Phenotyping of Genomic Selection Panel for Resistance to Foliar Fungal Diseases and Nutritional Quality traits in Groundnut

THESIS

Submitted to the

Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur

In partial fulfilment of the requirements

for the Degree of

DOCTOR OF PHILOSOPHY
In

AGRICULTURE
(GENETICS AND PLANT BREEDING)

By

SUNIL CHAUDHARI

Department of Plant Breeding and Genetics

College of Agriculture, Jabalpur 482004
Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, MP

2017

CERTIFICATE – I

This is to certify that the thesis entitled **"Phenotyping of Genomic Selection Panel for Resistance to Foliar Fungal Diseases and Nutritional Quality Traits in Groundnut"** submitted in partial fulfilment of the requirement for the degree of **"DOCTOR OF PHILOSOPHY IN AGRICULTURE" (Genetics & Plant Breeding)** of Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur is a record of the bonafide research work carried out by **Mr. Sunil Chaudhari** under my guidance and supervision. The subject of the thesis has been approved by the Student's Advisory Committee and the Director of Instructions.

All the assistance and help received during the course of investigation have been duly acknowledged by him.

Place: Jabalpur
Date: 31/07/2017

Dr. D. Khare
Chairman of the Advisory Committee

THESIS APPROVED BY THE STUDENT'S ADVISORY COMMITTEE

Committee	Name	Signature
Chairman	**Dr. D. Khare**	....
Co-Chairman	**Dr. P. Janila**	....
Member	**Dr. A. N. Shrivastava**	....
Member	**Dr. S. S. Shukla**	....
Member	**Dr. H. L. Sharma**	....

Thesis is approved by

(Dr. D. K. Mishra)
Professor and Head
Name Seal and Signature

Univ. Prof. & Head
Deptt. of Plant Breeding & Genetics
J N K V V, Jabalpur (M P)

CERTIFICATE – II

This is to certify that the thesis entitled **"Phenotyping of Genomic Selection Panel for Resistance to Foliar Fungal Diseases and Nutritional Quality traits in Groundnut"** submitted by **Mr. Sunil Chaudhari** to the Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur in partial fulfilment of the requirements for the degree of **"Doctor of Philosophy in Agriculture (Genetics & Plant Breeding)"** in the Department of **Plant Breeding & Genetics** has been, after evaluation, approved by the External Examiner and by the Student's Advisory Committee after an oral examination on the same.

Name : Dr. Sudam C. Patil
Designation : Principal Scientist & Head
Address : RORS, Jalgaon

Signature
External Examiner

Place : Jabalpur
Date : 31/03/2017

MEMBER OF THE STUDENT'S ADVISORY COMMITTEE

Committee	Name	Signature
Chairman	Dr. D. Khare	
Co-Chairman	Dr. P. Janila	
Member	Dr. A. N. Shrivastava	
Member	Dr. S. S. Shukla	
Member	Dr. H. L. Sharma	
Head of the Department	Dr. D. K. Mishra	Univ. Prof. & Head Deptt. of Plant Breeding & Genetics J N K V V, Jabalpur 482004 (M. P.
Director Instruction	Dr. D. Khare	

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This is to certify that Mr. Sunil Chaudhari has satisfactorily completed the research work related to this thesis entitled **"Phenotyping of Genomic Selection Panel for Resistance to Foliar Fungal Diseases and Nutritional Quality Traits in Groundnut"**. His thesis contains results of original research work and it is of high standards to warrant its presentation to the examination. I also certify that neither the thesis nor its part, thereof, has been previously submitted by him for a degree at any other university.

Place :
Date :

Dr. P. Janila
SENIOR SCIENTIST,
Groundnut Breeding,
ICRISAT, Patancheru, Hyderabad

Headquarters: Patancheru 502 324, Andhra Pradesh, India
Tel +91 40 30713071 **Fax** +91 40 30713074 +91 40 30713075 **Email** icrisat@cgiar.org
Liaison Office: CG Centers Block, NASC Complex, Dev Prakash Shastri Marg, New Delhi 110 012, India
Tel +91 11 32472306 to 08 **Fax** +91 11 25841294

ICRISAT-Nairobi
(*Regional hub ESA*)
PO Box 39063, Nairobi,
Kenya
Tel +254 20 7224550
Fax +254 20 7224001
Email icrisat-nairobi@cgiar.org

ICRISAT-Bamako
(*Regional hub WCA*)
BP 320
Bamako, Mali
Tel +223 20 709200
Fax +223 20 709201
Email icrisat-w-mali@cgiar.org

ICRISAT-Niamey
BP 12404
Niamey, Niger (Via Paris)
Tel +227 20 722529, 20 722725
Fax +227 20 734329
Email icrisatsc@cgiar.org

ICRISAT-Bulawayo
Matopos Research Station
PO Box 776,
Bulawayo, Zimbabwe
Tel +263 383 311 to 15
Fax +263 383 307
Email icrisatzw@cgiar.org

ICRISAT-Lilongwe
Chitedze Agricultural Research Station
PO Box 1096
Lilongwe, Malawi
Tel +265 1 707297/071/067/057
Fax +265 1 707298
Email icrisat-malawi@cgiar.org

ICRISAT-Maputo
c/o IIAM, Av. das FPLM No 2698
Caixa Postal 1906
Maputo, Mozambique
Tel +258 21 461657
Fax +258 21 461581
Email icrisatmoz@panintra.com

www.icrisat.org

Declaration and Undertaking by the Candidate

I, Sunil Chaudhari S/o Shri Hukumchand Chaudhari certify the work embodied in thesis entitled "Phenotyping of Genomic Selection Panel for Resistant to Foliar Fungal Diseases and Nutritional Quality traits in Groundnut" is my own first hand bonafide work carried out by me under the guidance of Dr. D. Khare and Dr. P. Janila at International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Hyderabad during *Rabi* 2014-15 to *Rabi* 2015-16.

The matter embodied in the thesis has not been submitted for the award of any other degree/diploma. Due credit has been made to all the assistance and help.

I, undertake the complete responsibility that any acts of misinterpretation, mistakes and errors of fact are entirely of my own.

I, also abide myself with the decision taken by my advisor for the publication of material extracted from the thesis work and subsequent improvement, on mutually beneficial basis, provided the due credit is given, thereof.

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Subject : Genetics and Plant Breeding

Department : Plant Breeding and Genetics

College : College of Agriculture, Jabalpur

Year of thesis submission : 2017

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Date : 31/07/2017
Place : Jabalpur

Dr. D. Khare
(Major Advisor)

Sunil Chaudhari
(Student)

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LIST OF SYMBOLS AND ABBREVIATIONS

Symbol	Legend
&	And
@	At the rate of
^{o}C	Degree Celsius
C.D.	Critical Difference
cm	Centimeter
C.V.	Coefficient of Variation
D.F.	Degree of Freedom
et al.	And others
etc	and the rest
Fig.	Figure (s)
g	Gram
ha	Hectare
HI	Harvest Index
i.e.	That is
kg	Kilogram (s)
m	Meter (s)
No.	Number (s)
NS	Non-significant
t	Tonnes
RH	Relative humidity
S.Em.±	Standard error of mean
M.S.S.	Mean sum of square
Viz.	Namely
%	Percent
±	Plus or Minus
LLS	Late leaf spot
GSP	Genomic Selection Panel

ACKNOWLEDGEMENT

I consider myself fortunate for having worked under the guidance and supervision of Dr. D. Khare, Director Research Services, Jawaharlal Nehru Krishi Vishwa Vidyalaya (JNKVV), Jabalpur, Madhya Pradesh and the chairman of my advisory committee. He had been a source of constant inspiration and support. His critical comments, personal interest, encouraging words and moral support throughout the study period have enabled me to furnish this assignment despite of ups and downs and to complete my research successfully. This dissertation could not have been completed without my chairperson who not only served as my supervisor but also encouraged me throughout my academic program and allowed me to conduct my research work at International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Hyderabad.

I am thankful for my co-advisor, Dr. P. Janila, Senior Scientist, Groundnut Breeding, ICRISAT, Patancheru for providing an opportunity to conduct my doctoral thesis research at ICRISAT and for excellent research facilities with the conductive environment. Her constant encouragements enabled me to learn and grow throughout my research work. It was purely her influence and help that enabled me to venture out disciplined during the course of my investigation. She had been extremely understanding about my problems and short-comings. I must also thank her for insistence on maintaining high standards in all things. I am privileged to be one of her students.

I am heartily thankful to Prof. V.S. Tomar, Hon. Vice-chancellor; Dr. S.S. Tomar, Former Director Research Services, JNKVV, Jabalpur (M.P.) and Dr. Om Gupta, Dean, College of Agriculture, Jabalpur, Madhya Pradesh, Dr. Abhishek Shukla, Deputy Director Instruction, JNKVV, Jabalpur for granting permission to conduct my doctoral thesis research at ICRISAT. I wish to thank Dr. D.K., Mishra, Principal Scientist and Head, Department of Plant Breeding and Genetics, College of Agriculture, Jabalpur (M.P.) with all members of department for their support. I am Thankful to Dr. P.K. Moitra, Principal Scientist, Dr. Stuti Mishra and all the members of Department of Plant Breeding and Genetics, College of Agriculture, Jabalpur for their help in academic work. I am also thankful to Dr. Sudam S. Patil, Principal Scientist and Head, Regional Oilseed Research Station, Jalgaon, Maharashtra and Dr. N. Shoba, Principal Scientist and Head of Coconut Research Station, Aliyarnagar, Tamil Nadu with their team for providing support, guidance and facilities to conduct the experimental trial at their respective locations.

It is my immense pleasure to express my utmost gratitude and reverence to Mr. Suyash B. Patil, Ph.D. Scholar, Chinese Academy of Agriculture Science, Beijing China. His advice, support, and encouragement have no doubt enabled me to overcome all the hurdles during research work. His vision and adept discussion technically and otherwise helped me to learn and understand the challenges of this field and the potential it has. I take the pride in having been associated with such a teacher.

I feel immense pleasure to express my sincere thanks to Dr. S.N. Nigam for sharing his valuable thoughts and pioneer experience. I am grateful to Dr. T.V. Murali for providing valuable inputs in the thesis, Mr. Y.D. Yadgiri, Mr. Surrendra Singh, Mr. T Ravindra Kumar, Mr. V. Papaih, Mr. P.B. Yadgiri, Mr. Nawaz, Mr. Ranjit, Mr. Ramesh, Mr. Rafi, Mrs. Suwarna, Mrs. Aparna, Mrs. Aundal and other staff members of Groundnut Breeding, ICRISAT for their help in conducting the research trials. I am also thankful to Dr. Rajeev Varshney, Program Director, CEG and Dr. M.K. Pandey, Scientist, Groundnut Genomics for their support during molecular work. I am thankful to Mrs. Richa, (Head, LSU), Mrs. Shripada, Mr. S. Damodar and all other staff of Learning System Unit, Library, and Housing and Food Services, ICRISAT, Patancheru. I am thankful to Satbeer Singh, Rajendragouda Patil, Dnyaneshwar Deshmukh, Sudarshan Patil, Pronob Paul, Mahesh, Yashoda Jadhav, Preeti Sundaram, Madhupani Sen, Sweta Panchal, Ph.D. Research Scholars of ICRISAT for their valuable support and discussion to solve problems during the course of present investigation.

In no particular order many thanks to my friends Mukesh Engla, Jayntilal Malgaya, Jagdish Patidar, Rahul Gawshinde, Tikamchand Rathore, Pravin Patel, Jainpal Rathore, Avinash Jha, Akanksha Tiwari, Madhu Prakash and Pratibha Choudhary for their help and making this duration memorable.

Any appreciable word would be less to thank my parents Mrs. Bhuribai Chaudhari and Shri Hukumchand Chaudhari and grand-parents late Mrs. Geeta Bai Chaudhari and Shri Devchand Chaudhari for the blessings they showered on me. My career would not have progressed in this direction and to this level without their generous help, understanding and encouragement. Their love and affection brought me to the level where I am today and also kindled my enthusiasm to carry out my research.

I feel a wave of sentiment toward my ever looking brothers Er. Gajanan Chaudhari, Mr. Shree Ram Birla, Mr. Dilip Birla and my fiance, Miss Pooja Punasiya, the dearest persons of my life, who have a dream for me and I feel contented to have completed an important step towards their dream, whose unending effects, instinct support and morale boost provided by them, to reach up to this point, lie in each letter of this thesis. I also wish to thank all well-wishers whose names are not mentioned here but are important to me.

Place : Jabalpur
Date : July 2017 **(Sunil Chaudhari)**

Chapter-I

Introduction

The cultivated groundnut (*Arachis hypogaea* L.; Family Leguminosae, native to Brazil) one of the most important oilseed crops of the world is presently cultivated in more than 100 countries throughout tropical, subtropical and warm temperate regions (Janila *et al.,* 2013a). It is an allotetraploid (2n=4x=40) with "A" and "B" genomes from two diploid progenitors, *A. duranensis,* and *A. ipaensis,* respectively (Kochert *et al.,* 1996). Except the cultivated species (*A. hypogaea*) and *A. monticola* in section *Arachis* and certain species in section *Rhizomatosae* that are tetraploid, all the other species representing all the nine sections are diploid (2n=2x=20). A single hybridization event between the diploid progenitors followed by chromosome doubling lead to the origin of cultivated groundnut about 3,500 years ago. It is classified into two subspecies, subsp. *fastigiata* Waldron and subsp. *hypogaea* Krap. Rig. The subsp. *fastigiata* contains four (*vulgaris*, *fastigiata*, *peruviana* and *aequatoriana*), whereas subsp. *hypogaea* contains two botanical varieties (*hypogaea* and *hirsuta*) with different expression in plant, pod and seed characteristics (Krapovickas and Gregory, 1994). The natural distribution of all the *Arachis* species is confined to Argentina, Bolivia, Brazil, Paraguay and Uruguay (Krapovickas, 1973).

As per the statistics of Food and Agriculture Organization (FAOSTAT, 2014), groundnut is cultivated nearly on 26.54 m hectare around the world with an annual production of 43.91 m tonnes and 1654 kg of nuts-in-shell productivity. The major producers are China, India and the USA which together account for two-thirds of the world output. Developing countries account for 82% of total groundnut area and 79% of production of the world. India ranks first in the area and second after China in production. In India, groundnut is grown on 4.68 m hectare area with the production of 6.55 m tonnes. The productivity of groundnut in India is quite low (1399 kg/ha) in comparison to Israel (7389 kg/ha), USA (4397 kg/ha), China (3492 kg/ha) and Argentina (2848 kg/ha) (FAOSTAT, 2014). The trend of area, production and productivity of groundnut in India during last decade showed that production of this crop widely fluctuates across years (Fig 1.1).

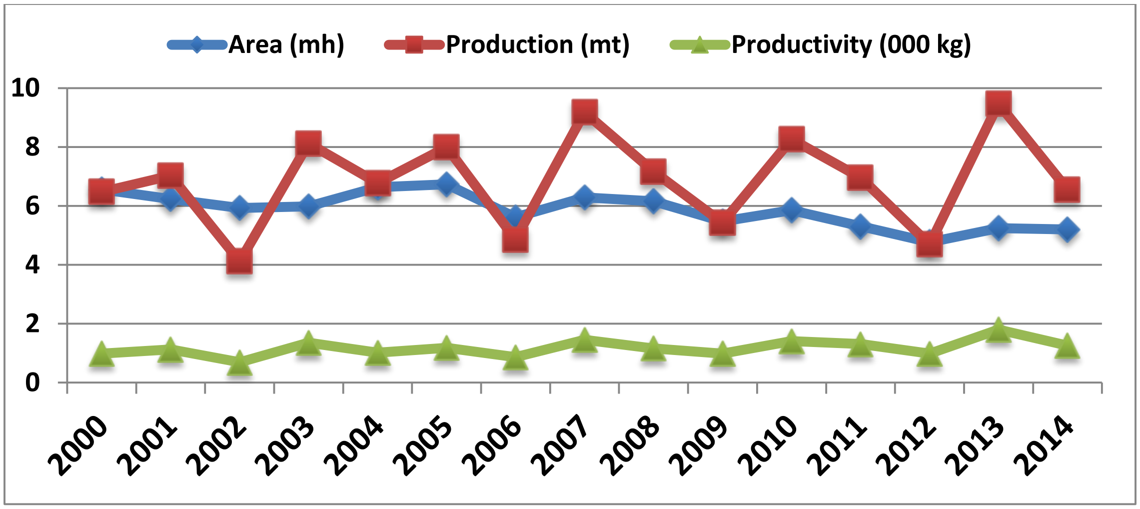

Fig.1.1 Area, production, and productivity of groundnut in India from 2000 to 2014 (FAOSTAT, 2014)

A wide gap exists between the genetic potential of the cultivars and realized yield mainly due to several biotic/abiotic stresses and fragile climatic conditions. Among the biotic stresses, two widespread foliar fungal diseases *viz*., late leaf spot (LLS) (*Phaeoisariopsis personata* Berk and Curt) and leaf rust (*Puccinia arachidis* Speg.) are together responsible for the reduction of 50-70% yield (Subrahmanyam *et al.,* 1984). Besides direct penalty for pod and seed yield through reduction in number of pods, pod and seed size, and weight, reduced in nutritional quality traits such as oil content and protein content are prominent under severe disease infection (Subrahmanyam *et al.,* 1984; Gupta *et al.,* 1987). Due to lack of resources and technical expertise required, farmers are not able to use the available methods of disease control (Subrahmanyam *et al.,* 1984). Exploitation of host plant resistance involving introgression of disease resistance using conventional breeding has been successful but labour intensive and time consuming.

Seed of groundnut contains about 35-54% oil, 21-36% protein and 6-24% carbohydrate (Cobb and Johnson, 1973). Groundnut oil contains 45-50% monounsaturated fatty acids, 30-35% polyunsaturated fatty acids and 17-18% saturated fatty acids (Ory *et al.,* 1992). For oil purpose, cultivars with high oil content and high O/L ratio are preferred, whereas, for confectionery purpose cultivars with low oil content, high O/L ratio and high protein content are preferred (Birthal *et al.,* 2010).

Many conventional breeding efforts have been made for improvement of complex polygenic traits such as yield, resistance/tolerance to stresses and nutritional quality, but the sufficient genetic gain couldn't be achieved in groundnut due to narrow genetic base. Integration of genomics tools with conventional breeding has been successful but lagged behind in groundnut in terms of genetic and genomic resources. The successful application of marker-assisted breeding in groundnut was conversion of cultivar Tifguard into 'high oleic Tifguard' (Chu *et al.,* 2011), introgression of QTLs resistance to rust and LLS (Janila *et al.,* 2016a) and mutant alleles of *ahFAD2* gene to improve the seed oil quality (Janila *et al.,* 2016b). The genes encoding fatty acid desaturase 2 (the key enzyme responsible for converting oleic acid to linoleic acid) in groundnut have been cloned and designated as *ahFAD2A* and *ahFAD2B* located at the linkage group a09 and b09 in A and B-genome, respectively (Jung *et al.,* 2000a & b). Therefore, it is important to screen breeding population for presence of both the mutant alleles of *ahFAD2* gene that can be used to develop new high oleic lines.

Genetics of rust resistance revealed recessive digenic inheritance (Vindhiyavarman *et al.,* 1993) and dominant single gene resistance (Singh *et al.,* 1984) whereas genetics of LLS resistance revealed its complex and polygenic nature (Dwivedi *et al.,* 2002) with combination of both nuclear and maternal gene effect (Janila *et al.,* 2013b). Complex nature of resistance to these diseases makes the identification of resistant and susceptible lines cumbersome through conventional screening techniques (Leal-Bertioli *et al.,* 2009). Incorporation of genomic tools in breeding program facilitates screening of large breeding populations and germplasm for desired genes and accelerates the rate of varietal development. Recently, many DNA markers were found to be putatively linked with rust (Varma *et al.,* 2005; Mace *et al.,* 2006; Khedikar *et al.,* 2010 and Sujay *et al.,* 2012) and LLS resistance gene

(Mace *et al.,* 2006; Shoba *et al.,* 2012b and Sujay *et al.,* 2012), and nutritional quality traits (Sarvamangala *et al.,* 2011). Validation of these markers will speed up the process of introgression of genes governing disease resistance and nutritional quality traits into preferred groundnut genotypes through its planned deployment in molecular breeding program (Sujay *et al.,* 2012). Therefore, identification of significant marker-traits association that can deploy in marker assisted breeding and assessment of molecular diversity for disease resistance and nutritional quality traits is important to develop new cultivars with improved disease resistance and nutritional quality.

Phenotyping of disease resistance and oil quality traits is cumbersome, time-consuming, high resource demanding and also most of the biochemical analysis used to quantify nutritional quality parameters are destructive methods and not suitable to evaluate individuals of segregating generations. Near-infrared spectroscopy (NIRS) can overcome this but it requires high investment in terms of money and technical resource. Therefore, it is necessary to go for easy and accurate method that helps to identify genotypes with these traits in early generation. Genomic selection (GS) is an emerging approach to increase selection intensity, accuracy and genetic gains in breeding program for improving complex polygenic traits through increasing frequency of favorable alleles in advance generation with the help of genomics estimated breeding value (GEBV) predicted using whole genome marker profile data and multi-environmental phenotypic data (Meuwissen *et al.,* 2001). To implement GS, multilocation phenotypic and genome-wide markers data on diverse population (genomic selection panel) are used to train a prediction model which is applied to a new set of selection candidates that have been genotyped with genome-wide markers. GS using only molecular information prior to phenotyping will be useful for increasing the rate of genetic gain by reducing the breeding cycle time, increasing the selection intensity and accuracy.

There are many factors that affect the accuracy of GS include the heritability of the trait, marker density, number of individuals in the training population, phenotypic and molecular diversity, and allelic richness in the genomic selection panel for desirable traits to capture each and every small effect QTLs involved in the expression of particular phenotype and proportion of genotype x environment interaction (GEI) (Daetwyler *et al.,* 2010). Considering GEI in construction of GS prediction model additionally, helps to identify wider adaptable end product at early generations. Looking towards the low heritability and bottlenecks associated in improvement of complex polygenic traits through conventional breeding methods, GS in groundnut for improving disease resistance, yield and nutritional quality would become a tractable and powerful approach facilitating selection of promising lines and parents on the basis of GEBVs. To implement GS approach, a comprehensive knowledge on presence of phenotypic and molecular diversity, and allelic richness in genomic selection panel for important agronomic and nutritional quality traits, their heritability, association among them and GEI for different traits are of paramount importance before construction of GS prediction model. Keeping these facts in view, the present investigation is aimed with following objectives:

1. Multi-location phenotyping of genomic selection panel for resistance to LLS and rust
2. Multi-location phenotyping of genomic selection panel for nutritional quality and yield parameters
3. To assess the association among the major observed traits
4. To evaluate genetic diversity and stability in the genomic selection panel for disease resistance, nutritional quality and yield components
5. To evaluate molecular diversity and allelic richness for rust, LLS and nutritional quality traits in GSP using SSR markers and analyze marker-trait association for validation of SSR markers

Chapter-II

Review of literature

Improvement of complex polygenic traits through conventional breeding has been difficult due to the involvement of multiple genes and their interaction with the environment. Advance genomic tools help to identify and incorporate quantitative trait loci (QTLs) of economically important traits to cultivated varieties. Presence of diversity among germplasm at both genetic and molecular level is crucial to identify suitable genotypes for use in breeding programs or for molecular studies aimed at identifying markers linked to QTLs/genes of interest. Focus on trait specific breeding has led to the development of genotypes that are suitable for one or few traits, but their overall assessment for other economically important traits is lacking. An assessment of diversity among germplasm and breeding lines for resistance to late leaf spot (LLS) and rust along with yield and nutritional quality traits across environments is critical to developing genomic selection prediction model. Therefore, the present study was aimed to evaluate genotypes of Genomic Selection Panel (GSP) for resistance to rust and LLS along with yield and nutritional quality traits across environments; to assess allelic richness for resistance to foliar fungal diseases and nutritional quality traits; and to identify potential marker-trait association that can deploy in marker-assisted breeding. The literature relevant to the objectives of the present study is reviewed in this chapter.

2.1 Groundnut

Groundnut is one of the most important oilseeds and food crop of the world. Various studies have shown that the cultivated groundnut originated by a single hybridization event between two wild diploid species with distinct genome giving rise to a sterile hybrid followed by a spontaneous duplication of chromosomes producing fertile tetraploid (groundnut) that remain reproductively isolated from its diploid wild ancestors (Kocher *et al.,* 1991; Jung *et al.,* 2003; Seijo *et al.,* 2004). Both pre and post zygotic hybridization barriers have been shown to restrict crossing between cultivated groundnut and wild *Arachis* species (Halward and Stalker, 1987).

2.1.1 Origin and Distribution

Genus *Arachis* was originated in South America and widely distributed in Argentina, Brazil, Paraguay and Uruguay. The cultivated groundnut (*A. hypogaea)* probably originated in the region of southern Bolivia and northern Argentina, as its progenitor *A. monticola*, the only wild allotetraploid species which is cross-compatible with *A. hypogaea* is found in this area (Krapovickas, 1969). The diploid species *A. duranensis* and *A. ipaensis* considered to be the most likely donors of A and B genomes of cultivated groundnut are restricted to northwest Argentina and southeast Bolivia (Krapovickas and Gregory, 1994 & 2007). Archeological evidence suggests that groundnut has been cultivated for over 3,500 years. The genus *Arachis* contains 81 identified species divided into nine taxonomic sections (*Arachis, Trierectoides, Erectoides, Extranervosae, Triseminatae, Heteranthae, Caulorrhizae, Procumbentes*, and *Rhizomatosae*) based on plant morphology, cross-compatibility and geographic origin/ distribution. Among these nine sections, *Arachis* has the largest number of species (32) including the cultivated groundnut (*A. hypogaea*) (Krapovickas and Gregory, 1994). Most of these species in this section are diploid with 2n=2x=20 and 2n=2x=18 whereas *A. hypogaea* (cultivated groundnut) and *A. monticola* in section *Arachis* are allotetraploid with 2n=4x=40 chromosome (Upadhyaya *et al.,* 2011a).

2.1.2 Major production constraints and target trait in groundnut

The main goal of groundnut breeding program is to develop new varieties that fulfill the requirements of farmers, consumers and traders. In Asia (India and China) and Africa, groundnut is predominantly used for oil extraction whereas in American and European markets it is used for making confections and butter. Groundnut suffers from several biotic and abiotic stresses that can cause serious damage to the crop and limit the productivity (Nigam, 2000). Groundnut is attacked by several foliar fungal diseases. Among them, late leaf spot caused by *Phaeoisariopsis personata* (Berk. & Curt.) Van Arx, early leaf spot (ELS) caused by *Cercospora arachidicola* Hori and rust caused by *Puccinia arachidis* Spegazzini are the major foliar fungal diseases cause severe yield loss worldwide. Aflatoxins are potent carcinogens produced by *Aspergillus flavus* and *A. parasiticus* in seed forcing several countries to have strict regimes on permissible levels of aflatoxins in their imports (Janila *et al.,* 2013a). Stem and pod rot, caused by *Sclerotium rolfsii*, is a potential threat to groundnut production in many warm, humid areas, especially where irrigated groundnut cultivation is expanding. Bacterial wilt caused by *Ralstonia solanacearum* is predominant among bacterial diseases of groundnut in South-East Asia, particularly China. Groundnut is also a host to several viral diseases, but only a few of them are economically important groundnut *viz.,* rosette disease in Africa, peanut bud necrosis disease in India, tomato spotted wilt virus in the USA, peanut stripe potyvirus in East and South East Asia, peanut stem necrosis disease in pockets in Southern India (Nigam *et al.,* 2012). Fresh seed dormancy is important especially in Spanish bunch types which are prone to pre-harvest sprouting. Pre-harvest sprouting can cause 10-20% yield loss (Nautiyal *et al.,* 2001) and predisposes the produce to the attack of fungus and microbes. A short period of dormancy of about 10–15 days is desirable (Janila *et al.,* 2013a).

Drought and heat are the most important abiotic stresses widespread in groundnut-growing areas. About 80% of the total groundnut area in the country is under rainfed condition. Development of water use efficient cultivars has been an important target trait. Breeding for short duration groundnut is an escape mechanism to avoid end of season moisture stress. Breeding for heat resilient crops has been gaining wide attention as heat tolerant genotypes can sustain production in heat stress environments that are expected to increase as a consequence of climate change. It is possible that moisture and temperature stress together may have adverse effects on productivity of groundnut in its semi-arid production environment (Janila *et al.,* 2013a). Drought during end of the season helps pre-harvest *Aspergillus* infection in the field that affects quality of produce (Janila *et al.,* 2013a).

The root knot nematodes, *Meloidogyne* spp. and the lesion nematodes, *Pratylenchus* spp. are important in groundnut (Sharma and McDonald, 1990). Aphids (*Aphis craccivora* Koch), several species of thrips (*Frankliniella schultzei*, *Thrips palmi*, and *F. fusca*), leaf miner (*Aproaerema modicella*), red hairy caterpillar (*Amsacta albistriga*), jassids (*Empoasca kerri* and *E. fabae*), and Spodoptera are important foliar insect pests and cause localized damage to groundnut during different growth stages (Wightman and Amin, 1988). Aphids and thrips are also vectors of important virus diseases. Termites, white grubs, and storage pests also cause damage to groundnuts. Among storage pests, groundnut borer or weevil (*Caryedon serratus*) and rust-red flour beetle (*Tribolium castaneum*) are important.

Groundnut based food products are now widely used in feeding programs to treat malnutrition and therefore, improving nutritional quality traits is gaining importance. In the case of roasted groundnut the flavor is an essential characteristic influencing consumer acceptance, and enhancing roasted groundnut flavor is an important target trait. The quality attributes preferred for confectionery grade varieties include high protein and sugar, low oil and aflatoxin contamination, attractive seed size and shape, pink or tan seed color, and ease of blanching and high oleic/linoleic fatty acid (O/L) ratio (Dwivedi and Nigam, 2005). High oleic trait is important for consumers' health and for food industry. For fodder purpose, the nitrogen content, metabolizable energy, and organic matter digestibility of haulms are important quality traits (Janila *et al.,* 2013a).

2.2 Variability, heritability and genetic advance

An estimate of nature and magnitude of genetic variability is a prerequisite for any crop improvement program. The variability observed in any population could be due to the genotype, environment, and genotype × environment interaction (G × E). The genetic and environmental components of variation were discussed by Johansen (1909) who attributed the variation in a segregating population to heritable and non-heritable factors, while the variation within pure lines was attributed to environmental factors. This was later confirmed by Nelson-Ehle (1909) and East (1916). The genetic variance is partitioned from total variance using the estimates of total variance in non-segregating population (Powers, 1942). The heritable variation was further divided into additive and non-additive variance, where non-additive fraction includes both dominant and inter-allelic interactions (Falconer, 1981). The broad sense heritability is the ratio of genotypic variance to the total variance in non-segregating population (Lush, 1945 and Hanson *et al.,* 1956). The genotypic variance also includes non-additive component which is not transmitted to the next generation. Hence, high heritability coupled with high genetic advance was reported to be more useful for making an effective selection in a population (Johnson *et al.,* 1955).

2.2.1 Yield and its contributing traits

Groundnut a crop of narrow genetic base struggles for natural variability because of tetraploid and highly self-pollinated nature. High magnitude of genotypic and phenotypic coefficient of variation (GCV and PCV) coupled with moderate to high heritability and genetic advance as percent of mean (GAM) for pod and kernel yield, hundred seed weight, percent sound mature kernels, number of primary branches per plant, days to maturity, shelling percent, haulm yield per plant and harvest index indicate the role of additive gene action for these traits (Manoharan *et al.,* 1990; Reddi *et al.,* 1991; Senapathi and Roy, 1991; Bansal *et al.,* 1992; Reddy and Gupta 1992; Pathirana, 1993; Reddy, 1994; Gowda *et al.,* 1996; Reddy *et al.,* 2001; Makhanlal *et al.,* 2003; Suneetha *et al.,* 2004; John *et al.,* 2005a; Shoba *et al.,* 2009; John *et al.,* 2009; Korat *et al.,* 2010; Padmaja *et al.,* 2013; Shridevi, 2014). However, moderate GCV and PCV with high heritability were observed for number of mature pods, plant height, hundred seed weight, pod yield per plant and harvest index (Ganeshan and Sudhakar, 1995; Islam and Rasul, 1998; Kavani *et al.,* 2004) and low for shelling percent, mature kernel percent and days to maturity (Gowda *et al.,* 1996; Azaharudheen and Gowda, 2013). High heritability for shelling percent and hundred seed weight; moderate for days to first flowering and low for pod yield per plant was reported by Upadhyaya *et al.* (2005) whereas, Swamy Rao (1979) reported low heritability and GAM for shelling percent and days to maturity. High heritability coupled with low GAM for shelling percent and sound matured kernel percent suggested that improvement of these traits is not possible by simple phenotypic selection (Uddin *et al.,* 1995; Hariprasanna *et al.,* 2008; Kavera 2009; Channayya *et al.,* 2011).

2.2.2 Foliar disease resistance

High GCV and PCV values coupled with high heritability and GAM were reported for LLS and rust in groundnut (Padmaja *et al.,* 2013; Khedikar, 2008; Kavani *et al.,* 2004, Venkataravana and Kumar, 2008; Ashis *et al.,* 2014) indicating the role of additive gene action (Venkataravana and Kumar, 2008; Ashis *et al.,* 2014). The inheritance of rust and LLS is controlled by several genomic regions with an additive effect on phenotype (Anderson *et al.,* 1986a; Singh *et al.,* 1984; Janila *et al.,* 2013b). Thus, identification of stable source of resistance followed by crossing and selection in early generations would be useful in developing resistant varieties (Narasimhulu *et al.,* 2013). Moderate GCV and PCV coupled with high heritability and moderate to high GAM for LLS and rust were reported by Vishnuvardhan *et al.* (2012).

2.2.3 Nutritional quality traits

Nutritional quality parameters such as oil content, protein content and fatty acids like oleic, linoleic, palmitic and stearic acid are important target traits in breeding programs. Genetic studies on these traits have reported high (Bovi *et al.,* 1983; Norden *et al.,* 1987; Vaddoria and Patel, 1990; Mishra *et al.,* 1992; Dwivedi *et al.,* 1994; Venkataraman *et al.,* 2001; Sarvamangala *et al.,* 2010) to low (Nadaf and Habib, 1987; Dwivedi *et al.,* 1993; Prakash *et al.,* 2000; Azharudheen, 2010; Channayya *et al.,* 2011) GCV and PCV values coupled with high heritability and low to moderate GAM. High heritability coupled with low GAM for oil content was also reported by Uddin *et al.* (1995) and Kavera (2009) and for protein content by Channayya *et al.* (2011). Low variability for these traits indicates the role of non-additive gene action in inheritance and the need to explore diversity among germplasm collection or wild species.

2.3 Trait associations

The genotypic correlation between traits may exist due to pleiotropy and/or association of loci governing variability for different traits located on the same chromosome. Knowledge on nature and extent of association between traits could be helpful in improving multiple traits and to formulate selection strategies in a breeding program.

2.3.1 Association among yield and its contributing traits

The economic yield of any crop depends on many component characters that can influence yield either jointly or singly and either directly or indirectly through other related characters. Selection for yield on the basis of per se performance alone may not be effective as that is based on the component characters associated with it, which is determined by correlation coefficient and path analysis. Pod and kernel yield had positive association with each other and other yield attributing traits such as number of pods per plant, number of mature pods per plant, hundred pod and seed weight, shelling out-turn, sound mature kernel percent, haulm yield and harvest index at genotypic and phenotypic levels (Tekale *et al.,* 1988; Patra and Mohanty, 1987; Alam *et al.,* 1985; Deshmukh *et al.,* 1986; Manoharan *et al.,* 1990; Vaddoria and Patel, 1990; Reddi *et al.,* 1991; Reddy and Gupta, 1992; Pushkaran and Nair; 1993; Sharma and Varshney, 1995; Moinuddin, 1997; Vasanthi *et al.,* 1998; Venkataravana *et al.,* 2000; Roy *et al.,* 2003; Kalmeshwar *et al.,* 2006; Channayya *et al.,* 2011; Shoba *et al.,* 2012a; Alam, 2014; Prabhu *et al.,* 2014; Gupta *et al.,* 2015a; Rasheed *et al.,* 2015; Vasanthi *et al.,* 2015). Shelling percentage and hundred kernel weight had negative significant association (Alam *et al.,* 1985). Genotypic correlation coefficients were reported higher than their corresponding phenotypic correlations indicating strong inherent association among the traits (Korat *et al.,* 2009).

Significant positive association of pod yield with kernel yield, test weight, plant height, number of pegs, number of matured pods and oil yield was also evident from findings of Kavani *et al.* (2004); Suvarna *et al.* (2004); Lakshmidevamma *et al.* (2004); Golakia *et al.* (2005) and Parmeshwarappa *et al.* (2008). A positive association was also observed between days to 50%

flowering and days to maturity (John *et al.,* 2005b; John *et al.,* 2009; Choudhary *et al.,* 2013).

2.3.2 Association among disease severity and yield traits

Disease severity score of LLS and rust showed a significant negative association with pod and seed yield, days to 50% flowering, days to maturity and haulm weight per plant indicating its negative impact on yield and its contributing traits (Iroume and Kanuft, 1987; Vasanthi *et al.,* 1998; Parmeshwarappa *et al.,* 2008; Vishnuvardhan *et al.,* 2012; Narasimhulu *et al.,* 2013; Alam, 2014). A positive association (0.48 to 0.60) among resistance to LLS and rust indicating that resistance to all three diseases can be incorporated into a single background by a single breeding effort (Anderson *et al.,* 1990; Vasanthi and Naidu, 1998). A significant positive relationship among LLS and rust scores along with their negative effect on pod and seed yield was also reported by Prabhu *et al.* (2014 & 2015).

2.3.3 Association among nutritional quality traits

Negative association of oil content with protein content (Yashoda, 2005; Kaveri *et al.,* 2008; Sarvamangala *et al.,* 2010; Ajay *et al.,* 2012), oil content with oleic acid content (Emeroglu and Mortuary, 1984; Kavera, 2009; Ajay *et al.,* 2012) and oleic acid with palmitic and linoleic acid (Bovi, 1983; Sekhon *et al.,* 1980; Bandyopadhyay and Desai 2000; Kaveri *et al.,* 2008; Sarvamangala *et al.,* 2010; Azharudheen and Gowda, 2013) was observed in several studies. A negative significant correlation between oil and protein content could be advantageous while developing cultivars for confectionery purpose where low oil and high protein is preferred (Sarvamangala *et al.,* 2010). In contradiction to many previous reports, a significant positive association between oil and protein content was reported by Kale *et al.* (1998); Parmer *et al.* (2002) and Azharudheen *et al.* (2013) indicating that simultaneous genetic improvement of both the nutrients might be effective. Genetic nature of fatty acid profile coupled with strong negative correlation between oleic and linoleic acids suggests that it is possible to obtain varieties with high oleic and low linoleic acid to increase their O/L ratio and oil stability which eventually leads to industrial acceptance (Hammonds *et al.,* 1997; Anderson *et al.,* 1998; Kavera, 2009).

2.3.4 Association among nutritional quality and yield traits

Oil yield was positively associated with number of pods per plant, hundred seed weight, seed yield per plant, number of primary branches per plant and number of seeds per pod (Bhagat *et al.,* 1986; Venkataravana *et al.,* 2000). However, a significant negative correlation of oil content with pod yield per plant, test weight, shelling percent and sound mature kernels and a positive significant correlation of oil yield with days to maturity and days to initiation of flowering was reported by Swamy *et al.* (2006). Pod yield was positively associated with 100-seed weight, oil and protein contents (Alam, 2014).

2.3.5 Association among nutritional quality and disease severity

Significant negative association of rust severity with protein and oil content was observed indicating their favourable association with rust resistance (Sarvamangla, 2009; Azaharuddin and Gowda, 2013). This also indicates that incidence of rust diseases will not only reduce pod yield, but also affect nutritional quality of groundnut kernels and selection for resistance may result in indirect improvement of these traits. In contrast, there was lack of association of all the nutritional quality traits with LLS (Azaharuddin and Gowda, 2013). Reduction in oil recovery, oil quality, protein and sugar due to disease severity of LLS and rust was also reported in earlier studies (Dwivedi *et al.,* 1993; Ghosh and Biswas, 1995; Motagi *et al.,* 2000a). Protein content was reduced from 16 to 12% due to foliar fungal diseases and also causes substantial losses in haulm yield and can affect the quality of fodder (Salako and Adu, 1990).

2.4 Diversity in groundnut

Based on compatibility features and genetic variability the genus *Arachis* was classified into four gene pools (Singh and Simpson, 1994). The first includes two tetraploid species (*A. hypogaea* and *A. monticola*) from section *Arachis;* II includes the remaining diploid species of section *Arachis* that shows strong cross-compatibility with *A. hypogaea*; III includes species from section *Procumbentes*, with weak cross-compatibility or incompatibility with *A. hypogaea*; and prescribes the most distantly related wild relatives to *A. hypogaea* and includes all species from the remaining seven sections of the genus *Arachis*. Despite the availability of broad genetic variations among species of the tertiary and quaternary (fourth) gene pools, the breeding community has been unable to exploit them because of incompatibility problems; thus, efforts need to be undertaken in finding efficient allele sharing methodologies for further improvement of cultivated groundnut. The origin of cultivated groundnut which is allotetraploid, followed by reproductive isolation with diploid wild relatives of further sections during domestication, left groundnut's primary gene pool with very limited genetic diversity. Earlier, genetic diversity studies using a range of molecular markers reported a very low level of diversity in the primary gene pool (Kochert *et al.,* 1996; Subramaninan *et al.,* 2000; Herselman *et al.,* 2003). Nevertheless, in the few other studies where large germplasm sets were used reported low levels of diversity in primary gene pools, while better genetic diversity still exists within the wild relatives (Varshney *et al.,* 2009a; Bera *et al.,* 2010; Upadhyaya *et al.,* 2011b; Khera *et al.,* 2013).

2.4.1 Diversity for yield and its contributing traits:

Several studies in the past quantified variability for morpho-agronomic traits (Vaddoria and Patel 1990; Reddy and Gupta, 1992; Pathirana, 1993; Senapati and Roy, 1998; Singh and Chaubey, 2003; Swamy *et al.,* 2003; John *et al.,* 2006; Kotzamanidis *et al.,* 2006; Sumathi and Muralidharan, 2007; Korat *et al.,* 2009; Sumathi *et al.,* 2009; Sadeghi *et al.,* 2011; Vekariya *et al.,* 2011; Nautiyal *et al.,* 2012). The two groups, subsp. *fastigiata* and *hypogaea* differed significantly for most of the morpho-agronomic traits with the *hypogaea* accessions having significantly greater mean pod length, pod width, seed length, seed width, yield per plant and 100-seed weight whereas *fastigiata* accessions showed higher plant height, leaflet length, leaflet width and shelling percentage (Upadhyaya, 2003). Evaluation of ICRISAT groundnut mini core (182 accessions) and Asia-specific groundnut core collection (504 accessions) for 20 agronomic traits showed sufficient variability for most of the traits (Madhura *et al.,* 2011; Swamy *et al.,* 2003; Upadhyaya *et al.,* 2005). Cluster analysis indicated no relationship between clustering pattern and subspecies among genotypes (Badigannavar *et al.,* 2002).

Genetic diversity studies using 21 to 184 genotypes reported three to 15 clusters based Mahalanobis D^2 statistic and PCA (Upadhyaya *et al.,* 2003; 2005 & 2006; Suneetha *et al.,* 2013; Nadaf *et al.,* 2014; Bhakal and Lal, 2015 and Gupta *et al.,* 2015b). Genetic diversity using principal component analysis (PCA) suggested that first two principal components explained most of variation present in the population (Upadhyaya, 2003; Upadhyaya *et al.,* 2006). The maximum contribution towards diversity was by hundred seed weight, harvest index, days to emergence and length of main axis and minimum contribution was by number of mature pods per plant, oil and protein content (Venkateswarlu, 2011; Vivekananda *et al.,* 2015). The diversity among the genotypes measured by intra-cluster and inter-cluster distance was sufficient for improvement of groundnut by hybridization and selection (Bhakal and Lal, 2015).

2.4.2 Foliar disease resistance

2.4.2.1 Late leaf spot (LLS)

LLS damage the crop by causing lesion formation, reduction in photosynthetic area and premature leaflet abscission. Leaf spot lesions can be seen on leaves, petioles, stems and peg, thus causing direct deterioration of developing pods (Reys and Romasata, 1940) and responsible for 10-50% reduction in pod yield (McDonald *et al.,* 1985). Depending upon weather conditions and cropping history, leaf spot symptoms usually appear between 45 to 60 days after planting. Symptoms of LLS appear as brown or black, circular spots up to 10 mm diameter lacking or with a less pronounced yellow halo on the upper leaf surface. Affected leaves turn pale green to yellow, wither and fall off the plant. Infection of LLS produces hormonal changes in the leaf that cause leaf drop. Defoliation usually occurs first on lower leaves, then progresses upward. When defoliation is severe, lesions appear on stems, petioles, and pegs as dark brown to black, oval-shaped blotches.

Inheritance of LLS resistance

Genetic studies to know inheritance of resistance to LLS were initiated as early as by Kornegay *et al.* (1980). Both, simple and complex inheritance of resistance to LLS is reported in the literature. Substantial additive genetic effects have been found for LLS among early generation progenies (Anderson *et al.,* 1986a). Tiwari *et al.* (1984) and Motagi *et al.* (2000b) reported a duplicate complementary recessive genes action whereas Nevill (1982) speculated a 5-gene model with significant non-additive gene action for resistance to LLS in groundnut. Both additive and dominance gene actions along with additive × additive type of epistasis contributed significantly to the inheritance of LLS resistance (Jogloy *et al.,* 1987 & 1999; Wambi *et al.,* 2014). Resistance to LLS is controlled by a combination of both, nuclear and maternal gene effects (Anderson *et al.,* 1986b). Among nuclear gene effects, additive effect controlled majority of the variation (Coffelt and Porter, 1986 and Janila *et al.,* 2013b). They also reported significant role of additive × dominance type of digenic epistatic effects. Additive and dominance maternal effects also contributed to the variation in the crosses indicated that the use of resistance donor as a female parent would be effective to tap maternal effects of resistance to LLS (Janila *et al.,* 2013b).

Host plant resistance for *Phaeoisariopsis personata*

Beside the complex nature of inheritance of LLS, several sources of resistance have been reported (Hassan and Beute 1977; Melouk *et al.,* 1984; Subrahmanyam *et al.,* 1985a; Gorbet *et al.,* 1990). High level of resistance to LLS has been found in wild species of groundnut (Stalker and Simpson, 1995). Among the wild *Arachis* species screened for LLS resistance, *A. chacoense* (PI 276325); *A. cardenasii* (PI 262141) and *A. stenosperma* (PI 338280) in section *Arachis* showed either an immune or a highly resistant reaction to the LLS (Subrahmanyam *et al.,* 1985b). However, cultivated groundnut was reported with moderate to high level of resistance to the major foliar fungal diseases (rust and LLS) with stable disease reaction across the environments (Subrahmanyam *et al.,* 1985b).

Sources of resistance to LLS have also been identified in cultivated groundnut (Chiteka *et al.,* 1988; Anderson *et al.,* 1993; Holbrook and Islebi, 2001) and used to develop breeding lines with resistance (Melouk *et al.,* 1984; Wells *et al.,* 1994; Xue and Holbrook, 1998 & 1999). Extensive screening of 13,000 accessions at ICRISAT identified 69 genotypes (20 from var. *peruviana*) as resistant against LLS (Subrahmanyam *et al.,* 1989; Mehan *et al.,* 1996). Resistance to LLS in groundnut has generally been associated with late maturity and undesirable pod and seed features (Nigam, 2000). Although, some breeding lines that had early maturity and tolerance to LLS have been documented (Branch and Culbreath, 1995 and Motagi *et al.,* 1996). Until the release of 'Southern Runner' in 1984, no commercial cultivars were available with promising resistance to LLS (Gorbet *et al.,* 1999). Successful examples of introgression of LLS resistance from wild into cultivated groundnut were the development of resistant varieties GPBD 4 and Mutant 28-2 (Gowda *et al.,* 2002a & b) and tolerant like Dh 8, K134, and ICGV 86590 (Gowda *et al.,* 1996). All other popular varieties like TMV2, JL 24, KRG1, R 8808, R9251, Dh40, Dh3-30, Dh43, TAG 24, S206 and S230 were reported to be susceptible (Reddy, 1988).

Evaluation of a mini core subset for LLS and rust at ICRISAT showed some accessions with moderate to highly resistant reaction against LLS and rust (Kusuma *et al.,* 2007; Sujay *et al.,* 2008; Sudani *et al.,* 2015) suggested that mini core collection can be used to improve the efficiency of identifying desirable traits and gene of interest in groundnut (Holbrook and Dong, 2005; Holbrook and Anderson, 1995).

2.4.2.2 Leaf rust in groundnut

Leaf rust disease has considerable economic importance in many groundnut growing regions of the world. Rust causes serious damage to the crop with pod yield losses up to 70% (Harrison, 1973; Subrahmanyam and McDonald, 1987). In India, many areas in Maharashtra, Andhra Pradesh and

Telangana, rust has been reported to cause 40-55% losses in pod yield in commonly grown susceptible cultivars (Ghuge *et al.,* 1981; Mayee, 1987; Subrahmanyam and McDonald, 1987). The disease can be particularly severe when it occurs together with LLS or it affects the crop early.

Symptoms of groundnut rust start from 8-10 days after infection with the occurrence of whitish flecks on the lower surface. A day later, yellowish flecks appear on the upper leaf surface and orange/brown colored pustules (uredinia) begin to form on the lower surface of the leaves. The pustules/uredinia are usually circular to elliptical, raised, and range from 0.3 to 2.0 mm in diameter. The pustules rupture after about 2 days of appearance to expose circular or oval uredospores which are dark orange at first but become cinnamon brown with maturity (Savary *et al.,* 1989). Necrosis develops in the area surrounding the pustules. Rust-damaged leaves become necrotic and dry up but remain attached to the plant. In the case of severe damage, plants have a burnt appearance.

Inheritance of rust resistance

Genetic basis of rust resistance in groundnut mainly depends on the genetic background and sources of resistance. Rust resistance is controlled by single recessive (Paramasivam *et al.,* 1990) or duplicate recessive genes (Bromfield and Bailey, 1972; Knauft and Norden, 1983; Knauft, 1987; Varman *et al.,* 1993) or by partially dominant gene (Middleton and Shorter, 1987). Genetic analysis of rust also revealed predominance of non-additive, additive × additive, and additive × dominance gene effects (Tiwari *et al.,* 1984; Reddy *et al.,* 1987 and Varman *et al.,* 1991). Additive gene effects and additive types of epistasis have also been found for rust resistance in groundnut (Singh *et al.,* 1984). In some diploid wild *Arachis* species, inheritance of rust resistance was reported as partially dominant (Singh *et al.,* 1984; Mondal *et al.,* 2007). Monogenic recessive mode of inheritance for rust resistance was also reported by Jakkeral *et al.* (2013).

Host plant resistance for *Puccinia arachidis*

There have been concerted efforts made to exploit genetic resistance to rust in groundnut (Wynne *et al.,* 1991 and Subrahmanyam *et al.,* 1985b & 1989). Effective screening of over 13,000 groundnut accessions at ICRISAT, India identified 160 genotypes with resistance to rust (Subrahmanyam *et al.,* 1982; 1983a & 1995; Mehan *et al.,* 1996; Singh *et al.,* 1997; Pensuk *et al.,* 2003). Most of these resistant genotypes were stable and belong to *Valencia* market type originating predominantly from Peru (Subrahmanyam *et al.,* 1989; Singh *et al.,* 1997). High levels of resistance, and in some cases, immunity have also been reported in many wild *Arachis* species (Subrahmanyam *et al.,* 1983a and Singh *et al.,* 1987). Several interspecific hybrids of diverse botanical backgrounds possess high levels of rust resistance and good agronomic potential (Singh *et al.,* 1997). Among the wild species, *A. batizocoi* (PI 298639, PI 338312), *A. duranensis* (PI 219823), *A. cardenasii* (PI 262141), *A. chacoense* (PI 276235), *A. pusilla* (PI 338449), *A. villosa* (PI 210554), and *A. correntina* (PI 331194) were found to be immune to rust (Subrahmanyam *et al.,* 1982). Several rust resistant cultivars *i.e.,* FDRS 10, ICGV's 86590, 93207 (Sylvia) and 87853 (Venus) bred at ICRISAT, have been released for cultivation in rust affected areas of India and Malesia (Nigam *et al.,* 1998; Nigam and Dwivedi, 2000). An extensive screening of 2000 genotypes under natural and artificial infection with *P. arachidis* reported 20 genotypes as resistant with disease severity score ranged from 2.0 to 3.0 on a 9 point scale (Singh *et al.,* 1997). Evaluation of a mini core collection (188 accessions) for foliar disease resistance also identified some accessions highly resistant to rust with better yield potential (Sujay *et al.,* 2008 and Sudini *et al.,* 2015).

Besides the complex inheritance and presence of environment, genotype × environment interactions and background effects of donor genotype on expression of QTLs governing resistance to rust and LLS, six best introgression lines have been developed namely ICGV's 13192, 13193, 13200, 13206, 13228 and 13229 with 39–79% higher mean pod yield and 25-89% higher mean haulm yield over their respective recurrent parents (Janila *et al.,* 2016a). Rust resistance in groundnut is of the slow rusting type, characterized by increased incubation period, reduced infection frequency, lesion diameter, spore germinability and low sporulation index (Subrahmanyam *et al.,* 1983b; Subrahmanyam *et al.,* 1993; Mehan *et al.,* 1994). These component characters can be used as a selection criterion to identify lines with resistance to rust.

2.4.3 Nutritional quality traits of groundnut

2.4.3.1 Oil content and fatty acid composition

Groundnut oil with high oleic and low linoleic acid are strongly preferred and demanded by consumers and traders due to its property of improving oil stability and health benefits. Thus, breeding groundnut variety with high O/L ratio has become one of the major goals of groundnut improvement. Oleic acid a monounsaturated fatty acid and linoleic a polyunsaturated fatty acid account for 75 to 80% of the total fatty acids in groundnut oil (Cobb and Johnson, 1973; Bruner *et al.,* 2001; Lopez *et al.,* 2001). Among the saturated fatty acids, which comprise the remaining 20% of the total fatty acids, palmitic acid (10%) has the largest proportion. Palmitic acid is considered to be a major contributor to increased levels of total blood cholesterol, especially low-density lipoprotein (LDL) (Worthington and Hammons, 1971; Groff *et al.,* 1996; Lukange *et al.,* 2007). Consumption of oils with reduced palmitic acid content is desirable to reduce the health risks of coronary diseases and breast, colon and prostate cancer properties associated with this fatty acid (Henderson, 1991; Willet, 1994). Linoleic acid is considered an unstable component and is responsible for poor flavour and undesirable oil odor, particularly in oils that are heated during use (Dutton *et al.,* 1951; Smous, 1979; Mounts *et al.,* 1988). Genotypes with reduced linoleic acid content have been developed which could enhance shelf-life and acceptability of groundnut and soybean oil (Wilcox *et al.,* 1984; Takagi *et al.,* 1990; Wilson, 1991; Byrum *et al.,* 1997).

About 80% of total groundnut produced in India is crushed for the extraction of oil. Hence, improvement in oil yield and quality is of interest to plant breeders (Motagi *et al.,* 2000a). The oil content of groundnut has been reported to range from 35.8 to 54.2% with an average of 45% (Pancholy *et al.,* 1978; Jambunathan *et al.,* 1985; Dwivedi *et al.,* 1990). Bhagat *et al.* (1984) reported high oil content in *Spanish* bunch (48.8%) compared to *Virginia* bunch (46.6%). Significant variability in oil content (41.7 to 61.3%) was identified among wild groundnut species. *Arachis magna* contained a significantly more oil (61%) than cultivated groundnut (50%) (Wang *et al.,* 2010). Among the botanical varieties of cultivated groundnut, var. *hypogaea* contained a higher amount of oil than *hirsuta* (Wang *et al.,* 2009). The *Virginia* types had higher oleic acid, protein content and O/L ratio with lower linoleic acid content than *Spanish* and *Valencia* types (Sekhon *et al.,* 1980; Norden *et al.,* 1987; Dwivedi *et al.,* 1993 Bansal *et al.,* 1993; Wang *et al.,* 2009; Mukri, 2012).

Significant difference among the genotypes with narrow variability for oil content was observed by Rajgopal *et al.* (2000); Manivel *et al.* (2000); Hassan and Ahmed (2012). Genotypes with large kernel size had low oil content and high protein content compared to those with small seed size (Prathiba and Uma, 1994; Sadhana and Snehalatha, 1998). Groundnut cultivars S 206, S 230, Dh 3-30, KRG1, Dh 8, GPBD 4 (Gowda *et al.,* 2002a), Mutant 28-2 (Gowda *et al.,* 2002b), TAG 24 (Kale *et al.,* 2000) were reported high oil contenting genotypes. Hammond *et al.* (1997) reported a wider range of performance of genotypes for palmitic acid (8.20 to 15.10%), stearic acid (1.10 to 7.20%), oleic acid (31.5 to 60.20%), linoleic acid (19.90 to 45.40%), arachidic acid (0.8 to 3.20%), eicosenoic acid (0.6 to 2.60%), behenic acid (1.80 to 5.40%) and lignoceric acid (0.50 to 2.50%).

The majority of groundnut cultivars reported having 45 to 50% oleic acid and 30 to 35% linoleic acid (Knauft *et al.,* 1993). In India, early maturing Spanish bunch varieties cover major area (about 70%) but they have poor oil quality with O/L ratio of ~1.0 to 1.2 (Raheja *et al.,* 1987; Bandyopadhyay and Desai, 2000). Two closely related natural mutant lines (435-2-1 and 435-2-2) had 80% oleic and 2% linoleic acid, with O/L ratio of 40:1 and iodine value of 74, one of them occurs commonly in groundnut germplasm (Norden *et al.,* 1987).

2.4.3.2 Protein content

The groundnut is an important source of edible oil and vegetable protein (Lusas, 1979). The development of nutritionally balanced foods is a promising approach to address the problem of dietary protein deficiency for growing population. The evaluation and screening of germplasm and wild species collections in the United States have indicated low genetic variability for oil and protein content and fatty acid composition (Hammonds *et al.,* 1997). An extensive study of over 8000 germplasm accessions at ICRISAT revealed a great variation for protein ranged from 16 to 34% (Dwivedi *et al.,* 1993). The wide range of protein content (15.5 to 32.9%) was reported by Rajgopal *et al.* (2000); Manivel *et al.* (2000); Mohan, (2002); Yashoda, (2005) and Yugandhar, (2005). Liao and Lei, (2004) released a black seed coat groundnut cultivar (Zhonghua 9) which contains 28.3% protein. Eighteen out of 184 accessions with higher nutritional traits such as protein content, oil content, oleic acid, and oleic to linoleic acid ratio with superior agronomic traits were identified by Upadhyaya *et al.* (2012). Seed width and protein content had the least contribution towards the total variation explained by first five PCs indicated low genetic variation for these traits (Upadhyaya *et al.,* 2003). Evaluation of mini core collection reported low-level of genetic variation for nutritional quality traits (Mukri *et al.,* 2014).

2.5 Genotype by Environment Interaction (GEI)

Breeders usually test a diverse array of genotypes under different environmental conditions, which implies genotype × environment interaction (GEI). According to Haldane (1947), GEI is important only if genotypes ranks differ from one environment to another. Since the 1970s, various attempts have been made to jointly capture the effects of G and GE interaction. Several methods have been developed to analyze GEI and to select genotypes that perform consistently across many environments (Becker and Leon, 1988; Kang, 1990; Kang and Gauch, 1996; Weber *et al.,* 1996). The earliest approach was the linear regression analysis (Yates and Cochran, 1938).

Finlay and Wilkinson (1963); Eberhart and Russell (1966) and Tai (1971) popularized variations of the regression approach, assuming an expected linear response of yield to environments. The merits and demerits of several methods were discussed by Kang and Miller (1984). Kang *et al.* (1987) concluded that Shukla's (1972) stability variance and Wricke's (1962) ecovalence were equivalent methods and they ranked genotypes identically for stability. These types of measures are useful to breeders and agronomists, as they provide the contribution of each genotype to total GEI. They can also be used to evaluate testing locations by identifying those locations with a similar GEI pattern (Glaz *et al.,* 1985). Other statistical methods that have received significant attention are pattern analysis (DeLacy *et al.,* 1996); the AMMI model (Gauch and Zobel, 1996), the shifted multiplicative model (Crossa *et al.,* 1996), the non-parametric methods of Huhn (1996), which are based on cultivar ranks, the probability of outperforming a check (Eskridge, 1996) and Kang's rank-sum method (Kang, 1988 &1993). The methods of Kang (1988, 1993) integrate yield and stability into one statistic that can be used as a selection criterion.

Among all the methods/models of stability analysis, GGE biplot (genotype and genotype × environment effect) technique is a versatile statistical/quantitative genetic methodology has recently been elucidated by Yan *et al.* (2000). The GGE biplot approach has captured the imagination of plant breeders and production agronomists like no other approach ever have. In addition to dissecting genotype × environment interactions, GGE biplot helps to analyze genotype-by-trait data, genotype-by-marker data, and diallel cross data (Yan *et al.,* 2000; Yan, 2001; Yan and Hunt, 2001, 2002; Yan and Rajcan, 2002). The relationship among the test environments and their comparison with respect to ideal environments can be evaluated. Stability and ranking of genotypes based on which won where pattern and comparison among genotypes with respect to ideal genotypes helps breeders to select genotypes with location specific adaptability.

2.5.1 GEI for yield traits in groundnut

In groundnut, yield and its major contributing traits, biotic and abiotic stress resistance/tolerance and nutritional quality traits are governed by a pool of major and minor genes along with environmental influence (Hardwick and

Wood 1972; Janila *et al.,* 2013a). Significant genotype × location, genotype × year and genotype × location × year interactions for yield and its components in groundnut have been reported in several studies (Punto and Lantinan, 1982, Senapathi and Roy, 1991; Ntare and Williams, 1998; Iwo *et al.,* 2002; Mekontchou *et al.,* 2006; Bucheyeki *et al.,* 2008; Khan *et al.,* 2009; Mothilal *et al.,* 2010a; Makinde and Ariyo, 2010; Dolinassou *et al.,* 2016; Patra *et al.,* 1995). Mathur *et al.* (1997) reported that shelling out-turn is a most stable character in groundnut and can be used as selection criteria. Similar findings for identification of genotypes for their stability for different traits under varying environmental conditions were also reported by Chunilal *et al.* (2006); Hariprasana *et al.* (2008) and Pradhan *et al.* (2010).

2.5.2 GEI for foliar disease resistance

In literature, significant differences among genotypes, environments, and genotype × environment interaction for resistance LLS and rust was reported (Singh and Sinha 1993; Reddy *et al.,* 1995; Thaware, 2009; Mothilal *et al.,* 2010b). Genotypes with stable expression of resistance to LLS across the eight environments were reported in different maturity groups (Iwo and Olorunju, 2009). Stable source of resistance to LLS and rust has been reported by Singh *et al.* (1997). Significant genotype, environment, and G × E interaction were reported for days to maturity, number of mature pods per plant, shelling percentage, 100 kernel weight and LLS severity (Chavan *et al.,* 2009; Godfrey and Olorunju, 2009). A lower area under the disease progress curve for percent defoliation was reported across years and locations (Gremillion *et al.,* 2011).

2.5.3 GEI for nutritional quality traits

Information about the influence of various factors on oil quality may be useful to guide the choice of location, sowing date, and crop management according to the purpose of the crop production. Significant genotypic differences and interactions with growing season and geographic location have been reported for oil, protein and fatty acid composition (Fore *et al.,* 1953; Worthington *et al.,* 1972; Holaday and Pearson, 1974; Mohamed-Som, 1974;

Mozingo and Steele, 1982; Norden *et al.,* 1987; Dwivedi *et al.,* 1993; Wang *et al.,* 2008; Sarvamangala 2009; Upadhyaya *et al.,* 2012; Azharudheen *et al.,* 2013; Dolinassou *et al.,* 2016). They suggested that temperatures after pegging could be the factor that affects oil composition to a greater extent. Considering proportion of variance due to genotype × environment (G × E) interaction to the total phenotypic variance, oil content was least stable followed by oleic acid whereas the protein and O/L ratio were the most stable nutritional traits (Upadhyaya *et al.,* 2005). The stability analysis resulted in the identification of a high oleic acid (>73%) containing genotype (ICG 2381).

Environmental factors such as soil and climatic variations and temperature are the most important factor affecting fatty acid composition (Cobb and Johnson, 1973; Sanders, 1982; Slack and Browse, 1984; Bansal, *et al.,* 1993). According to the report of Holaday and Pearson (1974), monounsaturated fatty acid content increases and polyunsaturated fatty acid content decreases with the increase of the soil temperature. This can be attributed to higher metabolic rate at elevated temperatures and decreased availability of oxygen that reoxidizes the desaturase enzyme system required to synthesize linoleate and linoleneate.

Seed maturity can also influence the fatty acid composition of groundnut. The actual impact of seed maturity was depended on genotype, climatic conditions, and genotype/climatic interactions. In general, oleic acid increases and linoleic acid decreases with seed maturity (Cobb and Johnson, 1973; Hinds, 1995; Young and Waller, 1972). In contrast to this, a reduction in oleic acid and an increase in linoleic acid with seed maturity was also reported by Hashim *et al.* (1993); Lynd and Ansman, (1989), whereas Knauft *et al.* (1987) observed no influence of maturity on oil chemistry. Besides fatty acid composition, early harvests decrease oil and protein yields and impaired oil quality (Nagaraj *et al.,* 1989).

The mean oleic acid concentration was observed high in *Virginia runner* followed by *Virginia bunch* and *Spanish bunch* genotypes (Picket and Holley, 1951; Worthington and Hammons, 1971; Taira, 1985; Raheja *et al.,* 1987; Lopez *et al.,* 2001). Very slight reduction in the variance components observed across the environments a lesser role of G × E interaction for fatty acid profile and O/L ratio (Azharudheen *et al.,* 2013). Similarly, the least influence of environment on oil content was reported by Prakash *et al.* (2000) and Venkataramana *et al.* (2001).

2.6 Molecular diversity in groundnut

Molecular marker and genomic tools are being used predominantly for assessment of molecular diversity, selection of parents and off-springs, and fast-track improvement of elite cultivars for desirable traits (Varshney and Tuberosa, 2007). In groundnut, different kinds of molecular markers including restriction fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPD) and amplified fragment length polymorphism (AFLP) were used in the past to assess the diversity and understand the relationships in various germplasm collections (Subramanian *et al.,* 2000; Dwivedi *et al.,* 2001; Herselman, 2003). The majority of these studies, however, revealed low level of DNA polymorphism, especially in cultivated groundnut. This may be attributed to the low level of genetic variation that existed in the germplasm collection, due to the origin of groundnut, or poor discriminatory power of marker systems such as RFLPs, RAPDs and AFLPs. However, microsatellite or simple sequence repeat (SSR) markers have shown higher polymorphic information content (PIC) with high reproducibility and co-dominant nature. Hence, these markers have been considered as the markers of choice in crop breeding (Gupta and Varshney, 2000). In recent years, considerable efforts of several research groups at international level resulted in development of several hundreds of SSR markers in groundnut (Hopkins *et al.,* 1999; He *et al.,* 2003; Fergusson *et al.,* 2004; Palmieri *et al.,* 2005; Moretzsohn *et al.,* 2004, 2005; Mace *et al.,* 2006; Proite *et al.,* 2007; Gimenes *et al.,* 2007; Wang *et al.,* 2007; Cuc *et al.,* 2008; Gautami *et al.,* 2009). These SSR markers have been found very useful to detect genetic diversity in groundnut germplasm including cultivated genotypes (Mace *et al.,* 2006, Tang *et al.,* 2007; Kameswara *et al.,* 2007).

High level of polymorphic variation among wild species but very little among cultivated groundnut was reported using RAPD and RFLP (Halward *et* *al.,* 1991). Polymorphism among the accession of cultivated groundnut with SSR and RAPD assay was reported by Hopkins *et al.* (1999) and Dwivedi *et al.* (2001), respectively. Ferguson *et al.* (2004) designed 226 SSR primers, out of which 192 were well amplified and 110 pairs revealed polymorphism (48.67%) in a diverse array of 24 cultivated groundnut accessions. The 110 primer pairs showed polymorphism at 123 loci, this is possible because of the presence of two genomes in an allotetraploid groundnut. Nearly 120 polymorphic loci and 3 to 19 alleles with an average of 6.9 alleles per primer pair were reported using 18 fluorescently labeled primer (f-SSR) against 48 cultivated *Valencia* groundnut genotypes (Krishna *et al.,* 2004). A total of 477 alleles were detected with an average of 15.4 alleles per locus using 31 SSR markers from 139 accessions (Barkley *et al.,* 2006). SSR marker clustered genotypes based on their botanical classification further support to the current taxonomy (Barkley *et al.,* 2007).

A high number of alleles (265) were detected in the range of 3 (Ah1TC6G09) to 20 (Ah1TC11H06) with an average of 10.6 alleles per locus and PIC value varied from 0.38 to 0.88 with an average of 0.70 for 25 SSR loci in 189 accessions (Varshney *et al.,* 2009a). A total of 59 unique alleles and 127 rare alleles were detected at almost all the loci studied. Cluster analysis grouped 189 accessions into four clusters (Varshney *et al.,* 2009a). A wider range of PIC value for polymorphic markers was ranged from 0.10 to 0.89 with an average of 0.31 to 0.61 per marker in earlier genetic diversity studies (Mace *et al.,* 2008; Cuc *et al.,* 2008; Gautami *et al.,* 2009; Varshney *et al.,* 2009a; Pandey *et al.,* 2012). PIC value reported being positively correlated with number of alleles per locus (Cuc *et al.,* 2008; Pandey *et al.,* 2012).

The study of molecular diversity for disease resistance in groundnut using 17 SSR primers reported six as polymorphic (Shoba *et al.,* 2010). Molecular diversity and association of SSR markers for rust and LLS resistance using 26 primers revealed 136 bands amplified with 76.5% polymorphism. Cluster analysis revealed two main clusters separated at 52% Jaccard's similarity coefficient according to disease reaction against LLS and rust (Mondal and Badigannavar, 2010). Genetic diversity and population structure of 196 groundnut cultivars using 146 SSRs revealed a total of 440 alleles with an average of 2.99 per marker and the average gene diversity index of 0.11 (Ren *et al.,* 2014). Eighty-six rare alleles with a frequency of less than 1% were identified in these cultivars.

Molecular diversity analysis using 35 SSRs in 12 mutant genotypes revealed an average of 3.57 polymorphic bands per primer (Goswami *et al.,* 2013). A comprehensive analysis of allelic diversity and population structure using diversity array technology markers (DArt) and SSR detected lower allele frequency and PIC in DArT (2.0 alleles/locus, 0.125 PIC) than SSRs (22.21 alleles/locus, 0.715 PIC) and clustered whole population into three sub-populations (Pandey *et al.,* 2014).

2.7 Marker-trait associations (MTAs)

Many agronomic traits are difficult to select and improve by conventional techniques. Hence, marker-assisted selection (MAS) offers an additional tool for obtaining improved varieties. Earlier, breeder depended on markers that had a morphological effect on plant. However, most morphological markers has several limitations such as dominance effects, epistatic relationships, developmental stage specificity and environmental influence. Molecular markers have proven to be a prominent tool to identify plants caring desirable genes leads to increase selection accuracy and intensity in the breeding program compared to conventional efforts of crop improvement. Further, scoring of molecular markers does not depend upon gene expression and are not affected by the environment, can be detectable using any plant tissue at any developmental stage reduces the time and space required for evaluation of plants. However, the successful exploitation of QTL regions reported to explain greater phenotypic variation for any traits requires a strong validation associated markers through the diverse population.

2.7.1 MTAs for yield and its contributing traits

The QTLs for different yield traits such as pod yield per plant, hundred seed weight, harvest index and haulm yield per plant with PV ranged from 10.2 to 20.6% in well water and stress condition was reported by Fonceka *et al.*

(2012). A total of 39 QTLs with 1.25 to 26.11% PV were also reported for pod and seed related traits (Chen *et al.,* 2016) Marker-trait association analysis through association mapping identified a total of 524 highly significant MTAs with wide range of PV (5.81-90.09%) for 36 traits. Out of these, 50 could be identified for four yield component traits *viz.,* seed length (nine MTAs, 11.81-13.29% PV), seed width (three MTAs, 14.91-30.09% PV), seed weight (five MTAs, 12.73%-26.08% PV) and pod yield (33 MTAs, 9.74-37.36% PV) (Pandey *et al.,* 2014a). Five QTLs were identified through family-based mapping approach for seed weight with PV ranged from 4.18-19.8% (Varshney *et al.,* 2009b; Ravi *et al.,* 2011). A total of 15 QTLs for pod length, 11 for pod width and 16 for hundred pod weight were reported with PV ranged from 3.68 to 27.84% (Luo *et al.,* 2017). Marker-trait association using Kruskal-Wallis ANOVA reported a significant association of five SSRs with kernel mass. Among these associated primers, TC3A12 and TC9H09 accounted for 28% and 12% of PV due to kernel mass and were associated with major QTLs (Goswami *et al.,* 2013). After validation, these MTAs can be used for improving yield and its component traits (Pandey *et al.,* 2014a).

2.7.2 MTAs for foliar disease resistance

Various efforts have been made in groundnut for mapping of QTLs linked to foliar disease resistance and their validation in different populations. A major QTL for rust (QTLrust01) potentially associated with candidate SSR marker IPAHM 103 was identified and validated using a wide range of resistant and susceptible breeding lines (Khedikar *et al.,* 2010). Another comprehensive QTL analysis across six environments detected 28 QTL for LLS and 15 QTL for rust (Sujay *et al.,* 2012). A major QTL for LLS, namely $QTLLLS_{01}$ (GM1573/GM1009-pPGPseq8D09) explained 10.27–62.34% phenotypic variance (PV) was detected in all the six environments. In the case of rust resistance, four new markers (GM2009, GM1536, GM2301 and GM2079) in addition to marker IPAHM103 showed significant association with the major QTL for rust (82.96% PV) (Sujay *et al.,* 2012). Similarly, the QTL region flanked by GM2009-IPAHM103 had very high PV of 44.5 % and 53.7% for LLS and rust response, respectively and another QTL region flanked by GM1839-

GM1009 on linkage group AhXII explained the phenotypic variance of 14.1–35.2% for LLS resistance (Kolekar *et al.,* 2016).

Two EST-SSR markers (SSR_GO340445 and SSR_HO115759) were detected closely linked to a rust resistance gene at 1.9 and 3.8 cM distances, respectively (Mondal *et al.,* 2012). Bulk segregant analysis and single marker analysis identified the markers (PM375, PM 384, pPGPseq5d5, PM 137, PM 3, PMc 588 and Ah 426) linked with LLS severity (Shoba *et al.,* 2012b). Validation of SSR markers linked to rust and LLS resistance revealed potentially associated markers (GM2009, GM2301, GM2079, GM1536, and IPAHM103 for rust; GM1954, GM1009 and GM1573 for LLS) that can be used in cultivar development through MAS (Gajjar *et al.,* 2014; Jekkeral *et al.,* 2014; Sukruth *et al.,* 2015). These markers were successfully used for introgression of QTLs resistance to rust and LLS into three popular cultivars (Janila *et al.,* 2016a).

2.7.3 MTAs for nutritional quality traits

There are limited reports available on the identification of QTL regions associated with nutritional quality traits. A QTL analysis detected seven QTLs for protein content (2.5–9.8% PV), eight QTLs for oil content (1.5–10.2% PV) and six common QTLs for oleic and linoleic acid (3.3–9.7% PV) (Sarvamangala *et al.,* 2011). Similarly, other studies also identified seven QTLs for oil content but they showed very low PV (1.5–9.5%) (Selvaraj *et al.,* 2009; Liang *et al.,* 2009; Wang *et al.,* 2011). A total of 25 MTAs were detected for oil content with PV ranged from 5.84% (gnPt-714399) to 40.37% (TC4G10), markers with high PV may be considered in developing cultivars with high oil content (Pandey *et al.,* 2014a). Two MTAs linked with single marker Seq5D05 could be detected for oleic acid with 16.42–20.8% PV while 22 MTAs were identified for O/L ratio with PV ranging from 13.7% (gnPt- 739706) to 47.45% (GM 2480) (Pandey *et al.,* 2014a). These MTAs explained lower PV than the earlier identified MTA conducted on US-mini core collection (53.57% PV) while MTAs identified for O/L ratio had high PV compared to study of Wang *et al.* (2011).

Inheritance of high oleic and low linoleic acid was shown to be under simple genetic control (Moore and Knauft, 1989) and duplicate recessive alleles (Ol_1 and Ol_2) are responsible for this character. Two major recessive genes have been identified in groundnut, which increases the oleic acid content to as high as 80% and reduces the linoleic acid content to around 2% (Moore *et al.,* 1989). Jung *et al.* (2000a & b) reported that high oleic groundnut resulted from reduction in the activity or transcript level of microsomal oleoyl-PC desaturase. They isolated two non-allelic but homeologous genes, *ahFAD2A* and *ahFAD2B* from the developing groundnut seed with normal oleic. Reduction in *ahFAD2B* transcript levels in the developing seeds is correlated with high oleic trait. Two mutant alleles of *FAD2* gene present on linkage group a09 (*ahFAD2A*) and b09 (*ahFAD2B*) control composition of three major fatty acids, oleic, linoleic and palmitic acid which together determine groundnut oil quality (Chu *et al.,* 2009; Chen *et al.,* 2010). Wang *et al.* (2011) further confirmed the potential role of two functional SNPs of *FAD2* gene in synthesis of higher oleic acid and O/L ratio.

Marker-trait association for oleic acid content also revealed that 60% of the variation in oleic or linoleic acid content can be explained by the genotypic effect of *ahFAD2A* and *ahFAD2B* genes (Wang *et al.,* 2013). Pandey *et al.* (2014b) found two marker intervals associated with *ahFAD2B* gene (26.54, 25.59, and 41.02% PV) and *ahFAD2A* gene (8.08, 6.86, and 3.78% PV) for oleic acid, linoleic acid, and O/L ratio. The successfully introgression of these two mutant alleles from SunOleic 95R into the genetic background of three elite cultivars (ICGV's 06110, 06142 and 06420) identified lines with high oleic acid similar to donor parent (Janila *et al.,* 2016b) All these reports indicate the presence of two mutant alleles of *AhFAD2* gene in inheritance of high oleic trait. Hence, the screening of entire breeding material for the presence of both the mutant alleles would be helpful to identify genotypes that can be used as a potential source of high oleic trait.

Chapter III
Material and Methods

The present investigation entitled "Phenotyping of Genomic Selection Panel for resistance to foliar fungal diseases and nutritional quality traits in groundnut" was carried out with the major aim of multilocation evaluation of Genomic Selection Panel (GSP) for two major foliar fungal diseases *viz.,* rust and late leaf spot (LLS) along with yield and nutritional quality traits which will further be used for construction of genomic selection prediction model in groundnut. The study was planned to conduct a preliminary evaluation of GSP for magnitude of genetic and molecular diversity, and allelic richness for complex polygenic traits like disease resistance and nutritional quality. A robust marker-trait association was also planned to validate marker on a diverse set of genotypes and identify significant markers that can be used in genomic assisted breeding. The details of material used and techniques adopted in the present study for recording of observations, analysis, and interpretation of data are briefly presented in this chapter.

3.1. Experimental material

The experimental material comprised of 340 genotypes of groundnut selected based on the diversity available for morphological and important economic traits in different subspecies and botanical varieties of cultivated groundnut. This population is designated as GSP constructed mainly for Genomic Selection with the help of whole genome-wide molecular marker and multi-location phenotypic data. Among these 340 genotypes of GSP, 227 genotypes belong to *Arachis hypogaea* subspecies *fastigiata* whereas 113 to *A. hypogaea* subspecies *hypogaea.* Among subspecies *fastigiata*, 212 genotypes belong to botanical variety *vulgaris*, 10 to *fastigiata*, 4 to *peruviana* and a single cultivar to botanical variety *aequatoriana* while among the 113 genotypes of subspecies *hypogaea*, 111 belongs to botanical variety *hypogaea* and each of one belongs to *hirsuta* and unknown botanical type. The GSP included genotypes representing 21 diverse geographical countries. Out of 340 genotypes, 51 were taken from 20 different countries whereas 289 were developed at 11 breeding centers of India. These genotypes represent most of the diversity at geographic distribution, botanical classification, and expression of economically important traits present in cultivated groundnut. The details of genotypes used in this study are given in Appendix I.

3.2 Environmental conditions

The present experiment was conducted at three locations in India *viz.,* International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Telangana, Regional Oilseed Research Station (ORS), Jalgaon, Maharashtra and Coconut Research Station (CRS), TNAU, Aliyarnagar, Coimbatore, Tamil Nadu during *Rainy* season 2015 for multi-location evaluation of GSP against two major foliar fungal diseases (rust and LLS), yield and nutritional quality traits (Figure 3.1). Additional post-rainy trial was conducted at ICRISAT Patancheru to evaluate genotypes for yield and nutritional quality traits under disease-free condition. Among these three experimental sites, OAR, Jalgaon and CRS, Aliyarnagar are natural disease hotspot for LLS and rust, respectively whereas, at ICRISAT, Patancheru artificial disease nursery was created by inoculating both the diseases through infector row technique. The details of environmental conditions of each location are given in Table 3.1.

3.3. Experimental design

The 340 genotypes of GSP constructed by ICRISAT were evaluated under four different environments in Alpha Lattice Design with two replications during *Kharif* 2015. Each replication was divided into 20 equal sized homogeneous blocks with the block size of 17 to reduce heterogeneity in the experiments through eliminating inter-block effect. Single row plots were planted with 4 m length and with inter and intra-row spacing of 30 and 10 cm, respectively. The sowing was done on broad bed system as recommended for groundnut cultivation with 4 rows per bed. Standard agronomic management practices were followed at each location: 60kg phosphorus pentoxide (P_2O_5) as a basal application, pre-emergence application of Pendimethalin (1kg active ingredient per ha) and irrigation soon after planting and subsequently when needed. Gypsum (500 kg/ha) was applied to the experimental field at peak flowering stage and protection was taken against insects whereas no protection measure applied to control foliar fungal diseases.

Table 3.1 Details of environmental conditions of each environment

Particulars		**Environments**			
		E_1	**E_2**	**E_3**	**E_4**
Seasons		Rainy 2015	Rainy 2015	Rainy 2015	Post-rainy 2015-16
Location		Coconut Research Station, Aliyarnagar, Tamil Nadu	Regional Oilseed Research Station, Jalgaon, Maharashtra	ICRISAT, Patancheru, Hyderabad, Telangana	
Latitude ('N)		10^0 29	21^0 03	17^0 53	
Longitude ('E)		76^0 58	75^0 34	78^0 27	
Altitude (MSL)		288.0	201.2	545.0	
Soil type		Sandy loam	Medium black	Sandy loam	
Climatic zone		Moderate rainfall	Moderate rainfall	Moderate rainfall	
Total rainfall (mm)		805.44	514.90	456.05	238.88
Temperature	Min ^{0}C	15.25	9.60	14.50	9.63
	Max ^{0}C	35.33	42.90	34.89	41.24
Humidity	Min (%)	48.86	30.57	36.85	19.00
	Max (%)	94.83	87.00	95.43	51.22
Date of sowing		July 7th 2015	June 23rd 2015	July 10th 2015	December 6th 2015

3.4 Methodology

3.4.1 Screening for diseases resistance to LLS and rust

The trial was conducted in disease screening nursery at three locations for screening of GSP against LLS and rust along with yield and nutritional quality traits. Aliyarnagar and Jalgaon are disease hotspots; hence infector rows of a highly susceptible cultivar TMV 2 was planted after every four broad beds to maintain uniform disease pressure without any artificial inoculation. However, an artificial disease-screening nursery was created that also has infector rows of TMV 2 after every four broad beds, and along the borders of the nursery to create optimum disease pressure for screening.

For artificial inoculation of the foliar pathogens, urediniospores of *Puccinia arachidis* (rust) and conidial suspension of *Phaeoisariopsis personata* (LLS pathogens) were collected separately using a cyclone spore collector

(Fischer Scientific co., USA) from naturally infected leaf lesions of the susceptible cultivar TMV 2 and inocula were stored at -20 ^{0}C (Figure 3.2a). Ten days before planting of the test material in the field, the groundnut cultivar TMV 2, susceptible to both diseases, were planted in polybags in the greenhouse to multiply the inoculum. Thirty-five days-old TMV 2 seedlings raised in the greenhouse were inoculated separately by spraying with urediniospores of rust and conidia of LLS at 5×10^{4} ml^{-1} (Figure 3.2b & 3.2c). The non-ionic detergent, Tween 20 was added to the spore solution as a surfactant at the rate of 0.05% of the spore solution. Water was sprinkled in and around the inoculated plants in the polybags and the plants were covered with polyethylene sheet during the nights for 7 days to maintain high humidity (95%) (Figure 3.2d). Severe rust and LLS developed on these plants in two weeks. When the test materials were around 50-days-old, infected plants in polybags were transplanted in the infector rows of the trial at one-meter distance and both conidia of LLS and urediniospores of rust were sprayed at a concentration of 5×10^{4} spores ml^{-1} on infector rows of the trial (Figure 3.2e & 3.2f). To promote disease development, sprinkler irrigation was provided to the trial daily for 30 min for a period of one month starting from the day of field inoculation with the pathogen.

The genotypes were evaluated through visual screening method and a modified 9 point scale for LLS (Fig 3.3 & Table 3.2) and rust severity (Fig 3.4 & Table 3.3) given by Subrahmanyam *et al.,* (1995).The visual scores (1-9) and the extent of leaf area destroyed (0-100%) are linearly related. Genotypes were scored for LLS and rust severity at 75, 90 and 105 days after sowing (DAS). Based on the disease severity scores at 90 and 105 DAS, genotypes were categorized into resistant (≤3), moderate resistance (4 to 5), susceptible (6 to 7) and highly susceptible (>7) (Sudani *et al.,* 2015).

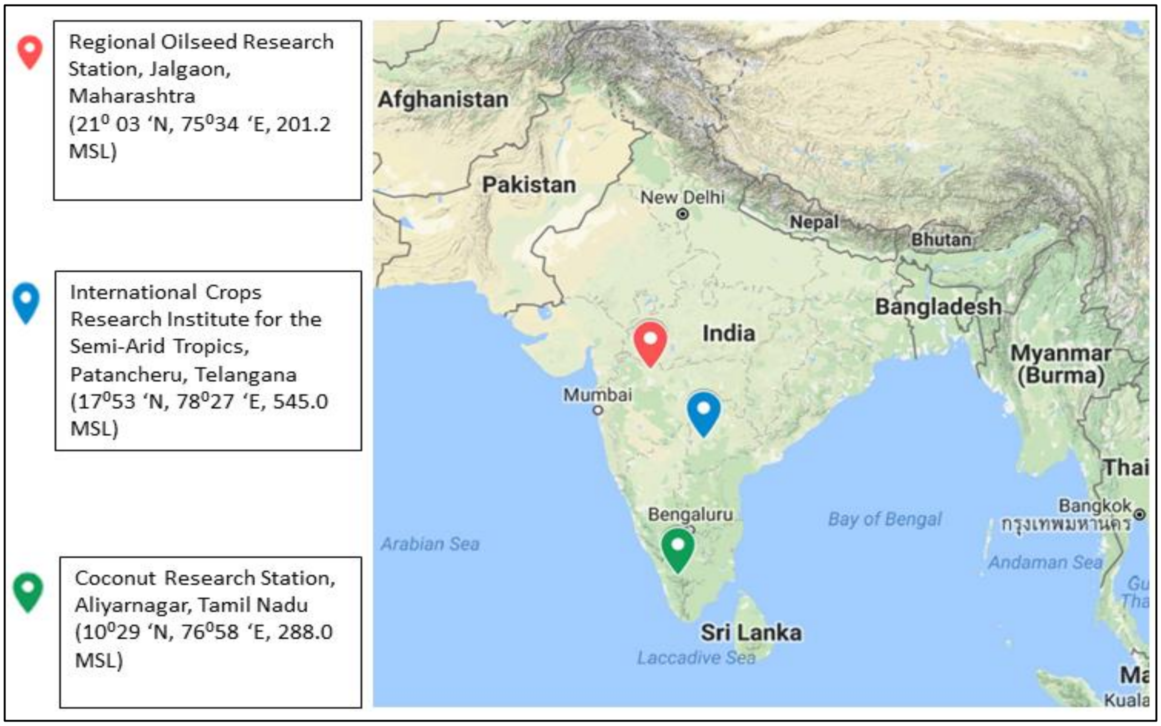

Figure 3.1 Map highlights the locations where experimental trials were conducted

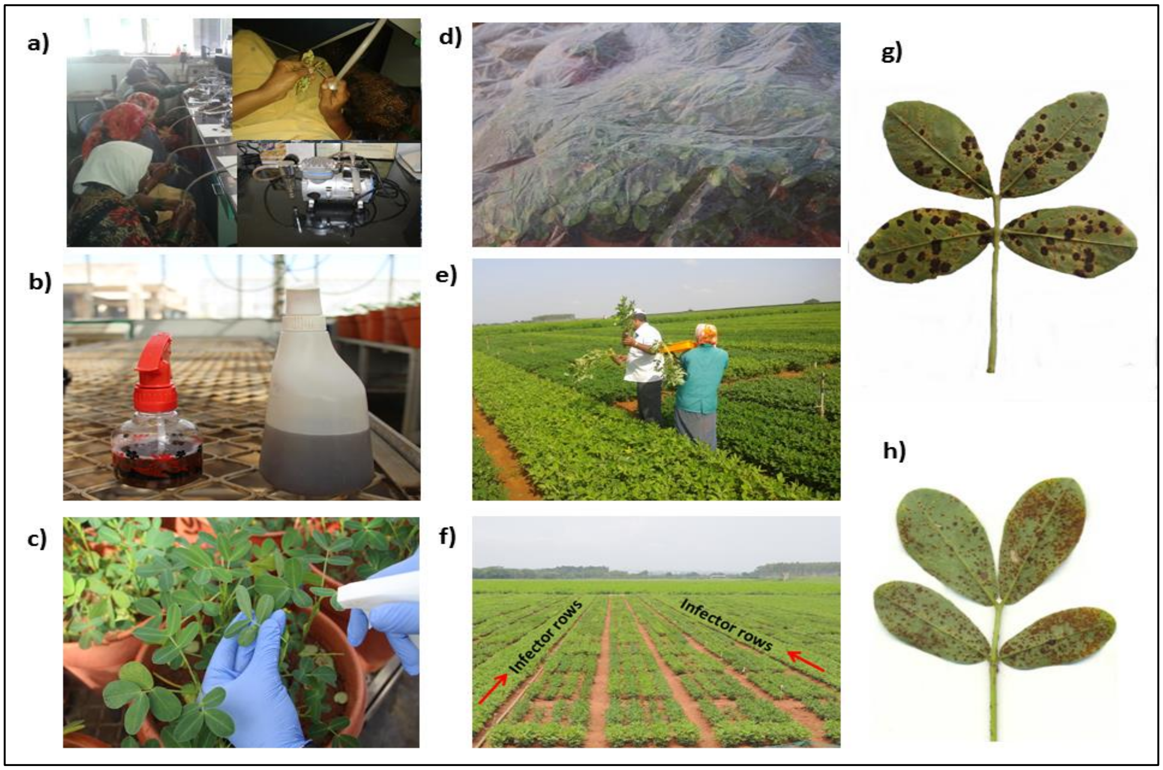

Figure 3.2 Procedure of artificial inoculation; **a)** Spore collection using a cyclone spore collector; **b)** Prepared solution of spores; **c)** Artificial inoculation of urediniospores of rust and conidia of LLS on plants; **d)** Plants were covered with polyethylene sheet during the night to maintain high humidity; **e)** Transplanting of diseased plants into infector rows of disease screening nursery; **f)** Layout of trial; **g & h)** Disease symptoms of LLS and rust, respectively

Table 3.2 Modified 9-point scale used for field screening of groundnut genotypes for LLS resistance (Subrahmanyam *et al.,* 1995)

Disease score	Description	Disease severity (%)*
1	No disease	0
2	Lesions present largely on lower leaves; no defoliation	1 -5
3	Lesions present largely on lower leaves, very few on middle leaves; defoliation of some leaflets evident on lower leaves	6-10
4	Lesions present on lower and middle leaves but severe on lower leaves; defoliation of some leaflets evident on lower leaves	11-20
5	Lesions present on lower and middle leaves, over 50% of defoliation of lower leaves	21-30
6	Severe lesions on lower and middle leaves; lesions present but less severe on top leaves; extensive defoliation of lower leaves; some defoliation on middle leaves	31-40
7	Lesions on all leaves but less severe on top leaves; defoliation of all lower and middle leaves	41-60
8	Defoliation of all lower and middle leaves; severe lesions on top leaves evident.	61-80
9	Almost all leaves defoliated, leaving bare stem; some leaflets may remain but show severe leaf spot	81-100

*Percentage leaf area damaged by LLS

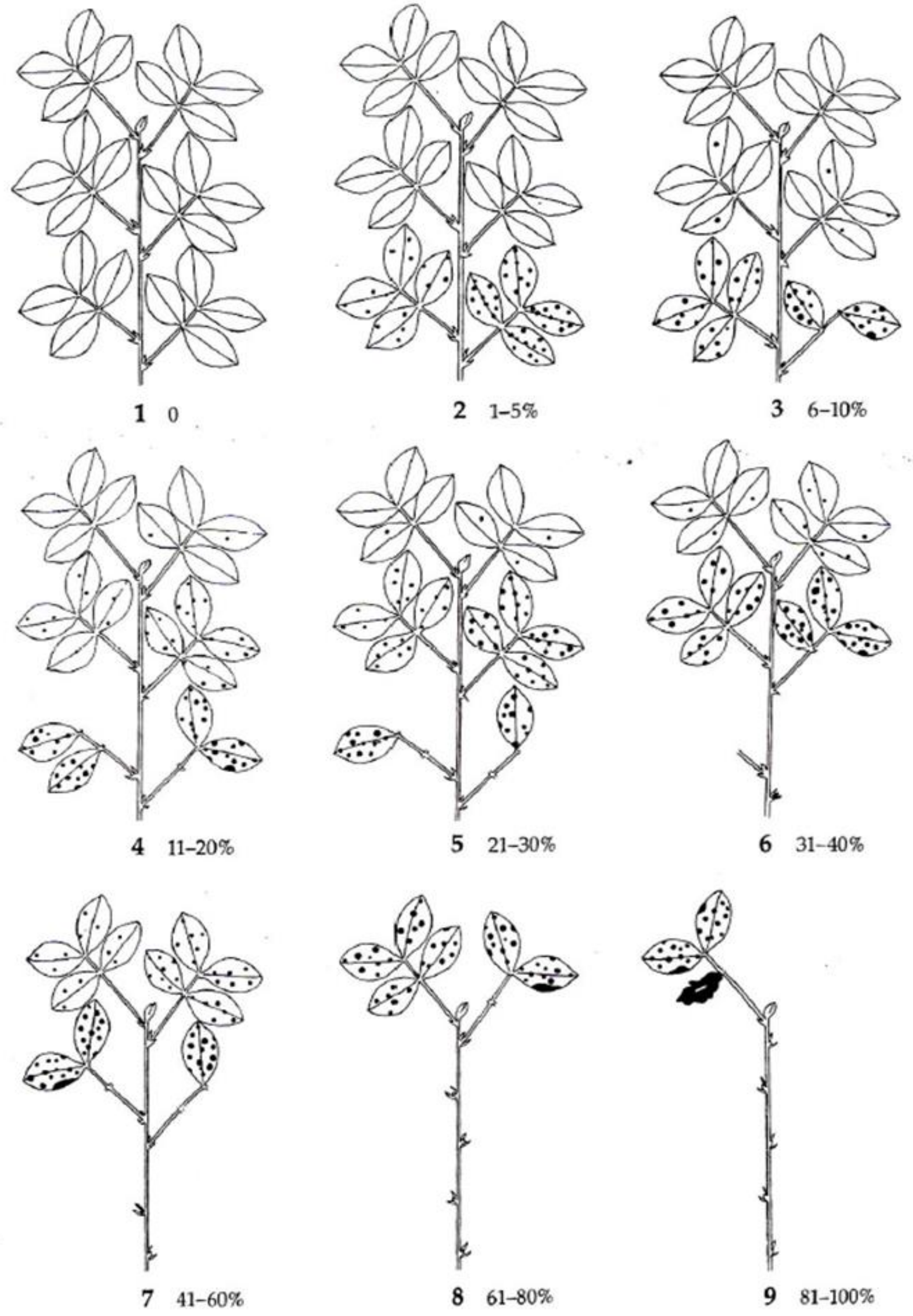

Figure 3.3 Diagram showing leaf symptoms and percent disease incidence used for scoring of genotypes against LLS disease resistance (Subrahmanyam *et al.,* 1995)

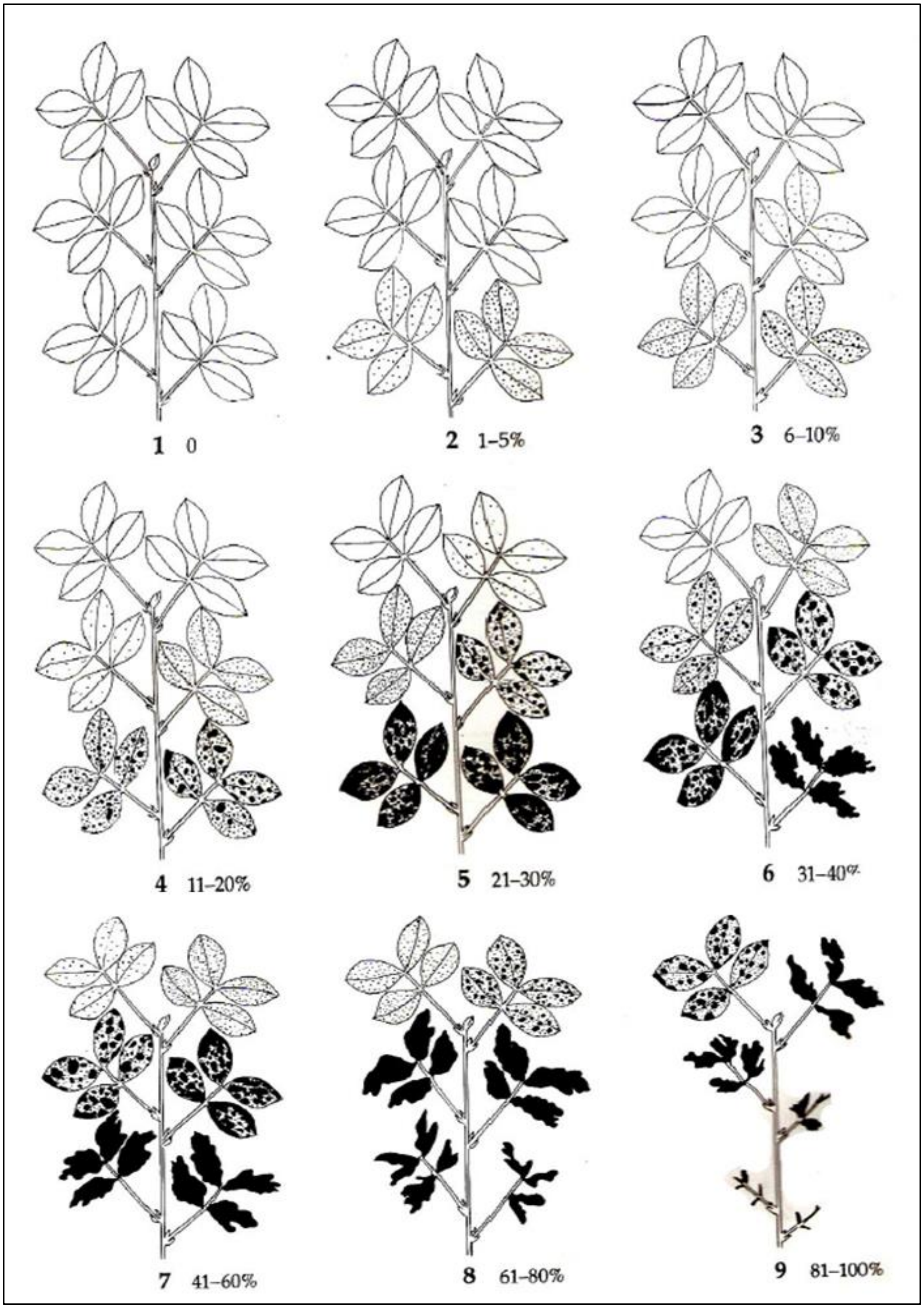

Figure 3.4 Diagram showing leaf symptoms and percent disease incidence used for scoring of genotypes against rust disease resistance (Subrahmanyam *et al.,* 1995)

Table 3.3 Modified 9-point scale used for field screening of groundnut genotypes for rust resistance (Subrahmanyam *et al.,* 1995)

Disease score	Description	Disease severity (%)*
1	No disease	0
2	Pustules sparsely distributed, largely on lower leaves	1-5
3	Many pustules on lower leaves, necrosis evident, very few pustules on middle leaves	6-10
4	Number of pustules on lower and middle leaves, severe necrosis on lower leaves	11-20
5	Severe necrosis of lower and middle leaves, pustules may be present on top leaves but less severe	21-30
6	Extensive damage to lower leaves, middle leaves, necrotic with dense distribution of pustules, pustules on top leaves	31-40
7	Severe damage to lower and middle leaves, pustules densely distributed on top leaves	41-60
8	100 per cent damage to lower and middle leaves, pustules on top leaves	61-80
9	Almost all leaves withered, bare stems seen	81-100

*Percentage leaf area damaged by rust

3.4.2 Observations on yield and its contributing traits

Observations on yield and its attributing characters were recorded on five randomly selected healthy plants excluding border plants from both the replications. The details of methods adopted for recording observations on different traits are

3.4.2.1 Days to 50% flowering: The number of days counted from the date of sowing to the day when 50% of the plants initiated flowers.

3.4.2.2 Days to physiological maturity: The number of days counted from date of sowing to the day when 80% of the plants got matured.

3.4.2.3 Plant height (cm): The plant height was recorded as the height of the main axis from ground level to apical leaflet in centimeters at 90 days after sowing.

3.4.2.4 Number of primary branches per plant: The total numbers of primary branches borne on the main axis were counted from five randomly selected healthy plants in each replication and mean was calculated.

3.4.2.5 Number of matured pods per plant at the time of harvest: The randomly selected five healthy plants were marked and harvested separately. Total number of matured pod produced in each of these five plants was counted and average was calculated.

3.4.2.6 Pod yield per plant (g): The weight of total pod per plant obtained after optimum drying of the pods harvested from five random plants was recorded and mean was calculated (g).

3.4.2.7 Seed yield per plant (g): The average weight of the total seeds obtained from shelling of mature pods of five selected plants was recorded from both the replications.

3.4.2.8 Shelling percent: The shelling percent was computed by taking 100 g random sample of dry pods of each genotype and it was shelled. Shelling outturn was computed by using the following formula

$$\text{Shelling percent} = \frac{\text{Kernel weight (g)}}{\text{Pod weight (g)}} \times 100$$

3.4.2.9 Hundred seed weight (g): A random sample of hundred well-developed seeds (avoiding shriveled and broken ones) was drawn from each replication and its weight was recorded in grams to get hundred seed weight.

3.4.2.10 Pod yield per hectare (kg): After optimum drying (~8%), the weight of total pods harvested from the whole plot of each genotype from each replication was recorded and calculated into pod yield per hectare.

3.4.2.11 Haulm yield per plant (g): Weight of total number of plants after optimum drying and threshing of pods was recorded from each replication and mean was computed by dividing final plant stand to get haulm yield per plant.

3.4.3 Nutritional quality analysis

All the genotypes of GSP were subjected to phenotyping for protein content, oil content and four major fatty acid *viz.,* palmitic acid (16:0), stearic acid (18:0), oleic acid (18:1) and linoleic acid (18:2) using near-infrared reflectance spectroscopy (NIRS). The oleic/linoleic acid (O/L ratio), an important oil quality determining parameter was calculated as follows.

$$\mathrm{O/L\ ratio} = \frac{\text{Oleic acid content (\%) (18: 1)}}{\text{Linoleic acid content (\%) (18: 2)}}$$

Near-infrared reflectance spectroscopy (NIRS)

Near infrared spectroscopy either in reflectance (NIRS) or transmittance mode (NITS) is a multi-trait technique of large scale applications in the analysis of nutritional quality traits of food and agricultural commodities (Shenk and Wasterhaus, 1995). In present study, oil and protein content along with four major fatty acids measured for each genotype using NIRS. The details about principle, spectral measurement, calibration of prediction equation, data analysis and validation of calibrated equation of NIRS are given below.

Principle

The detection and measurement of chemical composition of biological material based on the vibrational response of chemical bonds to NIR radiation.

Spectral measurement of NIR

All the samples were scanned on an NIR Systems model XDS monochromator (model XDS RCA, FOSS Analytical AB, Sweden, Denmark). Reflectance spectra (log1/R) from 400 to 2498 nm were recorded at 2 nm intervals. Each sample was subsequently scanned 32 times and the average spectrum was collected.

Data analysis

For analysis, about 30 to 60 g (depending on amount of seed available) of sound mature seed sample of each genotype was scanned in a rectangular cup. The cup was filled up sufficiently to allow good absorption of the incident light. In each scan, NIR light was allowed to fall on the bottom of the sample holder containing the groundnut seeds, where it penetrated and interacted with the samples. The reflected energy spectrum over the wavelength range of 400-2,498 nm that carried absorption information of the samples was collected. The instrument diagnostics was carried out to test the response of instrument, wavelength and NIR repeatability to avoid the effects of surrounding environment on the instrument performance. Mathematical procedures on the spectral information were carried out with WinISI II project manager software version 4.3 (Infrasoft International, Port Matilda, PA, USA).

Calibration

Before using NIR spectrophotometer for any quantitative analysis it has to be calibrated using chemical reference method with the application of multivariate regression models to interpret chemical information encoded in the spectral data. Original reflectance spectra were corrected prior to calibration by applying first and second derivative information, standard normal variate transformation, de-trend scatter correlation and four passes were used to eliminate outliers. Calibrations were performed based on spectral data from 400 to 2498 nm with an interval of 2 nm, to obtain the regression equations for fatty acid contents between spectral data and laboratory reference values using modified partial least squares (MPLS). For performing MPLS the number of parameters was set to ‘default’ and the number of cross-validation groups set to 8; with samples with a ‘H’ value larger than 4 (spectral outliers) and a (Student) ‘T’ value larger than 2.5 (sample which did not fit the calibration model) being eliminated (Shenk and Westerhaus, 1995).

Different mathematical pretreatment methods were tested on the calibration set and the best method was chosen based on the optimum results obtained for R^2 (determination coefficient of calibration) and 1-VR (coefficient of determination in cross-validation). Three mathematical treatments were used *viz.,* the raw data or the first or second derivatives of log 1/R data to remove background differences, combined with gap sizes in data points over which the derivative was calculated for enhancing spectral differences and a smoothing algorithm to reduces random noise in the spectral data (Savitzky and Golay, 1964). For example in the treatment 1,4,4,1 the first number indicates the order of derivative function (one is the first derivative of log 1/R); the second number is the gap (the length in nm); the third number represents the number of data points (segment length) used in the first smoothing and the fourth number is the number of data points in the second smoothing which is normally set at 1 for no second smoothing (Shenk and Westerhaus, 1993).

Calibrations were performed with five different mathematical treatments (1,2,2,1; 1,4,4,1; 1,8,8,1; 2,4,4,1; 2,8,8,1) using SNV + D (Standard Normal Variate + De-trend) scatter correction option. Scatter corrections are useful in reducing differences in the spectra related to physical characteristics such as particle size and path length of reflectance from the particle surface (Shenk and Westerhaus 1993). Four cycles of outlier elimination were allowed. Calibration models were assessed using statistics that included the standard error of calibration (SEC), the coefficient of determination in calibrations (R^2), the standard error of cross-validation (SECV), and the coefficient of determination in cross-validation (1-VR) (Shenk and Westerhaus, 1993). The optimum calibration equations were obtained based on the highest R^2 or 1-VR and the lowest SEC or SECV values.

Using the above-described procedure, calibration equations were developed using the readouts of wet chemistry methods. For developing calibration equations for oil content, 142 genotypes with varying oil content were analyzed using Soxhlet method. Similarly the oleic, linoleic and palmitic acid content in 208 $F_{2:3}$ population of the cross ICGV 06420 × SunOleic 95R was estimated using gas chromatography (GC). For developing calibration equation for protein content around 114 samples was estimated using Autoanalyzer for protein content. Different mathematical treatments were tested to identify the best calibration equation based on their coefficient of determination in calibration (R^2) and coefficient of determination of cross-validation (1-VR) values. The mathematical equation used, and the RSQ (R^2) and I-VR values of the developed equations is given in Table 3.4. The RSQ values for oil, protein and palmitic acid was 0.83, 0.87 and 0.88, respectively, while that for oleic and linoleic acid was 0.97. Similarly, the 1-VR values for the samples used in cross-validation of the developed equation were ranged from 0.75 for protein to 0.95 for oleic and linoleic acid indicating the suitability of the equation for predicting oil, protein, palmitic acid, oleic acid and linoleic acid in whole seed kernels. This equation is being routinely utilized at ICRISAT to analyze around 25,000-30,000 samples/season for the above quality traits and to screen samples based on their seed quality profile. The absorption spectrum of NIRS for two samples differing in their oleic acid contents is depicted in Figure 3.5.

Table 3.4 Calibration equations for predicting oil, protein and fatty acids (palmitic, oleic and linoleic acid) content in whole groundnut kernels using NIRS

Constituent	N	Mean	Range	Mathematical treatment	RSQ	1-VR
Oil (%)	142	48.69	40.08-57.31	1,4,4,1	0.83	0.80
Protein (%)	114	27.68	19.73-35.64	4,6,6,1	0.87	0.75
Palmitic acid (%)	208	11.42	6.77-16.06	2,4,4,1	0.88	0.80
Oleic acid (%)	208	52.12	23.44-80.79	2,4,4,1	0.97	0.95
Linoleic acid (%)	208	27.12	2.77-51.46	2,4,4,1	0.97	0.95

*N- Number of samples in calibration; **RSQ- coefficient of determination in calibrations; #1-VR- coefficient of determination in cross-validation

Validation of calibration statistics

The accuracy and precision of the selected calibration equation was monitored with the WinISI software using the external validation set (Windham *et al.,* 1989). The indicators for external validation were standard error of prediction (SEP); coefficient of determination in external validation (R^2) and SEP/SD values, which is the ratio of the standard error of prediction to standard deviation (SD) for the validation samples. The best-calibrated equation was used to phenotype GSP for nutritional quality traits.

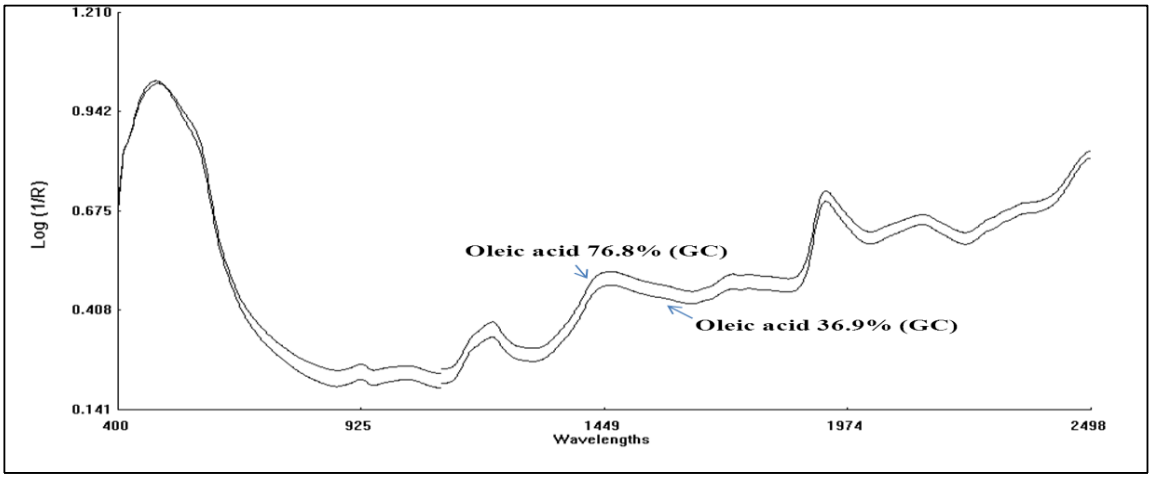

Figure 3.5 Raw absorption spectra of groundnut kernels representing two extreme oleic acid values

3.5 Molecular diversity, allelic richness and marker-traits association study

In order to construct better prediction model with high accuracy for Genomic Selection, molecular diversity and allelic richness must be evaluated to assess allelic variation for targeted loci. Hence, 336 genotypes of GSP were subjected for molecular diversity and allelic richness using 14 SSR markers reported to be linked with rust and LLS, and nutritional quality traits (Sarvamangla *et al.,* 2011; Goutami *et al.,* 2012 and Sujay *et al.,* 2012). The major aim was to check the allelic richness and molecular diversity for targeted traits, therefore the markers reported in previous studies with >10% phenotypic variance for rust, LLS and nutritional quality traits were selected in the present study. The steps involve in genotyping are explained under different headings.

3.5.1 DNA Isolation

Several procedures for genomic DNA isolation have been reported (Murray and Thompson, 1980; Dellaporta *et al.,* 1983; Tai and Tanksley, 1990). The procedure based on CTAB extraction buffer (Mace *et al.,* 2003) was used for genomic DNA isolation in this study.

A) Preparation

1. Two chrome-plated grinding balls (4 mm in diameter), pre-chilled at -20°C for about 30 minutes, were dispensed by an automatic ball dispenser to 12 × 8 well polypropylene strip extraction tubes with strip caps that were kept on ice.

2. 3% CTAB buffer was pre-heated at 65°C in water bath (Precision Scientific Model: Shaking Water Bath 50) before starting DNA extraction.

3. Leaf strips were collected from one-week-old seedlings from each genotype and cut into small pieces (approximately 30 mg), which were then transferred to an extraction tube fitted in a box. This was repeated for all 336 genotypes in three and half 96-well boxes.

B) Grinding and extraction

1. 450 μl of preheated 3% CTAB buffer was added to each extraction tube containing leaf sample and tightly capped with polyethylene strip caps.

2. Grinding was carried out using a Sigma Geno-Grinder (Spex Certiprep, USA) at 500 strokes/minute for 2 minutes.

3. Grinding was repeated until the color of the solution became pale green and leaf strip pieces were sufficiently macerated. After the first round of grinding, the boxes were checked for leakage by taking them out from the Geno-Grinder and were shaken for proper mixing of leaf tissues with buffer.

4. After grinding, the box with the tubes was fixed in a locking device and incubated at 65°C in a water bath for 40 minutes with occasional manual shaking.

C) Solvent extraction

1. 450 μl of Chloroform: Isoamyl alcohol (24:1) mixture was added to each tube, tubes were inverted twice for proper mixing and the samples were centrifuged at 5000 rpm for 10 minutes.

2. After centrifugation, the aqueous layer (approximately 300 μl) was transferred to a fresh tube (Marsh Biomarket).

D) Initial DNA precipitation

1. To each tube containing the aqueous layer, 7/10th volume (approximately 210 μl) of cold (kept at -20°C) Isopropanol was added. The solution was carefully mixed and the tubes were kept at -20°C for 10 minutes.

2. The samples were centrifuged at 5000 rpm for 15 minutes.

3. The supernatant was decanted under the fume hood and pellets were allowed to air dry for about 30 minutes.

E) RNase A treatment

1. In order to remove co-isolated RNA, pellets were dissolved into 200 µl of TE buffer (T_{10} E_1) and 3 µl of RNase A.
2. The solution was incubated at 37°C for 30 minutes or overnight at room temperature.

F) Solvent extraction

1. After incubation, 200 µl of Phenol: Chloroform: Isoamyl alcohol (25:24:1) was added to each tube, mixed and centrifuged at 5000 rpm for 10 minutes.
2. The aqueous layer in each tube was transferred to a fresh tube (Marsh Biomarket) and 200 µl of Chloroform: Isoamyl alcohol (24:1) was added to each tube, mixed and centrifuged at 5000 rpm for 10 minutes.
3. The aqueous layer was transferred to fresh tube (Marsh Biomarket).

G) DNA Precipitation

1. 15 µl (approximately 1/10th volume) of 3 M sodium acetate (pH 5.2) and 300 µl (2 volumes) of absolute ethanol (kept at -20°C) were added to each of the tubes and the mixture was subsequently incubated in a freezer (-20°C) for 5 minutes.
2. Following the incubation at -20°C, the tubes were centrifuged at 6200 rpm for 15 minutes.

H) Ethanol Wash

1. After centrifugation, the supernatant was carefully decanted from each tube in order to ensure that, the pellet remained inside the tube.
2. Subsequently, 200 µl of 70% ethanol was added to each of the tubes and it was followed by centrifugation at 5000 rpm for 5 minutes.

I) Final re-suspension

1. The supernatant was carefully decanted and the pellet was allowed to air dry for one hour.
2. Dried pellets were re-suspended in 100 µl of $T_{10}E_1$ buffer and kept overnight at room temperature to dissolve completely.
3. The re-suspended DNA samples were stored at 4°C.

3.5.2 Quantification of DNA concentration and quality check

To determine the quantity and quality of genomic DNA using agarose gel, an aliquot of 1 μl of DNA from each sample along with 5 ng of molecular weight marker (λ DNA, Amersham Biosciences) were initially analyzed by electrophoresis on 0.8% agarose gels containing ethidium bromide (0.5 μl/10 ml of gel) and run in 0.5X TBE (Tris Borate EDTA) buffer at a constant voltage (100 V) for one hour. The gel was viewed under UV illumination and recorded using an UVi Tech gel documentation system (DOL-008.XD, England). A smear of DNA indicated poor quality whereas a clear band indicated good quality DNA. After quality check, working stock of DNA with 5 ng/μl concentration was made by diluting with water for each sample.

3.5.3 Polymerase chain reaction (PCR)

PCR reactions were conducted in 96 and 384-well plates in a GeneAmp PCR system PE 9700 (Applied Biosystems, USA) DNA thermal cycler in volumes of 5 μl. A touchdown PCR program was used to amplify the DNA fragments. Fourteen SSR primers with M13 tail to bind with fluorescent labeled dye were used for genotyping of GSP (Table 3.5). Forward (2 pMol) and reverse (5 pMol) sequences of these SSR markers diluted and used for PCR reaction with each DNA sample of GSP. Initial denaturation for 5 minutes at 94°C (to minimize primer-dimer formation and to activate the Taq polymerase), subsequently 5 cycles of denaturation for 20 seconds at 94°C, annealing at 65°C for 30 seconds, the annealing temperature for each cycle is reduced by 1°C up to six cycle and extension at 72°C for 30 seconds after that 40 cycles of denaturation at 94°C for 20 seconds, annealing at 59°C for 20 seconds and extension at 72°C for 30 seconds followed by final extension at 72°C for 20 min and then maintain 4°C until removal of PCR plate. PCR amplification was checked on 1.2% agarose gels and PCR products of directly labeled primers and M13 tailed primers were separated by capillary electrophoresis on an ABI3730xl sequencer and their sizes were determined using GeneMapper® Version 4.0 software (Applied Biosystems, USA).

3.5.4 Genotyping using capillary electrophoresis

The PCR products amplified using fluorescence-labeled M13 tailed SSR primers were separated by capillary electrophoresis using an ABI Prism 3700 automatic DNA sequencer (Applied Biosystems Inc.). This has the ability to detect size differences of 1 bp using a fluorescence-based detection system, thus dispensing with the need for radioactivity or laborious manual Polyacrylamide or Agarose gel techniques.

For this purpose, forward primers were labeled with 6-FAM™ (Blue), VIC™ (Green), NED™ (Yellow) or PET™ (Red) fluorophores (Applied Biosystems). PCR products of primers labeled with different dyes or same fluorophore-labeled primers with non-overlapping amplicons (in terms of size) were pooled (post-PCR). The products of different fluorophore-labeled primers were pooled in different proportion (1.0 µl of 6-FAM–labeled product, 0.8 µl of VIC-labeled product, 1.4 µl of NED–labeled product, and 1.0 µl of PET-labeled product). The pooled PCR products were then mixed with 0.2 µl of GeneScan 500™ LIZ® internal size standard (Applied Biosystems) and 7.0 µl of Hi-Di™ Formamide (Applied Biosystems). The final volume was made up to 15 µl with sterilized double-distilled water. DNA fragments were denatured for 5 minutes at 95ºC (Perkin Elmer 9700, Applied Biosystem) and cooled immediately on ice and sent for fragment size analysis.

3.5.5 Fragment size fractionation

The PCR products with denatured DNA were electrophoresed and the capillary run was performed using the “Genscan2 POP6 Default” run module and “G5” filter-set. The analysis module used was “GS500 analysis”. The fragments were separated in a 50 cm capillary array using POP6 (Performance Optimized Polymer, Applied Biosystems) as separation matrix.

Table 3.5 Details of SSR primers used in the study

S. No.	Primer name	Repeat motif	Tm (^{0}C)	Product size	Primer sequence		Traits linked	References
1	GM1009	(CTC)5/ (CCG)5	59.6	411	F	TTTCCTTCTTTCCCTTCTTCTTC	LLS resistance	Nagy *et al.*, (2010); Sujay *et al.*, (2012)
					R	CGTTGTTGCCGTTAAACTGA		
2	GM2301	(AG)23	60.3	127	F	GTAACCACAGCTGGCATGAAC	Rust resistance	Nagy *et al.*, (2010); Sujay *et al.*, (2012)
					R	TCTTCAAGAACCCACCAACAC		
3	GM1954	(GA)11	59.7	115	F	GAGGAGTGTGAGGTTCTGACG	LLS resistance	Nagy *et al.*, (2010); Sujay *et al.*, (2012)
					R	TGGTTCATTGCATTTGCATAC		
4	GM1573	(TC)24	59.7	264	F	GAGACCGGAGACGGAGAGTAT	LLS resistance	Nagy *et al.*, (2010); Sujay *et al.*, (2012)
					R	ACGCCCATAGATTAACCCAGT		
5	GM 2079	CAG (6)	60.0	416	F	GGCCAAGGAGAAGAAGAAAGA	Rust resistance	Nagy *et al.*, (2010); Sujay *et al.*, (2012)
					R	GAAGGAGTAGTGGTGCTGCTG		
6	GM 1536	CT (10)	60.3	482	F	AAAGCCCTGAAAAGAAAGCAG	Rust resistance	Nagy *et al.*, (2009); Sujay *et al.*, (2012)
					R	TATGCATTTGCAGGTTCTGGT		
7	PM36	(AG)19	60.0	243	F	ACTCGCCATAGCCAACAAAC	Protein and oil content (%)	He *et al.*, (2003); Sarvamangla *et al.*, (2011)
					R	CATTCCCACAACTCCCACAT		
8	TC3E02	(CT)26+(CA)7 +(CA)5	56.0	273	F	TGAAAGATAGGTTTCGGTGGA	Protein content (%)	Moretzsohn *et al.*, (2005); Sarvamangla *et al.*, (2011)
					R	CAAACCGAAGGAGGAACTTG		
9	TC6E01	(GA)22	58.0	171	F	CTCCCTCGCTTCCTCTTTCT	Oil content (%), pod and seed weight	Sarvamangla *et al.*, (2011); Goutami *et al.*, (2012)
					R	ACGCATTAACCACACACCAA		
10	TC6H03	(AG)21	58.0	223	F	TCACAATCAGAGCTCCAACAA	Protein content (%)	Moretzsohn *et al.*, (2005); Sarvamangla *et al.*, (2011)
					R	CAGGTTCACCAGGAACGAGT		
11	TC1D02	(TC)30	56.0	264	F	GATCCAAAATCTCGCCTTGA	Haulm yield, Dry pod yield	Moretzsohn *et al.*, (2005); Goutami *et al.*, (2012)
					R	GCTGCTCTGCACAACAAGAA		
12	TC1D12	(TC)9	60.6	169	F	CCCTTTCATTCTCCCTTTCC	Protein content (%)	Moretzsohn *et al.*, (2005); Sarvamangla *et al.*, (2011)
					R	TTCTCCTGCACTAGGTTTCCA		
13	GM630	(ATA)11	60.0	341	F	CAGCAATTCAGCAAACTAATGAA	Pod and seed yield per plant, Haulm yield	Budiman *et al.*, (2006); Goutami *et al.*, (2012)
					R	TCCTCCCACGTCCTTTTATTT		
14	IPAHM 103	(AG)17	59.7	160	F	GCATTCACCACCATAGTCCA	Rust resistance, Oil content	Cuc *et al.*, (2008); Khedikar *et al.*, (2010)
					R	TCCTCTGACTTTCCTCCATCA		

Tm= Annealing temperature

3.5.6 Data Processing and Scoring of genotypes for amplicon size

GeneMapper® version 4.0 software (Applied Biosystems, USA) was used to size the peak pattern in relation to the internal size standard, GeneScan 500™ LIZ®. The principle behind this is that standards are run in the same lane or capillary injection as the samples, which contain fragment of unknown sizes labeled with different fluorophores. GeneMapper® version 4.0 Software automatically calculates the size of unknown DNA fragments by generating a calibration sizing curve based upon the migration times of the known fragments in the standard. The unknown fragments are mapped onto the curve and the sample data is converted from migration times to fragments size. The peaks were displayed with base pair values and height (amplitude) in a chromatogram. The height of the chromatogram peaks (representing the alleles) obtained through capillary electrophoresis is directionally proportionate to the signal strength, which in turn is determined by the amount of amplified product in the sample. True picks of all 14 SSR markers were identified and scored for each genotype using GeneMapper® version 4.0 software (Applied Biosystems, USA).

3.6 Screening of GSP for *ahFAD2A* & *ahFAD2B* mutant alleles

A total of 336 genotypes of GSP were screened for presence of mutant alleles of *ahFAD2* gene using allele-specific polymerase chain reaction (AS-PCR) developed by Chen *et al.,* (2010). Two different primer pairs were required for amplifying the mutant alleles of *ahFAD2A* and *ahFAD2B* genes along with one additional primer pair to amplify a common allele for wild-type allele as an internal control. The primer combination, F435-F, and F435SUB-R, amplified 203 bp fragment for the mutant allele (substitution from G:C to A:T) in the A-genome, while the primer combination, F435-F and F435INS-R amplified 195 bp fragment for the mutant allele (A:T insertion) in the B-genome. The primer combination, F435-F and F435IC-R was used as internal control to confirm successful amplification by amplifying 250 bp fragment for wild-type allele (Table 3.6). The PCR was set up in 10 µl volume using 5 ng of genomic DNA together with 5 picomole primer (forward and reverse each), 1X PCR buffer (Sib Enzyme, Russia), 5 mM $MgCl_2$, 0.03 U/l of Taq DNA polymerase (Kapa Biosystems Inc, USA), and 0.2 mM dNTPs for amplification of targeted region in ABI thermal cycler (Applied Biosystems, USA). The PCR program included initial denaturation step for 3 min at 94ºC, first 5 cycles at 94ºC for 20 s, 65ºC for 20 s and 72ºC for 30 s, with 1ºC decrease in temperature each cycle. The remaining 40 cycles were performed at 94ºC for 20 s with constant annealing temperature (59ºC) for 20 s. The condition for primer extension was set at 72ºC for 30 s and final extension at 72ºC for 20 min. The amplified PCR products were then separated by electrophoresis at 150V for 1 h on a 3% agarose gel (SeaKem LE Agarose, USA) in 1X TBE buffer. The ethidium bromide was used for staining the fragments and UV light was used for visualizing the stained fragments for easy scoring. While running the agarose gel, 100 bp DNA ladder (Life technologies, USA) was used as size reference for amplified fragments. Genotypes were scored and categorized based on the presence and absence of *ahFAD2A* and *ahFAD2B* mutant allele. The frequencies of both the mutant alleles in GSP were calculated and mean phenotypic performance of genotypes for fatty acids composition (oleic, linoleic, palmitic, stearic and O/L ratio) across the environments was compared with respect to presence/absence of allele.

Table 3.6 Details of allele-specific primers used to screen Genomic Selection Panel of groundnut for mutant alleles of *ahFAD2* gene (Chen *et al.,* 2010)

Gene	Primer	Sequence	Wild allele size	Mutant allele size
ahFAD2	F345F	ATCCAAGGCTGCATTCTCAC	250	-
	F345IC-R	ACTTCGTCGCGGTCG		
ahFAD2A	F345F	ATCCAAGGCTGCATTCTCAC	-	203
	F345SUB-R	TGGGACAAACACTTCGTT		
ahFAD2B	F345F	ATCCAAGGCTGCATTCTCAC	-	195
	F345INS-R	AACACTTCGTCGCCTCT		

3.7 Statistical analysis

3.7.1 Phenotypic data analysis

3.7.1.1 Analysis of variance

The analysis of variance for different characters was carried out using Alpha lattice design as suggested by Cochran and Cox (1957) in SAS version 9.2 (SAS Institute Inc 2013).

The phenotypic observations Zijkl on accession l in replicate j of block k of location i was modeled as:

$$\mathbf{Z_{ijkl} = \mu + e_i + (e/r)_{ij} + (e/r/b)_{ijk} + g_i + (eg)_{il} + \varepsilon_{ijkl}}$$

Where,

µ: is the grand mean;

e_i is the fixed effect of location i;

g_j is the fixed effect of genotype l;

$(e/r)_{ij}$ is the fixed effect of replication j nested with in location i;

$(e/r/b)_{ijk}$ is the random effect of block k nested with in replication j and location i and is ~ NID(0, σ^2b);

$(eg)_{il}$ is the fixed effect of the interaction between genotype l in location i;

ε_{ijkl} is the random residual effect and ~ NID(0, $\sigma^2\varepsilon$).

Table 3.7 Skeleton of analysis of variance (ANOVA) for alpha lattice design

Source of variation	DF
Environment	e-1
Replication	e (r-1)
Block	er (b-1)
Genotype	g-1
Genotype x Environment	(g-1)(e-1)
Residual	e (rt-rb-t+1)
Total	ert-1

Where, r = Number of replications, k2 Number of treatments (genotypes)

The adjusted variable mean differences were tested for significance as follows

Source of variation	Degree of freedom	Sum of squares	Mean squares	F ratio
Genotypes (adjusted)	k2-1	SSg	MSg	MSg/MSe
Error (intra block)	(k-1) (rk-k-1)	SSE	MSe	

The computed F value was compared with the table F value at (k2-1) and (k-1) (rk-k-1) degrees of freedom for 5% and 1% level of significance.

To test significance of the differences between any two adjusted genotypic means, the standard error of mean was computed using the formula

S.E= [2MSe/r (1+2ku/k+1)] 0.5

Where S.E = Standard error of mean

MSe = Mean sum of squares for error (intra block)

r = Number of replications

k = Number of genotypes in each sub-block

u = Weightage factor computed

3.7.1.2 Population mean and variances

A. Arithmetic mean: Best Linear Unbiased Predictions (BLUPs) were calculated for each accession for all quantitative traits at individual as well as combined across environments using SAS version 9.2.

B. Range: The minimum and maximum values for each trait in the Genomic Selection Panel were calculated.

C. Variance: It measures the variability and defined as the average of square of deviations from the mean.

$$\sigma^2 = \frac{1}{n}\sum (X_i - X)^2$$

Where, σ^2 =variance, Xi =observation, X = mean

D. Standard Deviation (SD): It is dispersion of individual values(X) around the population mean.

SD = $\sqrt{\sigma^2}$

E. Standard Error of Mean (SEm): It is dispersion of family mean around the estimated population mean.

$$\text{Standard Error} = \frac{\text{SD}}{\sqrt{\text{n}}}$$

Where,

SD = Standard deviation

n = number of observations

In fact, S.E. is the SD of mean i.e. represented by X±SEm.

F. Coefficient of variation (CV)

The coefficient of variation is the best statistical method to compare the amount of variation present in population for different traits. Different traits are represented by different units so that by converting units of all characters on the same scale, we can compare the amount of variation in terms of CV which is expressed as percentage ratio.

$$\text{CV (\%)} = \frac{\text{SD}}{\overline{\text{X}}} \times 100$$

3.7.1.3 Estimation of genetic variability parameters

Genetic variability among the genotypes for all recorded characters were estimated as mentioned below.

A. Genotypic coefficient of variability (GCV)

$$\text{GCV \%} = \frac{\sigma\text{g}}{\overline{\text{X}}} \times 100$$

B. Phenotypic coefficient of variability (PCV)

$$\text{PCV \%} = \frac{\sigma\text{p}}{\overline{\text{X}}} \times 100$$

C. Environmental coefficient of variability (ECV)

$$\text{ECV \%} = \frac{\sigma\text{e}}{\overline{\text{X}}} \times 100$$

Where,

σg = Genotypic standard deviation

σp = Phenotypic standard deviation

σe = Environmental standard deviation

$\overline{\text{X}}$ - Grand mean of the character.

PCV and GCV were classified based on the scale given by Robinson *et al.,* (1949) and presented below:

Low = 0-10%

Moderate = 10-20%

High = >20%

D. Heritability (h^2)

It is the ratio of genetic variance to the phenotypic variance. The estimates of heritability in the broad sense were obtained by applying formula given by Singh and Chaudhary (1977).

$$h^2 = \left(\frac{\sigma^2 g}{\sigma^2 p}\right) \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

As suggested by Johnson *et al.,* (1955), heritability values are categorized as follows:

Low : less than 30%

Moderate : 30-60%

High : more than 60%

E. Genetic advance (GA)

Genetic advance was computed by using the formula elucidated by Johnson *et al.,* (1955)

$$\text{Genetic advance} = \frac{\sigma^2 g}{\sigma^2 p} \times K$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

K = selection difference a constant value of which is 2.06

F. Genetic advance over percent mean (GAM)

GA % over mean = $\left(\frac{\mathrm{GA}}{\mathrm{mean}}\right) \times\ 100$

GAM was categorized as low, moderate and high as given by Johnson *et al.,* (1955).

Low = 0-10%

Moderate =10-20%

High = >20%

3.7.1.4 Correlation coefficient

Both genotypic and phenotypic correlation coefficient were worked out to determine the degree of association among important yield and nutritional quality traits. The correlations between all pairs of traits were determined through variance and covariance components using formula suggested by Webber and Moorthy (1952).

$$\mathrm{r}_{\mathrm{p(xy)}}\ = \frac{\mathrm{Cov_p(X, Y)}}{\sqrt{\mathrm{Vpx, Vpy}}}$$

$$\mathrm{r}_{\mathrm{g(xy)}}\ = \frac{\mathrm{Cov_g(X, Y)}}{\sqrt{\mathrm{Vgx, Vgy}}}$$

Where,

r_p and r_g are phenotypic and genotypic correlations, respectively.

Cov_p (x, y) and Cov_g (x, y) are phenotypic and genotypic covariance between the characters, x and y

V_{px} and V_{py} are the phenotypic variances for the characters x and y

V_{gx} and V_{gy} are the genotypic variances for the characters x and y

The calculated value of ‘r’ was compared with ‘t’ table value with (n-2) degree of freedom at 5 and 1 percent level of significance.

3.7.2 Genetic diversity analysis

3.7.2.1 Principal component analysis (PCA)

It is a way of identifying patterns in data and expressing the data in such a way as to highlight their similarities and differences. Since patterns in data can be hard to find in data of high dimension, where the luxury of graphical representation is not available, PCA could be one of the powerful tools for analyzing such high dimension data. Besides graphical presentation of pattern of variation in the dataset, PCA can compress the data by reducing the number of dimensions without much loss of information.

The PCA analysis reduces the dimensions of a multivariate data to a few principal axes, generates an Eigenvector for each axis and produce component scores for the characters (Senath and Sokal., 1973). Factor analysis uses covariance matrix of characters to generate factor loadings and communalities using the method of principal component extraction (Harman, 1967 and Ariyo, 1992)

In the present study, PCA was performed based on quantitative traits at the individual as well as across the environments to find out the relative importance of different traits in capturing the variation in GSP. The observations for each trait were standardized by subtracting mean from each observation and subsequently dividing by its standard deviation. This resulted in standardized values for each trait of each genotype with average 0 and standard deviation of 1. Best linear unbiased predictions (BLUPs) were used to perform PCA using GenStat version 15. The PCs that scored eigenvalue greater than one and had major contribution towards explaining total genetic variability in the data set were used for cluster analysis. A hierarchical cluster analysis for individual environment separately and for pooled data was performed using scores of the first six principal components (PCs) following Ward (1963) clustering method.

3.7.3 GGE biplot analysis

To evaluates the phenotypic stability and adaptability, the GGE biplot analysis performed, considering the simplified model for two main principal components. In this approach, the effects of genotype (G) and genotype by environment (GE) were considered as random in the model. In this case, the best linear unbiased predictions (BLUP) were calculated and used for GGE biplot analysis.

The components of genotypic variance, environmental variance, GE interaction variance and residual were estimated by general linear mixed model of ANOVA using software package SAS version 9.2. GGE biplot analysis based on which won where pattern, a ranking of genotypes based on mean and stability and the relationship among test environments and between genotype and environments was done using GenStat version 15 (Yan and Kang, 2003). Out of 340, a total of 109 genotypes which had disease severity score <3 for either of the diseases at ICRISAT and Aliyarnagar were subjected to stability analysis using GGE biplot to find stable source of disease resistance to rust and LLS, and yield and nutritional quality traits.

The model for a GGE biplot (Yan, 2002) based on singular value decomposition (SVD) of first two principal components is:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij} \qquad [1]$$

where Y_{ij} is the measured mean (DBH) of genotype i in environment j, μ is the grand mean, β_j is the main effect of environment j, $\mu + \beta_j$ being the mean yield across all genotypes in environment j, λ_1 and λ_2 are the singular values (SV) for the first and second principal component (PC1 and PC2), respectively, ξ_{i1} and ξ_{i2} are eigenvectors of genotype i for PC1 and PC2, respectively, η_{j1} and η_{j2} are eigenvectors of environment j for PC1 and PC2, respectively, ε_{ij} is the residual associated with genotype i in environment j.

PC1 and PC2 eigenvectors cannot be plotted directly to construct a meaningful biplot before the singular values are partitioned into the genotype and environment eigenvectors. Singular-value partitioning is implemented by,

$$g_{i1} = \lambda_1^{f1} \xi_{i1} \text{ and } eij = \lambda_1^{1-f1} \eta_{1j} \qquad [2]$$

Where f_1 is the partition factor for PC1, Theoretically f_1 can be a value between 0 and 1, but 0.5 is most commonly used.

To generate the GGE biplot, the formulae [1] was presented as:

$$\mathbf{Y_{ij} - \mu - \beta_j = g_{i1}e_{1j} + g_{i2}e_{2j} + \varepsilon_{ij}} \qquad \mathbf{[3]}$$

If the data was environment-standardized, the common formula for GGE biplot was reorganized as follows:

$$\mathbf{Y_{ij} - \mu - \beta_j / s_j = \Sigma\, g_{i1}e_{1j} + \varepsilon_{ij}} \qquad \mathbf{[4]}$$

Where, $\mathbf{s_j}$ is the standard deviation in environment j, l =1, 2,…,*k*, $\mathbf{g_{i1}}$ and $\mathbf{e_{1j}}$ are PC1 scores for genotype i and environment j, respectively.

We used environment standardized model [4] to generate biplot of “which-won where”. For the analysis of relationship between the trials, genotype, and test environments, we used unstandardized model [3]. The analyses were conducted and biplot generated using the “GGE biplot” function of GenStat version 15.

3.7.4 Molecular data analysis

The allele sizes for all markers for each genotype were used to analysis basic statistics using Power Marker version 3.25 (Liu and Muse, 2005). The summary statistics includes analysis of polymorphic information content (PIC), allelic richness as determined by total number of the detected alleles, number of alleles per locus, occurrence of unique, rare, common and most frequent alleles, gene diversity and heterozygosity (%).

3.7.4.1 Polymorphic information content (PIC)

The polymorphic information content (PIC) was estimated as below (Botstein *et al.,* 1980).

$$\widehat{\mathrm{PIC}}_{l} = 1 - \sum_{u=1}^{k} \acute{P}_{lu}^{\,2} - \sum_{u=1}^{k-1} \sum_{v=u+1}^{k} \acute{P}_{lu}^{\,2} \acute{P}_{lv}^{\,2}$$

3.7.4.2 Gene diversity

Gene diversity often referred to as expected heterozygosity, is defined as the probability that two randomly chosen alleles from the population are different. An unbiased estimator of gene diversity at the lth locus is

$$\widehat{\mathrm{D}}_{\mathrm{l}} = (1 - \sum_{u=1}^{k} \acute{\mathrm{P}}_{\mathrm{lu}}{}^{2}) \Big/ \left(1 - \frac{1+\mathrm{f}}{\mathrm{n}}\right)$$

3.7.4.3 Heterozygosity

Heterozygosity is simply the proportion of heterozygous individuals in the population. At a single locus and it was estimated as

$$\widehat{\mathrm{H}}_{\mathrm{l}} = 1 - \sum_{u=1}^{k} \widehat{\mathrm{P}_{\mathrm{luu}}}$$

3.7.4.4 Allele and genotype frequencies

The sample allele frequencies are calculated as$\tilde{P}_u = n_u/(2n)$, with the variance estimated as

$$\mathrm{Var}\left(\widetilde{\mathrm{P}}_{\mathrm{u}}\right) \hat{=}\cdot \frac{1}{2\mathrm{n}}\left(\widetilde{\mathrm{P}}_{\mathrm{u}} + \widetilde{\mathrm{P}}_{\mathrm{uu}} - 2\widetilde{\mathrm{P}}_{\mathrm{u}}^{2}\right)$$

Where $\hat{=}\cdot$ means “estimated by”.

The sample genotype frequencies $\tilde{P}_{uv}$ are calculated as n_{uv}/n. Both $\tilde{P}_u$ and $\tilde{P}_{uv}$ are unbiased maximum likelihood estimates of the population frequencies. Confidence interval for allele and genotype frequency was formed by resampling individuals from the data set.

3.7.4.5 Unique, rare and common alleles

Unique alleles are those that are present in one accession or in one group of accessions but absent in other accessions or group of accessions. Rare alleles are those whose frequency is ≤ 1 percent in the investigated materials. Common alleles are those occurring between 1-20 percent in the investigated materials while those occurring >20 percent was classified as most frequent alleles (Upadhyaya *et al.,* 2008).

3.7.4.6 Clustering

The unweighted neighbor-joining tree was constructed based on the simple matching dissimilarity matrix of 14 SSR markers genotyped in 336 genotypes of GSP using DARwin 5.0.156 program (Perrier and Jacquemoud Collet, 2006).

3.7.4.7 Principle coordinate analysis (PCoA)

The PCoA of genotypes of GSP was performed based on genetic distance values obtained from DARwin distance matrix using GENAlex 6.41 (Peakall and Smouse, 2006).

3.7.4.8 Analysis of molecular variance (AMOVA)

Analysis of molecular variance was performed to partition molecular variance within and among the subspecies of cultivated groundnut and populations identified by the cluster analysis based on 999 permutations using the software GENAlex 6.41 (Peakall and Smouse, 2006)

3.7.4.9 Population structure analysis

A set of 14 SSR markers identified to be linked with resistance to rust, LLS, and nutritional quality traits were used to know structure of population and admixture for targeted genomic regions. In order to infer precise population structure of GSP for targeted genomic regions, only molecular data were used without considering pre-existing available information on diversity based on botanical classification, geographical information in the analysis. The analysis was performed using the software package STRUCTURE 2.3.4. The program STRUCTURE implements a model-based clustering method for inferring population structure using genotype data consisting of unlinked markers to identify k clusters to which the program then assigns each individual genotype. The method was introduced by Pritchard *et al.,* (2000) and extended by Falush *et al.,* (2003 & 2007). To determine most appropriate k value, burn-in Markov Chain Monte Carlo (MCMC) replication was set to 10,000 and data were collected over 100,000 MCMC replications in each run. Ten independent runs were performed setting the number of population (k) from 2 to 10 using a model allowing for no admixture and correlated allele frequencies. The basis of this kind of clustering method is the allocation of individual genotypes to k clusters in 4such a way that Hardy-Weinberg equilibrium and linkage equilibrium are valid within clusters, whereas these kinds of equilibrium are absent between clusters. The k value was determined by LnP(D) in STRUCTURE output and an ad hoc statistic jk based on the rate of change in LnP(D) between successive k

(Evanno *et al.,* 2005). The final subpopulations were determined based on rate of change in LnP(D) between successive k and stability of grouping pattern across five-run.

3.7.4.10 Marker-trait association

Association of SSR marker data with the trait of interest was tested using the general linear mixed model (GLM) as described by Yu *et al.,* (2006) using TASSEL 2.1. This method simultaneously takes multiple levels of both gross level population structure (Q) and finer scale phenotypic data into account. The statistical model can be described in Henderson's notations (Henderson, 1975) as follows:

$$y = X\beta + Zu + e$$

Where,

y = the vector of observations

$\boldsymbol{\beta}$ = unknown vector containing fixed effects including genetic marker and population structure (Q)

u = unknown vector of random additive genetic effects from multiple backgrounds

QTL for individuals or lines

X and Z = the know design matrices

E = unobserved vector of random residuals.

The population structure analysis was conducted by running STRUCTURE and the population structure matrix (Q) was constructed at K=3. The BLUPs were determined for each accession for all quantitative traits for individual and pooled across environments were used for the association analysis as phenotypic data input. Higher disease severity score among both the replication was considered as the final score of that genotype for a particular location and taken for analysis whereas mean of all three locations used as pooled disease score across locations. However, four environment data of yield and nutritional quality traits were used for marker-trait association analysis for individual as well as pooled across environments. The SSR markers associated with the trait of interest were identified based on P value of marker, which determines whether a marker is associated with the desired trait. The R^2 (marker) indicating the fraction of the total phenotypic variation explained by the marker. Only those makers which having $P \leq 0.05$ were selected as significant markers associated with the trait of interest.

CHAPTER IV
Results

Phenotyping was done on Genomic Selection Panel (GSP) for yield traits, resistance to foliar fungal diseases (LLS and rust) and nutritional quality traits in four environments. Rainy season trials were conducted at Aliyarnagar (Tamil Nadu) and Jalgaon (Maharashtra) under natural disease epiphytotic, whereas at ICRISAT, Patancheru (Telangana), it was under artificial disease pressure created through infector row technique. Besides, the rainy season experiments, another trial was conducted at ICRISAT, Patancheru during the post-rainy season of 2015-16 to evaluate all genotypes under disease free condition. The phenotypic data collected from each individual environment as well as pooled were used to assess genetic diversity present in the GSP for traits evaluated and to identify the stable source of disease resistance, yield and nutritional quality traits through GGE biplot technique of stability analysis. The genotypes of GSP were subjected to molecular diversity analysis using 14 SSR markers data linked to rust, LLS and nutritional quality traits to assess molecular diversity and allelic richness present in GSP for the targeted loci. Marker-trait association analysis was done to evaluate association among SSR genomic region and phenotype across the environments. The experimental results of present investigation are presented under following headings

4.1 Analysis of variance

4.2 Mean and genetic parameters

4.3 Correlation among traits

4.4 Principal component analysis

4.5 Stability of disease resistance, yield, and nutritional traits

4.6 Molecular diversity

4.7 Marker-trait association (MTA)

4.8 Screening of GSP for mutant alleles of *ahFAD2* gene

4.1. Analysis of variance

Analysis of variance for disease resistance, yield and nutritional quality traits of GSP evaluated in four different individual environments and pooled are presented in Table 4.1 to 4.4. Partitioning of variance using ANOVA indicated that genotypes included in the present study differed significantly for all the traits in each individual environment as well as across the environments. There was a significant effect of environment reported for all the traits and a significant genotype × environment interaction for disease resistance (Table 4.3), yield, and nutritional quality traits (Table 4.4).

4.1.2 Homogeneity of variances

The observations on disease severity to LLS and rust were recorded at three different stages (75, 90 and 105 days after sowing) across the three different environments during the rainy season, whereas all other quantitative traits measured in four environments separately including a post-rainy trial at ICRISAT, Patancheru. The homogeneity of error variances across the environments was tested using widely accepted Bartlett's and Levene's test of homogeneity of variances. The results of both the tests showed that residual variances were heterogeneous between environments for disease severity scores, yield and nutritional quality traits (Table 4.5). Among both the test, Levene's test is better than Bartlett's test because it does not have any assumption of normalized data. Looking to the heterogeneity of variances for all the traits the replicated data was analyzed with the general linear mixed model (GLM) of ANOVA using proc glm function of SAS to model heterogeneity of error variance. Best linear unbiased prediction (BLUP) of mean (adjusted mean) (Schonfeld and Werner, 1986) were estimated from replicated data of genotypes from each individual as well as pooled across the environments. Pooled analysis of variance was carried out to check the variance due to environments and genotype × environments to make a decision about the assessment of stability of genotypes for disease resistance and yield traits. These BLUP values were further used for genetic diversity, stability, and marker-trait association study.

Table 4.1 Analysis of variance of Genomic Selection Panel of groundnut evaluated at Aliyarnagar (E_1), Jalgaon (E_2), ICRISAT rainy 2015 (E_3) and ICRISAT post-rainy 2015-16 (E_4)

Source	df	ENV	DFF	LLS75	LLS90	LLS105	Rust75	Rust90	Rust105	PH	NPB
Replication	**1**	**E_1**	21.18**	0.289**	0.205**	0.003	0.239**	0.118**	0.045*	735.86**	0.094**
		E_2	130.60**	0.013	0.014	0.214**	0.001	0.181**	0.595**	2.05	0.230**
		E_3	10.63	0.323**	0.013	0.006	0.135**	0.008	0.018*	56.38**	0.028
		E_4	152.48**	-	-	-	-	-	-	456.25**	0.020
Block (Replication)	**38**	**E_1**	4.58**	0.006	0.004	0.005	0.006	0.005	0.005	22.77**	0.008**
		E_2	4.14	0.002	0.018**	0.017**	0.001	0.021**	0.026	27.05**	0.010
		E_3	8.06**	0.007	0.003	0.002	0.006	0.005	0.002	23.80**	0.003
		E_4	3.66	-	-	-	-	-	-	4.48	0.010
Genotypes	**339**	**E_1**	8.56**	0.015**	0.025**	0.013**	0.036**	0.043**	0.018**	60.41**	0.009**
		E_2	13.65**	0.002	0.016**	0.023**	0.001**	0.019**	0.045**	91.92**	0.020**
		E_3	15.33**	0.025**	0.017**	0.012**	0.033**	0.030**	0.020**	60.72**	0.014**
		E_4	18.80**	-	-	-	-	-	-	44.08**	0.020**
Error	**301**	**E_1**	1.04	0.005	0.003	0.004	0.006	0.004	0.004	4.13	0.002
		E_2	3.43	0.002	0.005	0.005	0.001	0.007	0.012	10.34	0.010
		E_3	2.48	0.005	0.002	0.002	0.006	0.003	0.002	5.54	0.003
		E_4	2.19	-	-	-	-	-	-	2.86	0.010

Where * & ** represents significant at 5 and 1 % probability level

df = Degree of freedom; DFF= Days to 50% flowering, LLS75, LLS90 & LLS105 = Disease severity score of late leaf spot recorded at 75, 90 and 105 days after sowing, respectively; Rust75, Rust90 & Rust105= Disease severity score of rust recorded at 75, 90 and 105 days after sowing, respectively; PH = Plant height (cm); NPB= Number of primary branches plant^{-1}.

Table 4.1 Contd...

Source	DF	ENV	NPP	PYPP	SYPP	SH %	DM	HSW	PYH	HLM
Replication	**1**	**E_1**	33.55	98.39	21.41	202.71**	37.65	20.67	4965700.30**	-
		E_2	47.13	17.59	7.44	1.76	1972.01**	3.62	329537.80	-
		E_3	7.86	38.02	3.00	1162.31**	454.62**	2059.09**	213728.70	20.65
		E_4	393.79**	137.98**	62.08**	37.33	74.45**	224.67**	11775725.90**	97.10
Block (Replication)	**38**	**E_1**	16.10**	10.70	3.90*	9.47	2.82	8.98*	138719.90	-
		E_2	7.96	3.35	1.07	8.95	2.06	6.52	177394.70	-
		E_3	18.80	6.35	3.02	20.69	2.47	18.54	110286.10	13.47
		E_4	7.39	2.91	1.35	10.14	4.13	14.95**	213011.60	8.76
Genotypes	**339**	**E_1**	50.78**	29.14**	11.36**	57.06**	47.34**	113.05**	858484.80**	-
		E_2	67.35**	33.41**	13.18**	58.32**	119.17**	80.91**	1190905.20**	-
		E_3	46.03**	27.08**	10.35**	62.68**	121.2**	97.59**	883273.30**	32.49**
		E_4	33**	14.50**	6.18**	84.37**	121.13**	103.40**	997904.90**	91.38**
Error	**301**	**E_1**	7.14	4.43	1.76	7.24	3.14	4.07	105842.70	-
		E_2	7.94	4.47	1.82	5.16	1.82	6.03	118057.20	-
		E_3	11.49	5.40	2.54	23.42	4.20	12.18	80643.80	9.04
		E_4	4.34	1.86	0.78	6.72	3.46	4.51	138198.10	6.85

Where * & ** represents significant at 5 and 1 % probability level

df = Degree of freedom; NPP= Number of pods plant^{-1}; PYPP= Pod yield plant^{-1} (g); SYPP= Seed yield plant^{-1} (g); SH %= Shelling percent; DM= Days to physiological maturity; HSW= Hundred seed weight (g); PYH= Pod yield hectare^{-1} (kg/ha); HLM= Haulm weight plant^{-1} (g); E_1= Aliyarnagar; E_2= Jalgaon; E_3=ICRISAT rainy 2015; E_4= ICRISAT post-rainy 2015-16.

Table 4.2 Analysis of variance for nutritional quality traits of Genomic Selection Panel of groundnut evaluated at Aliyarnagar (E_1), Jalgaon (E_2), ICRISAT rainy 2015 (E_3) and ICRISAT post-rainy 2015-16 (E_4)

Source	df	ENV	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
Replication	**1**	**E_1**	0.22	0.01	0.57	0.32	0.09	0.19*	0.01
		E_2	0.002	0.255	0.025	0.099	0.004	0.033	0.002
		E_3	0.035	2.887**	1.551	6.13	0.126**	2.044**	0.744**
		E_4	0.325**	1.352**	1.22**	2.054**	0.018	0.644**	0.042**
Block (Replication)	**38**	**E_1**	0.04	0.11	0.09	0.07	0.02	0.02	0.01
		E_2	0.027	0.053	0.145	0.121	0.013	0.021	0.003
		E_3	0.016	0.036	0.043	0.044	0.01	0.028	0.012
		E_4	0.05**	0.088**	0.109	0.152**	0.007	0.019	0.004
Genotypes	**339**	**E_1**	0.095**	0.13**	0.36**	0.28**	0.05**	0.05**	0.01**
		E_2	0.088**	0.10**	0.441**	0.291**	0.057**	0.064**	0.007**
		E_3	0.116**	0.063**	0.345**	0.288	0.047**	0.269**	0.105**
		E_4	0.071**	0.088**	0.285**	0.273**	0.042**	0.041**	0.009**
Error	**301**	**E_1**	0.03	0.06	0.08	0.06	0.01	0.02	0.01
		E_2	0.021	0.055	0.08	0.059	0.01	0.018	0.002
		E_3	0.014	0.03	0.035	0.031	0.006	0.025	0.018
		E_4	0.019	0.037	0.074	0.063	0.008	0.012	0.002

Where * & ** represents significant at 5 and 1 % probability level; df = Degree of freedom

Table 4.3 Pooled analysis of variance for disease severity score of late leaf spot and rust recorded in Genomic Selection Panel at three different locations

Source	df	LLS75	LLS90	LLS105	Rust75	Rust90	Rust105
Environment	2	12.554**	12.97**	10.174**	10.496**	10.853**	27.029**
Replication (ENV)	3	0.208**	0.078**	0.074**	0.125**	0.102**	0.219**
Block (ENV × REP)	114	0.005	0.008**	0.008**	0.004	0.01**	0.011**
Genotypes	339	0.024**	0.042**	0.03**	0.04**	0.068**	0.059**
Genotype × Environment	678	0.009**	0.008**	0.008**	0.014**	0.011**	0.011**
Error	903	0.004	0.003	0.004	0.004	0.005	0.006

Where LLS75, LLS90 & LLS105 = Disease severity score of late leaf spot recorded at 75, 90 and 105 days after sowing, respectively; Rust75, Rust90 & Rust105= Disease severity score of rust recorded at 75, 90 and 105 days after sowing, respectively; * & ** represents significant at 5 and 1 % probability level; df= Degree of freedom; ENV= Environment and REP= Replication;

Table 4.4 Pooled analysis of variance for yield and nutritional quality traits recorded in Genomic Selection Panel at four different environments

Source	Environment	Rep (ENV)	Block (ENV × REP)	Genotypes	Genotype × Environment	Error
Degree of freedom	3	4	152	339	1017	1204
Yield and its contributing traits						
Days to 50% flowering	26111.81**	78.72**	5.11**	35.82**	6.42**	2.28
Plant height (cm)	51540.32**	312.64**	19.53**	161.24**	30.72**	5.71
Number of primary branches	0.89**	0.09**	0.01**	0.04**	0.01**	0.01
Number of mature pods per plant	3723.42**	120.58**	12.57**	95.54**	32.62**	7.73
Pod yield per plant (g)	2644.64**	73.00**	5.83	44.50**	19.20**	4.04
Seed yield per plant (g)	893.01**	23.48**	2.34	17.83**	7.52**	1.73
Shelling percent (%)	1326.11**	351.03**	12.31	132.62**	42.43**	10.63
Hundred seed weight (g)	370.62**	577.01**	12.25**	259.17**	42.9**	6.7
Days to maturity	167711.34**	634.68**	2.87	274.45**	41.93**	3.15
Pod yield per hectare (kg)	7700211.4**	4321173.2**	159853.1	2105123.5**	590881.7**	110685
Nutritional quality traits						
Oil (%)	25.567**	0.146**	0.034**	0.243**	0.04**	0.021
Protein (%)	84.246**	1.126**	0.07**	0.172**	0.066**	0.044
Oleic acid (%)	19.853**	0.841**	0.096*	1.104**	0.101**	0.066
Linoleic acid (%)	52.384**	2.15**	0.096**	0.861**	0.081**	0.053
Palmitic acid (%)	2.116**	0.059**	0.011	0.154**	0.012**	0.009
Stearic acid (%)	18.078**	0.887**	0.058**	1.086**	0.091**	0.037
O/L ratio	8.528**	0.403**	0.018	0.174**	0.027**	0.015

Where * & ** represents significant at 5 and 1 % probability level; ENV= Environment and REP= Replication;

Table 4.5 Levene's test for homogeneity of variance for all the traits under study

Traits		Mean Square		F Value	Probability level
		Environment	Error		
Foliar disease resistance	**df**	**2**	**2037**		
LLS75		1.705	0.003	653.66	<.0001
LLS90		0.057	0.004	12.81	<.0001
LLS105		0.307	0.004	75.88	<.0001
Rust75		3.447	0.004	955.97	<.0001
Rust90		0.207	0.005	39.60	<.0001
Rust105		0.821	0.006	127.13	<.0001
Yield and its contributing traits	**df**	**3**	**2716**		
Days to 50% flowering		116.20	2.682	43.33	<.0001
Plant height (cm)		331.60	16.21	20.46	<.0001
Number of primary branches		0.028	0.003	10.50	<.0001
Number of pods per plant		205.10	10.82	18.95	<.0001
Pod yield per plant (g)		175.90	6.07	29.01	<.0001
Seed yield per plant (g)		53.61	2.42	22.15	<.0001
Shelling percent (%)		221.90	14.28	15.54	<.0001
Hundred seed weight (g)		184.10	22.89	8.04	<.0001
Days to maturity		1126.10	19.83	56.80	<.0001
Pod yield per hectare (kg)		1025619	220104	4.66	0.003
Nutritional quality traits	**df**	**3**	**2716**		
Oil content (%)		0.1691	0.0222	7.62	<.0001
Protein content (%)		0.4799	0.0281	17.07	<.0001
Oleic acid (%)		0.6585	0.0817	8.06	<.0001
Linoleic acid (%)		0.0718	0.073	0.98	0.3996
Palmitic acid (%)		0.0292	0.0125	2.34	0.0718
Stearic acid (%)		1.3758	0.1205	11.41	<.0001
O/L Ratio		0.0159	0.0134	1.18	0.3147

Where LLS75, LLS90 & LLS105 = Disease severity score of late leaf spot recorded at 75, 90 and 105 days after sowing, respectively; Rust75, Rust90 & Rust105= Disease severity score of rust recorded at 75, 90 and 105 days after sowing, respectively.

4.2 Mean performance and genetic parameters

The data on quantitative traits were analyzed using general linear mixed model and BLUPs or adjusted means were estimated for each genotype at individual as well as across four environments through SAS version 9.2. The BLUPs for each trait at individual and across the environments are presented in Appendix II to XII. The nature and magnitude of variation for individual traits was assessed by the genotypic and phenotypic coefficient of variation (GCV & PCV), heritability in broad sense (h^2_{bs}) and genetic advance as percent mean (GAM) from each environment and pooled across the environments. The results of mean and range of genotype performance with genetic parameters for each trait under study, are presented below.

4.2.1 Severity score for late leaf spot and rust

Disease severity score for LLS and rust recorded at three different stages *viz.,* 75, 90 and 105 days after sowing (DAS) at all the three environments during rainy 2015 was largely depend on the amount of inoculum available for infection and favorable environmental conditions for disease establishment and spread. Disease pressure was high (≥8 disease severity score recorded for both rust and LLS at 90 DAS on susceptible cultivar TMV2) at Aliyarnagar and ICRISAT whereas it was low at Jalgaon (5 disease severity score in TMV2 for both the diseases at 90 DAS) for both the diseases due to unfavorable environmental conditions.

Late leaf spot

At Aliyarnagar

The disease scores of LLS at Aliyarnagar varied from 1 to 4 at 75 DAS, from 2 to 8 at 90 DAS and from 3 to 9 at 105 DAS with an average disease score of 1.90, 4.60 and 7.10 at 75, 90 and 105 DAS, respectively. Moderate GCV (17.06%) and high PCV (23.65) with moderate heritability (52.00%) and high GAM (25.34%) was reported at 75 DAS whereas moderate GCV (15.14%) and PCV (16.53%) with high heritability (83.86%) and GAM (28.55%) was reported at 90 DAS. However, low GCV (7.54%) and PCV (10.40%) with moderate heritability (52.64%) and GAM (11.27%) were reported at 105 DAS

(Table 4.6). The genotypes which had ≤3 disease severity score on 1-9 scale at 90 DAS were considered as resistant while four to five were moderately resistant, six to seven susceptible and genotypes which had >7 disease severity score were considered as highly susceptible to both the diseases. Out of 340 genotypes of GSP, 67 reported as resistant, 167 as moderately resistant, 104 as susceptible and 2 genotypes as highly susceptible to LLS at 90 DAS (Fig 4.1 & Table 4.7) whereas six genotypes were reported as resistant, 34 as moderately resistant, 126 as susceptible and 174 genotypes as highly susceptible to LLS at 105 DAS at Aliyarnagar (Fig 4.2).

At Jalgaon

Low disease pressure was observed at Jalgaon compared to Aliyarnagar and ICRISAT during rainy 2015. The disease score of genotypes of LLS varied from 1 to 3 at 75 DAS, 1 to 6 at 90 DAS, from 2 to 8 at 105 DAS with an average disease score of 1.07, 3.27 and 4.80 at 75, 90 and 105 DAS, respectively. Low GCV (2.24%) and PCV (10.78%) coupled with very low heritability (4.34%) and GAM (0.96%) was reported at 75 DAS whereas moderate GCV (12.84%) and PCV (17.44%) with moderate heritability (54.17%) and GAM (19.46%) was reported at 90 DAS (Table 4.6). Moderate GCV (13.35%) and PCV (16.40%) with high heritability (66.30%) and GAM (22.39%) were reported for LLS at 105 DAS at Jalgaon. Among the environments, disease pressure was quite low at Jalgaon with maximum disease score of 5 recorded in susceptible cultivar TMV2 at 90 DAS, therefore genotypes were not categorized into resistant and susceptible based on the data recorded at Jalgaon.

At ICRISAT rainy season 2015

The disease scores of genotypes for LLS at ICRISAT varied from 1 to 6 at 75 DAS, from 2 to 9 at 90 DAS and from 4 to 9 at 105 DAS with an average disease score of 3.27, 6.65 and 8.17 at 75, 90 and 105 DAS, respectively. A moderate GCV (17.12%) and high PCV (20.74%) coupled with high heritability (68.09%) and GAM (29.09%) was observed at 75 DAS whereas moderate GCV (10.13%) and PCV (11.28%) coupled with high heritability (80.76%) and moderate GAM (18.76%) was observed at 90 DAS (Table 4.6). A low GCV (7.71%) and PCV (8.53%) coupled with high heritability (81.55%) and moderate GAM (14.34%) were observed for LLS at 105 DAS at ICRISAT during rainy 2015. Nine genotypes were reported as resistant, 67 as moderately resistant, 148 susceptible and 116 reported as highly susceptible to LLS at 90 DAS (Fig 4.1 & Table 4.9). None of the genotypes showed resistance to LLS up to 105 DAS at ICRISAT during rainy 2015 while 19 genotypes were reported as moderately resistant, 47 as susceptible and 274 as highly susceptible to LLS at 105 DAS (Fig 4.2).

Pooled across the environments

The disease scores of genotypes for LLS across the environments varied from 1 to 4 at 75 DAS, from 2 to 7 at 90 DAS and from 4 to 8 at 105 DAS with an average disease score of 2.07, 4.85 and 6.68 at 75, 90 and 105 DAS, respectively. A moderate GCV (13.62 & 11.42%) and PCV (16.68 & 12.70%) coupled with high heritability (66.61 & 80.90%) and GAM (22.89 & 21.17%) was observed at 75 and 90 DAS, respectively whereas low GCV (8.06%) and PCV (9.42%) coupled with high heritability (73.25%) and moderate GAM (14.21%) was observed at 105 DAS (Table 4.6). Thirty-one genotype identified as resistant, 162 as moderately resistant, 147 susceptible whereas none of the genotypes reported as highly susceptible to LLS at 90 DAS (Fig 4.1 & Table 4.11). None of the genotypes showed a resistant reaction against LLS up to 105 DAS while 38 exhibited moderately resistant, 176 susceptible and 126 highly susceptible reactions against LLS at 105 DAS across the environments (Fig 4.2).

Leaf rust

At Aliyarnagar

The disease severity scores of genotypes for rust at Aliyarnagar varied from 1 to 5 at 75 DAS, from 1 to 8 at 90 DAS, from 2 to 9 at 105 DAS with an average of 2.40, 4.90 and 6.90 at 75, 90 and 105 DAS, respectively. High GCV (26.43% & 19.67%) and PCV (30.66% & 21.22%) coupled with heritability (74.29% & 85.95%) and GAM (46.93% & 37.57%) was reported for rust at 75 and 90 DAS, respectively whereas low GCV (9.96%) and moderate PCV (12.05%) coupled with high heritability (68.26%) and moderate GAM (16.95%) was reported at 105 DAS (Table 4.6). Out of 340 genotypes of GSP, 87 reported as resistant, 96 as moderately resistant, 154 as susceptible and 3 genotypes as highly susceptible to rust at 90 DAS (Fig 4.1 & Table 4.8) whereas 11 genotypes showed resistant, 58 moderately resistant, 151 susceptible and 140 highly susceptible reaction against rust at 105 DAS at Aliyarnagar (Fig 4.2).

At Jalgaon

Low disease pressure was observed for rust at Jalgaon compared to Aliyarnagar and ICRISAT during rainy 2015. The disease score of genotypes of rust varied from 1 to 3 at 75 DAS, 1 to 6 at 90 DAS, from 2 to 8 at 105 DAS with an average disease score of 1.01, 3.01 and 4.29 at 75, 90 and 105 DAS, respectively. Low GCV (4.01%) and PCV (5.35%) coupled with moderate heritability (56.08%) and low GAM (6.18%) was reported at 75 DAS whereas moderate GCV (14.20%) and PCV (20.39%) with moderate heritability (48.54%) and high GAM (20.39%) were reported at 90 DAS. However, high GCV (23.73%) and PCV (31.01%) with moderate heritability (58.57%) and GAM (37.41%) were reported for rust at 105 DAS at Jalgaon (Table 4.6). Due to low disease pressure at Jalgaon with maximum disease score of six recorded on susceptible cultivar TMV 2 at 90 DAS, genotypes were not categorized into resistant and susceptible at Jalgaon.

At ICRISAT rainy season 2015

The disease severity scores of genotypes for rust at ICRISAT varied from 1 to 6 at 75 DAS, from 2 to 8 at 90 DAS, from 3 to 9 at 105 DAS with an average of 3.05, 5.81 and 7.68 at 75, 90 and 105 DAS, respectively. High GCV (21.36%) and PCV (25.09%) coupled with high heritability (72.43%) and GAM (27.70%) was observed at 75 DAS whereas moderate GCV (14.73%) and PCV (16.15%) coupled with high heritability (83.27%) and GAM (27.70%) was observed at 90 DAS. However, low GCV (10.41%) and PCV (11.43%) coupled with high heritability (82.89%) and moderate GAM (19.53%) were observed at

105 DAS (Table 4.6). Out of 340 genotypes of GSP, 51 reported as resistant, 75 as moderately resistant, 148 as susceptible and 48 as highly susceptible to rust at 90 DAS (Fig 4.1 & Table 4.10) whereas three genotypes showed resistant, 43 moderately resistant, 69 susceptible and 225 highly susceptible reaction against rust at 105 DAS at ICRISAT during rainy 2015 (Fig 4.2).

Pooled across the environments

The disease severity scores of genotypes for rust across the environments varied from 1 to 4 at 75 DAS, from 2 to 7 at 90 DAS, from 3 to 8 at 105 DAS with an average of 2.14, 4.56 and 6.30 at 75, 90 and 105 DAS, respectively. Moderate GCV (17.19%) and high PCV (21.51%) coupled with high heritability (63.82%) and GAM (28.28%) was observed at 75 DAS whereas moderate GCV (15.13 & 12.52%) and PCV (16.71 & 13.96%) coupled with high heritability (82.00 & 80.45%) and GAM (28.22 & 23.13%) was observed at 90 and 105 DAS (Table 4.6). Out of 340 genotypes, 66 reported as resistant, 138 as moderately resistant, 136 as susceptible whereas none of the genotypes was reported as highly susceptible to rust at 90 DAS across the environments (Fig 4.1 & Table 4.12) whereas eight genotypes exhibited resistant, 59 moderately resistant, 173 susceptible and 100 highly susceptible reaction against rust at 105 DAS across the environments (Fig 4.2).

Source of resistance under different maturity duration

Genotypes resistant to LLS and rust were reported in different maturity groups. A single genotype (ICGV 86699) resistant to LLS and rust was reported with early maturity (~100 days) at ICRISAT and Aliyarnagar. Similarly many other genotypes showed resistance against LLS and rust with different maturity duration (varied from 100 to 130) at ICRISAT and Aliyarnagar during rainy season 2015 (Fig 4.3 to 4.6).

Table 4.6 Mean, range and genetic parameters for disease severity scores to LLS and rust of Genomic Selection Panel of groundnut evaluated across the environments

Traits	Mean	Range		GCV (%)	PCV (%)	h^2_{bs} (%)	GAM (%)
		Min	Max				
Aliyarnagar							
LLS 75	1.9	1	4	17.06	23.65	52.00	25.34
LLS 90	4.6	2	8	15.14	16.53	83.86	28.55
LLS 105	7.1	3	9	7.54	10.40	52.64	11.27
Rust 75	2.4	1	5	26.43	30.66	74.29	46.93
Rust 90	4.9	1	8	19.67	21.22	85.95	37.57
Rust 105	6.9	2	9	9.96	12.05	68.26	16.95
Jalgaon							
LLS 75	1.1	1	3	2.24	10.78	4.34	0.96
LLS 90	3.3	1	6	12.84	17.44	54.17	19.46
LLS 105	4.8	2	8	13.35	16.40	66.30	22.39
Rust 75	1.0	1	3	4.01	5.35	56.08	6.18
Rust 90	3.0	1	6	14.20	20.39	48.54	20.39
Rust 105	4.3	2	8	23.73	31.01	58.57	37.41
ICRISAT rainy 2015							
LLS 75	3.3	1	6	17.12	20.74	68.09	29.09
LLS 90	6.7	2	9	10.13	11.28	80.76	18.76
LLS 105	8.2	4	9	7.71	8.53	81.55	14.34
Rust 75	3.1	1	6	21.36	25.09	72.43	37.44
Rust 90	5.8	2	8	14.73	16.15	83.27	27.70
Rust 105	7.7	3	9	10.41	11.43	82.89	19.53
Pooled across the environments							
LLS75	2.1	1	4	13.62	16.68	66.61	22.89
LLS90	4.9	2	7	11.42	12.70	80.90	21.17
LLS105	6.7	4	8	8.06	9.42	73.25	14.21
Rust75	2.1	1	4	17.19	21.51	63.82	28.28
Rust90	4.6	2	7	15.13	16.71	82.00	28.22
Rust105	6.3	3	8	12.52	13.96	80.45	23.13

LLS75, LLS90 & LLS105= Disease severity score of late leaf spot at 75, 90 and 105 days, respectively; Rust75, Rust90 & Rust105= Disease severity score of rust at 75, 90 and 105 days, respectively; Min= Minimum; Max= Maximum; GCV = Genotypic co-efficient of variation (%); PCV= Phenotypic co-efficient of variation (%); h^2_{bs} = Heritability in broad sense (%); GAM= Genetic advance as percent of mean (%)

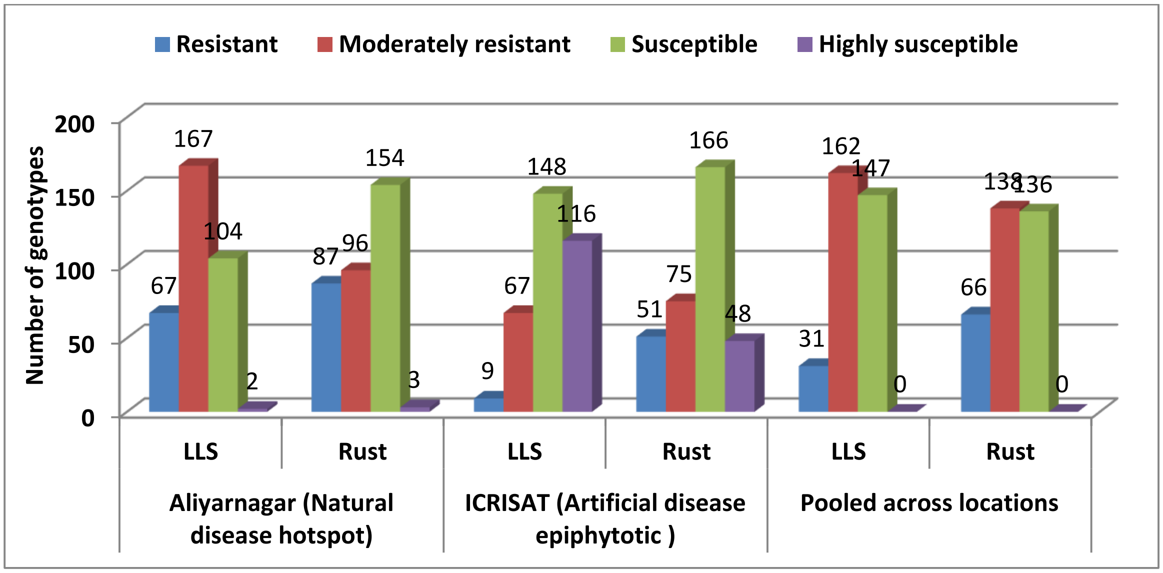

Figure 4.1 Categorization of genotypes based on reaction against rust and LLS at 90 days after sowing (DAS) at Aliyarnagar, ICRISAT and pooled across the locations during rainy 2015

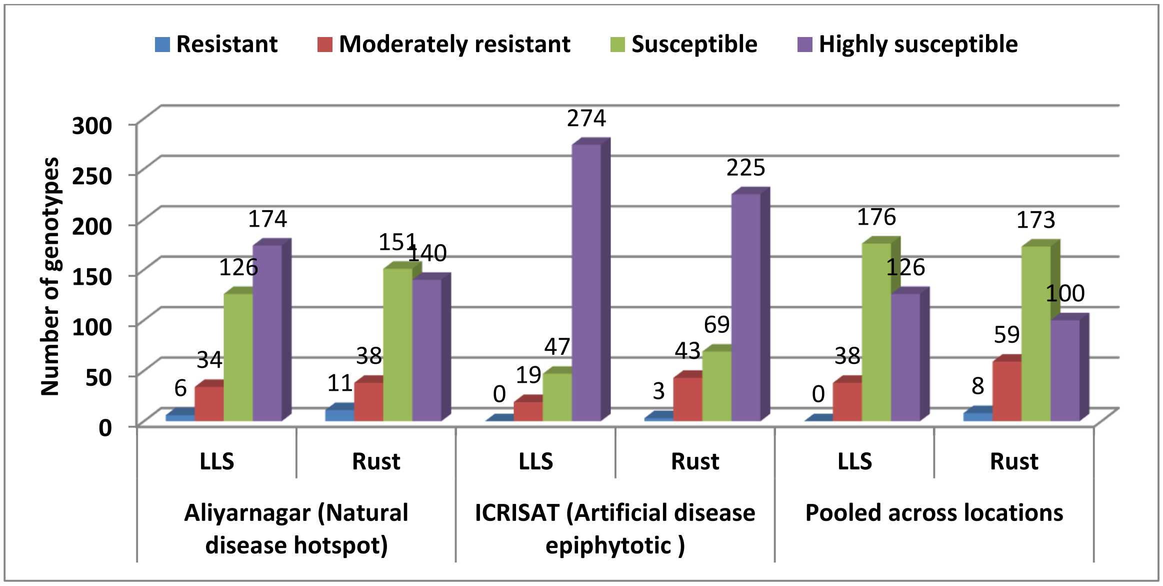

Figure 4.2 Categorization of genotypes based on reaction against rust and LLS at 105 days after sowing (DAS) at Aliyarnagar, ICRISAT and pooled across the locations during rainy 2015

Table 4.7 Disease reaction of genotypes of Genomic Selection Panel of groundnut against LLS based on field evaluation at 90 DAS during rainy 2015 at Aliyarnagar

Reaction*	Number	Genotypes
Resistant	67	ICGs 10053, 11337, 11426, 12370, 12625, 13895, 2381, 6022, 6646, ICGVs 00005, 00068, 00191, 00246, 00248, 00346, 00350, 00362, 01273, 01274, 01276, 01328, 01361, 02317, 01495, 02323, 02411, 02446, 03043, 03042, 04087, 05032, 05036, 05100, 05141, 05163, 06040, 06042, 06142, 06422, 07120, 07235, 86699, 87846, 97165, 99029, 99051, 99052, 99085, 99160, 24 M-86, 39 × 49 -77, 39 × 49-81-1, 49 M- 1-1, 49 M-16, 49 × 39-74, 49 × 39-8, GPBD 4, M 28-2, SPS 11, SPS 15, SPS 2, SPS 20, SPS 21, SPS 7, SPS 9, SPS 8
Moderately resistant	167	ICGs 10036, 10185, 11088, 11322, 11651, 12276, 12509, 12672, 14466, 14475, 14482, 14705, 14834, 15415, 15419, 156 , 2106, 2773, 2857, 3053, 3102, 3140, 4527, 4343, 532, 5662, 5663, 5891, 5745, 6766, 721, 8285, 8517, 8751, ICGVs 00290, 00343, 00351, 00371, 00387, 00440, 01005, 01060, 01124, 01263, 01265, 01464, 02022, 02144, 02189, 02206, 02242, 02266, 02286, 02287, 02290, 02321, 02434, 03056, 03064, 03128, 03136, 03397, 04044, 04115, 05057, 04149, 05161, 05176, 06049, 06099, 06100, 06110, 06175, 06347, 06188, 06420, 06423, 06424, 07023, 07145, 07148, 07166, 07220, 07168, 07223, 07227, 07246, 07268, 07368, 86015, 86325, 86352, 86564, 86590 , 87160, 87187 , 88145, 88438, 90320, 92195, 92267, 93216, 93280, 93920, 94118, 95058, 94169, 95290, 97045, 97058, 97092, 97115, 97116, 97120, 97182, 97128, 97183, 97261, 98105, 98163, 98184, 98294, 98373, 99233, 98432, 24 × 37-2275, 24 × 39-31 MR, 26 M 156-2, 26 × 37-IV- 9IR, 26 × M-223-1, 26 × M-95-1 RI, 27 × 49- 12, 27 × 49- 14, 27 × 49- 16, 27 × 49- 27-1, 39 × 49 -8, 49 M-2-2, 49 × 27-37, 49 × 37- 99(b) tall, 49 × 37-134, 49 × 37-90, 49 × 39-21-1, 49 × 39-21-2, 49 × 39-21-2(a), BAU 13, CS 39, CSMG 84-1, DTG 3, Gangapuri, ICR 48, M 110-14, M 28-2, MN1-35, Somnath, SPS 1, SPS 13, SPS 14, SPS 3, TDG 10, TDG 13, TDG 14, TG 39, TG 42, TG LPS 3, TKG 19A, TPG 41
Susceptible	104	ICG 10701, 111, 12879, 12991, 14985, 15190, 1668, 1834, 1973, 2031, 3027, 3312, 3343, 3421, 3584, 3673, 3746, 434, 442, 4543, 4729, 4955, 875, 5221, 9315, 9507, 11 , 76, 44, ICGV 00321, 00349, 01232, 01393, 01478, 02125, 02194, 02251, 02271, 02298, 03184, 03207, 03398, 04018, 04124, 05198, 06234, 06431, 07210, 07217, 07247, 07273, 07359, 09112, 13238, 13241, 13242, 13245, 86011, 86072, 86143, 87354, 87378, 87921, 89104, 93437, 91114, 93470, 94361, 95070, 95377, 95469, 96466, 96468, 97262, 97232, 99083, 99181, 99195, 26 M- 119-1, 26× 27-164, 49 × 27-13 (ii), 49 × 27-19, 49 × 37-91, 49 × 37-135, 49 × 37-97-1, 49 × 39-20-2, DH 86, DTG 15, Faizpur 1-5, J 11, JL 24, Mutant 3, SPS 10 , SPS 17, SPS 6, SunOleic 95R, TAG 24, TG 19, TG 41, TG 49, TG LPS 4, TG LPS 7, TMV 2 NLM,
Highly susceptible	2	TMV 2, ICGV 91116

* Genotypes were categorized based on resistance/susceptible reaction to LLS disease on a 1-9 scale where Resistant (R) =1-3; Moderately resistant (MR) = 4-5; Susceptible (S) = 6-7; Highly susceptible (HS) = 8-9 disease severity rating scale

Table 4.8 Disease reaction of genotypes of Genomic Selection Panel of groundnut against rust based on field evaluation at 90 DAS during rainy 2015 at Aliyarnagar

Reaction*	Number	Genotypes
Resistant	87	ICG 11337 , 11426, 2381, 6766, 8751, ICGV 00005, 00068, 00191, 00246, 00248, 00346, 00362, 01265, 01273, 01274, 01276, 01361, 01464, 02242, 02266, 02287, 02317, 02323, 02321, 02411, 02446, 03042, 03064, 03043, 04087, 04115, 05032, 05036, 05057, 05141, 05155, 05161, 05163, 06040, 06042, 06099, 06100, 06142, 06175, 06420, 06422, 06423, 06424, 07120, 07145, 07148, 07223, 07227, 07235, 86590 , 86699, 87846, 93280, 94118, 97120, 97128, 97182, 98105, 98184, 99051, 98373, 99052, 99085, 99160, 99233, 24 × 39-31 MR, 39 × 49 -8, 39 × 49-81-1, 49 M- 1-1, 49 M-16, 49 × 27-37, 49 × 39-21-1, 49 × 39-74, CS 39, GPBD 4, SPS 11, SPS 2, SPS 20, SPS 21, SPS 7, SPS 8,
Moderately resistant	96	ICG 10036, 10053, 10185, 11088, 12276, 12370, 12625, 13895, 14466, 14834, 15190, 15415, 15419, 2773, 2857, 3053, 4343, 4527, 532, 5662, 6022, 6646, ICGV 00290, 76, 00350, 00351, 00387, 01060, 00440, 01124, 01328, 01393, 01478, 01495, 02194, 02206, 02286, 02434, 03056, 03128, 03136, 03207, 03397, 03398, 04044, 05198, 06188, 06234, 07166, 07168, 07210, 07220, 07246, 07247, 86564, 87921, 88438, 90320, 93216, 93920, 95469, 97092, 97115, 97116, 97165, 98432, 98163, 99029, 99195, 24 M-86, 24 × 37-2275, 26 × 37-IV- 9IR, 26 × M-95-1 RI, 27 × 49- 12, 39 × 49 -77, 27 × 49- 16, 49 M-2-2, 49 × 27-13 (ii), 49 × 37-134, 49 × 37-90, 49 × 39-21-2, 49 × 39-21-2(a), 49 × 39-8, ICR 48, DH 86, M 110-14, M 28-2, M 28-2, MN1-35, SPS 1, SPS 14, SPS 15, SPS 17, SPS 9, SunOleic 95R, TAG 24,
Susceptible	154	ICG 10701, 111, 11322, 11651, 12509, 12672, 12879, 12991, 14475, 14482, 14705, 14985, 156 , 1668, 1834, 1973, 2031, 2106, 3027, 3102, 3140, 3312, 3421, 3343, 3584, 3673, 3746, 442, 434, 4543, 4955, 5221, 5663, 5745, 721, 8285, 8517, 875, 9315, 9507, 9961, ICGS 11 , ICGS 44, ICGV 00321, ICGV 00343, 00349, 00371, 01005, 01232, 01263, 02022, 02038, 02125, 02144, 02189, 02251, 02271, 02290, 02298, 03184, 04018, 04124, 04149, 05176, 06110, 06049, 06347, 06431, 07023, 07268, 07273, 07359, 07368, 13238, 09112, 13241, 13242, 13245, 86011, 86015, 86072, 86143, 86352, 86325, 87160, 87187 , 87354, 87378, 88145, 89104, 91114, 91116, 92195, 92267, 93437, 93470, 94169, 94361, 95058, 95070, 95290, 95377, 96466, 96468, 97045, 97183, 97058, 97232, 97261, 97262, 98294, 99083, 99181, 26 M- 119-1, 26 × M-223-1, 26 M 156-2, 26× 27-164, 27 × 49- 14, 27 × 49- 27-1, 49 × 27-19, 49 × 37- 99(b) tall, 49 × 37-135, 49 × 37-97-1, BAU 13, 49 × 39-20-2, CSMG 84-1, DTG 15, DTG 3, Faizpur 1-5, Gangapuri, J 11, JL 24, Mutant 3, Somnath, SPS 10 , SPS 13, SPS 3, SPS 6, TDG 10, TDG 13, TDG 14, TG 19, TG 39, TG 41, TG 42, TG 49, TG LPS 3, TG LPS 4, TG LPS 7, TKG 19A, TMV 2, TMV 2 NLM, TPG 41,
Highly susceptible	3	49 × 37-91, ICG 4729, ICGV 07217,

* Genotypes were categorized based on Resistant/susceptible reaction to rust disease on a 1-9 scale where Resistant (R) =1-3; Moderately Resistant (MR) = 4-5; Susceptible (S) = 6-7; Highly susceptible (HS) = 8-9 disease severity rating scale

Table 4.9 Disease reaction of genotypes of Genomic Selection Panel of groundnut against LLS based on field evaluation at 90 DAS during rainy 2015 at ICRISAT

Reaction*	Number	Genotypes
Resistant	9	GPBD 4, ICGVs 00068, 00246, 00248, 02411, 06142, 86699, SPS 11, SPS 20,
Moderately resistant	67	ICGs 11337 , 12370, 12625, 6022, ICGS 76, ICGVs 00191, 00362, 01273, 01274, 01276, 01328, 01361, 02317, 02323, 02446, 03042, 03043, 04087, 05032, 05036, 05100, 05141, 06175, 05163, 06420, 06422, 06423, 07145, 07120, 07166, 07220, 07223, 07235, 07246, 86590 , 87846, 97128, 98105, 99029, 99051, 99052, 99085, 99160, M 110-14, M 28-2, 24 × 39-31 MR, 24 M-86, 26 × M-95-1 RI, 39 × 49 -77, 39 × 49 -8, 39 × 49-81-1, 49 × 37-134, 49 × 37-90, 49 × 39-74, 49 M- 1-1, 49 M-16, CS 39, M 28-2, SPS 1, SPS 14, SPS 15, SPS 2, SPS 21, SPS 7, SPS 9, SPS 8,
Susceptible	148	ICGs 10036, 10053, 10185, 11088, 111, 11322, 11426, 12276, 12509, 12672, 14475, 14482, 14705, 14834, 15190, 15415, 15419, 156 , 1834, 2381, 2857, 3027, 3746, 3053, 4343, 4527, 5221, 5662, 532, 5663, 5745, 5891, 6646, 6766, 8285, 875, 8751, 9961, ICGVs 00005, 00290, 00343, 00346, 00350, 00351, 00371, 00440, 01005, 01060, 01124, 01263, 01265, 01393, 01464, 01478, 01495, 02144, 02189, 02206, 02242, 02286, 02287, 02290, 02321, 02434, 03064, 03056, 03128, 03136, 03184, 03397, 03398, 04044, 04115, 05057, 04124, 05155, 05161, 05176, 05198, 06040, 06042, 06099, 06188, 06100, 06424, 07168, 07210, 07227, 07268, 07359, 07368, 09112, 86015, 86325, 86564, 87160, 87187 , 87921, 90320, 92195, 93216, 93280, 93920, 94118, 94169, 95377, 95058, 95469, 97045, 97092, 97115, 97116, 97120, 97165, 98163, 97183, 98184, 98373, 98432, 99233, 24 × 37-2275, 26 × 37-IV- 9IR, 26 × M-223-1, 26 × 27-164, 26 M 156-2, 27 × 49- 12, 27 × 49- 14, 27 × 49- 16, 49 × 27-37, 49 × 37-135, 49 × 39-21-1, 49 × 39-21-2, 49 × 39-21-2(a), 49 × 39-8, 49 M-2-2, BAU 13, CSMG 84-1, DH 86, Gangapuri, ICR 48, MN1-35, Somnath, SPS 17, TDG 13, TDG 14, TG 42, TKG 19A,
Highly susceptible	116	ICGs 10701, 11651, 12879, 12991, 13895, 14466, 14985, 1668, 1973, 2031, 2106, 2773, 3102, 3140, 3312, 3343, 3421, 3584, 3673, 434, 442, 4543, 4955, 4729, 8517, 9315, 9507, ICGS 44, ICGS 11 , ICGVs 00321, 00349, 00387, 01232, 02022, 02125, 02194, 02251, 02266, 02271, 02298, 03207, 04018, 04149, 06049, 06110, 06234, 06347, 06431, 07023, 07148, 07217, 07273, 13238, 13241, 13242, 13245, 86011, 86072, 86143, 86352, 87354, 87378, 88145, 88438, 91114, 89104, 91116, 92267, 93437, 93470, 94361, 95070, 95290, 96468, 96466, 97058, 97182, 97232, 97261, 97262, 98294, 99083, 99195, 99181, 26 M- 119-1, 27 × 49- 27-1, 49 × 27-13 (ii), 49 × 27-19, 49 × 37- 99(b) tall, 49 × 37-91, 49 × 37-97-1, 49 × 39-20-2, DTG 15, DTG 3, Faizpur 1-5, J 11, JL 24, Mutant 3, SPS 10 , SPS 13, SPS 3, SPS 6, SunOleic 95R, TAG 24, TDG 10, TG 39, TG 19, TG 41, TG 49, TG LPS 3, TG LPS 4, TG LPS 7, TMV 2, TMV 2 NLM, TPG 41,

* Genotypes were categorized based on Resistant/susceptible reaction to LLS disease on a 1-9 scale where Resistant (R) =1-3; Moderately Resistant (MR) = 4-5; Susceptible (S) = 6-7; Highly susceptible (HS) = 8-9 disease severity rating scale

Table 4.10 Disease reaction of genotypes of Genomic Selection Panel of groundnut against rust based on field evaluation at 90 DAS during rainy 2015 at ICRISAT

Reaction*	Number	Genotypes
Resistant	51	GPBD 4, ICG 11337 , 12625, 8751, ICGS 76, ICGVs 00068, 00246, 00248, 00362, 01265, 01273, 01274, 01276, 01361, 01464, 02317, 02323, 02411, 02446, 03043, 05036, 05100, 05141, 05163, 05155, 06142, 06422, 06423, 07220, 07120, 07223, 07235, 07247, 86699, 87846, 99029, 99051, 99052, 99160, 39 × 49-81-1, 49 × 37-134, 49 × 39-74, 49 M- 1-1, 49 M-16, SPS 11, SPS 2, SPS 20, SPS 21, SPS 7, SPS 8,
Moderate resistant	75	ICGs 10036, 11088, 11426, 12276, 12370, 15190, 15415, 15419, 2381, 2857, 6022, 6646, ICGVs 00005, 00191, 00290, 00346, 00351, 01060, 01328, 01393, 02242, 02287, 03042, 02434, 03056, 03064, 03128, 03397, 03136, 04087, 04115, 04124, 05032, 05057, 06175, 06188, 06420, 06424, 07145, 07166, 07227, 07246, 86325, 86564, 86590 , 87921, 93280, 93920, 94118, 97115, 97120, 97165, 98105, 98184, 98373, 99085, 24 × 39-31 MR, 24 M-86, 26 × M-223-1, 26 × M-95-1 RI, 27 × 49- 12, 39 × 49 -8, 49 × 37-90, 49 × 39-21-1, BAU 13, 49 M-2-2, CS 39, M 110-14, M 28-2, M 28-2, SPS 1, SPS 14, SPS 9, TDG 14,
Susceptible	166	ICGs 10053, 10185, 111, 11322, 11651, 12509, 12672, 13895, 14466, 14475, 14482, 14705, 14834, 14985, 156 , 1834, 1973, 2031, 2773, 3027, 3053, 3102, 3343, 3312, 3673, 3746, 4343, 4527, 442, 4543, 4955, 5221, 532, 5662, 5891, 6766, 721, 8285, 875, 9507, 9961, ICGS 44, ICGVs 00343, 00350, 00371, 00387, 00440, 01005, 01124, 01263, 01478, 01495, 02038, 02125, 02144, 02189, 02194, 02206, 02251, 02271, 02286, 02290, 02321, 03184, 03398, 03207, 04018, 04044, 04149, 05176, 05198, 06040, 06042, 06099, 06100, 06347, 06234, 07023, 07168, 07210, 07217, 07268, 07273, 07359, 07368, 09112, 13238, 13241, 13245, 86011, 86015, 86352, 87160, 87354, 87187 , 87378, 88145, 90320, 91116, 92195, 92267, 93216, 93437, 94169, 95058, 95290, 95377, 95469, 96466, 97045, 97058, 97092, 97116, 97182, 97183, 97261, 97262, 98163, 98294, 98432, 99083, 99195, 99233, ICR 48, J 11, JL 24, MN1-35, Somnath, Mutant 3, 24 × 37-2275, 26 × 37-IV- 9IR, 26 M- 119-1, 26 M 156-2, 26 × 27-164, 27 × 49- 14, 27 × 49- 16, 39 × 49 -77, 49 × 27-13 (ii), 49 × 27-19, 49 × 27-37, 49 × 37-99(b) tall, 49 × 37-135, 49 × 37-97-1, 49 × 39-20-2, 49 × 39-21-2, 49 × 39-21-2(a), 49 × 39-8, CSMG 84-1, DH 86, DTG 15, Faizpur 1-5, Gangapuri, SPS 10 , SPS 13, SPS 15, SPS 17, SPS 6, TDG 13, TG 39, TG 42, TG LPS 3, TG LPS 4, TMV 2 NLM, TKG 19A, TPG 41,
Highly susceptible	48	ICGs 10701, 12879, 12991, 1668, 2106, 3140, 3421, 3584, 434, 4729, 5663, 8517, 9315, ICGS 11 , ICGVs 00321, 00349, 01232, 02022, 02266, 02298, 06049, 06110, 07148, 06431, 13242, 86072, 86143, 89104, 88438, 91114, 93470, 94361, 95070, 96468, 99181, SPS 3, SunOleic 95R, TAG 24, TDG 10, TG 19, TG 41, TG 49, TG LPS 7, TMV 2, 27 × 49- 27-1, 49 × 37-91, DTG 3,

* Genotypes were categorized based on Resistant/susceptible reaction to LLS disease on a 1-9 scale where Resistant (R) =1-3; Moderately Resistant (MR) = 4-5; Susceptible (S) = 6-7; Highly susceptible (HS)= 8-9 disease severity rating scale

Table 4.11 Disease reaction of genotypes of Genomic Selection Panel of groundnut against LLS based on field evaluation during rainy 2015 across the three environments

Reaction*	Number	Genotypes
Resistant	31	49 M- 1-1, 49 M-16, GPBD 4, ICG 11337 , ICG 6022, ICGVs 00068, 00246, 00248, 00362, 01274, 01328, 02323, 02446, 02411, 03043, 04087, 05036, 05100, 05141, 05163, 06142, 07235, 86699, 99051, 99052, 99160, M 28-2, SPS 11, SPS 2, SPS 20, SPS 8,
Moderate Resistant	162	24 × 39-31 MR, 24 M-86, 26 × 37-IV- 9IR, 26 × M-223-1, 26 × M-95-1 RI, 26 M 156-2, 27 × 49- 12, 27 × 49- 14, 27 × 49- 16, 39 × 49 -77, 39 × 49 -8, 39 × 49-81-1, 49 × 37-134, 49 × 27-37, 49 × 37-90, 49 × 39-21-1, 49 × 39-21-2, 49 × 39-21-2(a), 49 × 39-74, 49 × 39-8, 49 M-2-2, BAU 13, CS 39, CSMG 84-1, DH 86, Gangapuri, ICGs 10036, 10053, 10185, 11322, 11426, 12276, 12370, 12509, 12625, 13895, 14466, 14475, 14482, 14705, 14834, 15415, 15419, 156 (M 13), 2381, 2773, 2857, 4527, 4343, 5221, 532, 5662, 5745, 5891, 6646, 721, 6766, 8285, 875, 8751, 9961, ICGS 76, ICGVs 00005, 00191, 00290, 00346, 00350, 00351, 00371, 01060, 01124, 01265, 01273, 01276, 01361, 01393, 01464, 01495, 02189, 02242, 02286, 02287, 02290, 02317, 02321, 02434, 03042, 03056, 03064, 03128, 03136, 03397, 04044, 04115, 05032, 05057, 05155, 05161, 06040, 06042, 06099, 06100, 06110, 06175, 06188, 06422, 06423, 06420, 06424, 07120, 07145, 07148, 07166, 07168, 07220, 07223, 07227, 07246, 07247, 07368, 86325, 86590 , 87160, 87187, 87846, 90320, 93216, 93920, 93280, 94118, 95058, 97045, 97058, 97092, 97115, 97116, 97120, 97128, 97165, 97182, 98105, 98163, 98184, 98373, 99029, 98432, 99085, ICR 48, M 110-14, M 28-2, MN1-35, Somnath, SPS 1, SPS 14, SPS 15, SPS 21, SPS 7, SPS 9, TDG 13, TDG 14, TKG 19A, TPG 41,
Susceptible	147	24 × 37-2275, 26 × 27-164, 26 M- 119-1, 27 × 49- 27-1, 49 × 27-19, 49 × 37- 99(b) tall, 49 × 37-135, 49 × 37-97-1, DTG 3, Faizpur 1-5, ICGs 10701, 11088, 11651, 111, 12672, 14985, 15190, 1668, 1834, 2106, 3027, 3053, 3102, 3140, 3421, 3746, 434, 4955, 5663, 8517, ICGS 11, ICGS 44, ICGVs 00343, 00387, 00440, 01005, 01263, 01478, 02022, 02125, 02144, 02206, 02251, 02266, 02271, 02298, 03184, 03398, 03207, 04018, 04124, 04149, 05176, 05198, 06049, 06347, 06234, 06431, 07023, 07210, 07268, 07359, 09112, 13238, 13241, 13245, 86011, 86015, 86072, 86143, 86352, 86564, 87354, 87378, 87921, 88145, 88438, 89104, 91114, 92195, 92267, 93437, 94169, 94361, 95070, 95290, 95377, 95469, 96468, 97183, 97232, 97261, 98294, 99083, 99195, 99233, JL 24, Mutant 3, SPS 10 , SPS 13, SPS 17, SPS 3, SPS 6, SunOleic 95R, TDG 10, TG 39, TG 41, TG 19, TG 42, TG 49, TG LPS 3, TG LPS 4, TG LPS 7, TMV 2 NLM, 49 × 27-13 (ii), 49 × 37-91, 49 × 39-20-2, DTG 15, ICGs 12879, ICGs 12991, 1973, 2031, 3312, 3343, 3584, 3673, 4543, 442, 4729, 9315, 9507, ICGVs 00321, 00349, 01232, 02038, 02194, 07217, 07273, 13242, 91116, 93470, 96466, 97262, 99181, J 11, TAG 24, TMV 2,
Highly susceptible	0	

* Genotypes were categorized based on Resistant/susceptible reaction to LLS disease on a 1-9 scale where Resistant (R) =1-3; Moderately Resistant (MR) = 4-5; Susceptible (S) = 6-7; Highly susceptible (HS) = 8-9 disease severity rating scale

Table 4.12 Disease reaction of genotypes of Genomic Selection Panel of groundnut against rust based on field evaluation during rainy 2015 across the three environments

Reaction*	Number	Genotypes
Resistant	66	39 × 49-81-1,49 × 39-74,49 M- 1-1,49 M-16,CS 39,GPBD 4,ICG 11337 ,ICG 11426,ICG 8751,ICGVs 00005, 00068, 00191, 00248, 00246, 00346, 00362, 01265, 01273, 01274, 01276, 01361, 01464, 02317, 02323, 02411, 02446, 03042, 03043, 03064, 04087, 05032, 05036, 05057, 05100, 05141, 05155, 05163, 06142, 06175, 06422, 06423, 06424, 07120, 07145, 07220, 07223, 07227, 07247, 07235, 86590 , 86699, 87846, 97128, 98105, 98373, 99051, 99029, 99052, 99085, 99160,SPS 11,SPS 2,SPS 20,SPS 21,SPS 7,SPS 8,
Moderate Resistant	138	24 × 37-2275,24 × 39-31 MR,24 M-86,26 × M-223-1,26 × M-95-1 RI,27 × 49- 12,27 × 49- 14,39 × 49 -77,39 × 49 -8,49 × 27-37,49 × 37-134,49 × 37-90,49 × 39-21-2,49 × 39-21-1,49 × 39-21-2(a),49 × 39-8,49 M-2-2,BAU 13,CSMG 84-1,DH 86,ICGs 10036, 10053, 11088, 111, 12276, 12370, 12509, 12625, 13895, 14466, 14475, 14482, 14834, 15190, 15415, 15419, 2381, 2773, 2857, 3027, 3053, 4343, 4527, 532, 5662, 5745, 6022, 6766, 6646, 8285, 875,ICGS 76,ICGVs 00290, 00350, 00351, 00440, 00387, 01060, 01124, 01263, 01328, 01393, 01478, 01495, 02194, 02206, 02242, 02266, 02286, 02287, 02290, 02321, 02434, 03056, 03128, 03136, 03207, 03397, 03398, 04044, 04115, 04124, 05161, 05176, 05198, 06040, 06042, 06099, 06100, 06188, 06420, 07148, 07166, 07168, 07210, 07246, 07368, 13241, 86325, 86564, 87187, 87921, 88438, 90320, 93216, 93920, 94118, 93280, 95469, 96466, 97045, 97058, 97092, 97115, 97116, 97120, 97165, 97182, 98163, 98184, 98294, 98432, 99083, 99195, 99233,M 110-14,M 28-2,MN1-35,M 28-2,SPS 1,SPS 14,SPS 15,SPS 17,SPS 9,TDG 13,TDG 14,TG 42,TG LPS 4, 01274,
Susceptible	136	26 × 27-164,26 × 37-IV- 9IR,26 M- 119-1,26 M 156-2,27 × 49- 16,27 × 49- 27-1,49 × 27-13 (ii),49 × 27-19,49 × 37-97-1,49 × 39-20-2,DTG 15,DTG 3,ICGs 10185,Gangapuri, 11322, 11651, 12672, 12879, 12991, 14705, 156 (M 13), 1668, 2031, 2106, 3102, 3140, 3312, 3343, 3673, 3746, 4543, 4955, 5221, 5663, 5891, 721, 8517, 9507, 9961,ICGS 11,ICGS 44,s 00321, 00343, 00349, 00371, 01232, 02022, 02125, 02038, 02144, 02189, 02251, 02271, 02298, 03184, 06049, 04018, 06234, 06347, 07023, 07217, 07268, 07273, 07359, 09112, 13238, 13242, 13245, 86011, 86015, 86072, 86143, 86352, 87160, 87354, 87378, 88145, 89104, 91116, 92195, 92267, 93437, 94169, 94361, 95058, 95290, 95377, 97183, 97232, 97261, 97262, ICR 48, JL 24, Somnath, SPS 13, SPS 3, SPS 6, SunOleic 95R, TAG 24, TG 39, TG 49, TG LPS 3, TKG 19A, TMV 2 NLM, TPG 41, 49 × 37-135, 49 × 37-91, 49 × 37- 99(b) tall, Faizpur 1-5, ICGs 10701, 14985, 1834, 1973, 3421, 3584, 434, 442, 4729, 9315, ICGVs 01005, 04149, 06110, 06431, 91114, 93470, 95070, 96468, J 11, 99181, Mutant 3, SPS 10 , TDG 10, TG 19, TG 41, TG LPS 7, TMV 2,
Highly susceptible	0	

* Genotypes were categorized based on Resistant/susceptible reaction to LLS disease on a 1-9 scale where Resistant (R) =1-3; Moderately Resistant (MR) = 4-5; Susceptible (S) = 6-7; Highly susceptible (HS) = 8-9 disease severity rating scale

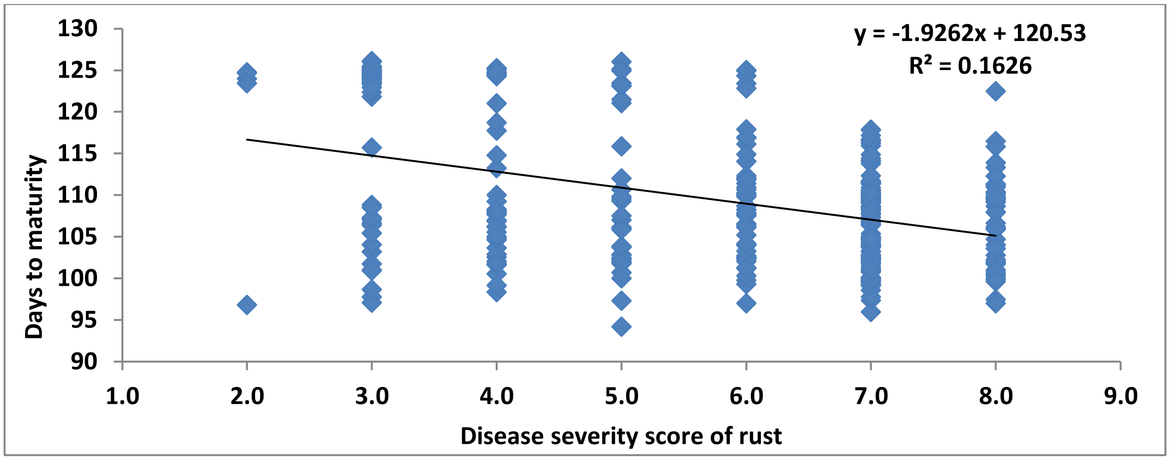

Figure 4.3 Disease reactions of genotypes for rust at 90 days after sowing with respect to days to maturity at ICRISAT during rainy 2015

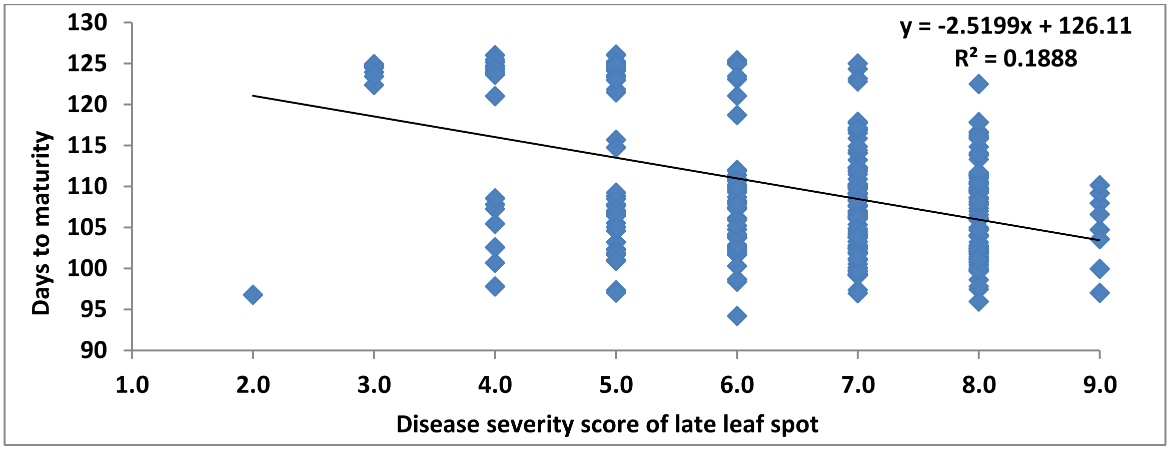

Figure 4.4 Disease reactions of genotypes for late leaf spot at 90 days after sowing with respect to days to maturity at ICRISAT during rainy 2015

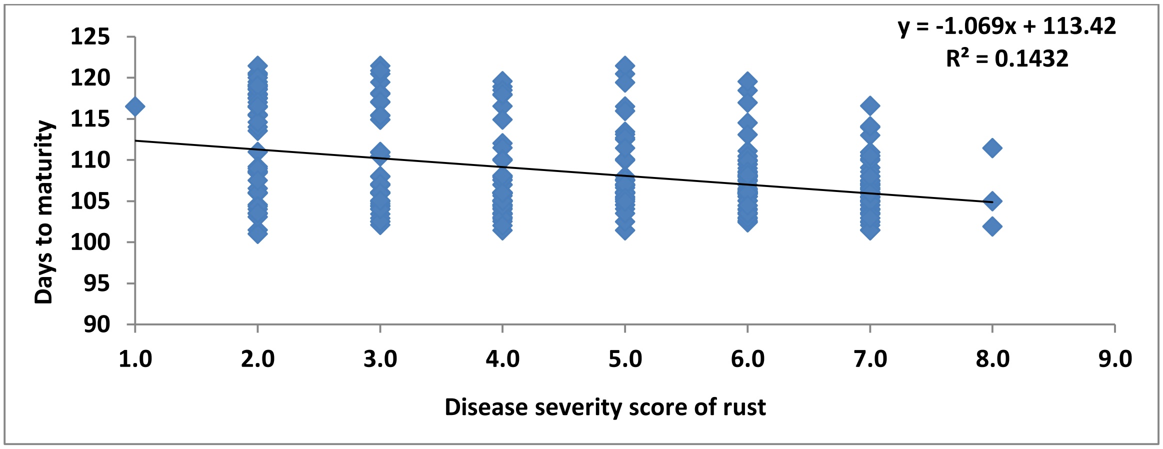

Figure 4.5 Disease reactions of genotypes for rust at 90 days after sowing with respect to days to maturity at Aliyarnagar during rainy 2015

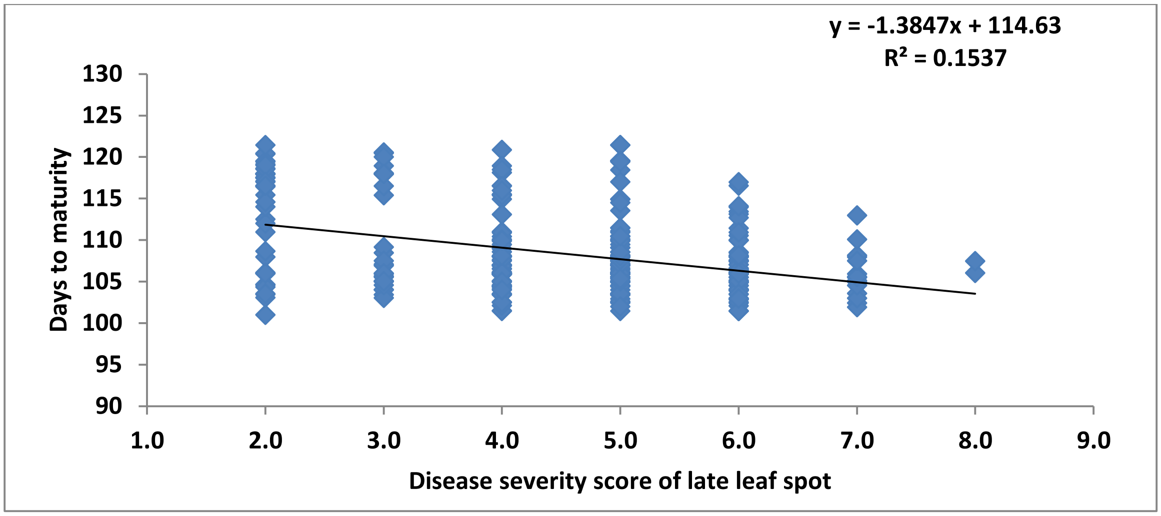

Figure 4.6 Disease reactions of genotypes for late leaf spot at 90 days after sowing with respect to days to maturity at Aliyarnagar during rainy 2015

4.2.2 Yield and its contributing traits

Days to 50% flowering

Genetic variation for days to 50% flowering was low as indicated by narrow range, low GCV and PCV coupled with high heritability and low to moderate GAM in each individual environment as well as pooled across environments. The days were taken for 50% flowering varied from 26 to 35 at Aliyarnagar, from 25 to 37 at Jalgaon, 23 to 37 at ICRISAT rainy 2015, from 34 to 53 at ICRISAT post-rainy 2015-16 and the average over the environments was from 29 to 38 days (Table 4.13). The location average over the genotypes was 30 days at Aliyarnagar, 29 days at Jalgaon, and 29 and 42 days at ICRISAT in rainy and post-rainy seasons, respectively. At Aliyarnagar, low GCV (6.45%) and PCV (7.29%) for days to 50% flowering with high heritability (78.40%) and moderate GAM (11.77%) was reported whereas low GCV (7.44%) and PCV (9.61%) coupled with moderate heritability (59.85%) and GAM (11.85%) was reported at Jalgaon. However, low GCV (8.67%) and PCV (10.20%) coupled with high heritability (72.23%) and moderate GAM (15.18%) was observed at ICRISAT during rainy 2015 and a similar trend of low GCV (6.82%) and PCV (7.67%) coupled with high heritability (79.21%) and moderate GAM (12.51%) was also recorded at ICRISAT during post-rainy 2015-16. A similar trend of low GCV (6.23%) and PCV (7.23%) with high heritability (76.20%) and moderate

GAM (11.20%) was observed from pooled analysis (Table 4.13). The genotype ICGV’s 06431, 04149, 87378, 13242, 07210, ICG’s 10701, 14985, 4543 and SPS 6 flowered earlier (26 days) compared to all other genotypes of GSP at Aliyarnagar, whereas ICGV’s 06049, 04149, 49 × 39-21-2 and SPS 9 recorded earliest (25 days) flowering genotypes at Jalgaon. The genotype ICGV 87378 (23 days) followed by ICGVs 91116 and 99181 and ICG 14985 (24 days) recorded as earliest flowering genotypes at ICRISAT during rainy 2015 compared to all other genotypes across the environments. All the genotypes flowered late in the post-rainy season compared to the rainy season at ICRISAT. Genotypes ICGV 13241 (34 days) followed by ICGV 01005 (35 days), ICGV 93470 and DTG 15 (36 days) recorded as early flowering genotypes during the post-rainy season at ICRISAT 2015-16. The genotypes ICGV 06431 followed by ICGV’s 99181, 91116, 04149 and 06049, DTG 15, TAG 24, ICG 3102 and ICGV 02189 flowered earlier (29 days) across the environments (Table 4.14).

Plant height (cm)

Genetic variation for plant height was high with moderate to high GCV, PCV, GAM and high heritability in each environment and across the environments. Plant height of different genotypes varied from 25.17 to 67.34 cm at Aliyarnagar, from 23.75 to 71.56 cm at Jalgaon, 20.56 to 59.70 cm at ICRISAT rainy 2015, from 12.93 to 37.90 cm at ICRISAT post-rainy 2015-16 and from 23.15 to 56.19 cm in pooled with an average of 36.70, 42.76, 35.40, 22.09 and 34.23 cm at Aliyarnagar, Jalgaon, ICRISAT rainy 2015, ICRISAT post-rainy 2015-16 and pooled across the environments, respectively (Table 4.13). At Aliyarnagar, moderate GCV (14.47%) and PCV (15.49%) with high heritability (87.21%) and GAM (27.83%) were reported for plant height. Similar moderate GCV (14.94 & 14.84%) and PCV (16.72 & 16.26%) coupled with high heritability (79.79 & 83.30%) and GAM (27.49 & 27.90%) was reported at Jalgaon and ICRISAT rainy 2015, respectively whereas high GCV (20.55%) and PCV (21.93%) coupled with high heritability (87.85%) and GAM (39.69%) was observed at ICRISAT post rainy 2015-16 (Table 4.13). However moderate GCV and PCV (12.60 & 14.77%) with high heritability (72.75%) coupled with high GAM (22.13%) were reported in pooled across the environments. The genotypes ICG 15419 (67.3 cm) recorded as maximum plant height followed by ICG 6022 (59.0 cm) and ICGV 01005 (54.9 cm) at Aliyarnagar whereas ICGV 30184 (71.6 cm) recorded highest plant height followed by ICG 6022 (69.8 cm) and 27 × 49-6 (66.6 cm) at Jalgaon. ICG 15419 (59.7 cm) recorded as tallest genotype followed by ICG 6646 (58.2 cm), ICG 6022 and ICG 8751 (57.0 cm) at ICRISAT during rainy 2015 whereas genotypes recorded minimum plant heights during the post-rainy season at ICRISAT 2015-16. The genotypes 27 × 49-16 (37.9 cm) followed by ICG 6646 (37.8 cm) and ICGV 02266 (37.7 cm) recorded as higher plant height compared to other genotypes at ICRISAT during post-rainy 2015-16. Genotypes ICG 15419 (56.2 cm) followed by ICG 6022 (53.6 cm), ICG 6646 (49.8 cm) and ICGV 03184 (49.1 cm) reported higher plant height across the environments (Table 4.15).

Number of primary branches per plant

Genetic variation for number of primary branches per plant was low with relatively narrow range, low GCV, PCV, and GAM with moderate to high heritability in each environment and across the environments. Number of primary branches per plant varied from 3 to 8 at Aliyarnagar, from 3 to 10 at Jalgaon, 4 to 10 at ICRISAT rainy and post-rainy 2015-16 and the average over the environments was from 4 to 8 (Table 4.13). The environment average over the genotypes for number of primary branches per plant was 5 at Aliyarnagar, 6 at Jalgaon, ICRISAT rainy and post-rainy 2015-16, and pooled across the environments. At Aliyarnagar, low GCV (8.82%) and PCV (10.92%) with high heritability (65.22%) and moderate GAM (14.68%) was reported for number of primary branches per plant whereas low GCV (9.27 & 10.04%) and moderate PCV (12.26 & 12.21%) coupled with moderate and high heritability (57.26 & 67.62%) and moderate GAM (14.46 & 17.00%) was reported at Jalgaon and ICRISAT rainy 2015, respectively. A similar trend of low GCV (9.57%) and moderate PCV (11.59%) coupled with high heritability (61.53%) and moderate GAM (14.69%) was observed at ICRISAT post-rainy 2015-16. A similar trend of low GCV and PCV (8.35 & 8.60%) with high heritability (81.03%) and moderate GAM (15.94%) was observed from pooled analysis across the environments.

The genotypes ICGV 09112 (8) recorded the highest number of primary branches at Aliyarnagar whereas ICGV 05141 (10) recorded at Jalgaon. The genotype 49 M-2-2 (10) recorded a higher number of primary branches at ICRISAT rainy season 2015 whereas ICGV 07246 (10) recorded at ICRISAT during the post-rainy season 2015-16. Pooled analysis reported genotype 49 M-2-2, ICGV's 07246, 01361 and 07247 (8) with higher number of primary branches across the environments (Table 4.15).

Number of matured pods per plant at the time of harvest

Number of matured pods per plant in groundnut is an important yield contributing trait and genotypes with a higher number of pods are desirable. Genetic variation for number of pods per plant in GSP was high as indicated by a wider range, high GCV and PCV coupled with high heritability and GAM in each environment and across the environments. Number of matured pods per plant varied from 3 to 35 at Aliyarnagar, from 4 to 38 at Jalgaon, 4 to 29 at ICRISAT rainy 2015, from 3 to 24 at ICRISAT post-rainy 2015-16 and the average over environments from 5 to 25. The average of environments over genotypes for matured pods per plant was 15 at Aliyarnagar, 16 at Jalgaon, 14 and 10 at ICRISAT rainy and post-rainy season, respectively and 14 was the average over environments (Table 4.13). At Aliyarnagar, high GCV (34.55%) and PCV (31.83%) with high heritability (75.36%) and GAM (56.92%) were reported for number of pods per plant. The similar trend of high GCV (34.65, 28.73 & 36.37%) and PCV (39.01, 37.06 & 41.50%) coupled with high heritability (78.91, 60.07 & 76.79%) and GAM (63.41, 45.86 & 65.65%) was reported at Jalgaon, ICRISAT rainy 2015 and ICRISAT post rainy 2015-16, respectively. Pooled analysis of four environment data also revealed a similar trend of high GCV and PCV (23.32 & 30.33%) with moderate heritability (59.09%) and high GAM (36.93%) for number of pods per plant across the environments (Table 4.13).

Table 4.13 Mean, range and genetic parameters for yield and its contributing traits of Genomic Selection Panel of groundnut evaluated across the environments

Traits	Mean	Range		GCV	PCV	h^2_{bs}	GAM
		Min	Max	(%)	(%)	(%)	(%)
Aliyarnagar							
Days to 50% flowering	30	26	35	6.45	7.29	78.40	11.77
Plant height (cm)	36.7	25.17	67.34	14.47	15.49	87.21	27.83
Number of primary branches plant^{-1}	5	3	8	8.82	10.92	65.22	14.68
Number of pods plant^{-1}	15	3	36	31.83	36.67	75.36	56.92
Pod yield plant^{-1} (g)	10.88	3.61	29.03	32.30	37.65	73.60	57.08
Seed yield plant^{-1} (g)	6.57	2.15	17.21	33.30	38.92	73.18	58.68
Shelling percent	60.56	38.97	71.3	8.23	9.35	77.47	14.92
Hundred seed weight (g)	32.6	19.64	66.22	22.68	23.51	93.05	45.06
Days to physiological maturity	108	101	121	4.34	4.64	87.56	8.37
Pod yield hectare^{-1} (kg)	1392.0	386.3	3809.2	43.92	49.71	78.05	79.92
Jalgaon							
Days to 50% flowering	30	25	37	7.44	9.61	59.85	11.85
Plant height (cm)	42.76	23.75	71.56	14.94	16.72	79.79	27.49
Number of primary branches plant^{-1}	6	3	10	9.27	12.26	57.26	14.46
Number of pods plant^{-1}	16	4	35	34.65	39.01	78.91	63.41
Pod yield plant^{-1} (g)	10.51	1.98	23.96	36.20	41.41	76.40	65.18
Seed yield plant^{-1} (g)	6.15	0.79	14	38.77	44.54	75.76	69.51
Shelling percent	58.09	42.05	70.16	8.88	9.70	83.77	16.73
Hundred seed weight (g)	33.66	13.61	55.16	18.18	19.58	86.14	34.75
Days to physiological maturity	122	107	140	6.27	6.36	97.01	12.72
Pod yield hectare^{-1} (kg)	1592.3	367.3	4864.4	46.00	50.81	81.96	85.78
ICRISAT rainy season 2015							
Days to 50% flowering	29	23	37	8.67	10.20	72.23	15.18
Plant height (cm)	35.4	20.56	59.7	14.84	16.26	83.30	27.90
Number of primary branches plant^{-1}	6	4	10	10.04	12.21	67.62	17.00
Number of pods plant^{-1}	14	4	29	28.73	37.06	60.07	45.86
Pod yield plant^{-1} (g)	10.21	2.54	21.09	32.24	39.45	66.76	54.26
Seed yield plant^{-1} (g)	5.85	1.54	13.49	33.77	43.38	60.58	54.14
Shelling percent	57.53	36.49	71.18	7.70	11.40	45.61	10.71
Hundred seed weight (g)	32.35	15.26	59.02	20.20	22.90	77.82	36.70
Days to physiological maturity	109	94	126	6.99	7.24	93.31	13.92
Pod yield hectare^{-1} (kg)	1569.0	356.7	3764.5	40.38	44.25	83.27	75.90
Haulm yield per plant^{-1}	16.1	7.1	29.26	21.27	28.30	56.49	32.93
ICRISAT post-rainy season 2015-16							
Days to 50% flowering	42	34	53	6.82	7.67	79.21	12.51
Plant height (cm)	22.09	12.93	37.9	20.55	21.93	87.85	39.69
Number of primary branches plant^{-1}	6	4	10	9.09	11.59	61.53	14.69
Number of pods plant^{-1}	10	3	24	36.37	41.50	76.79	65.65
Pod yield plant^{-1} (g)	6.63	1.94	19.87	37.92	43.13	77.27	68.66
Seed yield plant^{-1} (g)	3.98	0.74	11.62	41.30	46.83	77.78	75.03
Shelling percent	59.41	44.95	75.55	10.49	11.36	85.26	19.95
Hundred seed weight (g)	33.78	18.29	58.56	20.82	21.74	91.64	41.05
Days to physiological maturity	142	121	155	5.40	5.56	94.46	10.82
Pod yield hectare^{-1} (kg)	1641.4	409.0	4321.1	39.94	45.92	75.67	71.58

Traits	Mean	Range		GCV	PCV	h^2_{bs}	GAM
		Min	Max	(%)	(%)	(%)	(%)
Haulm yield plant^{-1} (g)	19.41	5.08	40.57	33.49	36.10	86.07	19.41
Pooled across the environments							
Days to 50% flowering	33	29	38	6.23	7.13	76.20	11.20
Plant height (cm)	34.23	23.15	56.19	12.60	14.77	72.75	22.13
Number of primary branches plant^{-1}	5.61	3.8	8.35	8.60	9.55	81.03	15.94
Number of pods plant^{-1}	13.82	4.93	25.35	23.32	30.33	59.09	36.93
Pod yield plant^{-1} (g)	9.56	3.86	17.3	22.48	31.23	51.81	33.33
Seed yield plant^{-1} (g)	5.64	2.13	11.16	24.23	33.32	52.88	36.30
Shelling percent	58.92	46.38	69.47	6.48	8.29	61.13	10.44
Hundred seed weight (g)	33.09	20.25	52.4	16.59	19.12	75.30	29.66
Days to physiological maturity	120.44	107	134	4.69	5.38	75.96	8.42
Pod yield hectare^{-1} (kg)	1549.9	478.3	3202.8	31.15	39.09	63.52	51.15
Haulm weight plant^{-1} (g)	17.76	8.51	30.37	21.89	28.90	57.38	34.16

Min= Minimum; Max= Maximum; GCV = Genotypic coefficient of variation (%); PCV= Phenotypic coefficient of variation (%); h^2_{bs} = Heritability in broad sense (%); GAM= Genetic advance as percent of mean (%)

The genotype ICGV 99051 (35) followed by 49 × 39-21-2(a) (34) and ICGV 02323 (30) recorded as higher number of pods per plant at Aliyarnagar whereas ICGV 07247 (35) followed by 49 × 39-74 (32) and ICGV 05163 (32) recorded higher number pods per plant at Jalgaon (Table 4.16). The genotypes 49 M-16 (29), 27 × 49-12 (28) and SPS 11 (28) recorded higher number of pods per plant at ICRISAT rainy 2015 whereas ICGV 07247 (24) followed by ICGV (22) and 49 M-16 (22) recorded higher number of pods per plant at ICRISAT during post-rainy 2015-16. Genotypes ICGV 07247, ICGV 01276 (25), 49 M-16 (23) and 49 × 39-21-2(a) (23) reported higher number of matured pods per plant across the environments (Table 4.16).

Pod yield per plant (g)

Genetic variation for pods yield per plant in GSP was also high as indicated by its wider range, high GCV and PCV coupled with heritability and GAM in the individual as well as across the environments. Pod yield per plant varied from 3.6 to 29.0 g at Aliyarnagar, from 1.98 to 23.96 g at Jalgaon, 2.5 to 21.1 g at ICRISAT rainy 2015, from 1.9 to 19.9 g at ICRISAT post-rainy 2015-16 and the average over environments from 3.9 to 17.3 g. The average of environments over genotypes for pod yield per plant was 10.9 g at Aliyarnagar, 10.5 g at Jalgaon, 10.2 and 6.6 g at ICRISAT rainy and post-rainy seasons, respectively (Table 4.13). High GCV (29.06%) and PCV (32.30%) with high heritability (73.60%) and GAM (57.08%) were reported for pod yield per plant at Aliyarnagar. A similar trend of high GCV (36.20, 32.24 & 37.92%) and PCV (41.41, 39.45 & 43.13%) coupled with high heritability (76.40, 66.76 & 77.27%) and GAM (65.18, 54.26 & 68.66%) was reported at Jalgaon, ICRISAT rainy 2015 and ICRISAT post-rainy 2015-16, respectively. However pooled analysis revealed high GCV and PCV with moderate heritability (51.81%) and high GAM (33.33%) for pod yield per plant across the environments (Table 4.13). The genotypes ICGV 05198 (29.0 g) followed ICGV 99051 (25.9 g) and ICGV 01478 (23.8 g) achieved higher pod yield per plant at Aliyarnagar whereas ICGV 05163 (24.0 g) followed by ICGV 03064 and ICGV 02323 (21.2 g) recorded higher pod yield per plant at Jalgaon. The pod yield per plant at ICRISAT during both rainy and post-rainy season was low compared to Aliyarnagar and Jalgaon. Genotype ICGV 06142 (21.1 g) followed by ICGV 02411 (21.0 g) and 49 M-16 (20.3 g) recorded higher pod yield per plant whereas CS 39 (19.9 g) followed by ICGV 07247 (17.0 g) and Faizpur 1-5 (14.9 g) recorded higher pod yield per plant at ICRISAT post-rainy 2015-16. Genotype ICGV 07247 (17.3 g) followed by ICGV 01276 (17.3 g), ICGV 05163 (16.8 g) and ICGV 02323 (16.3 g) reported higher pod yield per plant across the environments (Table 4.16).

Seed yield per plant (g)

High genetic variability for seed yield per plant in GSP was observed by its wider range, high GCV, PCV, heritability and GAM reported in individual and across the environments. Seed yield per plant varied from 2.2 to 17.2 g at Aliyarnagar, from 0.8 to 14.0 g at Jalgaon, 1.5 to 13.5 g at ICRISAT rainy 2015, from 0.7 to 11.6 g at ICRISAT post-rainy 2015-16 and the average over environments was from 2.1 to 11.2 g. The average of environments over genotypes was 6.6 g at Aliyarnagar, 6.2 g at Jalgaon, 5.9 and 4.0 g at ICRISAT rainy and post-rainy seasons, respectively (Table 4.13). High GCV (33.30%) and PCV (38.92%) with high heritability (73.18%) and GAM (58.68%) were reported for seed yield per plant at Aliyarnagar. A similar trend of high GCV (38.77, 33.77 & 41.30%) and PCV (44.54, 43.38 & 46.83%) coupled with high heritability (75.76, 60.58 & 77.78%) and GAM (69.51, 54.14 & 75.03%) was reported at Jalgaon, ICRISAT rainy 2015 and ICRISAT post-rainy 2015-16, respectively. However, pooled analysis revealed high GCV and PCV (24.23 to 33.32%) coupled with moderate heritability (52.88%) and high GAM (36.30%) for seed yield per plant across the environments (Table 4.13). The genotypes ICGV 05198 (17.2 g) followed ICGV 99051 (14.6 g) and ICGV 01478 (14.6 g) achieved higher seed yield per plant at Aliyarnagar whereas ICGV 06099 (14.0 g) followed by ICGV 05163 (13.9 g) and DH 86 (13.2 g) recorded higher seed yield per plant at Jalgaon. Genotype ICGV 02286 (13.5 g) followed by ICGV 02411 (13.3 g) and 49 M-16 (12.9 g) recorded higher seed yield per plant whereas CS 39 (11.6 g) followed by ICGV 07247 (11.6 g) and ICGV 03128 (9.1g) recorded higher seed yield per plant at ICRISAT post-rainy 2015-16. However, genotype ICGV 07247 (11.2 g) followed by ICGV 01276 (10.6 g), ICGV 02323 (10.5 g) and ICGV 06099 (10.3 g) reported higher seed yield per plant across the environments (Table 4.17).

Shelling percent

Shelling percent in groundnut is an important trait to determine seed yield from pod yield. Genetic variation in GSP for shelling percent was low as indicated by low GCV and PCV with moderate to high heritability and low to moderate GAM. Shelling percent was varied from 39 to 71% at Aliyarnagar, from 42 to 70% at Jalgaon, from 36 to 71% at ICRISAT rainy 2015, from 45 to 76% at ICRISAT post-rainy 2015-16 and the average over environments from 46 to 69%. The average of environments over genotypes for pod yield per plant was 61% at Aliyarnagar, 58% at Jalgaon and ICRISAT rainy 2015, and 59% at ICRISAT post-rainy and average across the environments (Table 4.13). Low GCV (8.23%) and PCV (9.35%) with high heritability (77.47%) and low GAM (14.92%) were reported for shelling percent at Aliyarnagar. The similar trend of low GCV (8.88%) and PCV (9.70%) coupled with high heritability (83.77%) and low GAM (16.73%) was reported at Jalgaon whereas low GCV (7.70%) and moderate PCV (11.40%) coupled with moderate heritability (45.61%) and low GAM (10.71%) was reported at ICRISAT rainy 2015. Low GCV (10.49%) and moderate PCV (11.36%) with high heritability (85.26%) and moderate GAM (19.95%) were recorded at ICRISAT post-rainy 2015-16. Pooled analysis also revealed a similar trend of GCV and PCV (6.48 & 8.29%) with high heritability

(61.13%) and low GAM (10.44%) for shelling percent across the environments (Table 4.13). The genotype ICG 156, BAU 13 and ICG 3312 recorded highest (71%) shelling percent at Aliyarnagar whereas ICGV 02038 (70%) followed by ICGV 07268 and SPS 7 (69%) had the highest shelling percent compared to all other genotypes at Jalgaon. Genotype ICGV 97262 (71%) followed by ICGV’s 03128 and 87187 (69%) was the best genotypes recorded higher shelling percent at ICRISAT during rainy 2015. Genotypes recorded higher shelling percent during the post-rainy season at ICRISAT compared to rainy season across the environments. Genotypes 49 × 39-74 (76%) recorded highest shelling percent followed by ICG 3584 and ICG 2106 (73%) at ICRISAT during post-rainy 2015-16. Genotype ICGV 95469 (70%) followed by ICGV 07268 (68%) ICGV 02038 (68%) and ICGV 95290 (68%) reported higher shelling percent across the environments (Table 4.17).

Hundred seed weight (g)

High genetic variability for hundred seed weight in GSP was observed with moderate to high GCV, PCV with high heritability and GAM in different environments. Hundred seed weight was varied from 19.64 to 66.22 g at Aliyarnagar, from 13.6 to 55.2 g at Jalgaon, from 15.3 to 59.0 g at ICRISAT rainy 2015, from 18.3 to 58.6 g at ICRISAT post-rainy 2015-16 and the average over environments was from 20.3 to 52.4 g. The average of environments over genotypes for hundred seed weight was 32.6 g at Aliyarnagar, 33.7 g at Jalgaon, 35.4 and 33.8 g at ICRISAT rainy and post-rainy seasons, respectively (Table 4.13). The average of hundred seed weight across the environments was 33.09 g. High GCV (22.68%) and PCV (23.51%) with high heritability (93.05%) and GAM (45.06%) was reported for hundred seed weight at Aliyarnagar whereas moderate GCV (18.18%) and PCV (19.58%) coupled with high heritability (86.14%) and GAM (34.75%) was reported at Jalgaon. At ICRISAT rainy 2015, high GCV (20.20%) and PCV (22.90%) coupled with high heritability (77.82%) and GAM (36.70%) was reported and a similar trend of high GCV (20.82%) and PCV (21.74%) with high heritability (91.64%) and GAM (41.05%) was recorded at ICRISAT post-rainy 2015-16. Genotypes ICGV 00440 (66.2g) followed 05198 (61.2g) and 49 × 37-97-1 (61.1g) had highest hundred seed weight at Aliyarnagar whereas ICGV 06234 (55.2g) followed by 49 M-1-1 (54.3g) and 49 × 37-99(b) tall (54.1 g) at Jalgaon. Genotypes ICGV 05198 (59.0 g) followed by 27 × M-223-1 (55.6 g) and TG 42 (54.0 g) reported as higher hundred seed weight at ICRISAT rainy 2015 whereas ICGV 06234 (58.6g) followed by ICGV 01478 (58.5g) and ICGV 06188 (56.5 g) at ICRISAT post-rainy 2015-16. However, pooled analysis also revealed moderate GCV and PCV (16.59 & 19.12%) with high heritability (75.30%) and GAM (29.66%) for hundred seed weight across the environments (Table 4.13). Genotypes ICGV 05198 (52.4g) followed by TG 42 (52.1g), ICGV 06188 (51.5g) and ICGV 00440 (51.0g) reported high hundred seed weight across the environments (Table 4.18).

Days to physiological maturity

Genetic variation for days to maturity in GSP was low across the environments as indicated by low GCV and PCV with heritability and low GAM in each environment and across the environments. Days to physiological maturity in GSP varied from 101 to 121 days at Aliyarnagar, from 107 to 140 days at Jalgaon, 94 to 126 days at ICRISAT rainy 2015, from 121 to 155 days at ICRISAT post-rainy 2015-16 and from 107 to 134 days in pooled across the environments with an average of 108, 122, 109, 142 and 120 days at Aliyarnagar, Jalgaon, ICRISAT rainy 2015, ICRISAT post-rainy 2015-16 and pooled across the environments, respectively (Table 4.13). At Aliyarnagar, low GCV (4.34%) and PCV (4.64%) with high heritability (87.56%) and low GAM (8.37%) were reported for days to maturity. The similar trend of low GCV (6.27, 6.99 & 5.40%) and PCV (6.36, 7.24 & 5.56%) coupled with high heritability (97.01, 93.31 & 94.46%) and moderate GAM (12.72, 13.92 & 10.82%) was reported at Jalgaon, ICRISAT rainy 2015 and ICRISAT post-rainy 2015-16, respectively. Pooled analysis of four environments also revealed low GCV and PCV (4.69 & 5.38%) with high heritability (75.96%) and low GAM (8.42%) for days to maturity. The genotypes ICGV 05155 followed by M 28-2 (101 days) and ICGV 95469 (102 days) matured earlier compared to all other at Aliyarnagar while genotypes ICGV 06234 (107 days) followed by TMV 2 and 26 × M-95-1 R1 (108 days) at Jalgaon. The genotypes 26 × M-223-1 (94 days) followed ICGV 87354 (96 days) and ICGV 86699 (97 days) matured earlier compared to all other genotypes across the environments whereas genotypes matured late during post-rainy season 2015-16. Genotypes ICGV 92195 (121 days) followed by ICGV 91116 (121 days) and 26 × M-95-1 R1 (122 days) matured earlier at ICRISAT during post-rainy 2015-16. Genotypes ICGV 92195 (107 days) followed by 26 × M-95-1 RI (108 days), 39 × 49-81-1 (109 days) and ICGV 13242 (109 days) matured earlier compared to other genotypes of GSP across the four environments (Table 4.14).

Pod yield per hectare (kg)

Genetic variation for the yield potential of genotypes in GSP was reported high with high GCV and PCV coupled with moderate to high heritability and high GAM in each environment and across the environments. Pod yield per hectare in GSP varied from 386 to 3809 kg at Aliyarnagar, from 367 to 4864 kg at Jalgaon, 356 to 3765 kg at ICRISAT rainy 2015, from 409 to 4321 kg at ICRISAT post-rainy 2015-16 and average over environments was from 478 to 3203 kg. The average of environments over genotypes for pod yield per hectare was 1392 kg at Aliyarnagar, 1592 kg at Jalgaon, 1569 and 1641 kg at ICRISAT rainy and post-rainy seasons, respectively (Table 4.13). At Aliyarnagar, high GCV (43.92%) and PCV (49.71%) with high heritability (78.05%) and GAM (79.92%) were reported for yield per plot. The similar trend of high GCV (46.00, 40.38 & 39.94%) and PCV (50.81, 44.25 & 45.92%) coupled with high heritability (81.96, 83.27 & 75.676%) and GAM (85.78, 75.90 & 71.58%) was reported at Jalgaon, ICRISAT rainy 2015 and ICRISAT post-rainy 2015-16, respectively. Pooled analysis also revealed a similar trend of high GCV and PCV (31.15 & 39.09%) with high heritability (63.52%) and GAM (51.15%) for pod yield across the environments. Among all individual environments and pooled, wide range for pod yield per hectare was observed at Jalgaon. The genotypes SPS 11 (3809 kg) followed by ICGV 05163 (3561 kg) and ICGV 06142 (3283 kg) recorded higher yield at Aliyarnagar whereas ICGV 03056 (4865 kg) followed by ICGV 03042 (4660 kg) and ICGV 03064 (4549 kg) recorded higher yield at Jalgaon. Among all the genotypes 49 M-16 (3765 kg) followed by ICGV 03064 (3484 kg) and ICGV 06142 (3478 kg) recorded higher pod yield per hectare at ICRISAT during rainy 2015 whereas CS 39 (4321 kg) followed by Faizpur 1-5 (3850 kg) and ICGV 07247 (3781 kg) reported higher yield per plant compared to other genotypes at ICRISAT post-rainy 2015-16. The mean performance of genotypes for pod yield per hectare during rainy and post-rainy season reported higher yield during the post-rainy season (disease free environment) compared to rainy season across the location (under disease pressure). However, an average of performance across the environments revealed that ICGV 07247 (3203 kg) followed by SPS 11(3130 kg), ICGV 03064 (3041 kg) and ICGV 06100 (2981 kg) reported higher pod yield per hectare across the environments (Table 4.18).

Haulm yield per plant (g)

Besides the important role of groundnut in the human diet, its fodder is an important component of feed for cattle. Foliar fungal diseases special rust and LLS are widely responsible for the reduction in fodder yield and quality across the growing regions. Hence, genotypes of GSP were evaluated for haulm yield per plant at ICRISAT Patancheru during rainy (diseased) and post-rainy season 2015-16 (disease free). High genetic variation in GSP was reported for haulm yield per plant in both the environments as revealed by high GCV and PCV coupled with moderate to high heritability and GAM. Haulm yield per plant in GSP varied from 7.1 to 29.3 g at ICRISAT during rainy 2015, from 5.1 to 40.6 g at ICRISAT during post-rainy 2015-16 and the average over environments was from 8.5 to 30.4 g. The average of environments over genotypes for haulm weight per plant was 16.1 and 19.4 g at ICRISAT during rainy and post-rainy seasons, respectively (Table 4.13). High GCV (21.27%) and PCV (28.30%) coupled with moderate heritability (56.49%) and high GAM (32.93%) was reported during rainy 2015 whereas high GCV (33.49%) and PCV (36.10%) with high heritability (86.07) and moderate GAM (19.41%) was reported during post-rainy season. Pooled analysis of haulm yield also revealed high GCV (21.89%) and PCV (28.90%) with moderate heritability (57.38%) and high GAM (34.16%) across the environments (Table 4.13). Mean performance for haulm yield per plant showed that genotypes recorded higher haulm yield during the post-rainy season (disease free) compared to the rainy season

Table 4.14 Performance of trait specific superior genotypes of Genomic Selection Panel across four environments for days to 50% flowering (DFF) and days to maturity (DM)

	Aliyarnagar		**Jalgaon**		**ICRISAT Rainy 15**		**ICRISAT Post-Rainy 15-16**		**Pooled**	
S. No.	**Genotypes**	**DFF**	**Genotypes**	**DFF**	**Genotypes**	**DFF**	**Genotypes**	**DFF**	**Genotypes**	**DFF**
1	ICGV 06431	26	ICGV 06049	25	ICGV 87378	23	ICGV 13241	34	ICGV 06431	29
2	ICGV 04149	26	49×39-21-2	25	ICGV 91116	24	ICGV 01005	35	ICGV 99181	29
3	TG LPS 4	26	SPS 9	25	ICG 14985	24	ICGV 93470	36	ICGV 06049	29
4	ICG 10701	26	ICGV 04149	25	ICGV 99181	24	DTG 15	36	ICGV 91116	29
5	ICG 14985	26	TG 49	26	ICG 15415	25	ICGV 07148	37	ICGV 04149	29
6	ICGV 87378	26	ICGV 91116	26	Gangapuri	25	27×49- 12	37	26×M-95-1 RI	29
7	ICG 4543	26	SPS 3	26	ICGV 99083	25	26×M-95-1 RI	37	DTG 15	29
8	SPS 6	26	TKG 19A	26	ICGV 88145	25	ICGV 06431	37	TAG 24	29
9	ICGV 13242	26	ICG 5221	26	26×M-223-1	25	TMV 2 NLM	37	ICG 3102	29
10	ICGV 07210	27	24×39-31 MR	26	J 11	25	TAG 24	37	ICGV 02189	29
Population mean		**30**		**30**		**29**		**42**		**33**
CV%		**3.4**		**6.09**		**5.4**		**3.5**		**4.6**
LSD at 5 %		**1.7**		**3.05**		**4.2**		**2.4**		**2.1**

S. No.	**Genotypes**	**DM**	**Genotypes**	**DM**	**Genotypes**	**DM**	**Genotypes**	**DM**	**Genotypes**	**DM**
1	ICGV 05155	101	39×49-81-1	107	26×M-223-1	94	ICGV 92195	121	ICGV 92195	107.4
2	M 28-2	101	TMV 2	108	ICGV 87354	96	ICGV 91116	121	26×M-95-1 RI	107.8
3	ICGV 95469	102	26×M-95-1 RI	108	ICGV 86699	97	26×M-95-1 RI	122	39×49-81-1	108.8
4	ICGV 13242	102	26×M-223-1	109	CSMG 84-1	97	ICGV 93437	122	ICGV 13242	109.0
5	26× 27-164	102	ICGV 86699	109	ICGV 13242	97	SPS 1	123	ICG 2031	110.5
6	ICGV 92195	102	ICGV 92195	110	39× 49-81-1	97	ICG 2031	123	ICGV 86011	111.0
7	ICGV 06424	102	ICGV 87354	110	26×M-95-1 RI	97	JL 24	123	49×39-74	111.0
8	ICGV 07217	102	ICGV 06424	111	ICGV 92195	97	ICGV 00321	124	ICGV 93470	111.1
9	ICG 532	102	ICGV 13242	111	ICG 3421	97	ICGV 06431	124	ICGV 02266	111.4
10	ICG 3421	102	CSMG 84-1	111	ICGV 13245	98	ICGV 07273	124	ICGV 02125	111.4
Population mean		**108.2**		**122.2**		**109.3**		**142.0**		**120.4**
CV%		**1.6**		**1.1**		**1.9**		**1.3**		**1.5**
LSD at 5 %		**2.9**		**2.2**		**3.4**		**3.1**		**2.5**

Table 4.15 Performance of trait specific superior genotypes of Genomic Selection Panel across four environments for number of primary branches (NPB) and plant height (PH)

	Aliyarnagar		Jalgaon		ICRISAT Rainy 15		ICRISAT Post-Rainy 15-16		Pooled	
S. No.	**Genotypes**	**NPB**	**Genotypes**	**NPB**	**Genotypes**	**NPB**	**Genotypes**	**NPB**	**Genotypes**	**NPB**
1	ICGV 09112	8	ICGV 05141	10	49 M-2-2	10	ICGV 07246	10	49 M-2-2	8.3
2	ICGV 07247	7	ICGV 07246	9	ICGV 07247	9	ICGV 06423	9	ICGV 07246	7.8
3	ICGV 03398	7	ICGV 07247	9	ICGV 07235	9	ICGV 07223	9	ICGV 01361	7.7
4	ICGV 03064	7	ICGV 99052	9	ICG 532	9	ICGV 07120	9	ICGV 07247	7.7
5	ICGV 06422	7	ICGV 01361	9	ICGV 03397	8	ICGV 04124	9	ICGV 07235	7.6
6	ICGV 07227	7	ICGV 04087	9	ICGV 07227	8	ICGV 97128	9	ICGV 07227	7.5
7	DH 86	7	ICGV 97128	9	ICGV 02321	8	ICGV 01495	9	ICGV 05057	7.4
8	ICGV 00346	7	ICGV 01265	9	ICGV 87187	8	49 M-2-2	9	ICGV 09112	7.4
9	ICGV 01495	7	ICGV 02323	9	ICGV 01478	8	ICGS 76	9	SPS 2	7.3
10	ICGV 98432	7	ICGV 00440	9	ICGV 03136	8	ICG 14466	9	SPS 7	7.3
Population mean		**5.0**		**6.0**		**6.0**		**6.0**		**5.6**
CV%		**10.6**		**8.0**		**6.9**		**7.2**		**7.2**
LSD at 5 %		**0.9**		**0.8**		**0.1**		**0.1**		**0.1**

S. No.	**Genotypes**	**PH (cm)**	**Genotypes**	**PH (cm)**	**Genotypes**	**PH (cm)**	**Genotypes**	**PH (cm)**	**Genotypes**	**PH (cm)**
1	ICG 15419	67.3	ICGV 03184	71.5	ICG 15419	59.7	27×49- 16	37.9	ICG 15419	56.2
2	ICG 6022	58.9	ICG 6022	69.7	ICG 6646	58.1	ICG 6646	37.7	ICG 6022	53.6
3	ICGV 01005	54.8	27×49- 16	66.5	ICG 8751	57.0	ICGV 02266	37.6	ICG 6646	49.8
4	ICGV 88145	54.0	ICG 15419	64.4	ICG 6022	56.9	ICGV 86011	37.6	ICGV 03184	49.1
5	ICG 8751	53.5	SPS 3	64.1	ICG 5221	50.8	TKG 19A	36.1	ICG 8751	47.1
6	ICG 6646	53.0	ICGV 04018	61.0	ICGV 00246	50.1	ICGV 07359	35.9	27×49- 16	46.7
7	ICG 12672	51.9	ICGV 96468	59.6	ICGV 99052	48.6	ICG 4955	35.3	ICGV 88145	45.8
8	ICGV 03184	49.9	ICG 3746	59.2	ICGV 01005	47.3	ICGV 87378	34.9	ICGV 01005	45.7
9	Somnath	49.7	TPG 41	59.1	BAU 13	47.1	ICG 15419	34.5	ICGV 04018	44.3
10	ICG 4955	49.2	ICGV 97165	58.2	ICG 12276	46.4	ICGV 00321	33.3	ICGV 91116	43.7
Population mean		**36.7**		**42.8**		**35.4**		**22.1**		**34.2**
CV%		**5.5**		**7.5**		**6.6**		**7.6**		**7.0**
LSD at 5 %		**3.3**		**5.3**		**8.7**		**2.8**		**3.3**

Table 4.16 Performance of trait specific superior genotypes of Genomic Selection Panel across four environments for number of pods per plant (NPP) and pod yield per plant (PYPP)

	Aliyarnagar		Jalgaon		ICRISAT Rainy 15		ICRISAT Post-Rainy 15-16		Pooled	
S. No.	**Genotypes**	**NPP**	**Genotypes**	**NPP**	**Genotypes**	**NPP**	**Genotypes**	**NPP**	**Genotypes**	**NPP**
1	ICGV 99051	35	ICGV 07247	35	49 M-16	29	ICGV 07247	24	ICGV 07247	25.4
2	49×39-21-2(a)	34	49×39-74	32	27×49- 12	28	ICGV 07246	22	ICGV 01276	24.5
3	ICGV 02323	30	ICGV 05163	32	SPS 11	28	49 M-16	22	49 M-16	23.2
4	ICGV 03128	30	ICGV 95070	31	ICGV 02286	27	ICGV 01276	21	49×39-21-2(a)	22.5
5	SPS 11	30	ICGV 07223	30	39× 49-81-1	26	CS 39	21	SPS 11	22.3
6	ICGV 04087	29	ICGV 00005	29	ICGV 01276	26	ICGV 07217	21	49×39-74	22.2
7	ICGV 01276	28	ICGV 02323	29	ICGV 99085	25	ICGV 07223	20	ICGV 02323	22.0
8	ICGV 03207	28	ICGV 00350	29	ICGV 03056	24	Faizpur 1-5	19	ICGV 05163	21.6
9	ICGV 06142	27	ICGV 06142	28	49×27-37	24	ICGV 03128	19	ICGV 01273	21.2
10	ICGV 07166	27	ICGV 06420	28	ICGV 06424	23	ICGV 00387	19	ICGV 06422	21.1
Population mean		**15**		**16**		**14**		**10**		**13.8**
CV%		**18.2**		**17.9**		**23.4**		**20.0**		**19.1**
LSD at 5 %		**4.4**		**4.6**		**5.6**		**3.4**		**3.9**

S. No.	Genotypes	PYPP (g)	Genotypes	PYPP (g)	Genotypes	PYPP (g)	Genotypes	PYPP (g)	Genotypes	PYPP (g)
1	ICGV 05198	29.0	ICGV 05163	24.0	ICGV 06142	21.1	CS 39	19.9	ICGV 07247	17.3
2	ICGV 99051	25.9	ICGV 03064	23.8	ICGV 02411	21.0	ICGV 07247	17.0	ICGV 01276	17.3
3	ICGV 01478	23.8	ICGV 02323	21.2	49 M-16	20.3	Faizpur 1-5	14.9	ICGV 05163	16.8
4	ICGV 03128	22.9	ICGV 07247	21.0	SPS 11	20.3	ICGV 03128	14.3	ICGV 02323	16.3
5	49×39-21-2(a)	22.1	ICGV 06100	20.8	ICGV 02286	19.9	ICGV 01495	14.2	SPS 11	16.3
6	SPS 11	21.8	ICGV 06099	20.8	ICGV 05141	19.9	ICGV 06234	14.2	ICGV 06099	16.2
7	ICGV 01263	21.5	ICGV 07223	20.5	ICGV 03064	19.8	ICGV 01276	13.7	ICGV 06100	16.2
8	ICGV 06099	21.4	ICGV 01274	20.2	ICGV 01276	19.7	ICGV 07166	13.2	ICGV 01495	16.2
9	ICGV 03207	21.3	ICGV 05036	19.9	ICGV 05057	19.6	ICG 11651	12.2	ICGV 06142	15.2
10	ICGV 98432	20.6	ICGV 94169	19.6	ICGV 03043	19.2	DTG 15	11.9	ICGV 03128	14.8
Population mean		**15.0**		**10.5**		**10.2**		**6.6**		**9.6**
CV%		**19.3**		**20.1**		**22.7**		**20.6**		**17.0**
LSD at 5 %		**3.5**		**3.4**		**3.8**		**2.2**		**2.8**

Table 4.17 Performance of trait specific superior genotypes of Genomic Selection Panel across four environments for seed yield per plant (SYPP) and shelling percent (SH%)

	Aliyarnagar		Jalgaon		ICRISAT Rainy 15		ICRISAT Post-Rainy 15-16		Pooled	
S. No.	**Genotypes**	**SYPP (g)**	**Genotypes**	**SYPP (g)**	**Genotypes**	**SYPP (g)**	**Genotypes**	**SYPP (g)**	**Genotypes**	**SYPP (g)**
1	ICGV 05198	17.2	ICGV 06099	14.0	ICGV 02286	13.5	CS 39	11.6	ICGV 07247	11.2
2	ICGV 99051	14.6	ICGV 05163	13.9	ICGV 02411	13.3	ICGV 07247	11.6	ICGV 01276	10.6
3	ICGV 01478	14.6	DH 86	13.2	49 M-16	12.9	ICGV 03128	9.1	ICGV 02323	10.5
4	ICGV 02323	14.6	ICGV 07247	13.2	SPS 11	12.7	ICGV 06234	8.2	ICGV 06099	10.3
5	ICGV 03207	13.9	ICGV 07223	13.0	ICGV 05141	12.7	ICGV 07217	8.0	SPS 11	10.0
6	ICGV 01276	13.6	ICGV 03064	12.9	ICGV 01276	12.1	ICGV 01495	8.0	ICGV 05163	9.7
7	ICGV 03128	13.5	ICGV 94169	12.6	ICGV 06142	11.8	ICG 4955	7.8	ICGV 01495	9.7
8	SPS 11	13.4	ICGV 01274	12.5	ICGV 05057	11.7	ICGV 06099	7.7	ICGV 03128	9.4
9	ICGV 06099	13.2	ICGV 06100	12.2	ICGV 03043	11.5	ICGV 06431	7.7	ICGV 06100	9.3
10	49×39-21-2(a)	13.1	ICGV 02323	11.9	ICGV 97128	11.4	Faizpur 1-5	7.7	ICGV 06142	9.0
Population mean		**6.6**		**6.1**		**5.9**		**4.0**		**5.6**
CV%		**20.2**		**21.9**		**27.2**		**22.1**		**18.3**
LSD at 5 %		**2.2**		**2.2**		**2.6**		**1.4**		**1.8**

S. No.	**Genotypes**	**SH%**	**Genotypes**	**SH%**	**Genotypes**	**SH%**	**Genotypes**	**SH%**	**Genotypes**	**SH%**
1	ICG 156	71.3	ICGV 02038	70.2	ICGV 97262	71.2	49×39-74	75.5	ICGV 95469	69.5
2	BAU 13	70.8	ICGV 07268	69.1	ICGV 03128	69.4	ICG 3584	73.3	ICGV 07268	68.2
3	ICG 3312	70.6	SPS 7	68.9	ICGV 87187	69.4	ICG 2106	73.2	ICGV 02038	67.9
4	ICGV 95469	70.6	ICGV 04018	68.8	26 M- 119-1	69.3	ICGV 03184	72.7	ICGV 95290	67.8
5	ICG 3746	70.5	ICG 12991	68.6	ICGV 07210	68.9	26× 27-164	72.3	ICG 2106	67.7
6	DH 86	70.4	ICGV 91116	67.9	ICGV 95469	68.7	JL 24	72.1	26×27-164	67.1
7	ICGV 02323	70.4	ICGV 02286	67.7	ICGV 95290	67.7	ICGV 97261	71.7	ICGV 03184	67.0
8	ICGV 02290	70.2	ICGV 95469	67.6	ICGV 97261	67.6	ICGV 02038	71.6	ICG 4955	66.9
9	ICG 2031	69.7	49 M- 1-1	67.4	ICGV 07217	67.4	ICG 3746	71.2	ICGV 03128	66.7
10	ICG 2106	69.6	ICGV 95290	67.3	ICG 4527	67.2	ICGV 95377	71.1	26 M- 119-1	66.6
Population mean		**60.7**		**58.1**		**57.5**		**59.4**		**58.9**
CV%		**4.4**		**3.9**		**8.4**		**4.4**		**5.5**
LSD at 5 %		**4.4**		**3.7**		**8.0**		**4.3**		**4.5**

Table 4.18 Performance of trait specific superior genotypes of Genomic Selection Panel across four environments for hundred seed weight (HSW) and pod yield per hectare (PYH)

	Aliyarnagar		**Jalgaon**		**ICRISAT Rainy 15**		**ICRISAT Post-Rainy 15-16**		**Pooled**	
S. No.	**Genotypes**	**HSW (g)**	**Genotypes**	**HSW (g)**	**Genotypes**	**HSW (g)**	**Genotypes**	**HSW (g)**	**Genotypes**	**HSW (g)**
1	ICGV 00440	66.2	ICGV 06234	55.2	ICGV 05198	59.0	ICGV 06234	58.6	ICGV 05198	52.4
2	ICGV 05198	61.2	49 M- 1-1	54.3	27× 49- 27-1	55.6	ICGV 01478	58.5	TG 42	52.1
3	49×37-97-1	61.1	49×37- 99(b) tall	54.1	TG 42	54.0	ICGV 06188	56.5	ICGV 06188	51.5
4	ICGV 01393	57.7	TG 42	51.9	ICGV 06188	52.0	ICGV 86564	53.5	ICGV 00440	51.0
5	TG 41	57.4	ICGV 06110	51.8	ICGV 07368	51.8	ICGV 00351	53.1	ICGV 05176	49.9
6	49×37- 99(b) tall	57.1	TG LPS 3	51.6	TPG 41	50.8	ICGV 07359	52.7	TG 41	49.7
7	TPG 41	56.8	TG 41	51.3	ICGV 03136	50.1	ICGV 97120	51.9	49×37-97-1	49.2
8	TG 42	56.3	ICGV 06188	50.0	TG 41	50.0	ICGV 05176	51.6	ICGV 06234	48.8
9	BAU 13	53.8	ICGV 05176	48.6	39×49 -8	49.9	ICGV 07368	51.1	ICGV 07368	48.7
10	ICGV 97045	53.7	BAU 13	48.6	ICGV 00440	49.4	ICGV 03136	51.1	ICGV 01478	48.0
Population mean		**32.6**		**33.7**		**32.4**		**33.8**		**33.1**
CV%		**6.2**		**7.2**		**10.8**		**6.3**		**7.8**
LSD at 5 %		**3.3**		**4.0**		**5.7**		**3.5**		**3.6**

S. No.	**Genotypes**	**PYH (kg)**	**Genotypes**	**PYH (kg)**	**Genotypes**	**PYH (kg)**	**Genotypes**	**PYH (kg)**	**Genotypes**	**PYH (kg)**
1	SPS 11	3809.3	ICGV 03056	4864.5	49 M-16	3764.5	CS 39	4321.2	ICGV 07247	3202.9
2	ICGV 05163	3560.6	ICGV 03042	4660.2	ICGV 03064	3484.0	Faizpur 1-5	3849.6	SPS 11	3129.5
3	ICGV 06142	3283.4	ICGV 03064	4549.0	ICGV 06142	3477.8	ICGV 07247	3780.9	ICGV 03064	3040.7
4	ICGV 06100	3269.2	ICGV 06420	4032.1	SPS 11	3418.1	ICGV 06234	3673.5	ICGV 06100	2981.1
5	ICGV 07246	3117.2	ICGV 01274	3982.1	ICGV 06100	3360.5	ICGV 01495	3655.5	ICGV 05163	2978.0
6	ICGV 00321	3108.6	ICGV 03128	3718.8	ICGV 05155	3257.3	ICGV 01276	3646.6	ICGV 05155	2952.5
7	DH 86	3063.7	ICGV 05155	3610.4	ICGV 05161	3149.8	ICGV 03128	3636.5	ICGV 01276	2923.8
8	ICG 2381	3049.9	ICGV 07247	3547.9	ICGV 05163	3142.3	ICGV 07166	3527.8	ICGV 03056	2898.6
9	ICGV 01478	3033.0	ICGV 00005	3546.3	ICGV 02321	3059.3	ICG 11651	3298.0	ICGV 07246	2827.2
10	ICGV 05198	3032.4	SPS 11	3528.5	ICGV 02411	3058.4	ICGV 97058	3073.7	ICGV 01495	2821.5
Population mean		**1396.8**		**1592.3**		**1569.0**		**1641.4**		**1549.9**
CV%		**23.3**		**21.58**		**18.1**		**22.6**		**19.5**
LSD at 5 %		**536.0**		**566.0**		**467.9**		**612.5**		**461.1**

(diseased environment). Genotype SPS 1 (29.3g) followed by ICG 14482 (28.4g) and SPS 21(28.2g) recorded higher haulm yield at ICRISAT during rainy 2015 whereas genotypes ICGV 86564 (40.5g) followed by ICGV’s 02290 (36.0g), 01273 (35.9g) and ICGV 05036 (35.9g) reported higher haulm yield during post-rainy season at ICRISAT. Pooled performance of genotypes reported ICGV 01464 (30.4g) followed by ICG 14475 (29.0g) and ICGV 86564 (28.5g) with higher haulm yield across the environments (Table 4.23).

4.2.3 Nutritional quality traits

Genotypes with higher nutritional value and quality in groundnut are in great demand, therefore, improving nutritional quality is now one of focused breeding objective of groundnut improvement. All the genotypes were evaluated for oil and protein content along with four major fatty acids through near infrared reflectance spectroscopy (NIRS). The mean, range and genetic parameters for nutritional quality traits are presented in Table 4.19. The range of performance of genotypes for all the nutritional quality traits was high but GCV and PCV were low for all the quality traits coupled with moderate to high heritability and low GAM at the individual as well as across the environments.

Oil content (%)

Narrow genetic variability in GSP observed for oil content with low GCV and PCV along with moderate to high heritability and low GAM across the environments. Oil content was varied from 45.0 to 64.2% at Aliyarnagar, from 46.1 to 64.9% at Jalgaon, from 38.2 to 59.9% at ICRISAT rainy 2015, from 42.0 to 60.6% at ICRISAT post-rainy 2015-16 and the average over environments was varied from 44.6 to 59.2%. The average of environments over genotypes was 53.5% at Aliyarnagar, 53.7% at Jalgaon, 48.5% and 49.1% at ICRISAT rainy and post-rainy seasons, respectively (Table 4.19). Very low GCV (2.51%) and PCV (3.38%) with moderate heritability (54.93%) and low GAM (3.83%) were reported for oil content at Aliyarnagar. The similar trend of low GCV (2.50 & 3.25%) and PCV (3.18 & 3.65%) coupled with high heritability (61.70 & 79.37%) and low GAM (4.04 & 5.97%) was observed at Jalgaon and ICRISAT rainy 2015, respectively whereas low GCV (2.29%) and PCV (3.02%) coupled with moderate heritability (57.43%) and very low GAM (3.58%) was observed for oil content at ICRISAT post-rainy 2015-16 (Table 4.19). The genotypes ICG 14482 (64.2%) followed by ICG 12625 (63.5%) and ICGV 99085 (62.7%) were the best genotypes had higher oil content compared to other genotypes at Aliyarnagar whereas genotypes ICGV 06420 (64.9%) followed by ICGV 99085 (62.5%) and ICGV 05155 (62.0%) recorded higher oil content at Jalgaon. Genotypes ICG 15419 (59.9%) followed by ICG 2381 (29.3%) and ICG 5221 (58.8%) reported higher oil content compared to other at ICRISAT during rainy season 2015 whereas ICG 2381 (60.6%) followed by ICGV 97045 (57.9%) and ICG 14475 (56.4%) were the best genotypes for oil content at ICRISAT during post-rainy season 2015-16. Pooled analysis of genotypes for oil content across the environments also revealed low values of GCV and PCV (2.39 & 2.67%) with high heritability (79.78%) and low GAM (4.39%). The average performance of genotypes across the environments revealed that genotypes ICG 15419 (59.18%) followed by ICG 2381 (58.97%), ICG 5221 (58.61%) and ICG 14482 (58.50%) reported high oil content across the environments (Table 4.20).

Protein content (%)

Narrow genetic variation in GSP was observed for protein content with low GCV, PCV coupled with moderate heritability and low GAM under different environments. Protein content in GSP varied from 13.5 to 28.4% at Aliyarnagar, from 13.2 to 27.8% at Jalgaon, from 19.2 to 29.8% at ICRISAT rainy 2015 and from 19.6 to 34.6% at ICRISAT post-rainy 2015-16. The average of environment over the genotypes was 20.2% at Aliyarnagar, 19.6% at Jalgaon, 24.1 and 26.7% at ICRISAT rainy and post-rainy seasons, respectively (Table 4.19). Low GCV (4.20%) and PCV (6.60%) with moderate heritability (40.55%) and low GAM (5.51%) were reported for protein content at Aliyarnagar. The similar trend of low GCV (2.65 & 3.08%) and PCV (4.37 & 4.85%) coupled with moderate heritability (36.84 & 40.33%) and low GAM (3.32 & 4.03%) was observed at ICRISAT rainy 2015 and ICRISAT post-rainy 2015-16, respectively whereas low GCV (3.38%) and PCV (6.27%) coupled with low heritability (29.04%) and low GAM (3.75%) was reported for protein content at Jalgaon. Protein content in different genotypes was observed high during the post-rainy season compared to rainy season across the environments. Genotypes ICGV 02038 (28.4%) followed by DTG LPS 3 (27.2%) and Faizpur 1-5 (26.7%) reported higher protein content at Aliyarnagar whereas ICGV 05198 (27.8%), 00321 and 02038 (25.1%) were the best genotypes for protein content at Jalgaon. ICG 14985 (29.8%) followed by ICGV 00362 (28.4%) and ICGV 05176 (28.0%) recorded higher protein content at ICRISAT during rainy 2015 whereas Faizpur 1-5 followed by ICG 2857 (34.1%) and ICGV 02038 (33.3%) reported higher protein content at ICRISAT during post-rainy season 2015-16. Pooled analysis of genotypes for protein content across the environments also revealed a similar trend of low GCV and PCV (2.98 & 3.71%) with high heritability (64.42%) and low GAM (4.93%). Pooled performance of genotypes showed that genotypes Faizpur 1-5 (27.7%) followed by ICGV 02038 (27.4%), ICGV 00321 (26.7%) and ICG 9507 (26.4%) reported higher protein content across the environments (Table 4.20).

Oleic acid (%)

Narrow genetic variation in GSP was observed for oleic acid content with low GCV, PCV coupled with moderate to high heritability and low GAM under different environments. Oleic acid in GSP varied from 29.4 to 74.4% at Aliyarnagar, from 21.3 to 80.5% at Jalgaon, from 31.4 to 76.0% at ICRISAT rainy 2015, from 30.3 to 76.1% at ICRISAT post-rainy 2015-16 and the average over environments from 31.2 to 78.8%. The average of environments over genotypes was 42.1% Aliyarnagar, 38.9% at Jalgaon, 42.9 and 43.9% at ICRISAT rainy and post-rainy seasons, respectively (Table 4.19). The wider range of oleic acid in GSP is due to a high oleic genotype SunOleic 95R which recorded >74% oleic acid across the environments. The range of oleic acid in GSP without SunOleic 95R became narrow from 29.4 to 60.3% at Aliyarnagar, from 21.3 to 56.9% at Jalgaon, from 31.4 to 62.4% at ICRISAT rainy 2015, from 30.3 to 58.5% at ICRISAT post-rainy 2015-16 and the average over environments from 31.2 to 57.4% indicating narrow genetic variability for this trait. Low GCV (5.80, 6.83, 6.02 & 4.91%) and PCV (7.19, 8.19, 6.66 & 6.41%) with high heritability (65.11, 69.51, 81.61 & 58.61%) and low GAM (9.64, 11.73, 11.19 & 7.74%) were reported for oleic acid content at Aliyarnagar, Jalgaon,

Table 4.19 Mean, range and genetic parameters for nutritional quality traits of Genomic Selection Panel of groundnut evaluated across the environments

Traits	Mean	Range#		GCV (%)	PCV (%)	h^2_{bs} (%)	GAM (%)
		Min	Max				
Aliyarnagar							
Oil content (%)	53.47	44.99	64.22	2.51	3.38	54.93	3.83
Protein content (%)	20.21	13.54	28.44	4.20	6.60	40.55	5.51
Oleic acid (%)	42.06	29.38	74.38	5.80	7.19	65.11	9.64
Linoleic acid (%)	39.68	5.30	51.25	5.22	6.49	64.56	8.63
Palmitic acid (%)	11.66	7.50	14.88	4.07	4.91	68.66	6.94
Stearic acid (%)	2.19	0.68	3.61	9.11	11.89	58.61	14.36
O/L ratio	1.13	0.58	14.03	16.28	19.72	68.15	27.69
Jalgaon							
Oil content (%)	53.66	46.05	64.88	2.50	3.18	61.70	4.04
Protein content (%)	19.64	13.23	27.81	3.38	6.27	29.04	3.75
Oleic acid (%)	38.89	21.33	80.47	6.83	8.19	69.51	11.73
Linoleic acid (%)	42.23	7.32	57.22	5.25	6.43	66.56	8.82
Palmitic acid (%)	11.93	6.49	14.48	4.43	5.24	71.42	7.71
Stearic acid (%)	2.10	0.27	3.88	10.48	14.00	56.10	16.18
O/L ratio	0.99	0.37	15.71	18.33	21.92	69.97	31.59
ICRISAT rainy 2015							
Oil content (%)	48.51	38.17	59.88	3.25	3.65	79.37	5.97
Protein content (%)	24.09	19.23	29.81	2.65	4.37	36.84	3.32
Oleic acid (%)	42.90	31.39	76.03	6.02	6.66	81.61	11.19
Linoleic acid (%)	36.13	6.12	46.91	5.97	6.64	80.94	11.07
Palmitic acid (%)	11.71	7.89	14.67	4.16	4.73	77.35	7.53
Stearic acid (%)	1.65	0.20	3.92	28.24	30.98	83.14	53.05
O/L ratio	1.26	0.68	12.76	16.49	19.49	71.57	28.73
ICRISAT post-rainy 2015-16							
Oil content (%)	49.05	41.96	60.63	2.29	3.02	57.43	3.58
Protein content (%)	26.74	19.57	34.57	3.08	4.85	40.33	4.03
Oleic acid (%)	43.87	30.32	76.06	4.91	6.41	58.61	7.74
Linoleic acid (%)	34.70	4.60	46.58	5.52	6.97	62.54	8.98
Palmitic acid (%)	12.50	7.08	15.09	3.66	4.45	67.82	6.21
Stearic acid (%)	2.33	0.75	4.79	7.97	10.69	55.53	12.23
O/L ratio	1.35	0.62	16.53	16.00	19.67	66.14	26.81
Pooled across the environments							
Oil content (%)	51.18	44.58	59.18	2.39	2.67	79.78	4.39
Protein content (%)	22.67	18.50	27.66	2.98	3.71	64.42	4.93
Oleic acid (%)	41.91	31.21	78.83	5.70	6.05	88.95	11.08
Linoleic acid (%)	38.21	5.61	47.60	5.28	5.60	88.61	10.23
Palmitic acid (%)	11.95	7.63	14.41	3.98	4.18	90.84	7.82
Stearic acid (%)	2.07	0.42	3.97	31.42	33.51	87.91	60.69
O/L ratio	1.17	0.66	14.09	10.17	11.25	81.68	18.94

Min= Minimum; Max= Maximum; GCV = Genotypic coefficient of variation (%); PCV= Phenotypic coefficient of variation (%); h^2_{bs} = Heritability in broad sense (%); GAM= Genetic advance as percent of mean (%); # = Nutritional quality traits were estimated by NIRS and could deviate by ±2.5.

ICRISAT rainy and post-rainy season, respectively. Pooled analysis of this trait also revealed a similar trend of low GCV (5.70%) and PCV (6.05%) with high heritability (88.95%) and moderate GAM (11.08%). Genotypes SunOleic 95R was the only genotype in GSP reported as high oleic (>70%) across the environments (Table 4.21).

Linoleic acid (%)

Narrow genetic variation in GSP for linoleic acid was observed with low GCV, PCV, GAM and high heritability at the individual as well as across the environments. Linoleic acid in GSP varied from 5.3 to 51.3% at Aliyarnagar, from 7.3 to 57.2% at Jalgaon, from 6.1 to 46.9% at ICRISAT rainy 2015, from 4.6 to 46.6% at ICRISAT post-rainy 2015-16 and the average over environments was from 5.6 to 47.6%. The average of environments over genotypes was 39.7% at Aliyarnagar, 42.2% at Jalgaon, 36.1 and 34.7% at ICRISAT rainy and post-rainy seasons, respectively (Table 4.19). SunOleic 95R was the only genotype recorded lowest linoleic acid (<6%) across the environments. The range of linoleic acid in GSP without SunOleic 95R varied from 24.1 to 51.3% at Aliyarnagar, from 26.7 to 57.2% at Jalgaon, from 23.3 to 46.9% at ICRISAT rainy 2015, from 21.8 to 46.6% at ICRISAT post-rainy 2015-16 and the average over environments was from 26.1 to 47.6%. Low GCV (5.22, 5.25, 5.97 & 5.52%) and PCV (6.49, 6.43, 6.64 & 6.97%) with high heritability (64.56, 66.56, 80.94 & 62.54%) and low GAM (8.63, 8.82, 11.07 & 8.98%) was reported for linoleic acid content at Aliyarnagar, Jalgaon, ICRISAT rainy 2015 and ICRISAT post-rainy 2015-16, respectively. Pooled analysis also revealed a similar trend of low GCV and PCV (5.28 & 5.60%) with high heritability (88.61%) and low GAM (10.23%) across the environments. The genotype SunOleic 95R recorded 5.3, 5.1, 6.1 & 4.6% linoleic acid at Aliyarnagar, Jalgaon, and ICRISAT rainy and post-rainy seasons, respectively (Table 4.22).

Palmitic acid (%)

There was significant difference among genotypes of GSP for palmitic acid observed under individual as well as across the environments but the magnitude of genetic variability for this trait was narrow as indicated by low GCV, PCV and GAM. Palmitic acid in GSP varied from 7.5 to 14.9% at Aliyarnagar, from 6.5 to 14.5% at Jalgaon, from 7.9 to 14.7% at ICRISAT rainy 2015, from 7.1 to 15.1% at ICRISAT post-rainy 2015-16 and the average over environments was from 7.6 to 14.4%. The average of environments over genotypes was 11.7% at Aliyarnagar, 11.9 at Jalgaon, 11.7 and 12.5 at ICRISAT rainy and post-rainy seasons, respectively (Table 4.19). Very low GCV (4.07, 4.43, 4.16 & 3.66%) and PCV (4.91, 5.24, 4.73 & 4.45%) with high heritability (68.66, 71.42, 77.35 & 67.82%) and low GAM (6.94, 7.71, 7.53 & 6.21%) was observed for palmitic acid content at Aliyarnagar, Jalgaon, ICRISAT rainy and post-rainy seasons, respectively. Pooled analysis also revealed a similar trend of low GCV and PCV (3.98 and 4.18%) with high heritability (90.84%) and low GAM (7.82%). Genotype ICG 15419 (7.5%) followed by ICG 5221 (7.7%) and ICG 6022 (8.1%) recorded lower palmitic acid compared to other genotypes at Aliyarnagar. Genotypes ICG 15419 followed by ICG 12625 (7.0%) and SunOleic 95R (8.5%) recorded lower palmitic acid compared to all other genotypes at Jalgaon. SunOleic 95R (7.9 & 7.08%) was recorded lowest palmitic acid at ICRISAT during rainy and post-rainy seasons followed by ICG 5221 and ICG 6022 (7.9%) during rainy season whereas ICG 2381 (8.2%) and ICG 6022 (8.5%) had low palmitic acid after SunOleic 95R during post-rainy season 2015-16. Pooled performance of genotypes across the environments showed that SunOleic 95R (7.6%) followed by ICG's 15419 (8.0%), 2381, 5221 and 6022 (8.3%) reported low palmitic acid across the environments (Table 4.22).

Stearic acid (%)

Genetic variability for stearic acid in GSP was high compared to other nutritional quality traits with moderate to high GCV and PCV coupled with moderate to high heritability and GAM under different environments. Stearic acid varied from 0.68 to 3.61% at Aliyarnagar, from 0.27 to 3.88% at Jalgaon, from 0.20 to 3.92% at ICRISAT rainy 2015, from 0.75 to 4.79% at ICRISAT post-rainy 2015-16 and the average of environments was from 0.42 to 3.97%. The average of environments over genotypes for stearic acid was from 2.18%

at Aliyarnagar, 2.10% at Jalgaon, 1.65 and 2.33% at ICRISAT rainy and post-rainy seasons, respectively (Table 4.19). Low GCV (9.11 & 7.97%) and moderate PCV (11.89 & 10.69%) with moderate heritability (58.61 & 55.53%) and GAM (14.36 & 12.23%) was reported for stearic acid content at Aliyarnagar and ICRISAT post-rainy 2015-16, respectively whereas moderate GCV (10.48%) and PCV (14.00%) coupled with moderate heritability (56.10%) and GAM (16.18%) was reported at Jalgaon. High GCV (28.24%) and PCV (30.98%) coupled with high heritability (83.14%) and high GAM (53.05%) were reported for stearic acid content at ICRISAT rainy 2015. A similar trend of high GCV and PCV (31.42 & 33.51%) with high heritability (87.91%) and GAM (60.69%) was reported in pooled analysis. The genotypes ICG 4955 (0.7, 0.3, 0.2 and 0.8%) reported lowest stearic acid at Aliyarnagar, Jalgaon, ICRISAT rainy and post-rainy seasons, respectively. The genotype ICG 4955 (0.4%) followed by ICG 3673 (1.0%), ICG 442 (1.0%), ICG 12672 (1.1%) and DTG 3 (1.1%) were also reported with low stearic acid across the environments (Table 4.23).

Oleic acid / Linoleic acid (O/L Ratio)

There was moderate variability reported for O/L ratio in GSP with moderate GCV and PCV with high heritability and GAM. It varied from 0.58 to 14.03 at Aliyarnagar, from 0.37 to 15.71 at Jalgaon, from 0.68 to 12.76 at ICRISAT rainy 2015, from 0.62 to 16.53 at ICRISAT during the post-rainy season and the average over environments was from 0.66 to 14.09. The average of environments over genotypes for linoleic acid was 1.13 at Aliyarnagar, 0.99 at Jalgaon, 1.26 and 1.35 at ICRISAT rainy and post-rainy seasons, respectively (Table 4.19). The wider range of O/L ratio in GSP was due to SunOleic 95R as it was recorded highest O/L ratio at Aliyarnagar (14.13), Jalgaon (15.71), ICRISAT rainy (12.76) and post-rainy (16.53) (Table 4.21). The O/L ratio in GSP without SunOleic 95R varied from 0.58 to 2.52 at Aliyarnagar, from 0.37 to 2.14 at Jalgaon, from 0.68 to 2.76 at ICRISAT rainy 2015, from 0.62 to 2.58 at ICRISAT during the post-rainy season and the average over environments was from 0.66 to 2.13. Moderate GCV (16.28, 18.33, 16.49 & 16.00%) and moderate to high PCV (19.72, 21.92, 19.49 &

Table 4.20 Performance of trait specific superior genotypes of Genomic Selection Panel across four environments for oil content (OC%) and protein content (PC%)

	Aliyarnagar		Jalgaon		ICRISAT Rainy 15		ICRISAT Post-Rainy 15-16		Pooled	
S. No.	**Genotypes**	**OC%**	**Genotypes**	**OC%**	**Genotypes**	**OC%**	**Genotypes**	**OC%**	**Genotypes**	**OC%**
1	ICG 14482	64.2	ICGV 06420	64.8	ICG 15419	59.9	ICG 2381	60.6	ICG 15419	59.2
2	ICG 12625	63.5	ICGV 99085	62.5	ICG 2381	59.3	ICGV 97045	57.9	ICG 2381	58.9
3	ICGV 99085	62.6	ICGV 05155	62.0	ICG 5221	58.8	ICG 14475	56.4	ICG 5221	58.6
4	ICG 6022	62.6	GPBD 4	62.0	ICGV 99085	57.9	ICG 12625	55.9	ICG 14482	58.5
5	ICG 15419	62.1	ICGV 00248	61.5	ICG 6022	57.6	ICG 14482	55.3	ICG 12625	58.3
6	ICG 14475	61.5	ICG 2381	61.3	GPBD 4	57.1	ICGV 05155	55.2	ICG 6022	58.3
7	ICGV 97128	60.9	ICG 5221	61.0	ICGV 00248	55.8	SPS 21	54.9	ICGV 99085	57.9
8	MN1-35	60.7	49 M-16	60.8	ICG 12625	55.6	ICG 15419	54.9	GPBD 4	57.8
9	ICG 12509	60.6	ICGV 00246	60.5	ICGV 06420	55.6	ICG 5221	54.5	ICGV 05155	57.6
10	SPS 21	60.6	ICGV 03042	60.3	SPS 9	55.3	ICG 3673	54.2	ICGV 97128	57.0
Population mean		**53.5**		**53.7**		**48.5**		**49.1**		**51.1**
CV%		**4.5**		**3.9**		**3.3**		**4.0**		**1.9**
LSD at 5 %		**4.0**		**3.5**		**2.6**		**3.2**		**2.8**

S. No.	**Genotypes**	**PC%**	**Genotypes**	**PC%**	**Genotypes**	**PC%**	**Genotypes**	**PC%**	**Genotypes**	**PC%**
1	ICGV 02038	28.4	ICGV 05198	27.8	ICG 14985	29.8	Faizpur 1-5	34.5	Faizpur 1-5	27.6
2	TG LPS 3	27.2	ICGV 02038	25.1	ICGV 00362	28.4	ICG 2857	34.0	ICGV 02038	27.3
3	Faizpur 1-5	26.6	ICGV 00321	25.1	ICGV 05176	28.0	ICGV 02038	33.2	TMV 2	26.9
4	ICGV 01276	25.5	ICGV 02271	24.7	ICGV 06142	28.0	ICGV 95290	33.0	ICGV 00321	26.6
5	ICGV 04018	25.3	ICG 9507	24.7	ICGV 06234	27.9	ICGV 97262	32.1	ICG 9507	26.4
6	ICR 48	24.6	ICGV 02144	24.6	ICGV 03398	27.9	ICGV 99195	31.5	ICGV 03398	26.3
7	ICGV 97182	24.6	26×M-223-1	24.6	ICGV 98294	27.6	ICGV 01005	31.1	ICGV 05176	26.2
8	27×49- 16	24.4	ICGV 05176	24.3	ICGV 98432	27.5	ICGV 00321	31.0	ICGV 06110	26.2
9	ICGV 98294	24.3	ICGV 03398	23.9	ICG 9507	27.5	ICGV 06188	30.9	ICGV 98294	25.9
10	ICGV 06110	24.2	ICGV 02022	23.7	DH 86	27.3	ICGV 07148	30.9	ICGV 95290	25.6
Population mean		**20.2**		**19.6**		**24.1**		**26.7**		**22.6**
CV%		**10.1**		**10.5**		**6.9**		**7.4**		**4.4**
LSD at 5 %		**3.3**		**3.4**		**3.4**		**3.3**		**2.7**

Table 4.21 Performance of trait specific superior genotypes of Genomic Selection Panel across four environments for oleic acid content (OA%) and oleic/linoleic acid ratio (O/L)

	Aliyarnagar		Jalgaon		ICRISAT Rainy 15		ICRISAT Post-Rainy 15-16		Pooled	
S. No.	**Genotypes**	**OA%**	**Genotypes**	**OA%**	**Genotypes**	**OA%**	**Genotypes**	**OA%**	**Genotypes**	**OA%**
1	SunOleic 95R	74.4	SunOleic 95R	80.4	SunOleic 95R	76.0	SunOleic 95R	76.0	SunOleic 95R	78.8
2	ICG 12276	60.3	ICG 14482	56.9	ICG 14482	62.4	ICGV 86699	58.4	ICG 14482	57.4
3	ICG 12509	58.5	ICG 12276	55.8	ICG 14475	59.2	ICG 11337	57.1	ICG 14475	54.2
4	ICG 14482	57.4	ICGV 97120	53.7	ICG 12625	57.2	ICG 6022	56.2	ICGV 97120	54.1
5	ICGV 97120	53.8	ICG 14475	53.1	ICG 12276	55.3	SPS 15	56.1	ICG 12276	53.7
6	24×37-2275	53.2	ICG 11426	51.9	ICG 6022	53.2	SPS 20	55.7	ICG 11426	52.4
7	ICGV 99085	52.8	ICGV 86143	50.2	ICG 11088	53.1	ICGV 97120	55.5	SPS 20	51.9
8	49 ×39-8	52.7	ICG 4955	49.6	ICG 12509	52.6	SPS 2	55.1	ICG 11337	51.6
9	ICG 11426	52.6	49 ×39-74	49.4	ICGV 97120	52.3	ICG 5221	54.8	ICG 6022	51.1
10	SPS 20	52.6	24 ×37-2275	49.2	ICGV 01328	52.2	ICGV 01124	54.6	ICG 12625	51.0
Population mean		**42.0**		**38.9**		**42.9**		**43.9**		**41.9**
CV%		**8.4**		**9.0**		**5.7**		**8.2**		**4.0**
LSD at 5 %		**5.8**		**5.8**		**4.0**		**5.9**		**4.6**

S. No.	**Genotypes**	**O/L**	**Genotypes**	**O/L**	**Genotypes**	**O/L**	**Genotypes**	**O/L**	**Genotypes**	**O/L**
1	SunOleic 95R	14.0	SunOleic 95R	15.7	SunOleic 95R	12.7	SunOleic 95R	16.5	SunOleic 95R	10.1
2	ICG 12276	2.5	ICG 12276	2.1	ICG 14482	2.7	ICGV 97045	2.5	ICG 12276	2.1
3	ICG 12509	2.0	ICG 14482	2.0	ICG 12276	2.3	ICGV 86699	2.3	ICG 14482	2.1
4	ICG 14482	1.9	ICGV 97120	1.7	ICG 14475	2.2	ICG 11337	2.3	ICGV 97120	1.8
5	ICGV 97120	1.7	ICG 1834	1.6	ICG 4955	1.8	SPS 15	2.2	ICG 11426	1.7
6	24 ×37-2275	1.7	ICG 11426	1.5	ICGV 01328	1.8	49×37- 99(b) tall	2.1	ICG 14475	1.7
7	ICR 48	1.7	ICG 14475	1.5	ICG 12625	1.8	SPS 2	2.1	ICG 11337	1.7
8	ICGV 06234	1.7	ICGV 86143	1.5	ICGV 97120	1.8	ICGV 01124	2.1	SPS 20	1.7
9	ICG 11426	1.6	24 ×37-2275	1.5	ICG 12509	1.8	ICGV 97120	2.1	ICGV 99085	1.6
10	ICGV 99085	1.6	ICG 4955	1.4	SPS 7	1.8	SPS 20	2.0	49 ×37- 99(b) tall	1.6
Population mean		**1.1**		**1.0**		**1.3**		**1.4**		**1.2**
CV%		**16.5**		**18.2**		**7.9**		**17.9**		**8.6**
LSD at 5 %		**0.3**		**0.3**		**0.1**		**0.4**		**0.1**

Table 4.22 Performance of trait specific superior genotypes of Genomic Selection Panel across four environments for linoleic acid (LA%) and palmitic acid content (PA%)

	Aliyarnagar		Jalgaon		ICRISAT Rainy 15		ICRISAT Post-Rainy 15-16		Pooled	
S. No.	**Genotypes**	**LA%**	**Genotypes**	**LA%**	**Genotypes**	**LA%**	**Genotypes**	**LA%**	**Genotypes**	**LA%**
1	SunOleic 95R	5.3	SunOleic 95R	5.1	SunOleic 95R	6.1	SunOleic 95R	4.6	SunOleic 95R	7.8
2	ICG 12276	24.0	ICG 12276	26.7	ICG 14482	23.3	ICGV 97045	21.8	ICG 12276	26.1
3	ICG 12509	28.6	ICG 14482	30.7	ICG 12276	23.3	ICG 11337	24.1	ICG 14482	28.6
4	ICR 48	29.8	ICG 1834	31.9	ICG 14475	26.4	ICGV 86699	24.6	ICGV 97120	29.3
5	ICG 14482	30.1	ICG 11426	32.1	ICG 4955	27.6	49×37- 99(b) tall	25.6	ICG 11426	29.9
6	24×37-2275	30.6	ICGV 97120	32.3	ICG 14985	27.7	ICGV 01124	26.4	ICGV 99085	31.0
7	ICGV 06234	30.8	ICGV 86143	32.7	ICGV 01328	27.7	SPS 2	26.4	ICG 5745	31.07
8	49×27-13 (ii)	30.8	TMV 2	32.9	ICGV 05198	28.0	ICG 5745	26.6	TMV 2	31.1
9	ICGV 97120	30.8	ICG 4955	33.4	49×37-97-1	28.1	ICG 442	26.6	49×37- 99(b) tall	31.1
10	ICGV 99085	31.4	24×37-2275	33.7	ICGV 01124	28.1	ICG 11426	26.6	ICGV 05198	31.2
Population mean		**39.7**		**42.2**		**36.1**		**34.7**		**38.2**
CV%		**7.7**		**7.3**		**5.7**		**8.4**		**3.7**
LSD at 5 %		**5.0**		**5.1**		**3.4**		**4.8**		**3.9**

S. No.	**Genotypes**	**PA%**	**Genotypes**	**PA%**	**Genotypes**	**PA%**	**Genotypes**	**PA%**	**Genotypes**	**PA%**
1	ICG 15419	7.5	ICG 15419	6.5	SunOleic 95R	7.9	SunOleic 95R	7.1	SunOleic 95R	7.6
2	ICG 5221	7.7	ICG 12625	6.9	ICG 5221	7.9	ICG 2381	8.1	ICG 15419	8.0
3	ICG 6022	8.1	SunOleic 95R	6.9	ICG 6022	7.9	ICG 6022	8.5	ICG 2381	8.2
4	ICG 12625	8.2	ICG 2381	7.3	ICG 15419	8.1	ICG 5221	9.1	ICG 5221	8.3
5	SunOleic 95R	8.5	ICG 5221	8.6	ICG 2381	8.4	ICG 15419	9.7	ICG 6022	8.3
6	ICG 6646	8.9	ICG 6022	8.8	ICG 12625	8.8	ICG 12625	10.1	ICG 12625	8.5
7	ICG 2381	9.3	ICG 6646	9.3	26×M-95-1 RI	9.9	ICGV 88438	10.3	ICG 6646	9.9
8	26×M-95-1 RI	9.4	ICGV 02446	9.6	ICGV 01393	9.9	GPBD 4	10.3	GPBD 4	10.0
9	ICGV 99085	9.5	ICG 11088	9.7	GPBD 4	9.9	ICG 11088	10.4	ICGV 99085	10.1
10	24×37-2275	9.5	24×37-2275	9.7	ICG 11088	10.0	ICG 14475	10.4	ICG 11088	10.2
Population mean		**11.7**		**11.9**		**11.7**		**12.5**		**11.9**
CV%		**5.4**		**5.4**		**4.5**		**5.0**		**2.6**
LSD at 5 %		**1.0**		**1.1**		**0.9**		**1.0**		**0.8**

Table 4.23 Performance of trait specific superior genotypes of Genomic Selection Panel across four environments for stearic acid content (SA%) and haulm weight per plant (HLM)

	Aliyarnagar		Jalgaon		ICRISAT Rainy 15		ICRISAT Post-Rainy 15-16		Pooled	
S. No.	**Genotypes**	**SA%**	**Genotypes**	**SA%**	**Genotypes**	**SA%**	**Genotypes**	**SA%**	**Genotypes**	**SA%**
1	ICG 4955	0.7	ICG 4955	0.2	ICG 4955	0.2	ICG 4955	0.7	ICG 4955	0.4
2	DTG 3	1.0	ICG 442	0.8	ICG 3673	0.2	ICG 12672	0.8	ICG 3673	0.9
3	ICG 3673	1.1	SPS 20	0.8	ICG 442	0.2	ICG 3673	0.9	ICG 442	1.0
4	ICG 12672	1.1	SPS 21	0.9	ICGV 13238	0.4	Gangapuri	1.0	ICG 12672	1.0
5	ICGV 86699	1.2	SPS 2	1.0	DTG 3	0.4	ICG 442	1.0	DTG 3	1.1
6	ICGV 09112	1.2	ICGV 01328	1.0	TAG 24	0.5	DTG 3	1.3	Gangapuri	1.1
7	Gangapuri	1.2	ICGV 07220	1.0	ICG 3746	0.5	ICGV 07220	1.5	ICGV 07220	1.2
8	SPS 2	1.2	ICG 8517	1.0	ICG 2773	0.5	49 M- 1-1	1.5	SPS 2	1.2
9	ICGV 97120	1.2	SPS 8	1.0	ICGV 89104	0.6	TG 49	1.5	ICG 8517	1.3
10	ICGV 01328	1.3	ICG 2773	1.1	26× 27-164	0.6	SPS 2	1.5	ICGV 01328	1.3
Population mean		**2.2**		**2.1**		**1.7**		**2.3**		**2.1**
CV%		**14.9**		**16.8**		**18.6**		**14.0**		**16.4**
LSD at 5 %		**0.5**		**0.6**		**0.5**		**0.5**		**0.5**

S. No.	**Genotypes**	**HLM (g)**	**Genotypes**	**HLM (g)**	**Genotypes**	**HLM (g)**	**Genotypes**	**HLM (g)**	**Genotypes**	**HLM (g)**
1	-	-	-	-	SPS 1	29.3	ICGV 86564	40.5	ICGV 01464	30.4
2	-	-	-	-	ICG 14482	28.4	ICGV 02290	36.0	ICG 14475	29.0
3	-	-	-	-	SPS 21	28.2	ICGV 01273	35.9	ICGV 86564	28.5
4	-	-	-	-	ICGV 99029	27.8	ICGV 05036	35.9	ICGV 05036	27.6
5	-	-	-	-	ICGV 00246	27.7	ICG 14475	34.8	ICGV 07120	27.6
6	-	-	-	-	ICGV 01464	27.7	ICGV 05176	34.1	ICGV 97045	27.5
7	-	-	-	-	ICGV 02411	26.7	ICGV 97045	33.5	ICGV 04087	27.5
8	-	-	-	-	ICGV 99052	26.2	ICG 15419	33.3	SPS 2	27.4
9	-	-	-	-	ICGV 07120	25.2	ICGV 00440	32.9	ICGV 07359	27.1
10	-	-	-	-	ICG 14466	24.9	ICGV 01464	32.8	ICGV 05176	26.9
Population mean						**16.1**		**19.4**		**17.8**
CV%						**18.7**		**13.5**		**15.9**
LSD at 5 %						**0.4**		**0.7**		**3.9**

19.67%) with high heritability (68.15, 69.97, 71.57 & 66.14%) and high GAM (27.69, 31.59, 28.73 & 26.81%) was observed for O/L ratio at Aliyarnagar, Jalgaon, ICRISAT rainy and post-rainy seasons, respectively (Table 4.21). Pooled analysis also revealed a similar trend of GCV and PCV (10.17 & 11.25%) with high heritability (81.68%) and moderate GAM (18.94%) for O/L ratio across the environments (Table 4.19).

4.3 Correlation analysis

The phenotypic and genotypic correlation among disease resistance (Disease severity scores of LLS and rust at 90 DAS), important yield and its component traits (Days to 50% flowering, number of pods per plant, pod and seed yield per plant, shelling percent, hundred seed weight, days to maturity and pod yield hectare), and nutritional quality traits of GSP were computed at individual as well as across the environments. The results of correlation analysis among the traits have been presented in Table 4.24 to 4.27.

4.3.1 Correlation between yield traits

The significant correlation between important yield and its contributing traits are given in Table 4.24. Pod yield per hectare had significant positive genotypic and phenotypic correlation with other yield component traits like number of mature pods per plant (r_g=0.49 to 0.89 & r_p=0.40 to 0.85), pod yield per plant (r_g=0.60 to 0.97 & r_p=0.49 to 0.84), seed yield per plant (r_g=0.57 to 0.96 & r_p=0.47 to 0.81) and hundred seed weight (r_g=0.21 to 0.44 & r_p=0.19 to 0.39) across the environments. Days to 50% flowering had positive significant correlation with days to maturity (r_g=0.12 to 0.67 & r_p=0.11 to 0.59) across the environments. Number of pods per plant had significant and positive correlation with pod yield per plant (r_g=0.75 to 0.89 & r_p=0.77 to 0.87), seed yield per plant (r_g=0.80 to 0.90 & r_p=0.74 to 0.87) and shelling percent (r_g=0.23 to 0.45 & r_p=0.15 to 0.36) across the environments. Pod yield per plant was positively and significantly associated with seed yield per plant (r_g=0.97 to 0.98 & r_p=0.94 to 0.98) and hundred seed weight (r_g=0.33 to 0.43 & r_p=0.32 to 0.41) across the environments. Hundred seed weight had significant positive correlation with days to maturity (r_g=0.15 to 0.57 & r_p=0.14 to 0.53). Pod yield per hectare had inconsistent association with days to maturity across the environments. It was positively correlated at Aliyarnagar (r_g=0.28 & r_p=0.23), ICRISAT rainy 2015 (r_g=0.24 & r_p=0.21) and pooled across the environments (r_g=0.24 & r_p=0.20) whereas negatively correlated at ICRISAT during post-rainy season 2015-16 (r_g=-0.34 & r_p=-0.31). Similarly, shelling percent also showed inconsistent association with pod yield per hectare. It had significant positive association at Jalgaon (r_g=0.28 & r_p=0.25) and ICRISAT during post-rainy 2015-16 (r_g=0.46 & r_p=0.42) whereas nonsignificant association in other environments (Table 4.24).

4.3.2 Correlation among disease severity scores and yield traits

The significant positive association of disease severity score of LLS was reported with disease severity scores of rust at 90 DAS across the environments (r_g=0.74 to 0.95 & r_p=0.47 to 0.88). The significant negative correlation of disease severity score of LLS was observed with number of mature pods per plant (r_g=-0.34 to -0.39 & r_p=-0.24 to -0.30), pod yield per plant (r_g=-0.31 to -0.57 & r_p=-0.24 to -0.42), seed yield per plant (r_g=-0.25 to -0.57 & r_p=-0.18 to -0.41) and yield per hectare (r_g=-0.45 to -0.52 & r_p=-0.37 to 0.43) across the environments except Jalgaon. It had a significant negative association with days to maturity (r_g=-0.34 to -0.50 & r_p=-0.23 to 0.44) across the environments. The disease severity score of rust also had significant negative correlation with number of mature pods per plant (r_g=-0.41 to -0.50 & r_p=-0.27 to -0.38), pod yield per plant (r_g=-0.41 to -0.67 & r_p=-0.30 to -0.49), seed yield per plant (r_g=-0.35 to -0.66 & r_p=-0.26 to -0.47), yield per hectare (r_g=-0.14 to -0.63 & r_p=-0.12 to 0.52) and days to maturity (r_g=-0.35 to -0.48 & r_p=-0.22 to 0.42) across the environments. Hundred seed weight had a significant negative correlation with disease severity scores of LLS (r_g=-0.30 & r_p=-0.26) and rust (r_g=-0.34 & r_p=-0.31) at ICRISAT during rainy 2015 while nonsignificant association in other environments (Table 4.25).

Table 4.24 Genotypic and phenotypic correlation among yield traits across the environments

Trait	ENV	DFF		NPP		PYPP		SYPP		SH		HSW		DM	
		r_g	r_p	r_g	r_p	r_g	r_p	r_g	r_p	r_g	r_p	r_g	r_p	r_g	r_p
NPP	E1	0.18**	0.11*												
	E2	0.03	-0.01												
	E3	-0.28**	-0.23**												
	E4	-0.42**	-0.38**												
	Pooled	-0.16**	-0.14**												
PYPP	E1	0.23**	0.14**	0.81**	0.81**										
	E2	0.02	-0.01	0.89**	0.87**										
	E3	-0.02	-0.06	0.78**	0.77**										
	E4	-0.42**	-0.38**	0.88**	0.86**										
	Pooled	0.04	0.02	0.75**	0.79**										
SYPP	E1	0.21**	0.12*	0.81**	0.80**	0.97**	0.97**								
	E2	-0.01	-0.04	0.90**	0.87**	0.98**	0.98**								
	E3	-0.04	-0.05	0.80**	0.74**	0.98**	0.94**								
	E4	-0.45**	-0.40**	0.87**	0.84**	0.98**	0.97**								
	Pooled	0.08	0.05	0.83**	0.82**	0.97**	0.97**								
SH	E1	-0.08	-0.05	0.1	0.08	0.04	0.04	0.26**	0.25**						
	E2	-0.18**	-0.16**	0.45**	0.36**	0.34**	0.29**	0.51**	0.47**						
	E3	-0.05	-0.02	0.23**	0.15**	0.09	0.08	0.31**	0.35**						
	E4	-0.35**	-0.30**	0.43**	0.39**	0.44**	0.41**	0.60**	0.57**						
	Pooled	-0.28**	-0.23**	0.43**	0.31**	0.09	0.12*	0.32**	0.34**						
HSW	E1	0.17**	0.13**	-0.12*	-0.06	0.33**	0.32**	0.30**	0.30**	-0.10	-0.06				
	E2	0.01	0.01	0.07	0.06	0.36**	0.34**	0.33**	0.32**	0.04	0.06				
	E3	0.30**	0.22**	-0.10	-0.05	0.40**	0.34**	0.33**	0.29**	-0.21**	-0.11*				
	E4	-0.13*	-0.12*	0.18**	0.18**	0.43**	0.41**	0.44**	0.43**	0.34**	0.35**				
	Pooled	0.27**	0.21**	-0.23**	-0.13*	0.34**	0.33**	0.22**	0.26**	-0.37**	-0.21**				
DM	E1	0.28**	0.23**	0.23**	0.17**	0.27**	0.20**	0.24**	0.17**	-0.15**	-0.13*	0.17**	0.15**		
	E2	0.12*	0.11*	0.01	-0.01	0.06	0.05	0.01	0.01	-0.21**	-0.19**	0.15**	0.14**		
	E3	0.32**	0.25**	0.04	0.04	0.31**	0.25**	0.28**	0.22**	-0.11*	-0.06	0.39**	0.33**		
	E4	0.67**	0.59**	-0.34**	-0.30**	-0.31**	-0.28**	-0.38**	-0.34**	-0.44**	-0.40**	0.57**	0.53**		
	Pooled	0.32**	0.27**	0.10	0.08	0.32**	0.24**	0.25**	0.19**	-0.22**	-0.18**	0.29**	0.26**		
PYH	E1	0.19**	0.14**	0.49**	0.40**	0.60**	0.49**	0.57**	0.47**	-0.10	-0.07	0.21**	0.19**	0.28**	0.23**
	E2	0.03	0.03	0.73**	0.65**	0.85**	0.73**	0.84**	0.73**	0.28**	0.25**	0.27**	0.25**	0.05	0.05
	E3	0.19**	0.18**	0.71**	0.56**	0.93**	0.79**	0.92**	0.74**	0.10	0.07	0.44**	0.39**	0.24**	0.21**
	E4	-0.44**	-0.40**	0.89**	0.85**	0.82**	0.76**	0.81**	0.79**	0.46**	0.42**	0.42**	0.39**	-0.34**	-0.31**
	Pooled	0.02	0.05	0.79**	0.68**	0.97**	0.84**	0.96**	0.81**	0.05	0.07	0.27**	0.27**	0.24**	0.20**

* & ** represents significance at <0.05 and <0.01 probability level, respectively; ENV=Environment; DFF= Days to 50% flowering; NPP= Number of mature pods per plant; PYPP= Pod yield per plant; SYPP= Seed yield per plant; SH= Shelling percent; HSW= Hundred seed weight; DM= Days to maturity; PYH= Pod yield per hectare; E_1 = Aliyarnagar; E_2= Jalgaon; E_3= ICRISAT rainy season 2015; E_4= ICRISAT post-rainy 2015-16; r_g= Genotypic correlation coefficient; r_p= Phenotypic correlation coefficient

Table 4.25 Genotypic and phenotypic correlation among disease severity scores of LLS and rust, and with yield traits across the environments

Trait	ENV	LLS90		Rust90	
		r_g	r_p	r_g	r_p
Disease severity score of rust at 90 DAS	E_1	0.84**	0.73**		
	E_2	0.74**	0.47**		
	E_3	0.92**	0.83**		
	Pooled	0.95**	0.88**		
Number of mature pods per plant	E_1	-0.36**	-0.29**	-0.47**	-0.37**
	E_2	-0.08	-0.09	-0.11*	-0.03
	E_3	-0.34**	-0.24**	-0.41**	-0.27**
	Pooled	-0.39**	-0.30**	-0.50**	-0.38**
Pod yield per plant	E_1	-0.31**	-0.24**	-0.41**	-0.30**
	E_2	0.04	0.03	-0.04	0.05
	E_3	-0.57**	-0.42**	-0.67**	-0.49**
	Pooled	-0.48**	-0.37**	-0.64**	-0.48**
Seed yield per plant	E_1	-0.25**	-0.18**	-0.35**	-0.26**
	E_2	0.08	0.07	-0.01	0.05
	E_3	-0.57**	-0.41**	-0.66**	-0.47**
	Pooled	-0.39**	-0.30**	-0.54**	-0.41**
Shelling percent	E_1	0.29**	0.23**	0.30**	0.24**
	E_2	0.30**	0.19**	0.24**	0.19**
	E_3	-0.03	-0.03	-0.01	-0.02
	Pooled	0.29**	0.21**	0.31**	0.23**
Hundred seed weight	E_1	0.01	0.02	-0.03	-0.02
	E_2	0.05	0.05	-0.07	-0.06
	E_3	-0.30**	-0.26**	-0.34**	-0.31**
	Pooled	-0.07	-0.09	-0.12*	-0.13*
Days to maturity	E_1	-0.45**	-0.39**	-0.44**	-0.38**
	E_2	-0.34**	-0.23**	-0.35**	-0.22**
	E_3	-0.50**	-0.43**	-0.44**	-0.39**
	Pooled	-0.50**	-0.44**	-0.48**	-0.42**
Pod yield per hectare	E_1	-0.45**	-0.37**	-0.58**	-0.47**
	E_2	-0.10	-0.10	-0.14**	-0.12*
	E_3	-0.52**	-0.43**	-0.63**	-0.52**
	Pooled	-0.47**	-0.40**	-0.62**	-0.52**

* & ** represents significance at <0.05 and <0.01 probability level, respectively

ENV= Environment; LLS90 & Rust90 = Disease severity score of late leaf spot and rust at 90 days after sowing, respectively; E_1 = Aliyarnagar; E_2= Jalgaon; E_3= ICRISAT rainy season 2015; r_g= Genotypic correlation coefficient; r_p= Phenotypic correlation coefficient;

4.3.3 Correlation among nutritional quality traits

Oil content had significant negative association with protein content (r_g= -0.28 to -0.61 & r_p=-0.31 to -0.57) across the environments. It had significant negative correlation with oleic acid (r_g=-0.12 to -0.24 & r_p=-0.12 to -0.25) and O/L ratio (r_g=-0.14 to -0.25 & r_p=-0.14 to -0.26) at Jalgaon, ICRISAT rainy 2015 and pooled across the environments. Protein content had inconsistent and low magnitude of positive and negative significant association with fatty acid composition across the environments. Among the fatty acids, oleic acid had strong significant negative association with linoleic (r_g= -0.93 to -0.96 & r_p=-0.93 to -0.96), palmitic (r_g=-0.60 to -0.73 & r_p=-0.62 to -0.73) and stearic acid. (r_g=-0.31 to -0.51 & r_p=-0.20 to -0.48) whereas strong positive with O/L ratio (r_g=0.91 to 0.98 & r_p=0.91 to 0.98) across the environments. Linoleic acid had positive significant association with palmitic (r_g= 0.46 to 0.61 & r_p=0.47 to 0.62) and stearic acid (r_g=0.33 to 0.47 & r_p=0.22 to 0.43) while a strong negative association with OL ratio (r_g=-0.90 to -0.99 & r_p=-0.90 to -0.99) across the environments. O/L ratio was significant negatively correlated with palmitic (r_g=-0.53 to -0.66 & r_p=-0.54 to -0.67) and stearic acid (r_g= -0.30 to -0.48 & r_p= -0.21 to -0.41) across the environments (Table 4.26).

4.3.4 Correlation among disease severity scores and nutritional quality traits

Disease severity score of LLS at 90 DAS had significant negative correlation with oil content (r_g= -0.26 to -0.52 & r_p= -0.26 to -0.44) and fatty acids such as linoleic (r_g=-0.15 to -0.23 & r_p=-0.14 to -0.20), palmitic (r_g=-0.16 to -0.43 & r_p=-0.13 to -0.38) and stearic acid (r_g= -0.31 to -0.52 & r_p=-0.28 to -0.45). However, it was positively associated with oleic acid (r_g=0.13 to 0.20 & r_p=0.12 to 0.18) and O/L ratio (r_g=0.15 & r_p=-0.13 to 0.14) with negligible magnitude across the environments. Similarly, disease severity scores of rust at 90 DAS also had negative correlation with oil content (r_g=-0.31 to -0.53 & r_p=-0.17 to -0.44), linoleic acid (r_g=-0.26 to -0.36 & r_p=-0.18 to -0.30), palmitic acid (r_g=-0.37 to -0.43 & r_p=-0.24 to -0.38) and stearic acid (r_g=-0.41 to -0.57 & r_p=-0.36 to -0.52) across the environments. However, it had significant positive association with oleic acid (r_g=0.25 to 0.32 & r_p=0.18 to 0.28) and O/L ratio

(r_g=0.23 to 0.27 & r_p=0.11 to 0.24) across the environments. Hundred seed weight had negative significant association with oil content (r_g=-0.22 to -0.35 & r_p=-0.11 to -0.27) whereas positive significant with protein content (r_g=0.29 to 0.44 & r_p=0.16 to 0.33) across the location except Jalgaon for oil content. Oil content had positive significant association with pod yield per plant (r_g=0.20 to 0.41 & r_p=0.17 to 0.36), linoleic acid (r_g=0.30 to 0.57 & r_p=0.36 to 0.49) and palmitic acid (r_g=0.12 to 0.42 & r_p=0.21 to 0.36) whereas negative with oleic acid (r_g=-0.29 to -0.56 & r_p=-0.23 to -0.48) and O/L ratio (r_g=-0.29 to -0.48 & r_p=-0.24 to -0.40) across the environments (Table 4.27).

Table 4.26 Genotypic and phenotypic correlation among nutritional quality traits across the environment

Trait	ENV	OC		PC		OAC		LAC		PAC		SAC		O/L ratio	
		r_g	r_p	r_g	r_p	r_g	r_p	r_g	r_p	r_g	r_p	r_g	r_p	r_g	r_p
PC	E1	-0.61**	-0.54**												
	E2	-0.58**	-0.52**												
	E3	-0.28**	-0.31**												
	E4	-0.60**	-0.57**												
	Pooled	-0.40**	-0.41**												
OAC	E1	0.01	-0.07	-0.17**	-0.12*										
	E2	-0.24**	-0.25**	0.02	-0.03										
	E3	-0.15**	-0.13**	-0.31**	-0.22**										
	E4	0.21**	0.11*	-0.19**	-0.11*										
	Pooled	-0.12*	-0.12*	-0.16**	-0.14*										
LAC	E1	0.19**	0.24**	0.01	-0.02	-0.95**	-0.95**								
	E2	0.37**	0.36**	-0.12*	-0.05	-0.96**	-0.96**								
	E3	0.30**	0.28**	0.15**	0.09	-0.96**	-0.95**								
	E4	-0.09	0.01	0.09	-0.01	-0.93**	-0.93**								
	Pooled	0.31**	0.30**	0.03	0.02	-0.96**	-0.96**								
PAC	E1	-0.01	0.05	0.27**	0.14**	-0.73**	-0.73**	0.61**	0.62**						
	E2	0.19**	0.17**	-0.02	0.03	-0.71**	-0.69**	0.58**	0.58**						
	E3	0.18**	0.14**	0.21**	0.18**	-0.60**	-0.62**	0.46**	0.47**						
	E4	-0.06	-0.07	0.07	0.09	-0.67**	-0.67**	0.53**	0.53**						
	Pooled	0.12*	0.13*	0.18**	0.15**	-0.67**	-0.67**	0.56**	0.56**						
SAC	E1	0.36**	0.43**	0.16**	0.05	-0.31**	-0.20**	0.33**	0.22**	-0.11*	-0.13*				
	E2	0.36**	0.40**	0.04	0.03	-0.39**	-0.33**	0.45**	0.35**	-0.12*	-0.12*				
	E3	0.50**	0.52**	0.39**	0.20**	-0.44**	-0.32**	0.47**	0.36**	0.11*	0.06				
	E4	0.34**	0.25**	-0.06	0.14**	-0.51**	-0.48**	0.47**	0.43**	-0.23**	-0.15**				
	Pooled	0.42**	0.44**	0.23**	0.16**	-0.38**	-0.35**	0.45**	0.41**	-0.09	-0.07				
O/L	E1	-0.08	-0.14**	-0.07	-0.05	0.97**	0.97**	-0.99**	-0.99**	-0.66**	-0.67**	-0.30**	-0.21**		
	E2	-0.25**	-0.26**	0.04	-0.01	0.98**	0.98**	-0.98**	-0.99**	-0.64**	-0.64**	-0.40**	-0.33**		
	E3	-0.20**	-0.19**	-0.22**	-0.15**	0.98**	0.97**	-0.99**	-0.99**	-0.53**	-0.54**	-0.43**	-0.33**		
	E4	0.15**	0.06	-0.12*	-0.05	0.93**	0.94**	-0.98**	-0.98**	-0.60**	-0.60**	-0.48**	-0.41**		
	Pooled	-0.14**	-0.14**	-0.06	-0.06	0.91**	0.91**	-0.90**	-0.90**	-0.56**	-0.56**	-0.33**	-0.30**		

* & ** represents significance at <0.05 and <0.01 probability level, respectively; ENV=Environment; OC= Oil content; PC= Protein content; OAC= Oleic acid content; LAC= linoleic acid content; PAC= Palmitic acid content; SAC= Stearic acid content; O/L= Oleic/linoleic acid ratio; E_1 = Aliyarnagar; E_2= Jalgaon; E_3= ICRISAT rainy season 2015; E_4= ICRISAT post-rainy 2015-16; r_g= Genotypic correlation coefficient; r_p= Phenotypic correlation coefficient

Table 4.27 Genotypic and phenotypic correlation among disease severity scores of LLS and rust, yield and nutritional quality traits across the environments

Trait	ENV	LLS90		Rust90		HSW		PYH	
		rg	rp	rg	rp	rg	rp	rg	rp
Oil content	E1	-0.41**	-0.26**	-0.36**	-0.26**	-0.34**	-0.20**	0.20**	0.17**
	E2	-0.26**	-0.20**	-0.31**	-0.17**	-0.25**	-0.16**	0.33**	0.26**
	E3	-0.52**	-0.43**	-0.50**	-0.44**	-0.06	0.10	0.41**	0.36**
	E4	-	-	-	-	-0.22**	-0.11*	-0.18**	-0.04
	Pooled	-0.51**	-0.44**	-0.53**	-0.44**	-0.35**	-0.27**	0.38**	0.33**
Protein content	E1	-0.18**	-0.13*	-0.21**	-0.16**	0.36**	0.20**	0.03	0.02
	E2	0.30**	0.21**	0.17**	0.10	0.29**	0.16**	-0.11*	-0.07
	E3	-0.18**	-0.13*	-0.20**	-0.16**	0.39**	0.23**	0.29**	0.20**
	E4	-	-	-	-	0.07	0.02	0.06	-0.05
	Pooled	0.13*	0.07	0.09	0.02	0.44**	0.33**	0.07	0.05
Oleic acid	E1	0.19**	0.18**	0.30**	0.26**	0.11*	0.08	-0.35**	-0.27**
	E2	0.13*	0.12*	0.25**	0.18**	-0.02	-0.04	-0.47**	-0.35**
	E3	0.17**	0.16**	0.30**	0.26**	-0.12*	-0.10	-0.52**	-0.43**
	E4	-	-	-	-	-0.12*	-0.10	-0.29**	-0.23**
	Pooled	0.20**	0.17**	0.32**	0.28**	0.01	0.01	-0.56**	-0.48**
Linoleic acid	E1	-0.19**	-0.17**	-0.29**	-0.26**	-0.13*	-0.1	0.33**	0.26**
	E2	-0.15**	-0.14**	-0.26**	-0.18**	-0.01	0.02	0.50**	0.36**
	E3	-0.15**	-0.14**	-0.27**	-0.24**	0.05	0.06	0.48**	0.40**
	E4	-	-	-	-	0.09	0.09	0.30**	0.25**
	Pooled	-0.23**	-0.20**	-0.36**	-0.30**	-0.07	-0.05	0.57**	0.49**
Palmitic acid	E1	-0.43**	-0.38**	-0.43**	-0.38**	-0.17**	-0.13*	0.28**	0.22**
	E2	-0.16**	-0.13*	-0.37**	-0.24**	-0.08	-0.05	0.30**	0.21**
	E3	-0.41**	-0.33**	-0.42**	-0.35**	0.12*	0.10	0.41**	0.32**
	E4	-	-	-	-	0.01	-0.02	0.12*	0.06
	Pooled	-0.31**	-0.29**	-0.39**	-0.34**	-0.07	-0.06	0.42**	0.36**
Stearic acid	E1	-0.52**	-0.45**	-0.57**	-0.52**	0.06	0.07	0.17**	0.14**
	E2	-0.04	-0.05	-0.08	-0.08	0.17**	0.17**	0.28**	0.22**
	E3	-0.46**	-0.38**	-0.54**	-0.46**	0.37**	0.35**	0.56**	0.46**
	E4	-	-	-	-	0.01	-0.01	-0.14**	-0.14**
	Pooled	-0.31**	-0.28**	-0.41**	-0.36**	0.1	0.14**	0.41**	0.36**
O/L ratio	E1	0.15**	0.13*	0.23**	0.21**	0.11*	0.09	-0.32**	-0.26**
	E2	0.01	0.01	0.26**	0.11*	-0.02	-0.04	-0.45**	-0.33**
	E3	0.15**	0.14**	0.27**	0.24**	-0.07	-0.06	-0.48**	-0.40**
	E4	-	-	-	-	-0.10	-0.10	-0.29**	-0.24**
	Pooled	0.15**	0.14**	0.25**	0.22**	0.02	0.01	-0.43**	-0.37**

* & ** represents significance at <0.05 and <0.01 probability level, respectively

ENV= Environment; LLS90 & Rust90 = Disease severity score of late leaf spot and rust at 90 days after sowing, respectively; HSW= Hundred seed weight; PYH= Pod yield per hectare; E_1 = Aliyarnagar; E_2= Jalgaon; E_3= ICRISAT rainy season 2015; E_4= ICRISAT post-rainy 2015-16; r_g= Genotypic correlation coefficient; r_p= Phenotypic correlation coefficient

4.4 Principal component analysis (PCA)

Genetic divergence or the presence of substantial genetic variation in the breeding population is one of the prerequisites for genetic gain in any crop improvement program. Therefore, genetic diversity in GSP was assessed across the four different environments using the scores of principal components which can be used to decide a sound breeding program for genetic improvement of this crop.

The PCA using BLUP values of important traits was performed which provided a reduced dimension model that could indicate measured differences among the genotypes of GSP. The purpose of the analysis was to obtain a small number of linear combinations of 20 quantitative traits which account for most of the variability in the data across the environments. The results revealed the importance of the first six PCs in discriminating the GSP in the individual environment and pooled since first six PCs had eigenvalues greater than or equal to 1.0 (Table 4.28a&b). The percentage of total variance explained by the first six PCs was 70.62% at Aliyarnagar, 71.74% at Jalgaon, 75.35% at ICRISAT during rainy 2015 and 79.49% at ICRISAT during post-rainy 2015-16 and 78.49% in pooled across the environments.

The PC1 was the most important component and accounted for more variation compared to other in all the four environments and pooled (26.06% at Aliyarnagar, 22.85% at Jalgaon, 32.69% at ICRISAT rainy 2015, 28.00% at ICRISAT post-rainy 2015-16 and 29.60% in pooled). The eigenvalues of PC1 were 4.95, 4.34, 6.54, 4.48 and 5.92 at Aliyarnagar, Jalgaon, ICRISAT rainy and post-rainy and pooled across the environments, respectively. The contribution of each trait towards total genetic variability explained by different PCs has been presented in Table 4.28a&b. The contribution of traits such as disease score of rust at 90 (13.99%) and 105 DAS (10.81%), disease scores of LLS 90 (11.37%) and 105 DAS (9.01%), pod yield per hectare (8.64%), number of pods per plant (7.31%) and pod yield per plant (6.45%) was more towards total variability explained by PC1 at Aliyarnagar whereas at Jalgaon, PC1 separates genotypes based on linoleic acid (15.30%), oleic acid (14.41%), pod yield per hectare (9.02%), number of pods per plant (9.09%), and rust (3.56 & 5.19%) and LLS (3.34 & 3.78%) severity scores at 90 and 105 DAS, respectively. Similar to Aliyarnagar, disease resistance to rust at 90 and 105 DAS (11.09 & 11.07%) followed by disease scores of LLS at 90 and 105 DAS (10.37 & 8.85%), pod yield per plant (8.97%) and pod yield per hectare (8.76%) contributed more towards the total variability explained by first PC at ICRISAT during rainy 2015. At ICRISAT during post-rainy 2015 major contribution towards first PC was made by pod yield per hectare (16.67%) followed by pod yield per plant (16.05%), number of pods per plant (14.90%), days to 50% flowering (6.98%), linoleic acid (6.88%) and oleic acid (6.51%). Similar to individual environments, PCA with pooled BLUPs also revealed disease score of rust at 90 and 105 DAS (12.68 & 12.09%) followed by disease scores to LLS at 90 and 105 DAS (10.75 & 9.68%), pod yield per plant (6.42%) and pod yield per hectare (6.27%) contributed more towards total variability explained by first PC (Table 4.28a). Most of the nutritional quality traits contributed more toward to variability explained by PC2, PC3 and PC4 whereas plant height, shelling percent, hundred seed weight and days to maturity contributed more for PC5 and PC6 in most of the environments and pooled (Table 4.28b). PCA analysis for all the four environments and pooled showed that disease severity scores of rust and LLS at 90 and 105 DAS, pod yield per hectare, pod yield per plant, number of pods per plant, hundred seed weight, days to maturity, oil content, protein content, oleic acid and linoleic acid had major contribution in all four environments, indicating their importance for characterization of genotypes.

4.4.1 Wards clustering analysis

The hierarchical cluster analysis (Ward, 1963) for individual environment and pooled was conducted using the scores of first six principle components. Different number of clusters were reported at different environments and pooled. The results obtained from cluster analysis of each individual environment and pooled have been presented in Table 4.29 to 4.38 and explained below.

4.4.1.1 Aliyarnagar, Tamil Nadu (Rainy 2015)

Ward's hierarchical cluster analysis based on scores of first six PCs which together explained 70.62% of total genetic variability resulted in grouping of entire GSP into seven clusters at dissimilarity value of ~200 (Table 4.29 & Fig 4.7). The cluster I comprised of 44 genotypes was dominated by high yielding genotypes with higher cluster mean for pod yield per hectare (2191.7 kg/ha), number of pods per plant (22.30) and pod yield per plant (16.34 g). Cluster II had 52 genotypes with lowest cluster mean for disease severity to LLS (2.81 & 5.23) and rust (2.62 & 4.85) both at 90 and 105 DAS, respectively and higher cluster mean for days to maturity (113) indicated that most of the resistant cultivars grouped together in this cluster (Table 4.30a). Cluster III was the largest cluster comprised of 98 genotypes and recorded higher cluster mean for shelling percent and lower cluster mean for days to 50% flowering indicating that most of the improved genotypes were grouped together in this cluster. Cluster IV grouped 36 genotypes identified for higher cluster mean for protein content and palmitic acid. Cluster V had 75 genotypes with lowest cluster mean for oil content and stearic acid whereas higher cluster mean for hundred seed weight indicating that most of genotypes of this cluster had low oil content and stearic acid with high seed mass at Aliyarnagar. Genotype SunOleic 95R maintained its own identity with highest oleic acid content (74.4%), lowest linoleic acid (5.3%), palmitic acid (8.5%) and higher O/L ratio (14.03) formed an individual cluster VI indicating greater dissimilarity with all other genotypes of GSP. While cluster VII comprised of 34 genotypes and recorded high cluster mean for oil content (57.0%) and lower for protein content (18.7%) indicating that genotypes with high oil content and low protein content grouped together in this cluster (Table 4.30b).

4.4.1.2 Jalgaon, Maharashtra (Rainy 2015)

The GSP evaluated at Jalgaon grouped into eight clusters in Ward's hierarchical clustering based on first six PCs that together accounted for 71.74% of total variability (Table 4.31 & Fig 4.8). The cluster I had 31 genotypes dominated with genotypes taken longer number of days to 50% flowering as revealed by high cluster mean for it. Cluster II comprised of 51 genotypes with lowest cluster mean for disease severity scores to LLS (2.71 & 3.94) and rust (2.41 & 3.18) both at 90 and 105 DAS and high cluster mean for days to maturity (128 day), pod yield per hectare (2769 kg) and oil content (57.4%) indicated that most of the resistant, high yielding and high oil containing cultivars grouped together in this cluster (Table 4.32a&b). Cluster III comprised of 63 genotypes identified for lower cluster mean for hundred seed weight (31.92 g) and protein content (18.4%). However, cluster IV grouped 18 genotypes of GSP identified for higher cluster mean for hundred seed weight (46.70 g) with better protein content (20.9%) compared to other clusters. Cluster V had 56 genotypes and recorded high cluster mean for protein content (21.6%) indicating that most of the genotypes of this cluster had higher protein content at Jalgaon. Similar to Aliyarnagar, SunOleic 95R maintained its own identity at Jalgaon with highest oleic acid content (80.47%), lowest linoleic acid (5.12%), palmitic acid (6.98) and high O/L ratio (14.03) grouped in separate cluster VI (Table 4.32b). While cluster VII & VIII comprised of 33 and 87 genotypes, respectively with low cluster mean for pod yield per hectare (1009 and 1299 kg), number of pods per plant (10.7 and 12.3) and pod yield per plant (6.80 and 8.96 g), respectively indicated that all the genotypes with lower yield potential were grouped together in these two clusters (Table 4.32a).

Table 4.28a Eigenvalues, percentage of total variation explained and eigenvectors of first six principal components (PCs) for different yield and its contributing traits of Genomic Selection Panel evaluated in four different environments

PCs	Eigenvalue	Variability explained (%)	Cumulative value (%)	Eigenvectors												
				DFF	LLS 90	LLS 105	Rust 90	Rust 105	PH	NPP	PYPP	SH	HSW	DM	PYH	HLM
Aliyarnagar																
PC1	4.95	26.06	26.06	-0.192	0.337	0.300	0.374	0.329	0.069	-0.270	-0.254	0.092	-0.019	-0.208	-0.294	-
PC2	2.70	14.19	40.24	0.166	-0.218	-0.192	-0.190	-0.174	-0.047	0.011	0.055	-0.146	0.123	0.182	0.029	-
PC3	1.91	10.07	50.31	-0.211	-0.095	-0.115	-0.037	-0.091	0.218	-0.096	-0.249	-0.026	-0.416	-0.053	-0.098	-
PC4	1.57	8.24	58.55	-0.135	0.176	0.174	0.123	0.168	0.171	0.415	0.517	0.325	0.164	-0.061	0.219	-
PC5	1.29	6.80	65.35	0.019	0.019	0.037	0.015	-0.009	0.392	-0.386	-0.106	-0.314	0.434	0.182	0.023	-
PC6	1.00	5.27	70.62	-0.251	0.014	-0.206	0.072	-0.075	0.620	0.001	0.061	0.180	0.050	0.389	0.102	-
Jalgaon																
PC1	4.34	22.85	22.85	0.083	-0.183	-0.195	-0.189	-0.228	0.048	0.301	0.282	0.047	0.039	0.126	0.300	-
PC2	3.35	17.63	40.48	-0.158	0.380	0.404	0.369	0.384	0.067	0.249	0.282	0.282	0.129	-0.178	0.240	-
PC3	1.98	10.44	50.92	-0.061	-0.141	-0.134	-0.038	-0.053	0.065	0.300	0.311	0.164	0.087	0.045	0.244	-
PC4	1.52	8.02	58.93	-0.280	0.038	0.062	0.123	0.132	0.315	-0.105	-0.245	-0.049	-0.446	-0.112	-0.175	-
PC5	1.40	7.39	66.32	-0.214	-0.059	-0.038	-0.025	-0.023	0.426	-0.180	0.019	-0.283	0.450	0.232	0.035	-
PC6	1.03	5.42	71.74	0.496	0.079	0.037	0.327	0.293	-0.227	-0.072	0.010	-0.312	0.213	0.409	-0.008	-
ICRISAT rainy season 2015																
PC1	6.54	32.69	32.69	-0.099	0.322	0.297	0.333	0.333	-0.036	-0.195	-0.299	-0.026	-0.155	-0.192	-0.296	-0.190
PC2	2.81	14.04	46.72	-0.214	0.216	0.250	0.167	0.204	-0.009	0.223	0.113	0.119	-0.125	-0.232	0.142	-0.244
PC3	2.06	10.30	57.02	-0.378	-0.002	-0.039	0.002	0.004	0.310	0.329	0.163	0.156	-0.265	-0.171	0.077	0.084
PC4	1.46	7.29	64.31	-0.125	0.056	0.152	0.031	0.118	-0.313	0.288	0.355	-0.060	0.374	-0.043	0.364	-0.255
PC5	1.20	6.01	70.32	-0.130	0.127	0.140	0.069	0.121	0.585	-0.192	0.015	-0.450	0.281	0.039	0.031	0.225
PC6	1.01	5.03	75.35	0.276	-0.115	0.039	-0.084	0.025	-0.190	-0.252	-0.205	0.214	0.152	-0.216	-0.083	-0.294
ICRISAT post-rainy season 2015-16																
PC1	4.48	28.00	28.00	-0.264	-	-	-	-	0.250	0.386	0.401	0.275	0.178	-0.232	0.408	-0.093

Table 4.28a Continue....

PCs	Eigenvalue	Variability explained (%)	Cumulative value (%)	Eigenvectors												
				DFF	LLS 90	LLS 105	Rust 90	Rust 105	PH	NPP	PYPP	SH	HSW	DM	PYH	HLM
PC2	2.77	17.30	45.30	-0.279	-	-	-	-	0.083	0.085	0.111	0.097	0.034	-0.286	0.117	-0.234
PC3	1.93	12.06	57.36	0.168	-	-	-	-	0.193	0.188	0.264	-0.019	0.203	0.286	0.234	0.488
PC4	1.49	9.31	66.66	-0.179	-	-	-	-	-0.096	0.014	-0.107	0.162	-0.366	-0.330	-0.084	-0.224
PC5	1.10	6.90	73.57	-0.079	-	-	-	-	0.059	-0.172	-0.007	0.066	0.322	-0.057	-0.002	-0.066
PC6	0.95	5.92	79.49	0.164	-	-	-	-	-0.453	-0.152	-0.061	0.610	0.537	0.028	-0.061	-0.096
Pooled across the environments																
PC1	5.92	29.60	29.60	-0.167	0.328	0.311	0.356	0.348	0.004	-0.209	-0.253	0.050	-0.058	-0.232	-0.250	-0.218
PC2	3.53	17.67	47.27	-0.244	0.226	0.242	0.174	0.196	0.073	0.303	0.241	0.277	-0.037	-0.219	0.250	-0.205
PC3	2.08	10.38	57.65	-0.275	-0.095	-0.098	-0.073	-0.065	0.156	0.261	0.071	0.203	-0.339	-0.190	0.091	-0.151
PC4	1.77	8.84	66.49	-0.107	0.059	0.098	0.018	0.062	0.145	0.154	0.412	0.045	0.514	0.109	0.364	0.114
PC5	1.43	7.14	73.63	-0.152	0.068	0.061	0.058	0.046	0.587	-0.270	-0.141	-0.266	0.018	0.003	-0.106	0.190
PC6	0.97	4.86	78.49	0.109	-0.087	0.004	-0.084	-0.028	-0.498	0.014	-0.037	-0.086	-0.033	-0.170	-0.019	-0.432

Where; DFF= Days to 50% flowering, LLS90, LLS 105, Rust90 & Rust105= Disease severity score of late leaf spot and rust recorded at 90 and 105 days after sowing respectively, PH = Plant height (cm), NPP= Number of pods plant^{-1}, PYPP= Pod yield plant^{-1} (g), SH %= Shelling percent, DM= Days to physiological maturity, HSW= Hundred seed weight (g), PYH= Pod yield hectare^{-1} (kg/ha), HLM = Haulm weight per plant (g)

Table 4.28b Eigenvalues, percentage of total variation explained and eigenvectors of first six principal components (PCs) for nutritional quality traits of Genomic Selection Panel of groundnut evaluated in four different environments

PCs	Eigenvalue	Variability explained (%)	Cumulative value (%)	Eigenvectors						
				Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
Aliyarnagar										
PC1	4.95	26.06	26.06	-0.152	-0.019	0.242	-0.246	-0.219	-0.121	0.160
PC2	2.70	14.19	40.24	0.039	-0.035	0.481	-0.470	-0.357	-0.033	0.403
PC3	1.91	10.07	50.31	0.549	-0.520	0.052	0.076	-0.101	0.170	-0.012
PC4	1.57	8.24	58.55	0.187	-0.140	0.075	-0.043	-0.220	0.335	0.045
PC5	1.29	6.80	65.35	0.051	0.183	-0.070	0.129	-0.226	0.481	-0.151
PC6	1.00	5.27	70.62	-0.192	-0.096	0.049	-0.037	0.075	-0.479	-0.119
Jalgaon										
PC1	4.34	22.85	22.85	0.259	-0.110	-0.380	0.391	0.299	0.177	-0.233
PC2	3.35	17.63	40.48	-0.038	0.119	-0.111	0.110	-0.008	0.085	-0.074
PC3	1.98	10.44	50.92	0.263	-0.296	0.364	-0.305	-0.313	0.068	0.426
PC4	1.52	8.02	58.93	0.455	-0.382	-0.039	0.132	-0.098	0.281	-0.089
PC5	1.40	7.39	66.32	-0.090	0.281	-0.015	0.030	-0.278	0.478	-0.041
PC6	1.03	5.42	71.74	0.146	-0.375	0.021	0.038	-0.086	0.043	-0.121
ICRISAT rainy season 2015										
PC1	6.54	32.69	32.69	-0.216	-0.083	0.205	-0.202	-0.218	-0.244	0.137
PC2	2.81	14.04	46.72	0.022	-0.004	-0.431	0.449	0.156	0.034	-0.369
PC3	2.06	10.30	57.02	0.431	-0.387	0.235	-0.114	-0.210	0.065	0.190
PC4	1.46	7.29	64.31	-0.144	0.270	0.144	-0.180	-0.232	0.122	0.280
PC5	1.20	6.01	70.32	0.000	0.170	-0.032	0.081	-0.243	0.320	-0.123
PC6	1.01	5.03	75.35	0.301	-0.171	-0.004	0.125	-0.352	0.539	-0.043

Table 4.28b Continue....

PCs	Eigenvalue	Variability explained (%)	Cumulative value (%)	Eigenvectors						
				Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
ICRISAT post-rainy season 2015-16										
PC1	4.48	28.00	28.00	-0.114	0.070	-0.255	0.262	0.132	-0.120	-0.196
PC2	2.77	17.30	45.30	-0.032	0.016	0.457	-0.415	-0.442	-0.112	0.380
PC3	1.93	12.06	57.36	0.356	-0.439	0.144	-0.144	-0.034	0.186	0.126
PC4	1.49	9.31	66.66	0.595	-0.440	-0.056	0.187	-0.053	0.113	-0.139
PC5	1.10	6.90	73.57	0.093	0.298	-0.078	0.093	-0.320	0.786	-0.110
PC6	0.95	5.92	79.49	0.011	-0.189	0.011	-0.033	0.039	-0.169	0.004
Pooled across the environments										
PC1	5.92	29.60	29.60	-0.192	0.033	0.225	-0.228	-0.217	-0.171	0.159
PC2	3.53	17.67	47.27	-0.022	0.073	-0.353	0.353	0.178	0.035	-0.297
PC3	2.08	10.38	57.65	0.469	-0.439	0.234	-0.120	-0.218	0.028	0.212
PC4	1.77	8.84	66.49	-0.115	0.186	0.222	-0.236	-0.276	0.159	0.279
PC5	1.43	7.14	73.63	0.204	0.018	-0.094	0.179	-0.212	0.496	-0.183
PC6	0.97	4.86	78.49	0.085	0.256	-0.043	0.064	-0.309	0.568	0.039

Table 4.29 Details of genotypes grouped into different clusters in Ward's hierarchical clustering at Aliyarnagar during rainy season 2015

Cluster	Number	Genotypes
Cluster I	44	49 × 39-21-2(a), 49 M- 1-1, 49 M-2-2, ICG 14466, ICG 721, ICGVs 00005, 00290, 01263, 01265, 01273, 01274, 01276, 01495, 02266, 02287, 02321, 02323, 03042, 03128, 03207, 04044, 04087, 04115, 05057, 05163, 06042, 06099, 06100, 06142, 06175, 06420, 07166, 07223, 07227, 07235, 07246, 07247, 93280, 93920, 97115, 98105, 98373, 99051, SPS 11
Cluster II	52	24 × 39-31 MR, 24 M-86, 39 × 49 -8, 49 M-16, GPBD 4, ICGs 11337, 11426, 2381, ICGVs 00068, 00191, 00246, 00248, 00346, 00362, 01060, 01328, 01361, 01464, 02317, 02411, 02434, 02446, 03043, 05032, 05036, 05100, 05141, 05155, 06040, 06422, 06423, 07120, 07145, 07148, 86590 , 86699, 87846, 97120, 97128, 97165, 98184, 99029, 99052, 99160, MN1-35, SPS 15, SPS 2, SPS 20, SPS 21, SPS 8, SPS 7, SPS 9
Cluster III	98	26 × 27-164, 26 M- 119-1, 49 × 37-135, DTG 15, Gangapuri, ICGs 10036, 12672, 12879, 12991, 14985, 15415, 1668, 1834, 1973, 2031, 2106, 3102, 3140, 3312, 3343, 3421, 3584, 3673, 3746, 434, 442, 4543, 4729, 4955, 8517, 8751, 9315, 9507, ICGS 11, ICGVs 00321, 00343, 00350, 01005, 01232, 02022, 02038, 02125, 02144, 02189, 02194, 02206, 02251, 02286, 03056, 04018, 03184, 04124, 04149, 05161, 06049, 06431, 07023, 07217, 07273, 13238, 13241, 13242, 13245, 86011, 86352, 87160, 87354, 87378, 88145, 89104, 91114, 91116, 92195, 92267, 93437, 93470, 94361, 95070, 95290, 95377, 96466, 96468, 97232, 97261, 97262, 99181, J 11, JL 24, Mutant 3, Somnath, SPS 10 , SPS 3, SPS 6, TAG 24, TG LPS 7, TG 19, TKG 19A, TMV 2 NLM
Cluster IV	36	49 × 27-19, 49 × 27-37, DH 86, Faizpur 1-5, ICGs 11651, 3027, 4527, 8285, 875, ICGS 44, ICGS 76, ICGVs 00349, 00371, 00387, 02271, 03136, 03397, 03398, 06347, 07168, 07268, 86015, 86143, 94118, 95469, 97092, 98163, 98294, 99195, 99233, M 110-14, M 28-2, SPS 1, TDG 14, TG LPS 3, TG LPS 4
Cluster V	75	24 × 37-2275, 27 × 49- 14, 27 × 49- 16, 27 × 49- 27-1, 49 × 27-13 (ii), 49 × 37- 99(b) tall, 49 × 37-91, 49 × 37-97-1, 49 × 39-20-2, BAU 13, CS 39, CSMG 84-1, DTG 3, ICGs 10053, 10185, 10701, 111, 11322, 12370, 13895, 14705, 14834, 15190, 156 (M 13), 2773, 2857, 3053, 4343, 532, 5663, 5745, 5891, 6766, 9961, ICGVs 00351, 00440, 01393, 01478, 02242, 02290, 02298, 03064, 05176, 05198, 06110, 06188, 06234, 07359, 07368, 86072, 09112, 86325, 86564, 87187, 88438, 90320, 93216, 94169, 95058, 97045, 97116, 97182, 97183, 98432, 99083, ICR 48, SPS 13, SPS 17, TDG 10, TG 39, TG 41, TG 42, TG 49, TMV 2, TPG 41
Cluster VI	1	SunOleic 95R
Cluster VII	34	26 × 37-IV- 9IR, 26 × M-223-1, 26 × M-95-1 RI, 26 M 156-2, 27 × 49- 12, 39 × 49 -77, 39 × 49-81-1, 49 × 37-134, 49 × 37-90, 49 × 39-21-1, 49 × 39-21-2, 49 × 39-74, 49 × 39-8, ICGs 11088, 12276, 12509, 12625, 14475, 14482, 15419, 5221, 5662, 6022, 6646, ICGVs 01124, 06424, 07210, 07220, 87921, 97058, 99085, M 28-2, SPS 14, TDG 13

Table 4.30a Cluster means for yield and its contributing traits used for assessment of genetic diversity at Aliyarnagar during rainy season 2015

Cluster	DFF	LLS90	LLS105	Rust90	Rust105	PH	NPP	PYPP	SH %	HSW	DM	PYH
Cluster I	31.36	3.70	6.52	3.09	6.23	34.15	22.30	16.34	61.51	34.12	109.73	2191.73
Cluster II	31.10	2.81	5.23	2.62	4.85	36.52	16.43	11.55	56.90	30.92	113.04	1869.36
Cluster III	28.29	5.76	7.71	6.44	7.85	39.99	12.80	8.89	63.54	27.95	106.04	1047.45
Cluster IV	30.72	5.19	7.61	5.22	7.28	33.85	14.95	11.53	61.16	33.43	105.47	1204.36
Cluster V	30.60	4.96	7.57	5.41	7.41	35.33	12.14	10.16	60.21	39.16	108.51	1213.71
Cluster VI	29.00	6.00	8.00	5.00	7.00	29.02	10.04	7.13	56.79	28.65	104.55	897.20
Cluster VII	29.85	4.00	7.03	4.53	6.88	36.75	12.99	9.57	57.51	30.90	107.49	1275.08

Where; DFF= Days to 50% flowering; LLS90, LLS 105, Rust90 & Rust105= Disease severity score of late leaf spot and rust recorded at 90 and 105 days after sowing, respectively; PH = Plant height (cm); NPP= Number of pods plant^{-1}; PYPP= Pod yield plant^{-1} (g); SH %= Shelling percent; DM= Days to physiological maturity; HSW= Hundred seed weight (g); PYH= Pod yield hectare^{-1} (kg).

Table 4.30b Cluster means for nutritional quality traits used for assessment of genetic diversity at Aliyarnagar during rainy season 2015

Cluster	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
Cluster I	54.44	20.68	38.19	42.41	12.32	2.35	0.92
Cluster II	55.47	20.05	40.45	41.29	12.23	2.21	1.02
Cluster III	53.62	19.42	41.74	40.06	11.68	2.12	1.07
Cluster VI	52.10	22.01	36.87	43.43	12.42	2.24	0.86
Cluster V	50.45	20.94	45.36	36.33	11.05	2.01	1.27
Cluster VI	52.15	21.53	74.38	5.30	8.50	2.13	14.03
Cluster VII	57.00	18.65	46.79	37.69	10.53	2.48	1.30

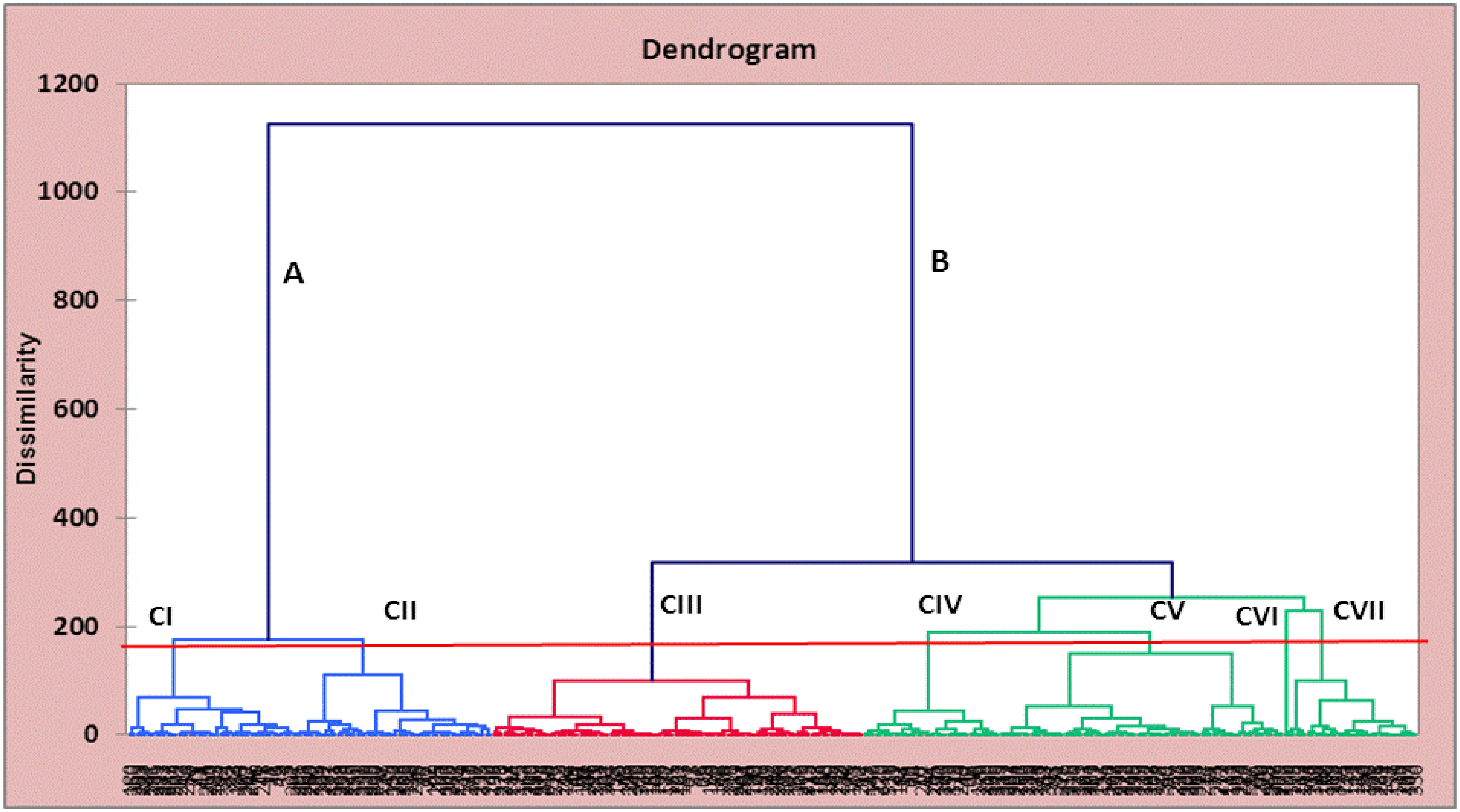

Figure 4.7 Hierarchical cluster analysis (Ward's method 1963) of 340 genotypes of Genomic Selection Panel of groundnut evaluated for disease resistance, yield and nutritional quality traits at Aliyarnagar during rainy season 2015

Table 4.31 Details of genotypes grouped into different clusters in Ward's hierarchical clustering at Jalgaon during rainy season 2015

Cluster	Number	Genotypes
Cluster I	31	49 × 37-90, DH 86, DTG 3, ICG 111, ICG 11322, ICG 5891, ICGVs 00068, 00290, 00346, 00371, 01361, 02287, 02317, 02446, 03207, 03397, 04044, 04115, 04124, 05057, 05141, 06175, 07148, 07227, 07246, 86590 , 87846, 98184, M 110-14, M 28-2, TDG 14
Cluster II	51	49 M-16, ICGV 00005, 00191, 00246, 00248, 00350, 00351, 01273, 01274, 01276, 02206, 02321, 02323, 02411, 03042, 03043, 03056, 03064, 03128, 04087, 05032, 05036, 05100, 05155, 05161, 05163, 06040, 06042, 06099, 06100, 06142, 06347, 06420, 06422, 06423, 06424, 07120, 07145, 07223, 07235, 07247, 87921, 95469, 97128, 97182, 98105, 98163, 99051, 99052, 99160, SPS 11
Cluster III	63	26 × 37-IV- 9IR, 26 M 156-2, 39 × 49 -77, 39× 49-81-1, 49 × 37-135, 49 × 39-21-2(a), 49 × 39-74, 49 × 39-8, DTG 15, ICGs 11088, 12672, 12879, 12991, 14985, 1668, 1834, 1973, 2031, 2106, 3102, 3312, 3421, 3584, 3746, 442, 4543, 4729, 4955, 9315, ICGVs 00349, 01005, 01495, 02298, 04149, 06431, 07210, 07268, 13238, 86011, 86072, 86325, 87378, 88145, 90320, 91114, 92195, 92267, 93280, 94169, 95070, 95058, 96468, 97120, 97261, 99181, ICR 48, J 11, JL 24, M 28-2, SPS 10 , TDG 10, TG 19, TG 49,
Cluster IV	18	27 × 49- 27-1, 39 × 49 -8, 49 × 27-13 (ii), 49 × 37- 99(b) tall, 49 × 37-91, 49 × 37-97-1, 49 × 39-20-2, 49 M- 1-1, ICGV 00321, 00440, 01478, 06110, SPS 13, TG 39, TG 41, TG 42, TG LPS 3, TG LPS 7
Cluster V	56	26 × M-223-1, 26 × M-95-1 RI, 26 M- 119-1, 26× 27-164, 49 × 39-21-1, Faizpur 1-5, Gangapuri, ICGs 10701, 14705, 15415, 3343, 3673, 434, 5663, 8517, 9507, ICGS 11 , ICGS 44, ICGV 00343, 00387, 01232, 02022, 02038, 02125, 02144, 02189, 02194, 02251, 02271, 02286, 03398, 06049, 07023, 07217, 07273, 13242, 13245, 86015, 86352, 91116, 93437, 93470, 94361, 95290, 96466, 97092, 97183, 97232, 97262, 99195, 98294, Mutant 3, SPS 6, TAG 24, TMV 2, TMV 2 NLM
Cluster VI	1	SunOleic 95R
Cluster VII	33	24 × 37-2275, 24 × 39-31 MR, 27 × 49- 14, 27 × 49- 16, 49 × 39-21-2, GPBD 4, ICGs 10053, 10185, 12625, 15419, 2381, 5221, 6022, 6646, ICGVs 01060, 01263, 02242, 03184, 04018, 06234, 86564, 94118, 95377, 97045, 99029, 99083, 99085, 99233, Somnath, SPS 20, SPS 3, TKG 19A, TPG 41
Cluster VIII	87	24 M-86, 27 × 49- 12, 49 × 27-19, 49 × 27-37, 49 × 37-134, 49 M-2-2, BAU 13, CS 39, CSMG 84-1, ICGs 10036, 11337 , 11426, 11651, 12276, 12370, 12509, 13895, 14466, 14475, 14482, 14834, 15190, 156 , 2773, 2857, 3027, 3053, 3140, 4343, 4527, 532, 5662, 5745, 6766, 721, 8285, 875, 8751, 9961, ICGS 76, ICGVs 00362, 01124, 01265, 01328, 01393, 01464, 02266, 02290, 02434, 05176, 03136, 05198, 06188, 07166, 07168, 07220, 07359, 07368, 09112, 13241, 86143, 86699, 87160, 87187 , 87354, 88438, 89104, 93216, 93920, 97058, 97115, 97116, 97165, 98373, 98432, MN1-35, SPS 1, SPS 14, SPS 15, SPS 17, SPS 2, SPS 21, SPS 7, SPS 8, SPS 9, TDG 13, TG LPS 4

Table 4.32a Cluster means for different yield and yield contributing traits used for assessment of genetic diversity at Jalgaon during rainy season 2015

Cluster	DFF	LLS90	LLS105	Rust90	Rust105	PH	NPP	PYPP	SH %	HSW	DM	PYH
Cluster I	32.38	2.77	3.71	2.52	3.35	38.76	16.31	10.39	58.42	33.18	123.32	1614.05
Cluster II	31.36	2.71	3.94	2.41	3.18	44.91	24.05	16.21	59.17	33.87	127.61	2769.11
Cluster III	29.31	3.98	5.89	3.90	5.76	42.96	18.37	11.95	61.56	31.92	117.96	1626.32
Cluster IV	31.06	4.06	6.00	4.00	5.94	35.50	15.56	12.86	56.84	46.70	125.44	1753.42
Cluster V	29.47	4.07	6.13	3.50	5.07	43.43	14.78	9.67	60.20	32.07	117.31	1500.70
Cluster VI	28.16	3.00	5.00	3.00	4.00	37.38	16.01	10.60	63.06	32.87	113.98	1415.28
Cluster VII	28.46	3.00	4.58	2.91	4.18	51.66	12.27	8.96	55.75	36.13	124.86	1298.63
Cluster VIII	31.12	2.70	3.90	2.43	3.41	40.52	10.68	6.80	54.56	32.39	123.30	1009.30

Where; DFF= Days to 50% flowering; LLS90, LLS 105, Rust90 & Rust105= Disease severity score of late leaf spot and rust recorded at 90 and 105 days after sowing, respectively; PH = Plant height (cm); NPP= Number of pods plant^{-1}, PYPP= Pod yield plant^{-1} (g); SH%= Shelling percent; DM= Days to physiological maturity; HSW= Hundred seed weight (g); PYH= Pod yield hectare^{-1} (kg)

Table 4.32b Cluster means for nutritional quality traits used for assessment of genetic diversity at Jalgaon during rainy season 2015

Cluster	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
Cluster I	54.54	19.07	34.85	45.64	12.44	2.22	0.77
Cluster II	57.43	18.65	31.72	48.57	13.06	2.38	0.66
Cluster III	54.09	18.36	42.10	39.79	11.34	2.02	1.08
Cluster IV	49.95	20.93	41.12	39.95	11.46	1.82	1.04
Cluster V	52.02	21.59	36.54	43.98	12.20	2.04	0.85
Cluster VI	54.24	19.02	80.47	5.12	6.98	1.89	15.71
Cluster VII	55.08	19.78	41.95	40.68	10.82	2.64	1.06
Cluster VIII	52.10	19.79	41.62	39.43	11.90	1.83	1.08

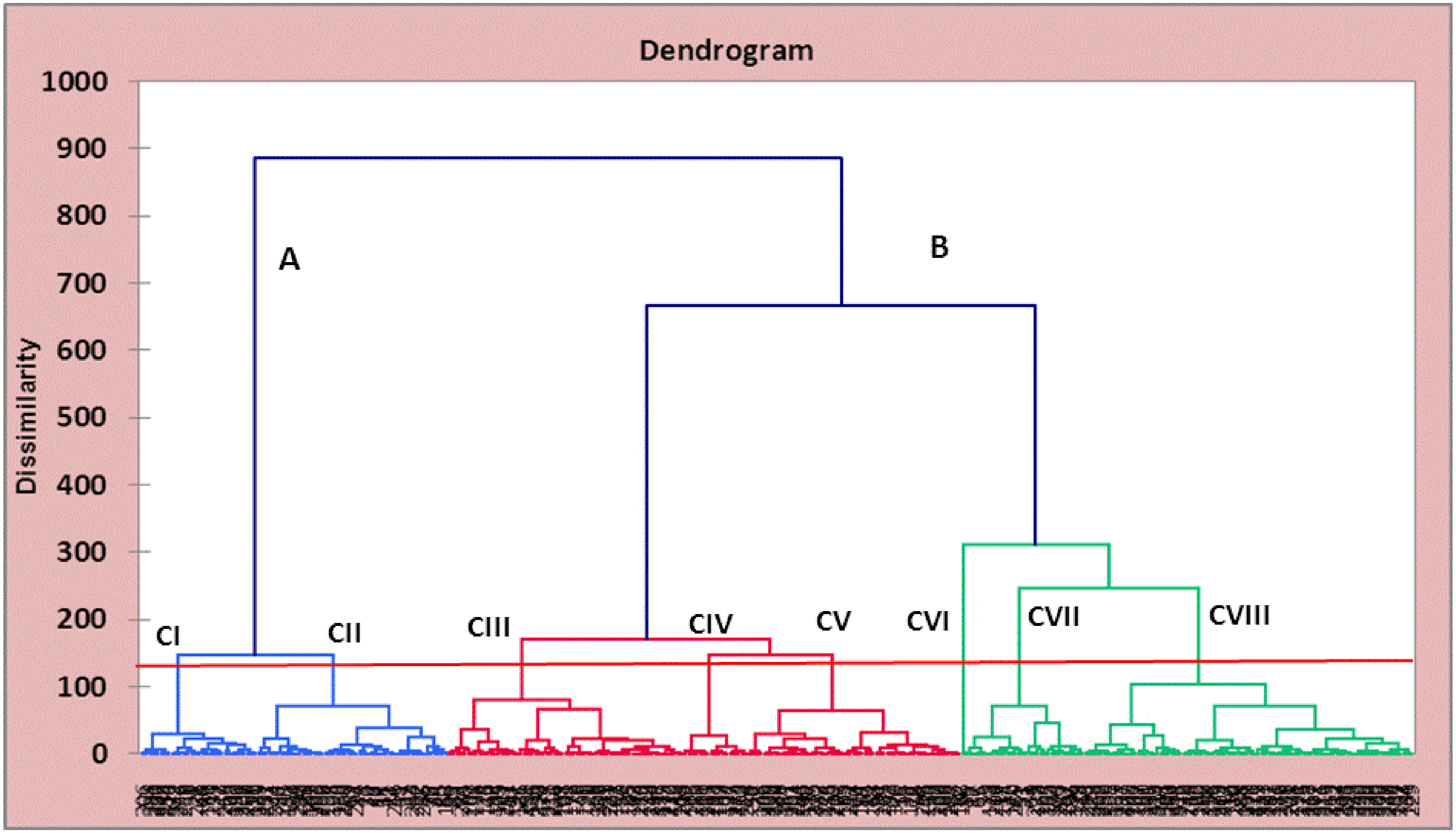

Figure 4.8 Hierarchical cluster analysis (Ward's method 1963) of 340 genotypes of Genomic Selection Panel of groundnut evaluated for disease resistance, yield and nutritional quality traits at Jalgaon during rainy season 2015

Table 4.33 Details of genotypes grouped into different clusters in Ward's hierarchical clustering at ICRISAT during rainy season 2015

Cluster	Number	Genotypes
Cluster I	78	24 × 37-2275, 26 M 156-2, 27 × 49- 14, 27 × 49- 16, 27 × 49- 27-1, 49 × 27-13 (ii), 49 × 27-19, 49 × 37- 99(b) tall, 49 × 37-91, 49 × 37-97-1, 49 × 39-20-2, 49 × 39-21-2, 49 M-2-2, BAU 13, DH 86, ICGs 10036, 10053, 10185, 111, 12370, 13895, 14466, 14834, 14985, 15190, 156 (M 13), 2773, 2857, 3027, 3053, 4343, 4527, 532, 5662, 5663, 5745, 6766, 721, 8285, 875, 9507, ICGVs 00321, 00343, 00440, 01393, 01464, 01478, 02298, 03136, 05176, 03398, 05198, 06110, 06188, 06234, 07359, 07368, 86143, 86564, 88438, 97045, 97116, 97165, 97183, 98432, 99083, SPS 13, SPS 17, SPS 3, TG 39, TG 41, TG 42, TG 49, TG LPS 3, TG LPS 4, TG LPS 7, TMV 2, TPG 41
Cluster II	61	26 × 37-IV- 9IR, 26 M- 119-1, 49 × 37-135, DTG 15, DTG 3, Gangapuri, ICGs 12672, 12991, 1668, 1973, 2031, 2106, 3102, 3140, 3343, 3584, 3673, 3746, 442, 4543, 4729, 4955, 6646, 8517, 8751, ICGVs 01005, 02022, 02038, 02189, 02194, 02251, 03207, 04018, 06049, 06431, 07148, 07273, 13238, 13241, 13242, 13245, 86352, 87354, 87378, 88145, 89104, 91114, 91116, 92195, 93470, 93437, 97232, 97261, J 11, JL 24, MN1-35, Mutant 3, SPS 10 , SPS 6, TAG 24, TMV 2 NLM
Cluster III	74	26 × 27-164, 26 × M-223-1, 39 × 49 -8, 49 × 37-134, 49 × 37-90, 49 × 39-21-1, 49 × 39-21-2(a), 49 × 39-8, CSMG 84-1, Faizpur 1-5, ICGs 10701, 11322, 11651, 12879, 14705, 1834, 3312, 3421, 434, 5891, 9315, 9961, ICGS 11, ICGS 44, ICGVs 00005, 00349, 00371, 00387, 01124, 01263, 02125, 02144, 02206, 02242, 02290, 03128, 03397, 04124, 04149, 06042, 06347, 07023, 07168, 07210, 07217, 07268, 09112, 86011, 86015, 86325, 86072, 87160, 87187, 90320, 93216, 93920, 94169, 94361, 95058, 95070, 95377, 95469, 96466, 96468, 97058, 97120, 97262, 99181, 99195, 13895, ICR 48, TDG 10, TDG 14, TG 19, TKG 19A
Cluster IV	1	SunOleic 95R
Cluster V	32	26 × M-95-1 RI, 27 × 49- 12, 39 × 49-81-1, 49 × 39-74, GPBD 4, ICGs 11088, 11337 , 11426, 12276, 12509, 12625, 14475, 14482, 15419, 2381, 5221, 6022, ICGVs 01328, 05141, 06424, 07220, 86699, 99085, SPS 1, SPS 14, SPS 15, SPS 2, SPS 20, SPS 21, SPS 7, SPS 8, 14985, SPS 9
Cluster VI	44	39 × 49 -77, 49 × 27-37, ICG 15415, ICGVs 00290, 00346, 00350, 00351, 01060, 01232, 01495, 02266, 02271, 02286, 02287, 02317, 02321, 02434, 03056, 03064, 03184, 04044, 04115, 05155, 05161, 06040, 06099, 06100, 07145, 07166, 07227, 87921, 92267, 93280, 94118, 95290, 97092, 97115, 97182, 98163, 98184, 98294, 99233, Somnath, TDG 13
Cluster VII	50	24 × 39-31 MR, 24 M-86, 49 M- 1-1, 49 M-16, CS 39, ICGS 76, ICGVs 00068, 00191, 00246, 00248, 00362, 01265, 01273, 01274, 01276, 01361, 02323, 02411, 02446, 03042, 03043, 04087, 05032, 05036, 05057, 05100, 05163, 06142, 06175, 06420, 06422, 06423, 07120, 07223, 07235, 07246, 07247, 86590 , 87846, 97128, 98105, 98373, 99029, 99051, 99052, 99160, M 110-14, M 28-2, M 28-2, SPS 11

Table 4.34a Cluster means for different yield and yield contributing traits used for assessment of genetic diversity at ICRISAT during rainy season 2015

Cluster	DFF	LLS90	LLS105	Rust90	Rust105	PH	NPP	PYPP	SH %	HSW	DM	PYH	HLM
Cluster I	30.94	7.14	8.59	6.50	8.28	33.03	9.65	7.86	54.56	36.29	110.97	1167.19	15.56
Cluster II	26.55	7.89	8.93	7.16	8.89	39.34	14.85	8.28	58.21	25.04	105.70	1089.42	15.80
Cluster III	28.82	7.22	8.78	6.53	8.51	33.65	14.05	9.08	59.61	30.73	105.22	1485.92	13.31
Cluster IV	26.94	8.00	9.00	8.00	9.00	28.17	12.04	7.08	62.16	25.68	100.28	977.85	15.39
Cluster V	29.85	4.97	6.38	4.09	5.84	37.35	14.69	10.54	57.88	32.16	111.77	1453.70	20.00
Cluster VI	28.56	6.68	8.57	5.50	7.55	36.91	19.13	13.88	56.28	33.83	106.56	2265.00	16.09
Cluster VII	30.70	4.58	6.46	3.32	5.28	34.45	17.94	14.55	59.05	36.51	118.46	2376.97	18.99

Where; DFF= Days to 50% flowering, LLS90, LLS 105, Rust90 & Rust105= Disease severity score of late leaf spot and rust recorded at 90 and 105 days after sowing, respectively, PH = Plant height (cm), NPP= Number of pods plant^{-1}, PYPP= Pod yield plant^{-1} (g), SH %= Shelling percent, DM= Days to physiological maturity, HSW= Hundred seed weight (g), PYH= Pod yield hectare^{-1} (kg), HLM = Haulm weight plant^{-1} (g)

Table 4.34b Cluster means for different nutritional quality traits used for assessment of genetic diversity at ICRISAT during rainy season 2015

Cluster	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
Cluster I	44.82	25.10	44.88	33.53	11.34	1.46	1.37
Cluster II	48.00	22.99	45.10	34.71	11.33	1.04	1.32
Cluster III	48.13	23.61	42.42	36.74	11.53	1.68	1.19
Cluster IV	46.06	25.37	76.03	6.12	7.89	1.45	12.76
Cluster V	53.59	22.66	50.36	31.59	11.46	1.89	1.64
Cluster VI	49.94	24.45	37.67	40.64	12.26	2.05	0.94
Cluster VII	50.97	25.10	36.97	40.52	12.73	2.14	0.92

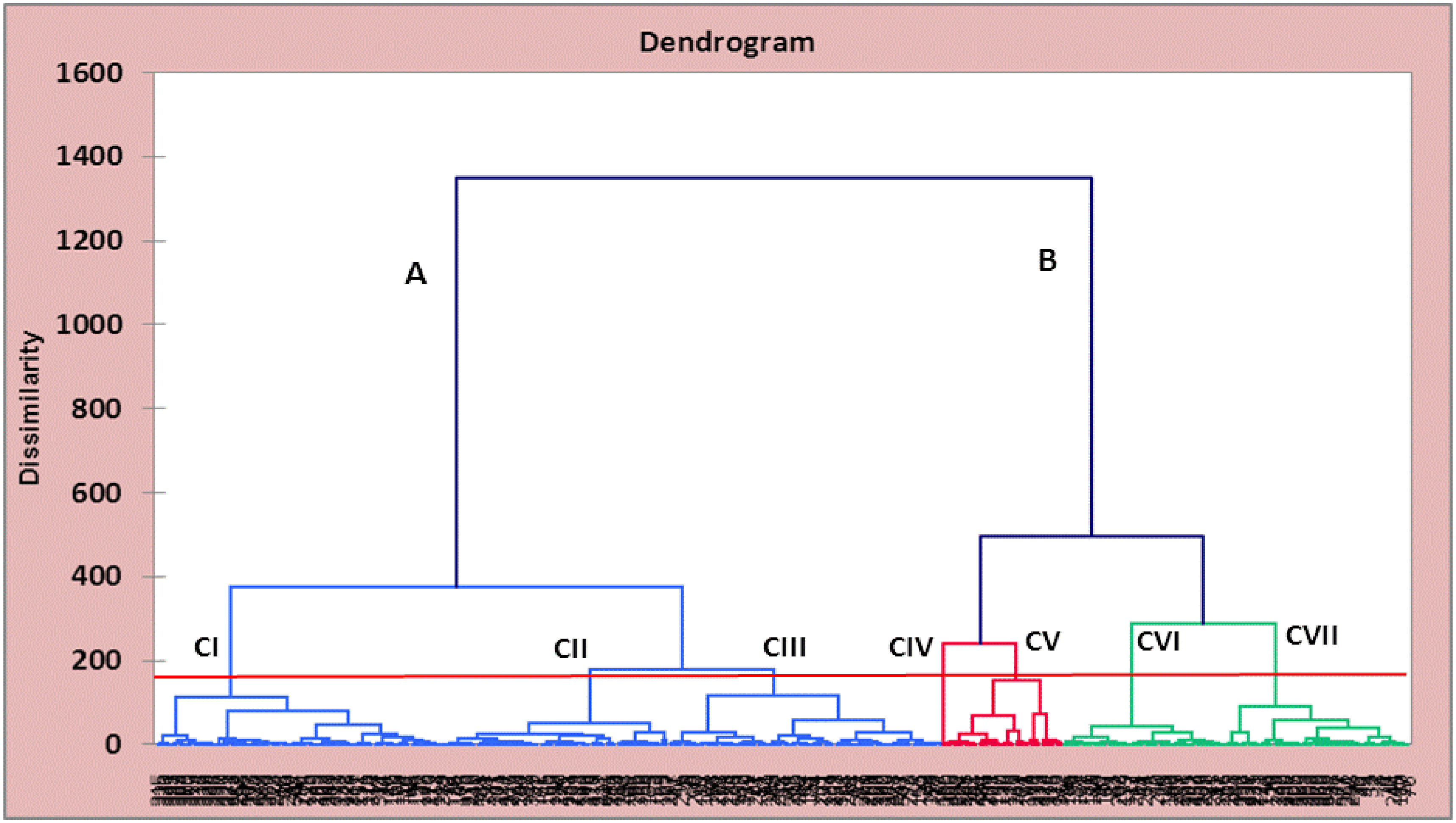

Figure 4.9 Hierarchical cluster analysis (Ward's method 1963) of 340 genotypes of Genomic Selection Panel of groundnut evaluated for disease resistance, yield and nutritional quality traits at ICRISAT during rainy season 2015

Table 4.35 Details of genotypes grouped into different clusters in Ward's hierarchical clustering at ICRISAT during post-rainy season 2015-16

Cluster	Number	Genotypes
Cluster I	1	SunOleic 95R
Cluster II	67	24 M-86, 26 × M-223-1, 49 × 37-90, 49 × 39-20-2, 49 × 39-21-2, 49 M- 1-1, 49 M-2-2, CSMG 84-1, ICGs 10036, 11322, 12370, 13895, 14466, 14834, 15190, 2773, 2857, 3027, 3053, 4343, 4527, 532, 5662, 5663, 5891, 6766, 875, 9507, ICGS 44, ICGVs 00068, 00246, 00362, 01265, 01393, 01464, 02287, 03397, 03398, 04115, 05100, 06040, 06110, 06142, 06175, 06420, 06424, 07168, 86143, 86590 , 95058, 87354, 95070, 97092, 97115, 97165, 97262, 98163, 99052, 99160, ICR 48, M 110-14, M 28-2, TDG 13, TDG 14, TG 39, TG 42, TG LPS 7
Cluster III	37	49 × 37- 99(b) tall, 49 × 39-21-1, GPBD 4, ICGs 10185, 11337 , 11426, 12276, 12625, 14475, 14482, 14985, 15419, 2381, 5221, 6022, 9961, ICGVs 00440, 01124, 02298, 03064, 05161, 07220, 86325, 86564, 86699, 87187, 88438, 97045, 97116, 98432, SPS 15, SPS 2, SPS 20, SPS 21, SPS 7, SPS 8, TG 41
Cluster IV	116	24 × 39-31 MR, 26 × M-95-1 RI, 26 M- 119-1, 27 × 49- 12, 39 × 49 -77, 39 × 49 -8, 39 × 49-81-1, 49 × 27-37, 49 × 37-135, 49 × 39-21-2(a), 49 × 39-74, 49 × 39-8, 49 M-16, DTG 15, DTG 3, Faizpur 1-5, Gangapuri, ICGs 10701, 111, 11651, 12672, 12879, 12991, 14705, 15415, 1668, 1834, 1973, 2031, 2106, 3102, 3140, 3312, 3343, 3421, 3584, 3673, 3746, 442, 4543, 4729, 4955, 8517, 9315, ICGVs 00321, 00349, 01005, 01060, 01232, 01276, 01274, 01328, 02022, 02038, 02125, 02189, 02194, 02251, 02266, 02286, 03207, 04018, 04149, 06049, 06431, 07023, 07148, 07166, 07210, 07217, 07273, 13238, 13241, 13242, 13245, 86011, 86015, 86352, 87160, 87378, 87921, 88145, 89104, 91114, 91116, 92195, 92267, 93216, 93437, 93470, 95290, 96466, 96468, 97183, 97261, 97232, 99181, 99195, 99233, J 11, JL 24, MN1-35, Mutant 3, Somnath, SPS 1, SPS 10 , SPS 11, SPS 14, SPS 3, SPS 6, SPS 9, TAG 24, TDG 10, TG 19, TG LPS 4, TMV 2 NLM
Cluster V	35	26 × 37-IV- 9IR, 27 × 49- 16, 27 × 49- 27-1, 49 × 27-19, 49 × 37-134, CS 39, ICGs 10053, 11088, 5745, 6646, ICGVs 00351, 01263, 01495, 02144, 02242, 03128, 05032, 05176, 05198, 06188, 06234, 07247, 07359, 07368, 90320, 93920, 94169, 95377, 97120, 98294, 99085, SPS 13, TG 49, TG LPS 3, TMV 2
Cluster VI	84	24 × 37-2275, 26 × 27-164, 26 M 156-2, 27 × 49- 14, 49 × 27-13 (ii), 49 × 37-91, 49 × 37-97-1, BAU 13, DH 86, ICGs 12509, 156 (M 13), 434, 721, 8285, 8751, ICGS 11, ICGS 76, ICGVs 00005, 00191, 00248, 00290, 00343, 00346, 00350, 00371, 00387, 01273, 01361, 01478, 02206, 02271, 02290, 02317, 02321, 02323, 02411, 02434, 02446, 03042, 03043, 03056, 03136, 03184, 04044, 04087, 04124, 05036, 05057, 05141, 05163, 05155, 06042, 06099, 06100, 06347, 06422, 06423, 07120, 07145, 07223, 07227, 07235, 07246, 07268, 09112, 86072, 87846, 93280, 94118, 94361, 95469, 97058, 97128, 97182, 98105, 98184, 98373, 99029, 99051, 99083, M 28-2, SPS 17, TKG 19A, TPG 41

Table 4.36a Cluster means for different yield and yield contributing traits used for assessment of genetic diversity at ICRISAT during post-rainy season 2015

Cluster	DFF	PH	NPP	PYPP	SH%	HSW	DM	PYH	HLM
Cluster I	41.00	16.95	4.50	2.77	49.81	29.51	144.00	687.45	16.60
Cluster II	44.89	18.92	5.74	3.50	53.69	29.23	146.61	829.10	20.15
Cluster III	43.81	20.40	7.03	4.42	55.15	29.85	145.99	1014.07	23.75
Cluster IV	39.57	23.16	12.39	7.64	63.52	33.00	133.52	1942.27	13.72
Cluster V	41.98	24.62	12.76	9.74	59.86	42.81	145.14	2384.79	21.74
Cluster VI	43.27	22.90	11.97	7.44	60.08	36.50	146.89	1851.92	23.83

Where; DFF= Days to 50% flowering, PH = Plant height (cm), NPP= Number of pods plant^{-1}, PYPP= Pod yield plant^{-1} (g), SH %= Shelling percent, DM= Days to physiological maturity, HSW= Hundred seed weight (g), PYH= Pod yield hectare^{-1} (kg), HLM = Haulm weight plant^{-1} (g)

Table 4.36b Cluster means for different nutritional quality traits used for assessment of genetic diversity at ICRISAT during post-rainy season 2015

Cluster	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
Cluster I	49.33	26.43	76.06	4.60	7.08	2.02	16.53
Cluster II	48.70	27.23	43.05	34.76	12.78	2.45	1.29
Cluster III	52.19	24.60	50.89	30.04	11.53	2.46	1.75
Cluster IV	48.67	27.46	43.17	35.73	12.38	2.16	1.23
Cluster V	47.13	27.16	47.59	31.10	11.92	2.28	1.57
Cluster VI	49.29	26.13	40.46	37.14	13.18	2.43	1.12

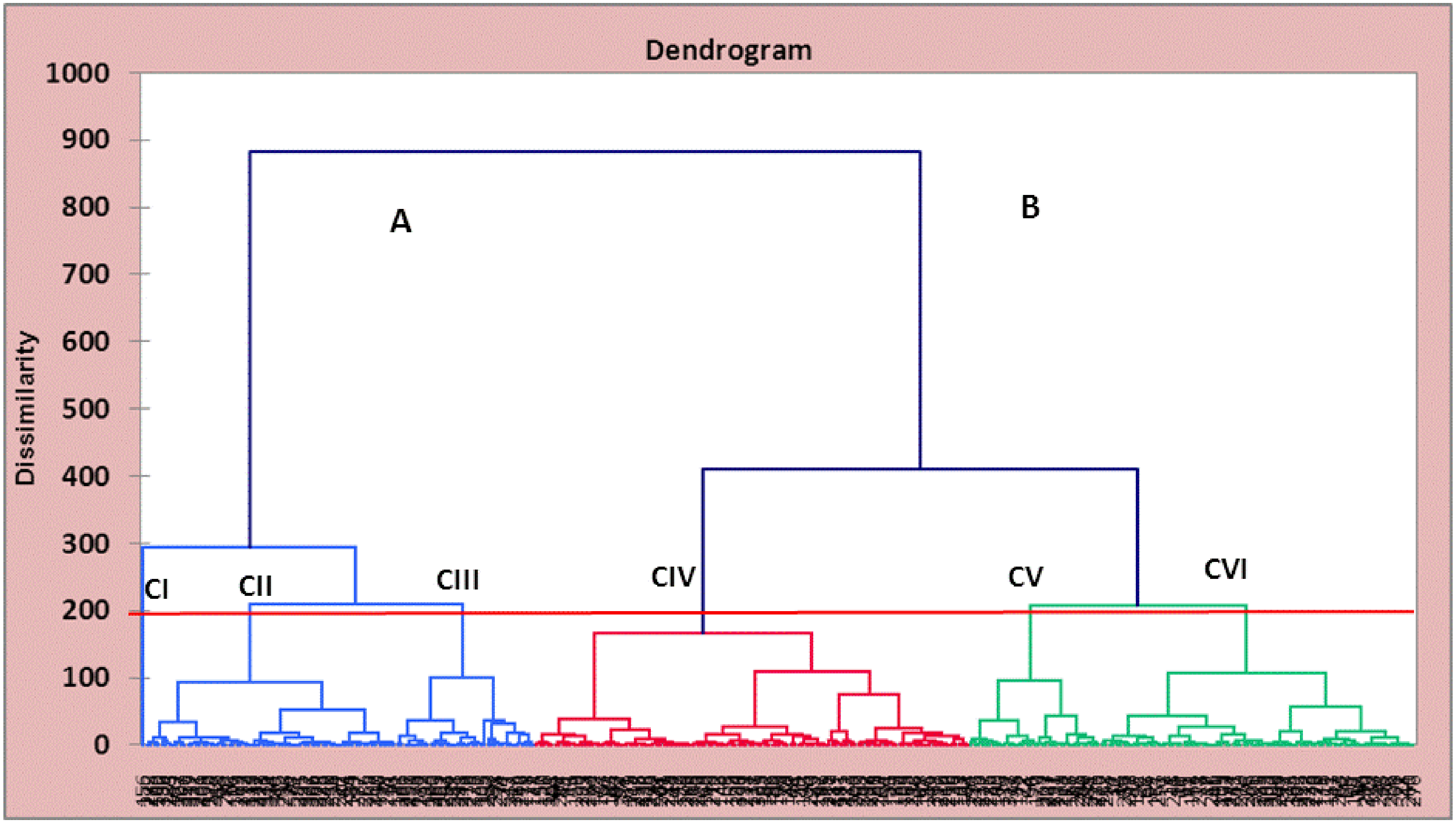

Figure 4.10 Hierarchical cluster analysis (Ward's method 1963) of 340 genotypes of Genomic Selection Panel of groundnut evaluated for disease resistance, yield and nutritional quality traits at ICRISAT during post-rainy season 2015-16

Table 4.37 Details of genotypes grouped into different clusters in Ward’s hierarchical clustering across the environments

Cluster	Number	Genotypes
Cluster I	49	49 M-16, ICGVs 00191, 00246, 00248, 00346, 01273, 01274, 01276, 01361, 01495, 02317, 02323, 02411, 03042, 03043, 03064, 03128, 04087, 05032, 05036, 05057, 05100, 05155, 05161, 05163, 06040, 06099, 06100, 06142, 06420, 06422, 06423, 07120, 07145, 07166, 07223, 07235, 07246, 07247, 86590 , 87846, 97128, 98105, 98184, 99029, 99051, 99052, 99160, SPS 11
Cluster II	66	24 × 39-31 MR, 24 M-86, 26 × M-223-1, 26 × M-95-1 RI, 26 M 156-2, 39 × 49 -77, 39 × 49 -8, 39× 49-81-1, 49 × 27-37, 49 × 37-90, 49 × 39-21-1, 49 × 39-21-2(a), 49 × 39-74, 49 M- 1-1, CS 39, ICG 10036, ICG 8751, ICGS 76, ICGVs 00005, 00068, 00290, 00350, 00351, 00362, 01060, 01263, 01265, 02206, 02242, 02266, 02286, 02287, 02321, 02434, 02446, 03056, 04044, 04115, 05141, 06042, 06175, 06424, 07148, 07227, 07268, 87921, 90320, 93216, 93280, 94118, 93920, 97115, 97165, 97182, 98163, 98294, 98373, 99233, M 110-14, M 28-2, M 28-2, SPS 1, SPS 14, SPS 9, TDG 13, TDG 14
Cluster III	112	26 M- 119-1, 26× 27-164, 27 × 49- 12, 49 × 37-135, 49 × 37-91, DH 86, DTG 15, DTG 3, Faizpur 1-5, Gangapuri, ICGs 10701, 11322, 11651, 12672, 12879, 12991, 14705, 15415, 1668, 1834, 1973, 2031, 2106, 3102, 3140, 3312, 3343, 3421, 3584, 3673, 3746, 434, 442, 4543, 4729, 4955, 8517, 9315, ICGS 11 , ICGS 44, ICGVs 00321, 00343, 00349, 00371, 00387, 01005, 01232, 02022, 02038, 02144, 02125, 02189, 02194, 02251, 02271, 03184, 03207, 03397, 03398, 04018, 04124, 04149, 06049, 06347, 06431, 07023, 07210, 07217, 07273, 13238, 13241, 13242, 13245, 86011, 86015, 86143, 86352, 87160, 87378, 88145, 91114, 91116, 92195, 92267, 93437, 93470, 94361, 95070, 95290, 95377, 95469, 96466, 96468, 97092, 97232, 97261, 97262, 99083, 99181, 99195, J 11, JL 24, Mutant 3, Somnath, SPS 10 , SPS 3, TAG 24, SPS 6, TDG 10, TG 19, TKG 19A, TMV 2 NLM
Cluster IV	90	24 × 37-2275, 26 × 37-IV- 9IR, 27 × 49- 14, 27 × 49- 16, 27 × 49- 27-1, 49 × 27-13 (ii), 49 × 27-19, 49 × 37- 99(b) tall, 49 × 37-134, 49 × 37-97-1, 49 × 39-20-2, 49 × 39-21-2, 49 × 39-8, 49 M-2-2, BAU 13, CSMG 84-1, ICGs 10053, 10185, 11088, 111, 12370, 12509, 13895, 14466, 14834, 14985, 15190, 156 , 2773, 2857, 3027, 3053, 4343, 4527, 532, 5662, 5663, 5745, 5891, 6766, 721, 8285, 875, 9507, 9961, ICGVs 00440, 01124, 01393, 01464, 02290, 01478, 02298, 03136, 05176, 05198, 06110, 06188, 06234, 07168, 07359, 07368, 09112, 86072, 86325, 86564, 87187 , 87354, 88438, 89104, 94169, 95058, 97045, 97058, 97116, 97120, 97183, 98432, ICR 48, MN1-35, SPS 13, SPS 17, TG 39, TG 41, TG 42, TG 49, TG LPS 3, TG LPS 4, TG LPS 7, TMV 2, TPG 41
Cluster V	1	SunOleic 95R
Cluster VI	22	GPBD 4, ICGs 11337 , ICG 11426, ICG 12276, ICG 12625, ICG 14475, ICG 14482, ICG 15419, ICG 2381, ICG 5221, ICG 6022, ICG 6646, ICGV 01328, ICGV 07220, ICGV 86699, ICGV 99085, SPS 15, SPS 2, SPS 20, SPS 21, SPS 7, SPS 8

Table 4.38a Cluster means for different yield and yield contributing traits used for assessment of genetic diversity across the environments

Cluster	DFF	LLS90	LLS105	Rust90	Rust105	PH	NPP	PYPP	SH	HSW	DM	PYH	HLM
Cluster I	34.06	3.57	5.56	2.80	4.63	34.75	18.38	13.22	58.98	34.73	127.41	2390.17	21.40
Cluster II	33.10	4.30	6.30	3.73	5.75	32.84	15.14	10.26	57.95	32.85	118.78	1684.43	17.39
Cluster III	31.24	5.83	7.49	5.75	7.31	35.68	14.09	8.93	61.63	30.11	116.20	1427.64	14.89
Cluster IV	34.32	5.08	6.91	4.96	6.65	32.63	10.66	8.26	56.87	36.82	122.21	1235.41	18.55
Cluster V	31.20	5.67	7.33	5.33	6.67	28.32	10.71	6.88	57.88	29.12	115.63	1001.71	15.99
Cluster VI	33.67	3.42	5.23	3.33	5.05	36.64	11.35	7.92	56.34	30.17	124.49	1208.85	22.17

Where; DFF= Days to 50% flowering, LLS90, LLS 105, Rust90 & Rust105= Disease severity score of late leaf spot and rust recorded at 90 and 105 days after sowing, respectively; PH = Plant height (cm), NPP= Number of pods plant^{-1}, PYPP= Pod yield plant^{-1} (g), SH %= Shelling percent, DM= Days to physiological maturity, HSW= Hundred seed weight (g), PYH= Pod yield hectare^{-1} (kg), HLM = Haulm weight plant^{-1} (g)

Table 4.38b Cluster means for different nutritional quality traits used for assessment of genetic diversity across the environments

Cluster	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
Cluster I	53.29	22.43	36.19	42.91	12.85	2.30	0.87
Cluster II	51.71	22.60	39.96	39.62	12.23	2.29	1.04
Cluster III	50.77	22.77	41.22	39.00	11.92	1.92	1.09
Cluster IV	49.01	23.07	44.83	35.10	11.54	1.95	1.32
Cluster V	50.60	22.99	78.83	5.61	7.63	1.86	14.09
Cluster VI	55.82	21.30	50.43	33.59	11.09	2.11	1.58

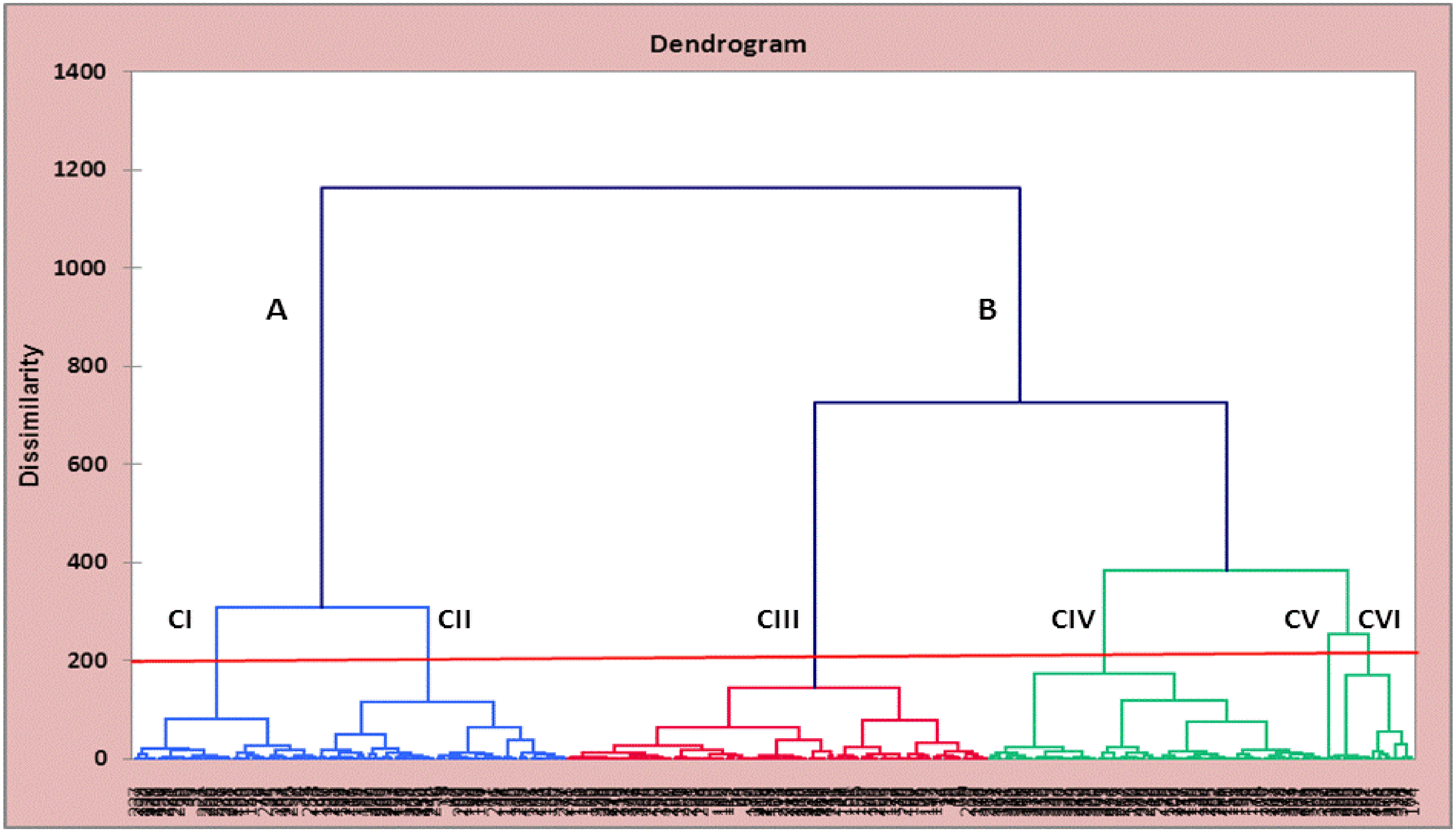

Figure 4.11 Hierarchical cluster analysis (Ward's method 1963) of 340 genotypes of Genomic Selection Panel of groundnut evaluated for disease resistance, yield and nutritional quality traits across the environments

4.4.1.3 ICRISAT, Patancheru (rainy season 2015)

A total 75.35% of genetic variability present in GSP was explained by first six PCs at ICRISAT during rainy 2015. Based on scores of these six PCs, entire GSP was grouped into seven clusters (Table 4.33 & Fig 4.9). The cluster I grouped 78 genotypes recorded lower cluster mean for number of pods per plant (9.65). Cluster II had 61 genotypes with lowest cluster mean for day to 50% flowering (26.6 days) and hundred seed weight (25.0 g) whereas cluster III comprised of 74 genotypes and recorded low cluster mean for haulm weight per plant (13.3 g). SunOleic 95R solely formed cluster IV with highest oleic acid content (76.0%) and O/L ratio (12.8), and lowest linoleic acid (6.1%) and palmitic acid (7.9%) (Table 4.34b). Cluster V had 32 genotypes and recorded high cluster mean for oil content (53.6%) and haulm weight per plant (20.0 g) with low cluster mean for protein content (22.7%) indicating that most of genotypes of this cluster reported higher oil and lower protein content at ICRISAT during rainy season. While cluster VI grouped 44 genotypes had higher cluster mean for pod yield per hectare (2265 kg), number of pods per plant (19.1) and comparatively higher cluster mean for disease severity scores of both diseases indicated that most of the genotypes of this cluster had better yield performance even under disease pressure (Table 4.34a). In contrast to all, cluster VII comprised of 50 genotypes and recorded low cluster mean for disease severity score of LLS and rust at 90 DAS (4.58 & 3.32) with higher cluster mean for pod yield per hectare (2377 kg) and days to maturity (118.5 days) indicated that most of the genotypes possess resistance to both the disease and high yield potential along with late maturity were grouped together in this cluster (Table 4.33 & 4.34a).

4.4.1.4 ICRISAT, Patancheru (post-rainy season 2015-16)

Ward's cluster analysis based on scores of first six PCs which together explained 79.49% of total genetic variability grouped entire GSP into six clusters (Table 4.35 & Fig 4.10). Cluster I had a single genotype SunOleic 95R recorded highest mean performances for oleic acid (76.1%), lowest linoleic acid (4.6%), palmitic acid (7.1%) and high O/L ratio (16.5) indicating its separate identity as high oleic genotype in GSP (Table 4.36b). Cluster II comprised of 67 genotypes and recorded higher cluster mean for days to 50% flowering (44.9 days) with low yield potential (829 kg/ha). 37 out 340 genotypes of GSP grouped in cluster III which recorded higher cluster mean for oil content (52.2%) and lower cluster mean for protein content (24.6%) indicating that genotypes of this cluster had better oil content. Cluster IV comprised of 116 genotypes recorded higher cluster mean for shelling percent (63.5%) and protein content (27.5%) with lowest cluster mean for days to maturity (133.5 days) and haulm weight per plant (13.7 g) indicates that most of the improved genotypes with higher shelling percent, protein content with early maturity were grouped together in this cluster. In contrast to other, cluster V comprised of 35 genotypes of GSP dominated with high yielding genotypes as revealed by higher cluster mean for pod yield per hectare (2385 kg) and hundred seed weight (42.8 g) but with lower cluster mean for oil content (47.1 %). However cluster VI had 84 genotypes and recorded higher cluster mean for days to maturity (146.8 day), haulm weight per plant (23.8g), linoleic acid (37.1%), palmitic acid (13.2%) and a lower cluster mean for oleic acid (40.5%) indicated that most of genotypes with late maturity and lower nutritional quality were grouped together in this cluster (Table 4.35 and 4.36a).

4.4.1.5 Diversity across the environments

Best linear unbiased predictions of mean performance of genotype across the environments were subjected to PCA to calculate different PCs and their contribution towards explaining total genetic variation of GSP. First six PCs together explained 78.49% of total genetic variation, the eigenvectors of these PCs for each genotype was used for clustering the genotypes using wards method of hierarchical clustering which grouped whole GSP into six clusters (Table 4.37 & Fig 4.11). Cluster I grouped 49 genotypes and recorded higher cluster mean for number of pods per plant (18.4), pod yield per plant (13.2 g) haulm weight per plant (21.4 g) and pod yield per hectare (2390 kg/ha) with lowest cluster mean for disease severity score to LLS (3.57) and rust (2.80) indicating that all the high yielding cultivars with resistance to both the diseases were grouped together in this cluster (Table 4.38a). Cluster II comprised of 66 genotypes recorded moderate level of performance for all the traits. Custer III was largest cluster comprised of 112 (32.9%) genotypes recorded high cluster mean for shelling percent (61.6%) and comparatively lower cluster mean for days to maturity (116.2 days). Cluster IV grouped 90 genotypes identified for higher cluster mean for hundred seed weight (36.8g) and protein content (23.1%) along with lower cluster mean for oil content (49.0%) indicated that most of the genotypes of this cluster had higher seed mass with high protein and low oil content across the environments. In contrast to other, cluster V had a single genotype SunOleic 95R recorded highest mean performances for oleic acid (78.8%), lowest linoleic acid (5.6%), palmitic acid (7.6%) and high O/L ratio (14.1) indicating its unique identity as high oleic genotype across the environments (Table 4.37). Cluster VI had 22 genotypes recorded high cluster mean for oil content (55.8%), haulm weight per plant (22.2g) whereas low cluster mean for protein content (21.3%) and pod yield per hectare (1208 kg) indicating that most of the genotypes of this cluster had higher oil content along with low protein content and low yield potential across the environments (Table 4.38a&b).

4.5 Stability analysis

In the present study, 340 genotypes of GSP evaluated for resistance to rust and LLS along with yield and nutritional quality traits across four environments. Of these, the genotypes which had less than three disease severity score for either of the diseases at ICRISAT and Aliyarnagar along with a susceptible check (TMV 2) were subjected to stability analysis to identify the stable source of disease resistance, yield and nutritional quality traits. The stability analysis of this subset (109 genotypes) was done using genotype and genotypes × environment (GGE) biplot technique proposed by Yan *et al.* (2000).

4.5.1 Pooled analysis of variance

The data of all the genotypes of GSP from three different environments *viz.,* Aliyarnagar, Jalgaon and ICRISAT during rainy 2015 were subjected to pooled analysis for disease severity scores whereas, besides these three environments, data from ICRISAT during the post-rainy season were also used for assessing the stability of genotypes for yield and nutritional quality traits.

Pooled analysis of variance revealed significant genotypic differences for all the traits (Table 4.3 & 4.4). The mean square attributable to environment and genotype × environment (G × E) interaction was highly significant for all traits under study. The significance of G × E interaction indicates there is a need to check the stability of genotypes for different traits. The GGE biplot analysis was performed for important traits like disease severity score of rust and LLS at 90 DAS, yield and its important contributing traits, and nutritional quality parameters. The data from multi-environment trials are usually large, and their graphical presentation helps understand the pattern involved in the particular data set. The GGE biplot allows visual examination of the GE interaction pattern of multi-environment data. To construct a meaningful biplot, PC1 and PC2 eigenvectors were plotted after partitioning of singular values into the genotype and environment eigenvectors. Theoretically, the partitioning factors can take any value between 0 and 1. However, for this analysis, a value of 0.5 was used to give equal importance to both the genotypes as well as environments.

4.5.2 Stability of late leaf spot resistance

The biplot analysis, as viewed by the environment vector of genotypes for disease severity to LLS has been presented in Fig 4.12, 4.14 and 4.16. The results of PCA of genotype × environment interaction (GEI) showed that the first two PCs in the biplot explained 87.51% and 89.94% of the total variation due to GEI for LLS and rust at 90 DAS, respectively.

(a) Polygon view of GGE biplot analysis for LLS scores at 90 DAS

The polygon view of a biplot is the best way to visualize the interaction patterns between genotypes and environments to show the presence or absence of crossover GE interaction which is helpful in estimating the possible existence of different mega-environments. Visualization of the "which won where" pattern of MET data is necessary for studying the possible existence of different mega-environments in the target environment. Fig. 4.12 represents a polygon view of MET data of genotypes for LLS scores at 90 DAS. In this biplot, a polygon was formed by connecting the vertex genotypes with straight lines and the rest of the genotypes placed within the polygon. The partitioning of GE interaction through GGE biplot analysis showed that PC1 and PC2 together accounted for 87.51 of GGE sums of squares for LLS at 90 DAS. The vertex genotypes in the biplot were 262, 238, 3, 73, 186, 269, 82, 321, 256 and 268. These genotypes were the best or the poorest genotypes for disease resistance/susceptibility in some or all of the environments because they were farthest from the origin of the biplot. From the polygon view of biplot analysis of MET data of three environments, the genotypes fell in four sections and the test environments fell in two sections. The first section contains the test environments Aliyarnagar and Jalgaon which had the genotype 73 (TMV 2) as the genotype recorded higher disease score at 90 DAS considered most susceptible to LLS across the environments whereas genotypes 262 (ICGV 86699) plotted left side of biplot indicates that this genotypes had lowest disease severity score to LLS. The second section contains the environments ICRISAT_R15 with the genotype 321 (ICG 13895) as the best plotted farthest side biplot.

(b) Mean and stability performance of genotypes for LLS score at 90 DAS

The ranking of 109 genotypes of GSP based on their disease severity score and stability performance are shown in Fig. 4.14. The line passing through the biplot origin is called the average environment axis (AEA), which is defined by the average PC1 and PC2 scores of all environments. A concentric circle drawn on AEA is called Average Environment Coordinate (AEC). The genotypes closer to concentric circle indicates higher mean performance. The line which passes through the biplot origin and is perpendicular to the AEA represents the stability of genotypes. Distance in either direction away from the biplot origin on this axis indicates greater GE interaction and reduced stability. The genotypes on the right side of this perpendicular line performed greater than mean disease severity score across the environments and the genotypes on the left side of this line had lesser score than mean across the environments. For selection, the stable resistant genotypes are those with lowest disease severity and least vector length from AEA. In the biplot, the genotypes plotted left side of biplot and have the shortest vector from the AEA are the superior and stable for disease resistance. The genotype 71 (GPBD 4), 238 (ICGV 00248), 84 (ICGV 06142), 152 (ICGV 02411), 237 (ICGV 00246), 246 (ICGV 00068), 293 (SPS 11), and 301 (ICG 11426) can be considered as stable genotypes with lower disease score and shortest vector length from AEA. The genotype 262 (ICGV 86699) had lowest disease score compared to other with greater vector length from AEA.

(c) Relationship among test environments

The summary of the interrelationships among the test environments has been presented in Fig 4.16. The lines that connect the biplot origin and the markers for the environments are called environment vectors. The angle between the vectors of two environments is related to the correlation coefficient between them. The cosine of the angle between the vectors of two environments approximates the correlation coefficient between them. Acute angles indicate a positive correlation, obtuse angles a negative correlation and right angles indicate no correlation. A short vector may indicate that the test environment is not related to other environments. Based on the angles between environment vectors, all the three environments (Aliyarnagar, Jalgaon, and ICRISAT_R15) were positively correlated with each other because of acute angles ($<90^0$) formed between them. The position of the environment on biplot revealed that ICRISAT_R15 was the best environments where genotypes got higher diseases scores followed by Aliyarnagar and Jalgaon. Jalgaon was the poorest environment plotted nearer to biplot origin indicates that genotypes recorded lower disease scores at Jalgaon. The ranking of environments in with respect to ideal test environments (Fig 4.16) revealed that the ICRISAT_R15 and Aliyarnagar are plotted on border of the inner circle in the biplot indicates that both had similar disease pressure and also revealed that both the environments are ideal for cultivar evaluation against LLS disease.

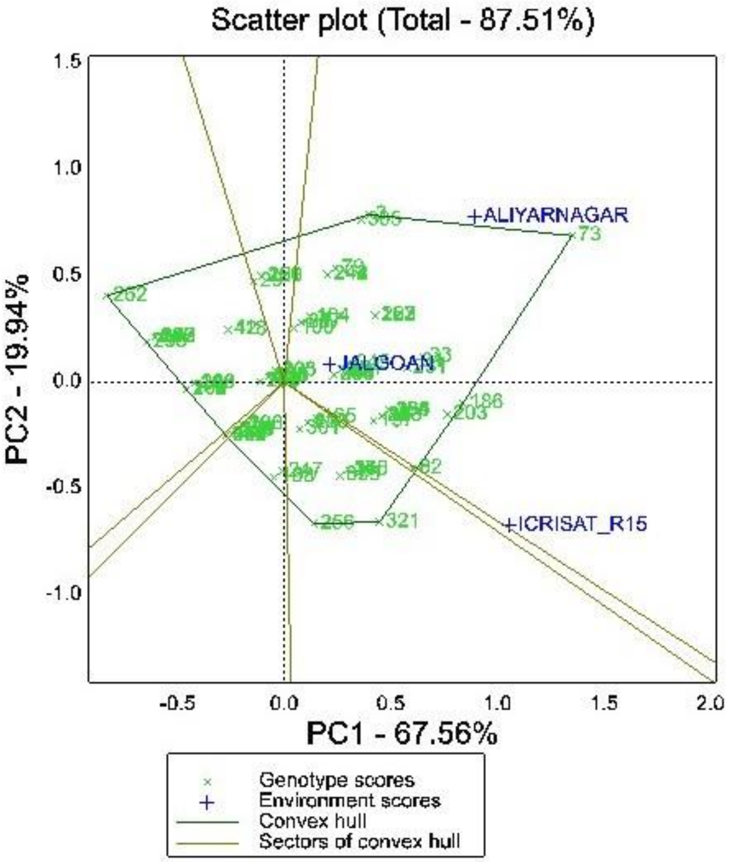

Figure 4.12 Polygon view of scattered biplot showing ranking of genotypes based on which won where pattern for disease severity against late leaf spot at 90 DAS across three locations

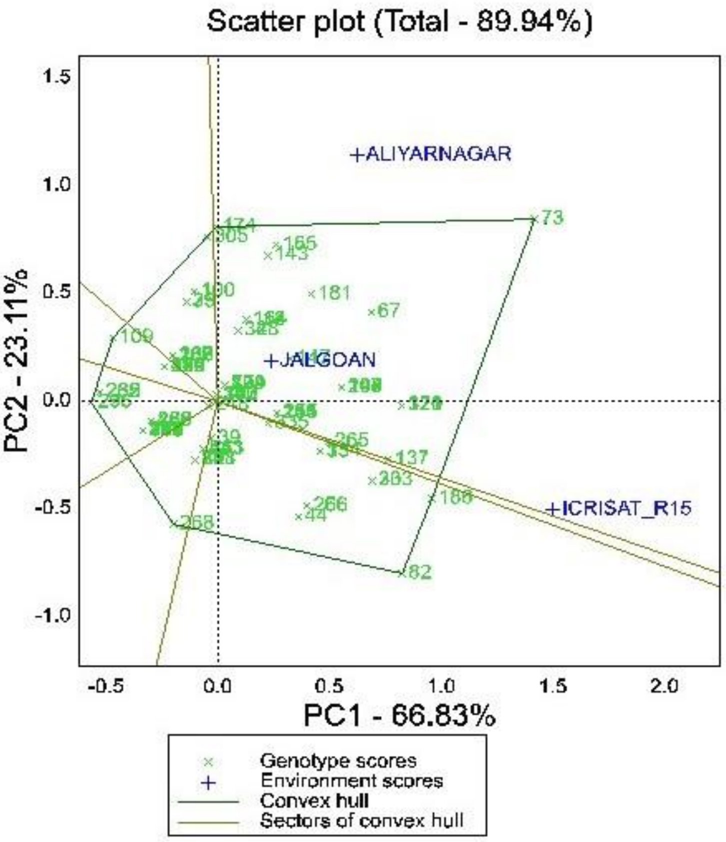

Figure 4.13 Polygon view of scattered biplot showing ranking of genotypes based on which won where pattern for disease severity against rust at 90 DAS across three locations

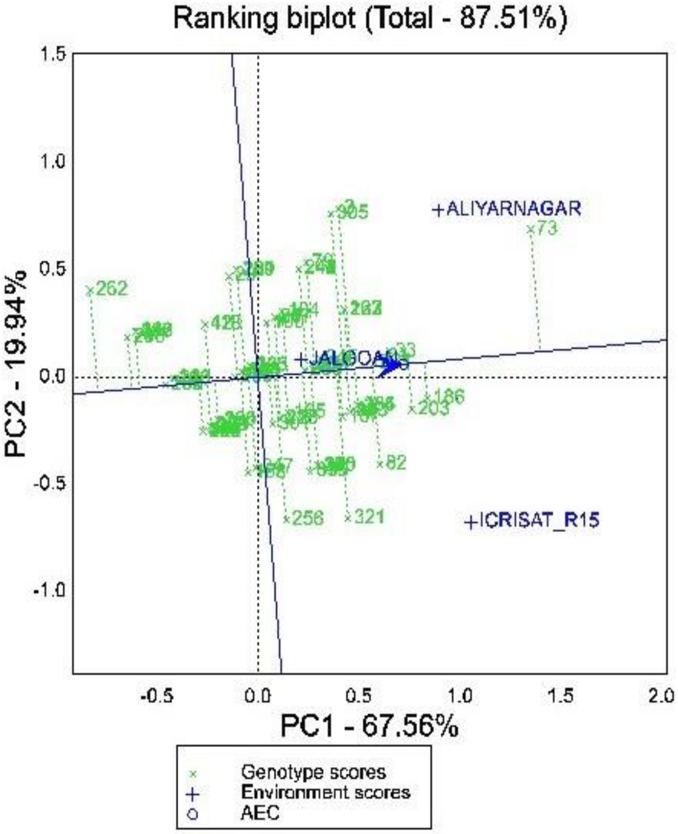

Figure 4.14 GGE biplot showing ranking of genotypes for mean performance and stability for disease severity score to LLS at 90 days after sowing across the three locations

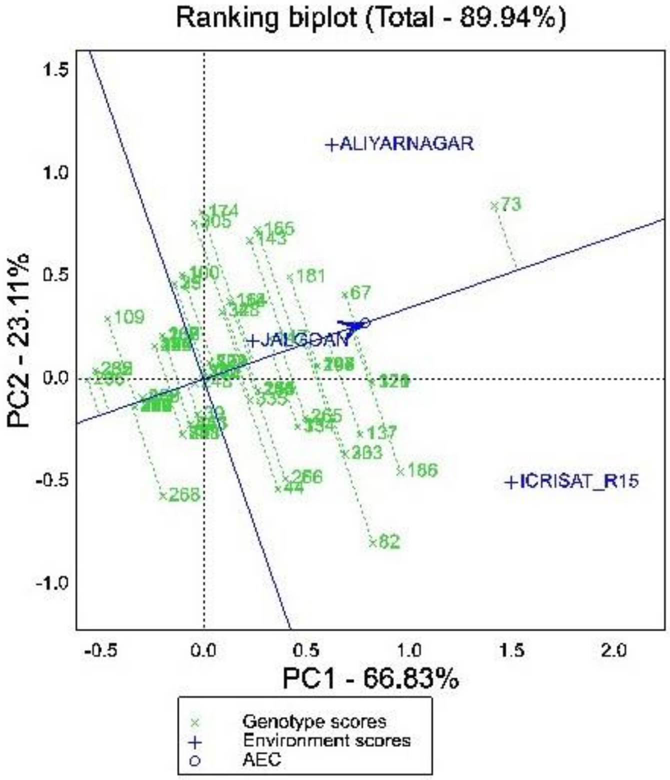

Figure 4.15 GGE biplot showing ranking of genotypes for mean performance and stability for disease severity score to rust at 90 days after sowing across the three locations

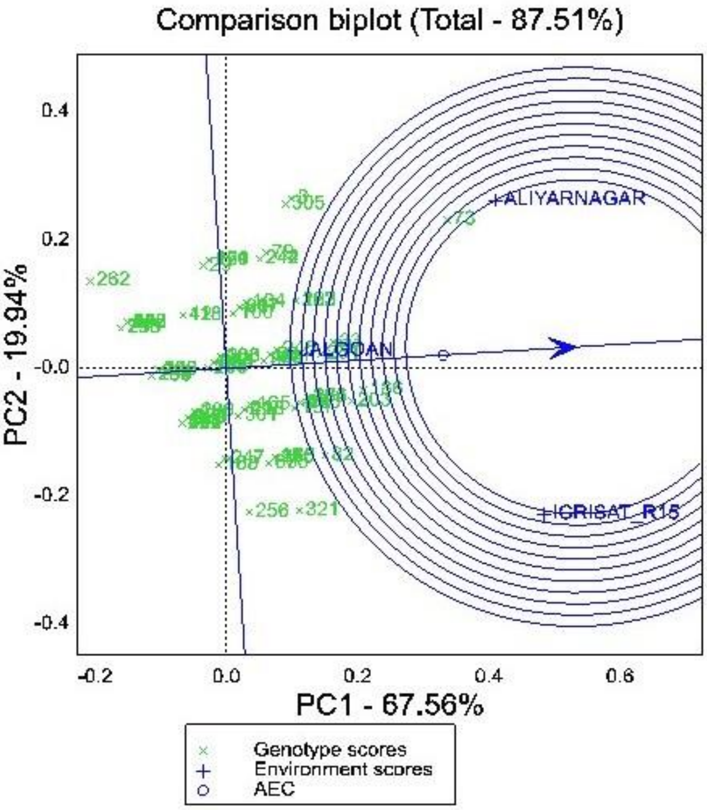

Figure 4.16 Comparison of environments with respect to ideal test environment for LLS severity. Area of inner circle of in biplot represents ideal test environment and the environment plotted within this circle are the best environment for cultivar evaluation

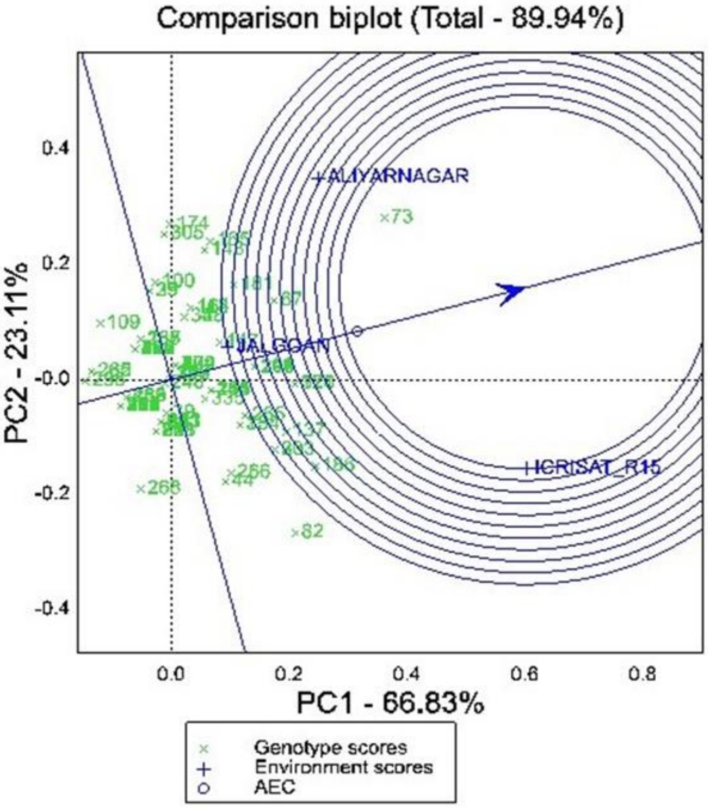

Figure 4.17 Comparison of environments with respect to ideal test environment for rust severity. Area of inner circle of in biplot represents ideal test environment and the environment plotted within this circle are the best environment for cultivar evaluation

4.5.3 Stability of rust resistance

The polygon view, ranking biplot, and comparison of environments biplots have been presented in Fig. 4.13, 4.15 and 4.17. The partitioning of GE interaction through GGE biplot analysis showed that PC1 and PC2 together accounted for 89.54% of GGE sum of squares for rust. The vertex genotypes in this study were 296, 109, 305, 174, 73, 186, 82 and 268. These genotypes were the best or the poorest genotypes for disease resistance/susceptibility to rust in some or all of the environments because they were farthest from the origin of the biplot. From the polygon view of biplot analysis of MET data of three environments, the genotypes fell in four sections and the test environments fell in two sections. The first section contains the test environments Aliyarnagar and Jalgaon while the second section consists ICRISAT_R15. The genotype 73 (TMV 2) plotted farthest from the biplot origin indicates that it had high disease severity score at 90 DAS across the environments whereas genotypes 236 (ICGV 99052) and 301 (ICG 11426) plotted farthest on left side of biplot indicates that this genotypes had lowest disease severity score across the environments (Fig 4.13).

The ranking of 109 genotypes of GSP based on their disease severity score to rust and stability performance are presented in Fig. 4.15. In the biplot, the genotypes plotted left side of biplot and have the shortest vector from the AEA are the better genotypes. The genotype 236 (ICGV 99052), 301 (ICG 11426), 235 (ICGV 99051), 262 (ICGV 86699), 71 (GPBD 4), 27 (ICGV 06422), 30 (ICGV 07223), 32 (ICGV 07235), 77 (ICGV 05100), 84 (ICGV 06142), 152 (ICGV 02411), 153 (ICGV 05155), 229 (ICGV 00362), 237 (ICGV 00362), 238 (ICGV 00248), 239 (ICGV 01361), 252 (ICGV 99160), 253 (ICGV 02323), 260 (ICGV 87846), 288 (SPS 2) , 291 (SPS 7), 293 (SPS 11), 296 (SPS 21) and 303 (ICGV 02446) had lower disease score with shortest vector length from AEA indicates their superiority for resistance to rust and stability across the environments. The genotype 109 (49 M-16) and 268 (ICGV 05032) had lower mean disease score but greater vector length from AEA. Genotypes 109 plotted near to Aliyarnagar whereas 268 near to ICRISAT indicated their high disease score at the respective location. The summary of the interrelationships among the test environments has been presented in Fig 4.17. Based on the angles between environment vectors, all the three environments (Aliyarnagar, Jalgaon, and ICRISAT_R15) were positively correlated with each other because of acute angles (<90^0) formed between them. The position of the environment on biplot revealed that ICRISAT_R15 was farthest on right side of the perpendicular line indicating that it was the best environments where genotypes got higher diseases scores followed by Aliyarnagar and Jalgaon. Jalgaon was the poorest environment plotted nearer to biplot origin indicates that genotypes recorded lower disease scores at Jalgaon. The ranking of environments in with respect to ideal test environments (Fig 4.17) also revealed that the ICRISAT_R15 and Aliyarnagar were the environments plotted on the border of inner circle in the biplot indicating that both had similar disease pressure for rust and are better for cultivar evaluation against rust.

4.5.4 Number of pods per plant

The polygon view and ranking biplot have been presented in Fig. 4.18 and 4.19, respectively. The partitioning of GE interaction through GGE biplot analysis showed that PC1 and PC2 together accounted for 77.04% of GGE sum of squares for number of pods per plant. The vertex genotypes in the biplot (235, 293, 180, 3, 203, 321, 163, 334, 301, 296 and 262) were the best or the poorest genotypes for number of pods per plant in some or all of the environments because they are farthest either of the side from the origin of biplot. Polygon view of biplot showed that genotypes fell in four sections whereas the test environments fell in two sections. The first section contains the test environments Aliyarnagar and ICRISAT_R15 while the second section consists ICRISAT_PR15 and Jalgaon indicates most of the genotypes fell in respective section were performed better in these environments. Among the environments, Jalgaon plotted farthest from the origin on biplot and discriminating itself from other environments indicating that genotypes recorded higher number of pods per plant at Jalgaon compared to other environments.

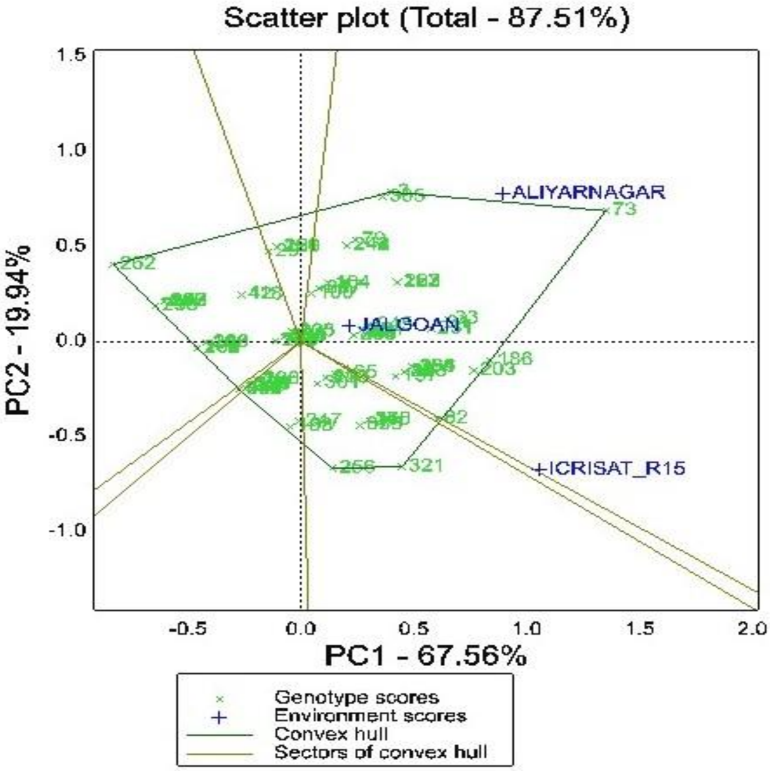

Figure 4.18 Polygon view of scattered biplot showing ranking of genotypes based on which won where pattern for disease severity score to late leaf spot across three locations

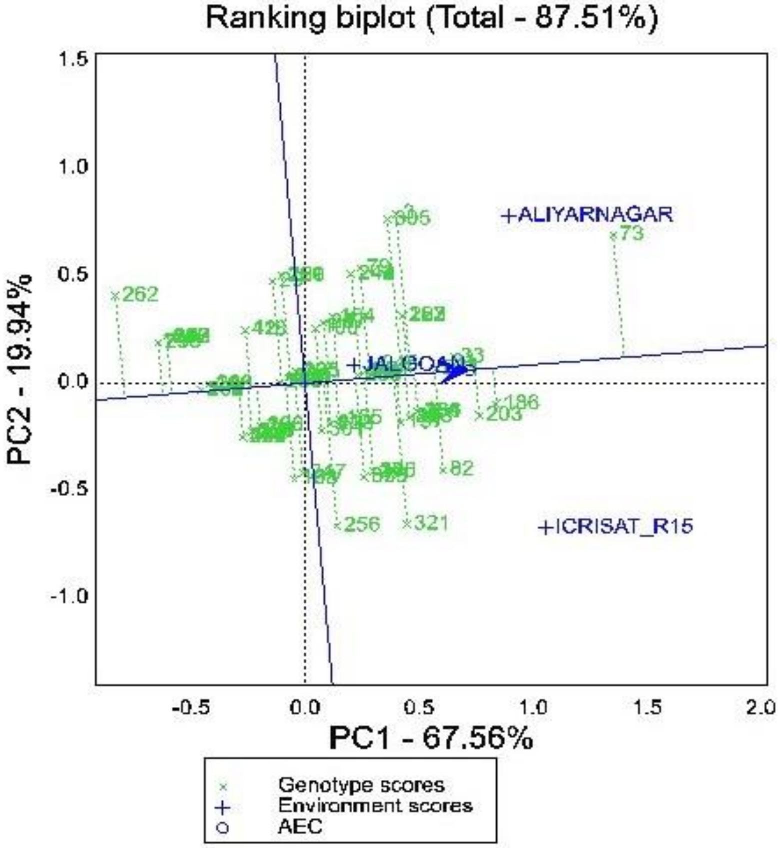

Figure 4.19 GGE biplot showing ranking of genotypes for mean performance and stability for disease severity score to late leaf spot across the three locations

The ranking of 109 genotypes of GSP based on mean and stability performance are presented in Fig. 4.19. In the biplot, the genotypes plotted right side of biplot and have the shortest vector from the AEA are better and stable genotypes for number of pods per plant. The genotype 109 (49 M-16), 253 (ICGV 02323), 26 (ICGV 05163), 42 (ICGV 01273), 153 (ICGV 05155), 27 (ICGV 06422), 45 (ICGV 03043), 266 (ICGV 06099), 32 (ICGV 07235), 84 (ICGV 06142), 13 (ICGV 93280), 235 (ICGV 99051), 41 (ICGV 00005), 44 (ICGV 02321), 136 (39 × 49-81-1), 154 (ICGV 06100), 1 (ICGV 06423), 37 (ICGV 07120), 43 (ICGV 01274), 76 (ICGV 03042) and 251 (ICGV 98105) are near to AEC with shortest vector length from AEA indicates their superior and stability for number of pods per plant across the environments. The genotype 3 (ICGV 07247), 180 (ICGV 01276), 293 (SPS 11), 135 (49 × 39-74) and 241 (ICGV 04087) were also high performing genotypes but greater vector length from AEA indicating that these genotypes had higher interaction with the environment. Among these, genotype 3 (ICGV 07247) and 135 (49 × 39-74) are closer to Jalgaon and ICRISAT_PR15 indicates their superior performance in both the location whereas 180 (ICGV 01276) performed better at ICRISAT_R15 and 293 (SPS 11) at Aliyarnagar indicated that these genotypes were adaptable to specific environments. Based on the angles between environment vectors, all the four environments were positively correlated with each other. Aliyarnagar and ICRISAT_R15 were closely related because of acute angles ($<90^0$) formed between them indicates that the genotypes performed almost similar in both the environments.

4.5.5 Shelling percent

The polygon view and ranking biplot for shelling percent have been presented in Fig. 4.20 and 4.21, respectively. The partitioning of GE interaction through GGE biplot analysis showed that PC1 and PC2 together accounted for 71.92% of GGE mean sums of squares for shelling percent. The vertex genotypes in the biplot (235, 293, 180, 3, 203, 321, 163, 334, 301, 296 and 262) were the best or the poorest genotypes for number of pods per plant in some or all the environments because they are farthest from the origin of the biplot. In the biplot, genotypes fell in four sections whereas the test environments fell in two sections. The first section contains the test environments Aliyarnagar, Jalgaon and ICRISAT_R15 while the second section consists ICRISAT_PR15 plotted farthest on right side of the biplot indicates most of the genotypes had lower shelling percent in all three diseased environments (Aliyarnagar, Jalgaon, ICRISAT_R15) compared to the post-rainy season at ICRISAT.

In ranking biplot, the genotypes plotted right side of biplot with shortest vector length from AEA are the better genotypes with high mean and stable shelling percent across the environments. The genotype 253 (ICGV 02323), 37 (ICGV 07120), 3 (ICGV 07247), 67 (ICGV 00350), 42 (ICGV 01273), 32 (ICGV 07235), 181 (ICGV 01328), 13 (ICGV 93280), 266 (ICGV 06099), 109 (49 M-16), 293 (SPS 11), 44 (ICGV 02321) and 71 (GPBD 4) are near to AEC with shortest vector length from AEA indicates their superiority and stability for shelling percent across the environments. The genotype 135 (49 × 39-74) and 87 (ICGV 94118) were also high performing genotypes but greater vector length from AEA towards ICRISAT_PR15 indicated that these genotypes had higher shelling percent at ICRISAT during post-rainy season 2015-16 (Fig 4.21).

4.5.6 Hundred seed weight

The polygon view and ranking biplot for shelling percent have been presented in Fig. 4.22 and 4.23, respectively. The partitioning of GE interaction through GGE biplot analysis showed that PC1 and PC2 together accounted for 81.65% of GGE mean sums of squares for hundred seed weight. The vertex genotypes in the biplot (24, 283, 104, 39, 183, 147, 328, 80 and 294) were the best or the poorest genotypes for hundred seed weight in some or all the environments because they are farthest from the origin of the biplot. From the polygon view of biplot of MET data of four environments, the genotypes fell in four sections whereas the test environments fell in two sections. The first section contains the test environments Aliyarnagar, Jalgaon and ICRISAT_R15 with a narrow-angle between them indicates that genotypes had similar performance for hundred seed weight in these three environments whereas the second section consists ICRISAT_PR15 discriminating itself from other environments plotted farthest on right side of the biplot indicates most of the

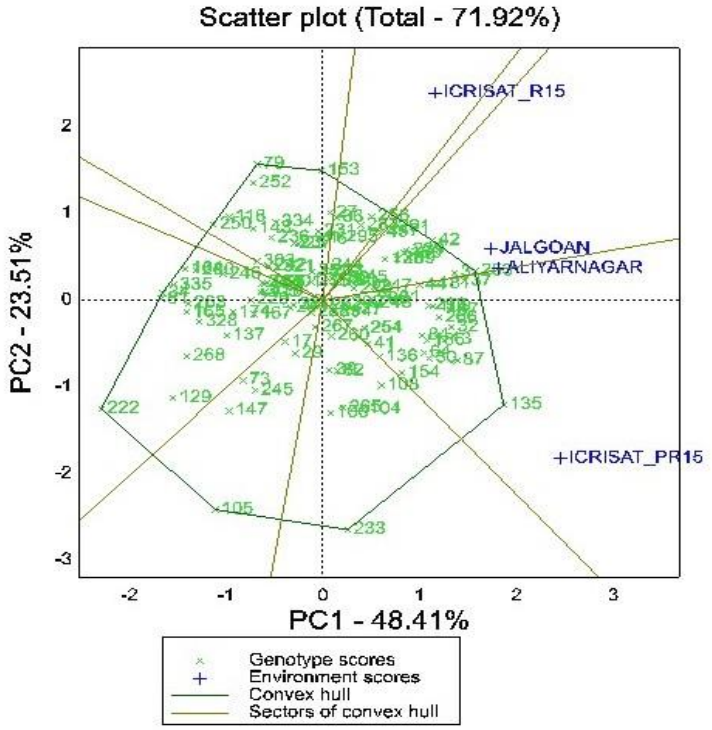

Figure 4.20 Polygon view of scattered biplot showing ranking of genotypes based on which won where pattern for shelling percent across three environments

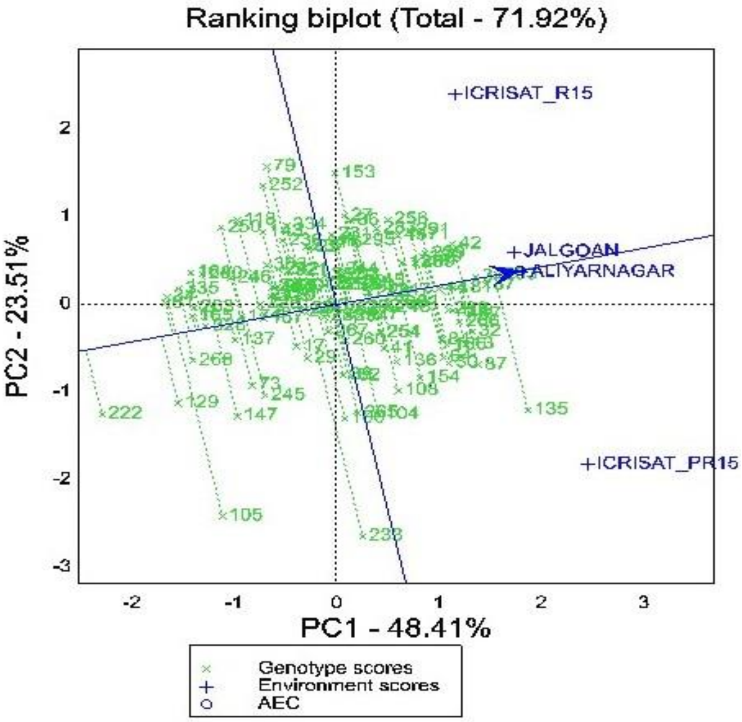

Figure 4.21 GGE biplot showing ranking of genotypes for mean performance and stability for shelling percent across the three environments

genotypes had higher hundred seed weight during post-rainy season at ICRISAT compared to rainy season across the environments (Fig 4.22).

The ranking of genotypes of GSP for hundred seed weight and stability performance are presented in Fig. 4.23. In the biplot, the genotypes plotted on right side of biplot with shortest vector length from the AEA are better genotypes. The genotype 283 (49 M- 1-1), 247 (ICGV 01495), 100 (49 × 37-134), 265 (ICGV 06040), 266 (ICGV 06099), 17 (ICGV 02242), 170 (ICG 10053), 228 (ICGV 00346), 105 (39 × 49 -77), 222 (ICGV 01464), 248 (ICGV 05057), 154 (ICGV 06100), 269 (ICGV 05141), 260 (ICGV 87846), 267 (CS 39), 263 (ICGV 98373) and 251 (ICGV 98105) are near to AEC with shortest vector length from AEA indicates their superiority and stability for hundred seed weight across the environments. The genotype 104 (39 × 49 -8), 39 (ICGV 97120), 253 (ICGV 02323) and 87 (ICGV 94118) were also high performing genotypes but greater vector length from AEA indicates their unstable performance for hundred seed weight across the environments.

4.5.7 Pod yield per hectare

The polygon view and ranking biplot for yield performance of selected genotypes of GSP have been presented in Fig. 4.24 and 4.25, respectively. The partitioning of GE interaction through GGE biplot analysis showed that PC1 and PC2 together accounted for 81.20% of GGE mean sums of squares for pod yield per hectare. The vertex genotypes in the biplot are 79, 24, 293, 3, 267, 165, 328, 334, 321, 34 and 335 indicating that these genotypes were the best or the poorest genotypes for pod yield per hectare in some or all the environments because they are farthest either of direction from the origin of biplot. The polygon view of MET data of four environments in the biplot showed that genotypes fell in four sections whereas the test environments fell in two sections. The first section contains the test environments Aliyarnagar and Jalgaon whereas the second section consists ICRISAT_R15 and ICRISAT_PR15. Among these four environments, ICRISAT post-rainy

(ICRISAT_PR15) discriminating itself from other environments indicates varying performance of genotypes during post-rainy season compared to all rainy seasons across the environments while among rainy seasons Jalgaon is furthest from origin of biplot compared to Aliyarnagar and ICRISAT_R15 which had similar position on biplot indicates that genotypes had higher yield performance at Jalgaon than Aliyarnagar and ICRISAT_R15 (Fig 4.24).

The ranking of genotypes for mean pod yield and stability are presented in Fig. 4.25. The ranking biplot of genotypes based on higher mean and stability revealed that genotype 154 (ICGV 06100) followed by 26 (ICGV 05163), 153 (ICGV 05155), 30 (ICGV 07223), 32 (ICGV 07235), 253 (ICGV 02323), 266 (ICGV 06099), 37 (ICGV 07120), 152 (ICGV 02411), 25 (ICGV 05161), 45 (ICGV 03043), 1 (ICGV 06423), 42 (ICGV 01273) and 27 (ICGV 06422) were the genotypes plotted near to AEC with shortest vector length from AEA indicating their superior performance and stability for pod yield per hectare. The genotype 3 (ICGV 07247), followed by 24 (ICGV 03064), 293 (SPS 11), 180 (ICGV 01276), 247 (ICGV 01495), 84 (ICGV 06142), 43 (ICGV 01274), 76 (ICGV 03042), 109 (49 M-16), 268 (ICGV 05032) were also high yielding genotypes but greater vector length from AEA indicates their unstable performance for pod yield per hectare. Among these, 3 (ICGV 07247), 180 (ICGV 01276), 247 (ICGV 01495) and 109 (49 M-16) are plotted nearer to environment Aliyarnagar and Jalgaon indicated that these genotypes have location specific adaptability under these environments whereas 24 (ICGV 03064), 293 (SPS 11), 84 (ICGV 06142), 43 (ICGV 01274) and 76 (ICGV 03042) plotted towards ICRISAT_PR15 indicates these were superior at ICRISAT during post-rainy season compared to other genotypes (Fig 4.25).

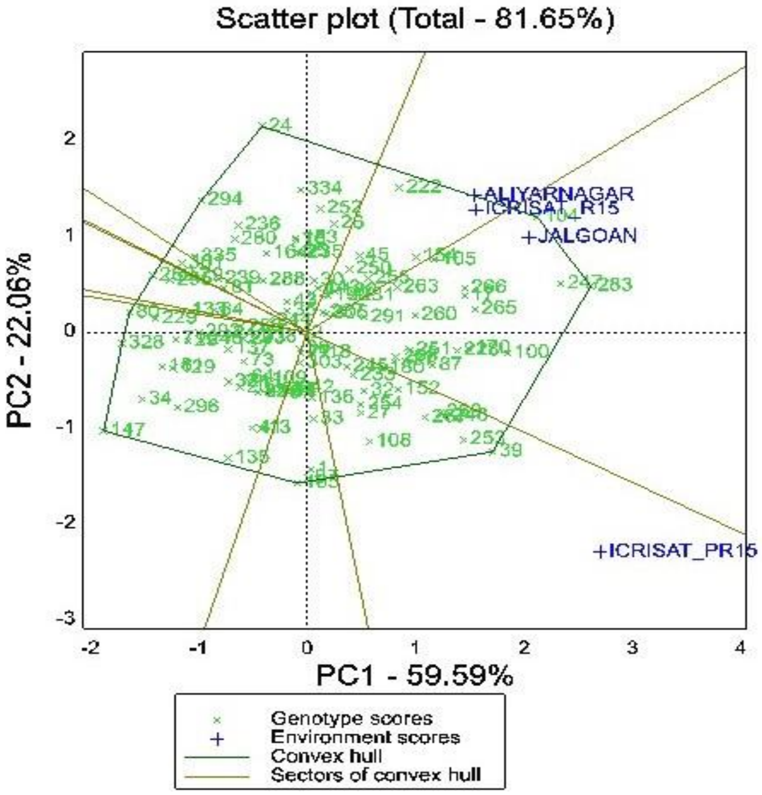

Figure 4.22 Polygon view of scattered biplot showing ranking of genotypes based on which won where pattern for hundred seed weight across three environments

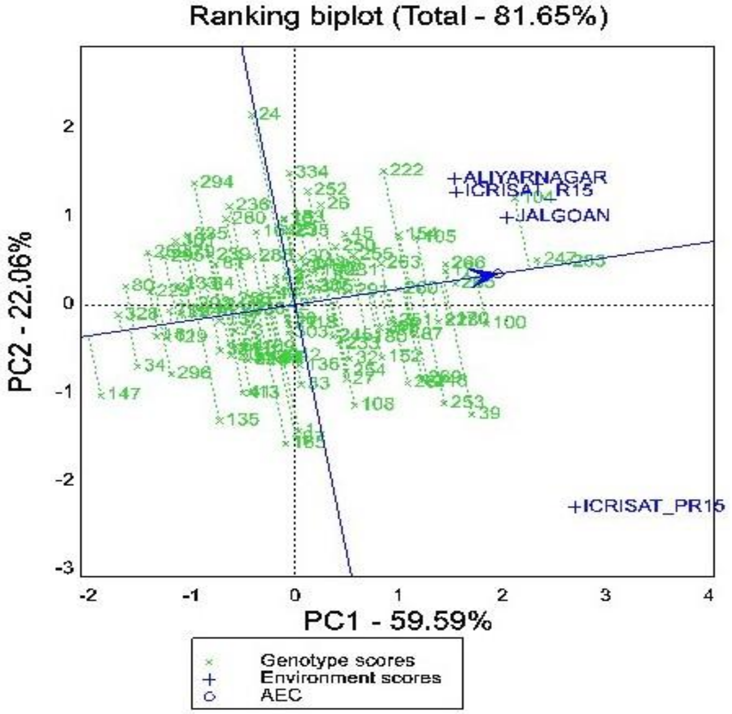

Figure 4.23 GGE biplot showing ranking of genotypes for mean performance and stability for hundred seed weight across the three environments

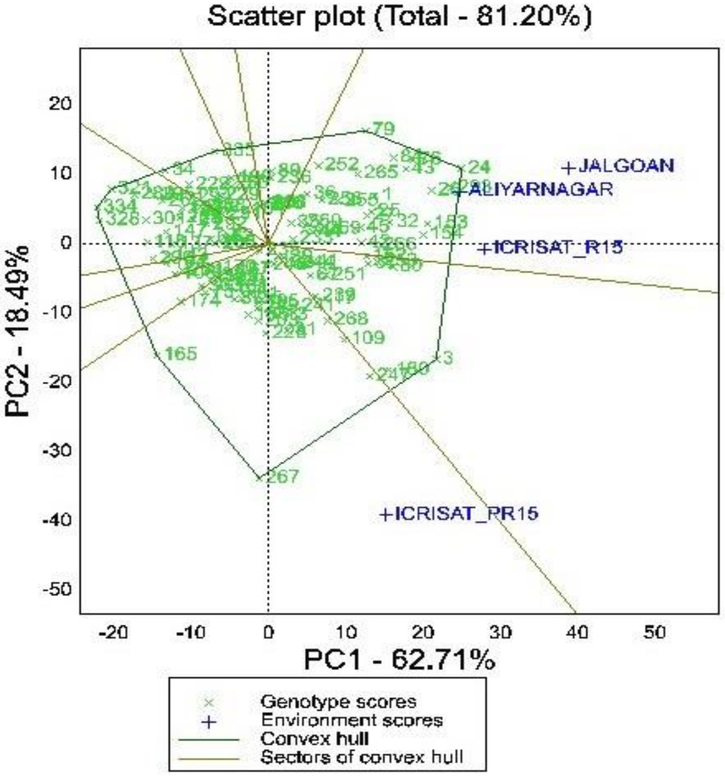

Figure 4.24 Polygon view of scattered biplot showing ranking of genotypes based on which won where pattern for pod yield hectare across three environments

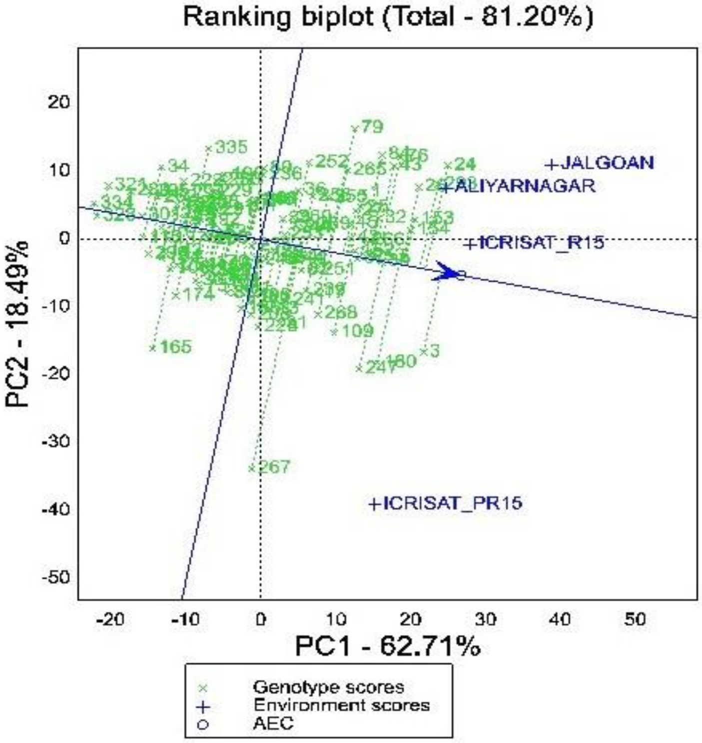

Figure 4.25 GGE biplot showing ranking of genotypes for mean performance and stability for pod yield per hectare across the three environments

4.5.8 Nutritional quality traits

The polygon view and ranking biplot for oil protein, oleic and linoleic acid have been presented in Fig. 4.26 to 4.33. The partitioning of GE interaction through GGE biplot analysis showed that PC1 and PC2 together accounted for 82.47, 71.73, 92.02 and 89.77% of GGE mean sums of squares for oil, protein, oleic and linoleic acid. The vertex genotypes in the biplot were 335, 73, 203, 167, 30, 164 and 335 for oil content (Fig 4.26) whereas 203, 180, 109, 84, 137, 82, 26, 153, 296 and 180 for protein content (Fig 4.28), 254, 296, 301, 38, 280, 262, 335, 76 and 24 for oleic acid (Fig 4.30) and 33, 301, 73, 135, 190, 251, 76, 79, 64, 288 and 262 for linoleic acid (Fig 4.32). These vertex genotypes were the best or the poorest genotypes for hundred seed weight in some or all the environments because they are farthest from the origin of the biplot. From the polygon view of biplot of MET data of four environments, the genotypes fell in four sections whereas the test environments fell in two sections for all nutritional quality traits. The first section contains the test environments Jalgaon, ICRISAT_R15 and ICRISAT_PR15 with a narrow-angle between them indicates that genotypes had similar performance for oil content in these three environment's whereas the second section consists Aliyarnagar discriminating itself from other environments (Fig 4.26). For protein content, the first section consisted environments Jalgaon and Aliyarnagar and second consisted ICRISAT_R15 and ICRISAT_PR15. Among these Aliyarnagar plotted farthest from biplot origin indicating that most of the genotypes had higher protein content at Aliyarnagar compared to other environments. Jalgaon, Aliyarnagar, and ICRISAT_R15 were in the first section whereas ICRISAT_PR15 discriminated itself from other environments in the biplot for oleic acid (Fig 4.28).

The ranking of selected genotypes of GSP for oil, protein, oleic and linoleic acid content based on mean and stability performance is presented in Fig. 4.27, 4.29, 4.31 and 4.33, respectively. In the biplot, the genotypes plotted right sides of biplots with shortest vector length from AEA are better genotypes. The genotype 153 (ICGV 05155) followed by 71 (GPBD 4), 244 (ICGV 97128),

296 (SPS 21), 238 (ICGV 00248), 84 (ICGV 06142), 76 (ICGV 03042), 293 (SPS 11), 147 (SPS 9), 109 (49 M-16), 29 (ICGV 07220), 152 (ICGV 02411), 80 (ICGV 06424), 154 (ICGV 06100), 26 (ICGV 05163) and 265 (ICGV 06040) are near to AEC with shortest vector length from AEA indicates their superior and stability performance for oil content (Fig 4.27). Genotypes 335 (ICG 2381), 174 (ICG 12625), 164 (ICG 6022), 64 (ICGV 99085) and 79 (ICGV 06420) were also higher oil containing genotypes but with greater vector length from AEA indicates their instability for oil content. The genotypes 180 (ICGV 01276) followed by 229 (ICGV 00362), 170 (ICG 10053), 109 (49 M-16), 293 (SPS 11), 118 (24 M-86), 231 (ICGV 02287), 253 (ICGV 02323), 186 (ICGV 02266), 44 (ICGV 02321) and 43 (ICGV 01274) were plotted right side of the biplot with shorter vector length from AEA indicating their superiority and stability for protein content across the environments compared to other genotypes (Fig 4.29). However genotypes, 39 (ICGV 97120) followed by 301 (ICG 11426), 295 (SPS 20), 280 (ICG 11337), 164 (ICG 6022), 174 (ICG 12625), 294 (SPS 15), 64 (ICGV 99085), 288 (SPS 2), 108 (49 × 39-8), 29 (ICGV 07220) and 71 (GPBD 4) were the high performing genotypes across the environments with least vector length from AEA for oleic acid (Fig 4.31). Low linoleic acid is desired traits in groundnut for higher nutritional quality with longer self-life therefore, genotypes plotted left side of the biplot with least vector length are the superior compared to others. In the biplot, genotype 39 (ICGV 97120), 301 (ICG 11426), 73 (TMV 2), 295 (SPS 20), 108 (49 × 39-8), 71 (GPBD 4), 29 (ICGV 07220), 288 (SPS 2), 262 (ICGV 86699) and 294 (SPS 15) had lower linoleic content with shorter vector length from AEA indicating their superiority and stability for low linoleic acid (Fig 4.33).

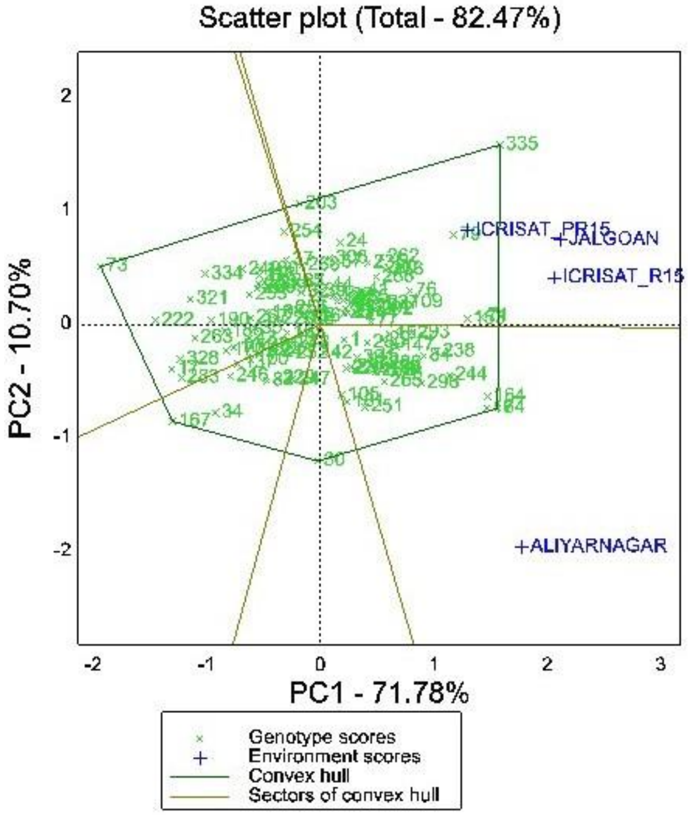

Figure 4.26 Polygon view of scattered biplot showing ranking of genotypes based on which won where pattern for oil content across four environments

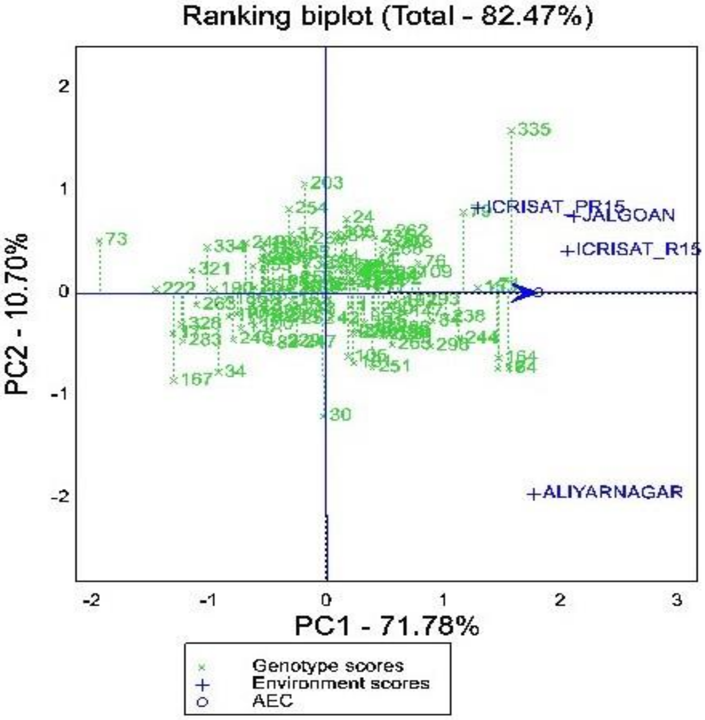

Figure 4.27 GGE biplot showing ranking of genotypes for mean performance and stability for oil content across four environments

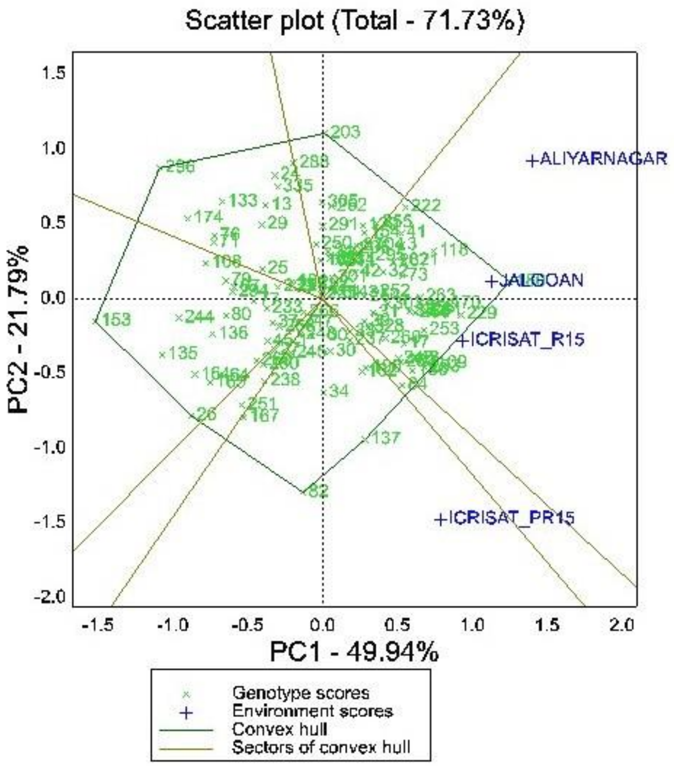

Figure 4.28 Polygon view of scattered biplot showing ranking of genotypes based on which won where pattern for protein content across four environments

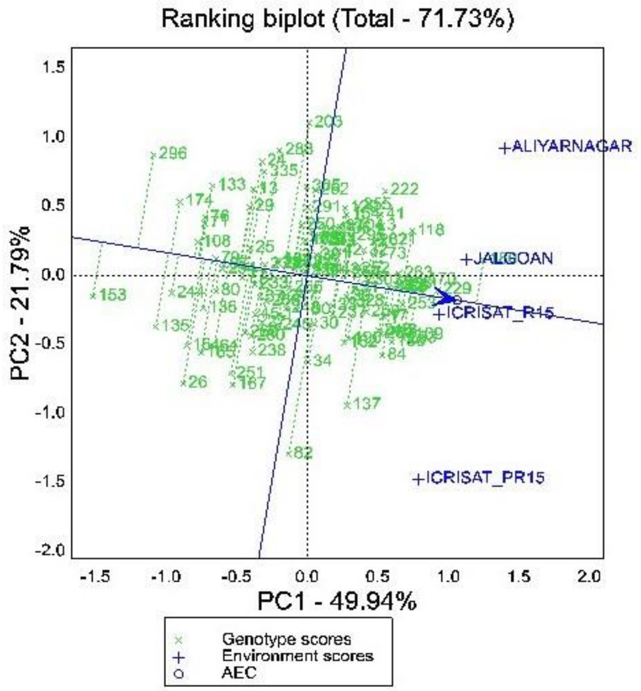

Figure 4.29 GGE biplot showing ranking of genotypes for mean performance and stability for protein content across four environments

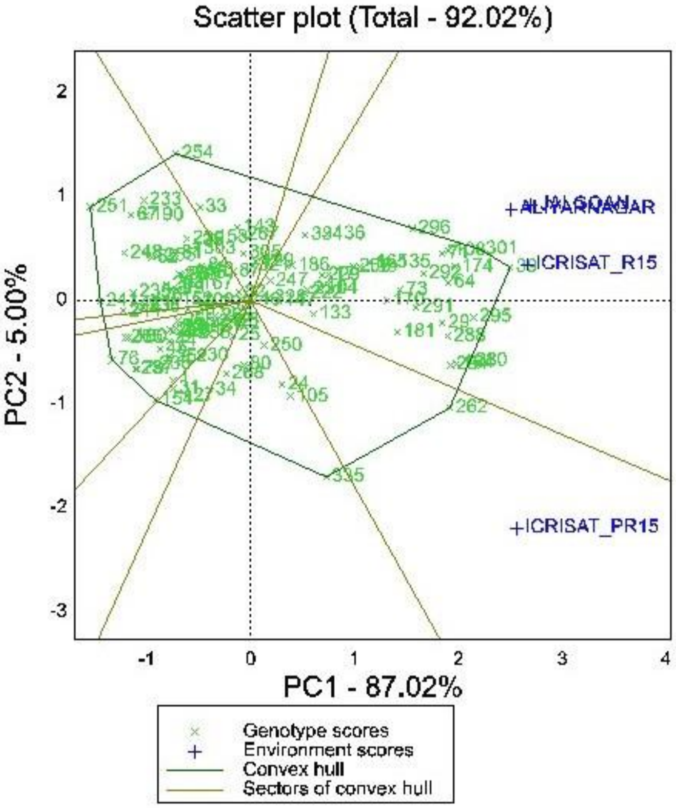

Figure 4.30 Polygon view of scattered biplot showing ranking of genotypes based on which won where pattern for oleic acid content across four environments

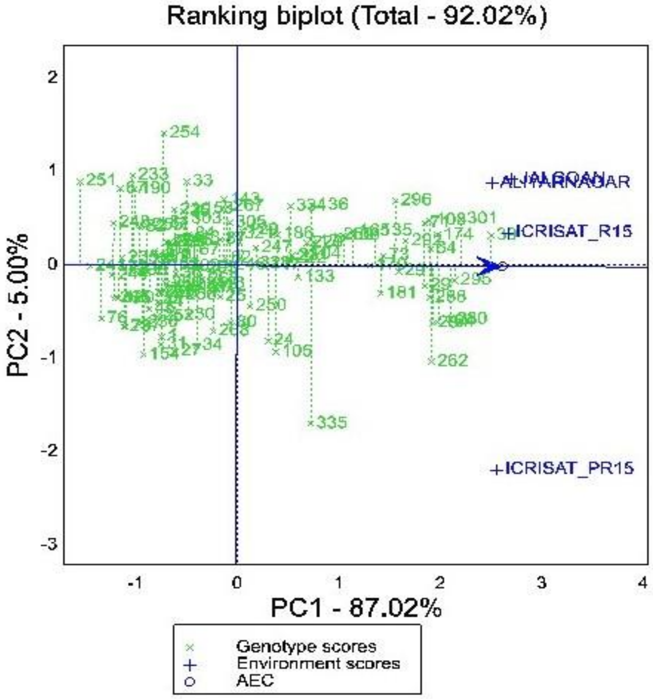

Figure 4.31 GGE biplot showing ranking of genotypes for mean performance and stability for oleic acid content across four environments

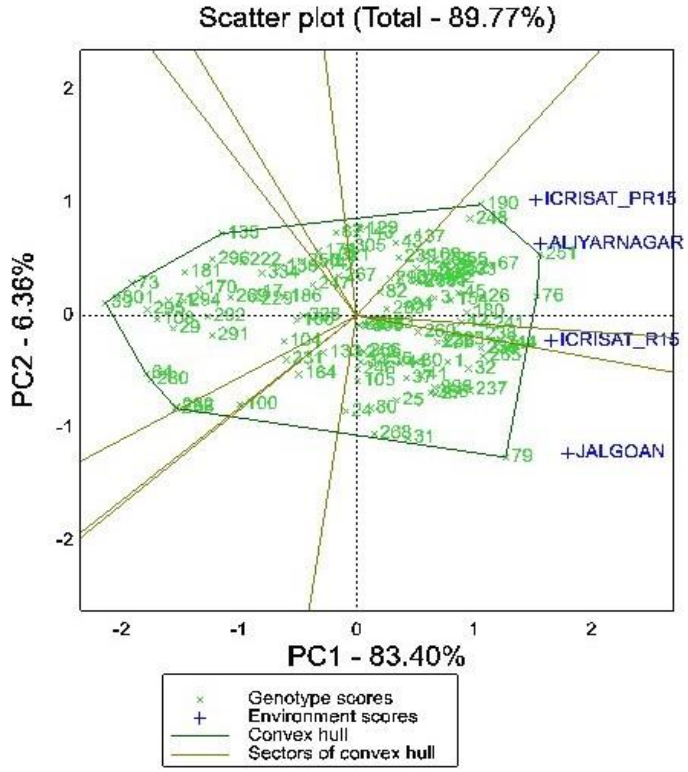

Figure 4.32 Polygon view of scattered biplot showing ranking of genotypes based on which won where pattern for linoleic acid content across four environments

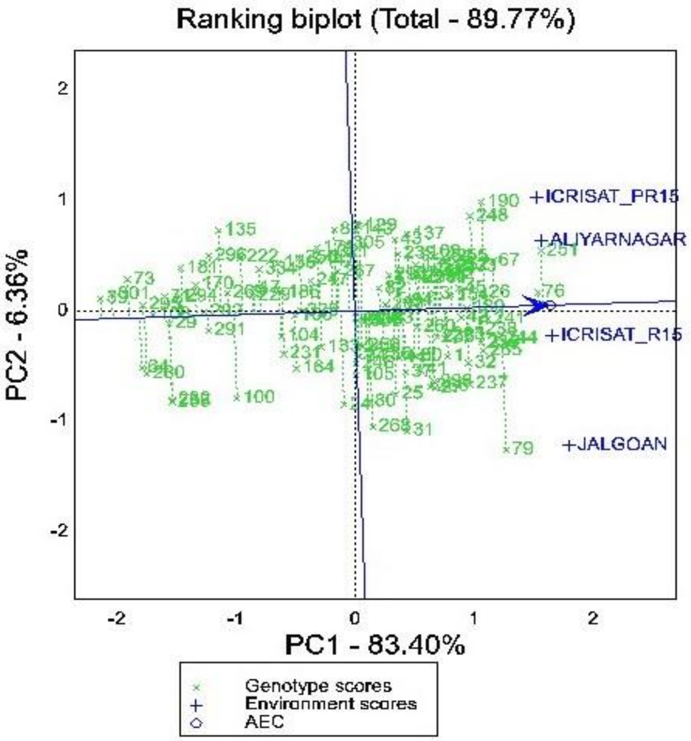

Figure 4.33 GGE biplot showing ranking of genotypes for mean performance and stability for linoleic acid content across four environments

4.6 Molecular diversity

In any plant breeding program, assessment of genetic divergence is an important and foremost objective. The threat to genetic erosion has led to a significant interest in the assessment of genetic diversity in germplasm collections. It helps in identifying the desirable parents for hybridization program. Molecular markers are useful complement to the morphological and physiological characterization of cultivars because they are plentiful, independent of tissue or environmental effects and allow cultivar identification early in plant development. A total of 336 genotypes of GSP subjected to genotyping with 14 SSR marker linked to rust and LLS, yield and nutritional quality traits to assess diversity in GSP at the molecular level and allelic richness for targeted loci. The results are presented below.

4.6.1 Analysis of molecular variance (AMOVA)

The distribution of molecular variance among and within the subspecies has been represented in Table 4.39. The AMOVA revealed that eight percent of the total molecular variance was due to variation among the sub-species while 92% was due to variation present among individuals within the sub-species (Table 4.39 & Fig 4.34).

4.6.2 Allelic richness and genetic diversity

The 14 SSR markers detected a total of 462 alleles in 336 genotypes of GSP (Table 4.40). The number of alleles per locus varied from 14 (GM 630) to 56 (IPAHM 103) with an average 33 alleles per locus. The marker IPAHM 103 (56 alleles) detected the highest number of alleles followed by GM 2301 (47 alleles), PM 36 (40 alleles), TC6H03 (37 alleles), and TC1D02 and GM 1954 (28 alleles). The polymorphic information content (PIC) values varied from 0.62 (GM 1573) to 0.92 (GM 1954) with an average of 0.80. All the markers were highly polymorphic with PIC values more than 0.60. Gene diversity varied from 0.65 (GM 1573) to 0.93 (GM 1954), with an average of 0.82. All the markers showed very high gene diversity for the locus under study. Among these 14 SSR markers, IPAHM 103 showed the highest number of alleles (56 alleles) with gene diversity of 0.91, heterozygosity of 0.31 and PIC value of 0.90 (Table 4.40 & Fig 4.34).

Table 4.39 Analysis of molecular variance (AMOVA) based on two subspecies using 14 SSR markers in Genomic Selection Panel of groundnut

Source	df	Sums of Square	Mean Squares	Estimated Variance	Percent of total variance
Among Subspecies	1	5.044	5.044	0.031	8%
Within Subspecies	334	122.121	0.366	0.366	92%
Total	335	127.165	-	0.397	100%

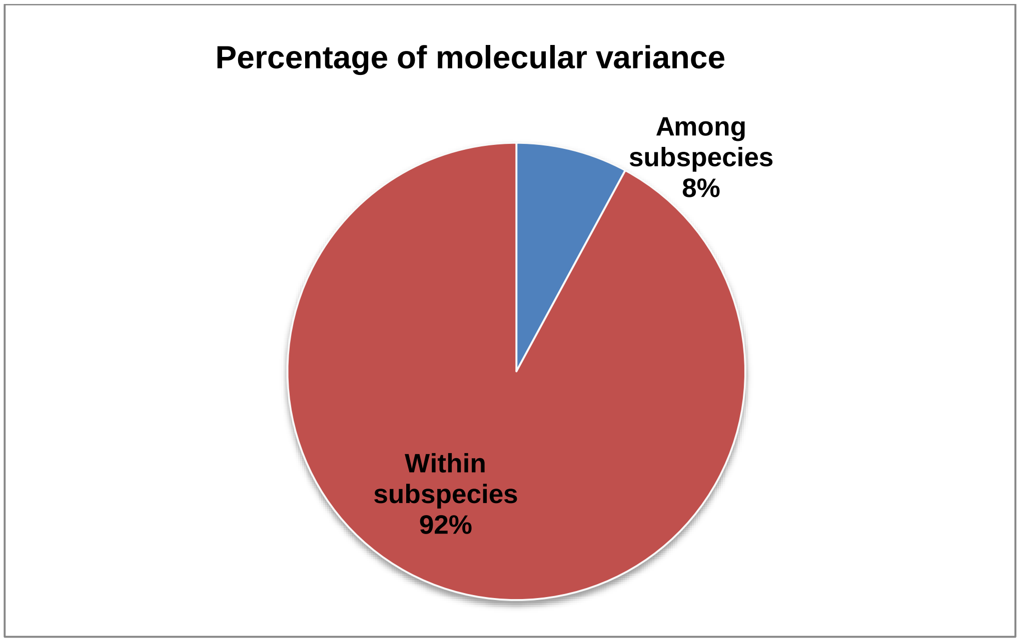

Figure 4.34 Percent molecular variance contributed towards total variance by among and with subspecies

4.6.3 Heterozygosity

A varying range of heterozygosity was detected in genotypes of GSP for 14 SSR genomic regions which varied from 0.00 (GM 630, GM 1536 and TC3E02) to 0.42 (GM 2301) (Table 4.40). Three out of 14 SSR markers detected no heterozygosity whereas six markers showed <0.10 heterozygosity and only five markers showed more than 0.10 heterozygosity. Among these five markers, GM 2301 detected highest heterozygosity (0.42) followed by IPAHM (0.31), GM 1009 (0.21), PM 36 (0.18) and GM 1573 (0.12).

4.6.4 Unique, rare, common and most frequent alleles

Out of 462 alleles detected in 336 genotypes of GSP for 14 SSR markers, 230 alleles were rare, 155 common and 18 were the most frequent alleles (Table 4.41 & Fig 4.37). A total of 59 unique alleles were detected in GSP varied from 0 to 20, which were present only in one genotype and absent in all other accessions (Table 4.41). The highest number of unique alleles were reported for GM 2301 (20) followed by TC1D12 (7), TC6E01 (5), IPAHM 103 (5) whereas there were no unique alleles reported on GM 1536, GM 630, and TC3E02. The number of rare alleles was varied from 6 (GM 630) to IPAHM 103 (34). The highest number of rare alleles were reported in IPAHM 103 (34) followed by PM 36 (27) and GM 1954 (17). Common alleles were detected for all the 14 SSR loci which varied from 5 to 19, the highest number of common alleles were reported in TC6H03 (19) followed by GM 1954 (18) and IPAHM 103 (16). In contrast, 11 out of 14 SSR loci showed the most frequent alleles, of which one SSR reported three, five SSRs reported two and other five SSR markers reported only one allele as most frequent (Table 4.41 & Fig 4.38).

4.6.5 Diversity in Genomic Selection Panel at sub-species level

The 336 genotypes of GSP included individuals from two different subspecies (ssp.) *viz.,* ssp. *fastigiata* (223 genotypes) and ssp. *hypogaea* (113 genotypes). Fourteen markers detected a total of 365 (79.00%) alleles in ssp. *fastigiata* whereas 332 (71.86%) out of 462 alleles reported in individuals belongs to ssp. *hypogaea*. Within the ssp. *fastigiata*, the number of alleles varied from 10 (GM 630) to 54 (IPAHM 103) with a mean of 26.07 alleles per SSR locus. In the ssp. *hypogaea*, the number of alleles per locus varied from 14 (GM 630) to 39 (IPAHM 103) with an average of 23.71. Comparison of number of alleles detected by different marker revealed that both the subspecies has different amount of diversity for the different locus. The markers GM 1954, 1573, 1009, 1536, PM 36, TC1D12 and IPAHM 103 detected higher number of alleles in ssp. *fastigiata* compared to *hypogaea* whereas GM 2301, TC1D02, TC3E01, TC6H03 and GM 630 reported higher number of alleles in ssp. *hypogaea* than ssp. *fastigiata*. Both the subspecies had similar diversity for GM 2079 with an equal number of alleles.

Table 4.40 Allelic richness, gene diversity, heterozygosity and polymorphic information content (PIC) for 14 SSR loci in Genomic Selection Panel of groundnut

Marker	**Major Allele Frequency**			**Number of Alleles**			**Gene Diversity**			**Heterozygosity**			**PIC**		
	fast	***hypo***	**Combined**	***fast***	***hypo***	**Combined**	***fast***	***hypo***	**Combined**	***fast***	***hypo***	**Combined**	***fast***	***hypo***	**Combined**
GM2079	0.44	0.22	0.37	16.00	16.00	24.00	0.68	0.87	0.78	0.04	0.01	0.03	0.63	0.86	0.75
GM1954	0.16	0.22	0.18	33.00	21.00	36.00	0.93	0.89	0.93	0.00	0.01	0.01	0.93	0.88	0.92
GM1573	0.51	0.63	0.55	18.00	16.00	24.00	0.67	0.59	0.65	0.16	0.04	0.12	0.63	0.57	0.62
GM1009	0.37	0.27	0.33	34.00	18.00	35.00	0.74	0.82	0.80	0.22	0.17	0.21	0.71	0.79	0.77
GM1536	0.47	0.47	0.47	22.00	12.00	24.00	0.70	0.70	0.70	0.00	0.00	0.00	0.66	0.66	0.67
GM2301	0.42	0.22	0.35	26.00	37.00	47.00	0.77	0.88	0.82	0.34	0.57	0.42	0.75	0.87	0.81
PM36	0.26	0.26	0.24	32.00	30.00	40.00	0.83	0.87	0.85	0.23	0.06	0.18	0.80	0.86	0.83
TC1D02	0.33	0.31	0.32	18.00	26.00	29.00	0.81	0.80	0.82	0.09	0.07	0.08	0.79	0.78	0.80
TC1D12	0.12	0.34	0.18	31.00	20.00	36.00	0.93	0.82	0.91	0.02	0.03	0.02	0.92	0.81	0.90
TC3E02	0.54	0.47	0.52	23.00	24.00	29.00	0.69	0.75	0.71	0.00	0.01	0.00	0.67	0.74	0.70
TC6E01	0.20	0.19	0.19	24.00	25.00	31.00	0.89	0.89	0.89	0.03	0.07	0.04	0.88	0.88	0.89
TC6H03	0.20	0.16	0.19	24.00	34.00	37.00	0.89	0.94	0.92	0.03	0.07	0.04	0.89	0.93	0.91
IPAHM103	0.20	0.19	0.20	54.00	39.00	56.00	0.90	0.89	0.91	0.33	0.28	0.31	0.89	0.89	0.90
GM630	0.39	0.26	0.34	10.00	14.00	14.00	0.73	0.85	0.78	0.00	0.00	0.00	0.68	0.83	0.75
Mean	**0.33**	**0.30**	**0.32**	**26.07**	**23.71**	**33.00**	**0.80**	**0.83**	**0.82**	**0.11**	**0.10**	**0.10**	**0.78**	**0.81**	**0.80**

Where *fast*= Subspecies *fastigiata* (223 genotypes); *hypo*= Subspecies *hypogaea* (113 genotypes); Combined represents diversity in entire Genomic Selection Panel (336 Genotypes)

The PIC values varied from 0.63 (GM 1573) to 0.93 (GM 1954) in ssp. *fastigiata* and 0.56 (GM 1573) to 0.93 (TC6H03) in ssp. *hypogaea*. Markers GM 2079, GM 1009, GM 2301, PM 36, TC3E02, TC6H03 GM 630 had higher PIC value in ssp. *hypogaea* compared to ssp. *fastigiata*. Gene diversity in ssp. *fastigiata* was varied from 0.67 to 0.93 whereas from 0.58 to 0.93 in ssp. *hypogaea*. Gene diversity among both the subspecies also revealed a similar trend where markers GM 2079, GM 1009, GM 2301, PM 36, TC3E02, TC6H03 and GM 630 had higher gene diversity in ssp. *hypogaea* compared to ssp. *fastigiata*. The heterozygosity for 14 SSR loci in GSP varied from 0.00 to 0.42 across the subspecies, eight out of 14 SSR had heterozygosity <0.10 in both the subspecies. Markers GM 1009, GM 1573, PM 36 and IPAHM 103 reported higher heterozygosity in ssp. *fastigiata* compared to ssp. *hypogaea* (Table 4.40)

4.6.6 Unweighted neighbor-joining tree

The neighbor-joining tree based on simple matching dissimilarity matrix between 336 genotypes of GSP using DARwin 6.0 version program highlighted broadly five clusters named as CI, CII, CIII CIV and CV (Table 4.42 & Fig 4.35).

The CI contained 79 of which 69 genotypes (88.4%) were from sub-species *fastigiata*. Genotypes of cluster CI were grouped into three sub-clusters named as CIa, CIb and CIc comprised of 37, 16 and 26 genotypes, respectively. Among these three sub-clusters, CIa comprised 91.6% genotypes developed at UAS Dharwad. However, the genotypes belong to var *peruviana* were grouped into sub-cluster CIb whereas sub-cluster III (CIc) grouped the genotypes having higher O/L ratio compared to all other clusters and sub-clusters. High oleic line SunOleic 95R was also present in this cluster. Cluster II (CII) consisted of 64 genotypes divided into two sub-clusters (CIIa and CIIb) of 44 and 20 genotypes, respectively. Among these, sub-cluster CIIb had lowest cluster mean for diseases severity to LLS and rust at 90 DAS across the environments indicating that the majority of resistance genotypes were grouped together in this cluster. The cluster CIII had 49 genotypes grouped into two sub-clusters of 38 and 11 genotypes. Among these two, sub-cluster CIIIb recorded higher cluster mean for oil and protein content compared to other clusters. The cluster CIV comprised of 48 genotypes represented by the ssp. *hypogaea* as all the genotypes grouped into this cluster belong to ssp. *hypogaea*. Beside this, sub-cluster CIVa was dominated with nearly 94.3% accessions belongs to mini core collection. Sub-cluster CIVb had higher cluster mean for oil content represents that genotypes of this cluster recorded higher oil content across the environments. Cluster V was the largest cluster grouped 96 genotypes into four sub-clusters comprised 36, 25, 25 and 10 genotypes, respectively. This cluster consisted of 93.75% genotypes belongs to ssp. *fastigiata* var *vulgaris*. All the high yielding genotypes were grouped together in sub-cluster CVd. The results of neighbor-joining tree corresponded well with the classification based on biological diversity (sub-species level) and expression of targeted traits across the environments (Table 4.43a&b). The clusters I and V were represented by genotypes from ssp. *fastigiata* var *vulgaris* whereas cluster IV was represented by ssp. *hypogaea*. However, clusters II and III had the genotypes from both the subspecies. It indicates that genotypes belong to these two clusters might be sharing similar pedigree or genomic regions (Fig 4.35).

4.6.7 Principal coordinates analysis (PCoA)

The PCoA with SSR markers was used to determine relatedness among the genotypes (Fig 4.36). The first two PCos explained 17.96% of the total variation among the 336 genotypes of GSP. Plotting the first two PCos and colour coding of genotypes according to subspecies and botanical varieties showed clear separation of the sub-species *fastigiata* (blue) and *hypogaea* (red). In PCoA, genotypes presented in different colors were corresponding to the clusters observed in the unweighted neighbor-joining tree. Most of the genotypes belong to subspecies *hypogaea* were grouped in quadrant I and IV whereas the genotypes belong to ssp. *fastigiata* var *vulgaris* were scattered in quadrants II, III and IV. The genotypes belong to botanical variety *peruviana* of ssp. *fastigiata* grouped together in quadrant III. However, quadrant IV had the genotypes from both the sub-species.

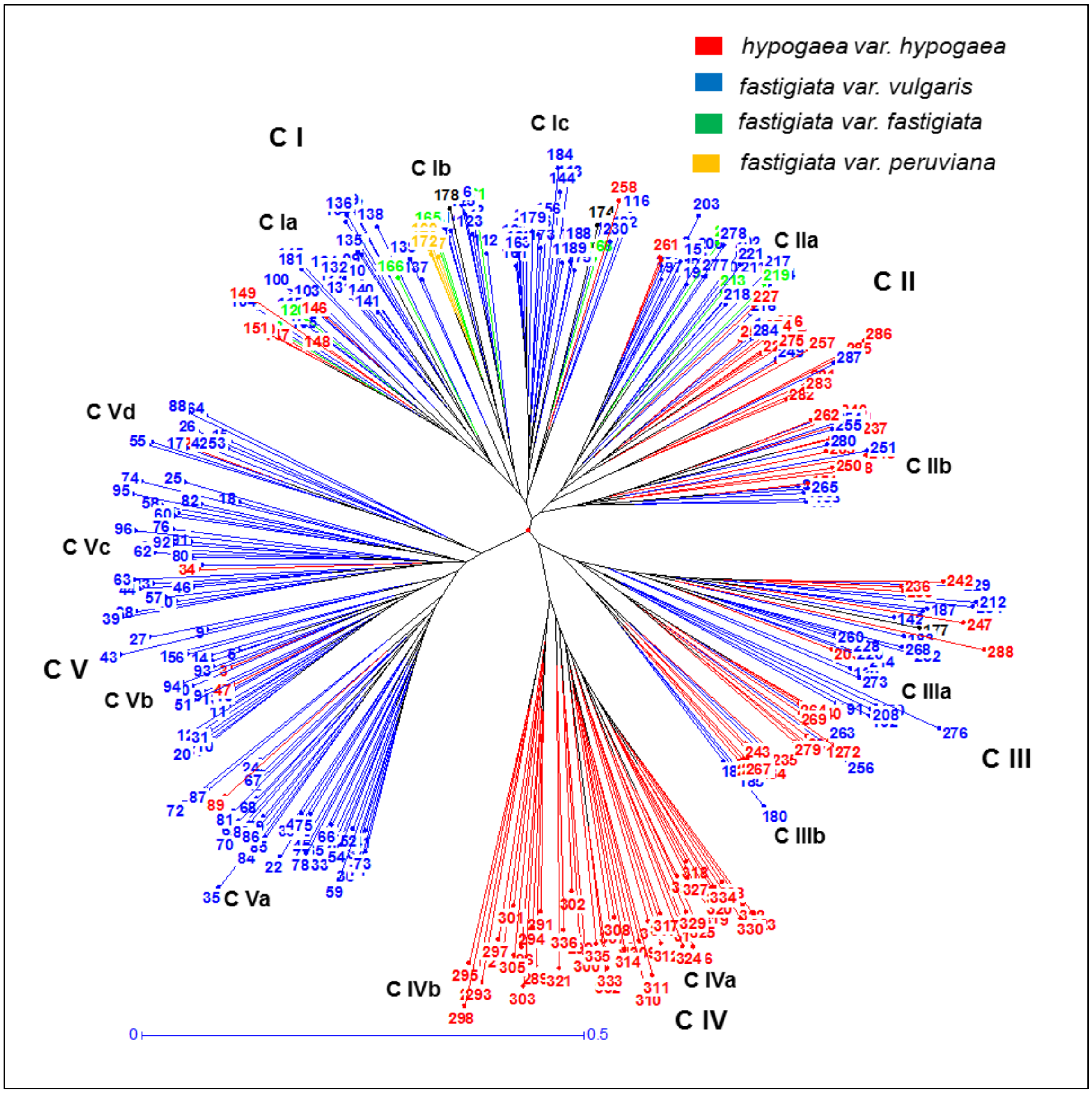

Figure 4.35 Unweighted neighbor-joining tree based on the simple matching dissimilarity matrix of 14 SSR markers genotyped in Genomic Selection Panel of groundnut

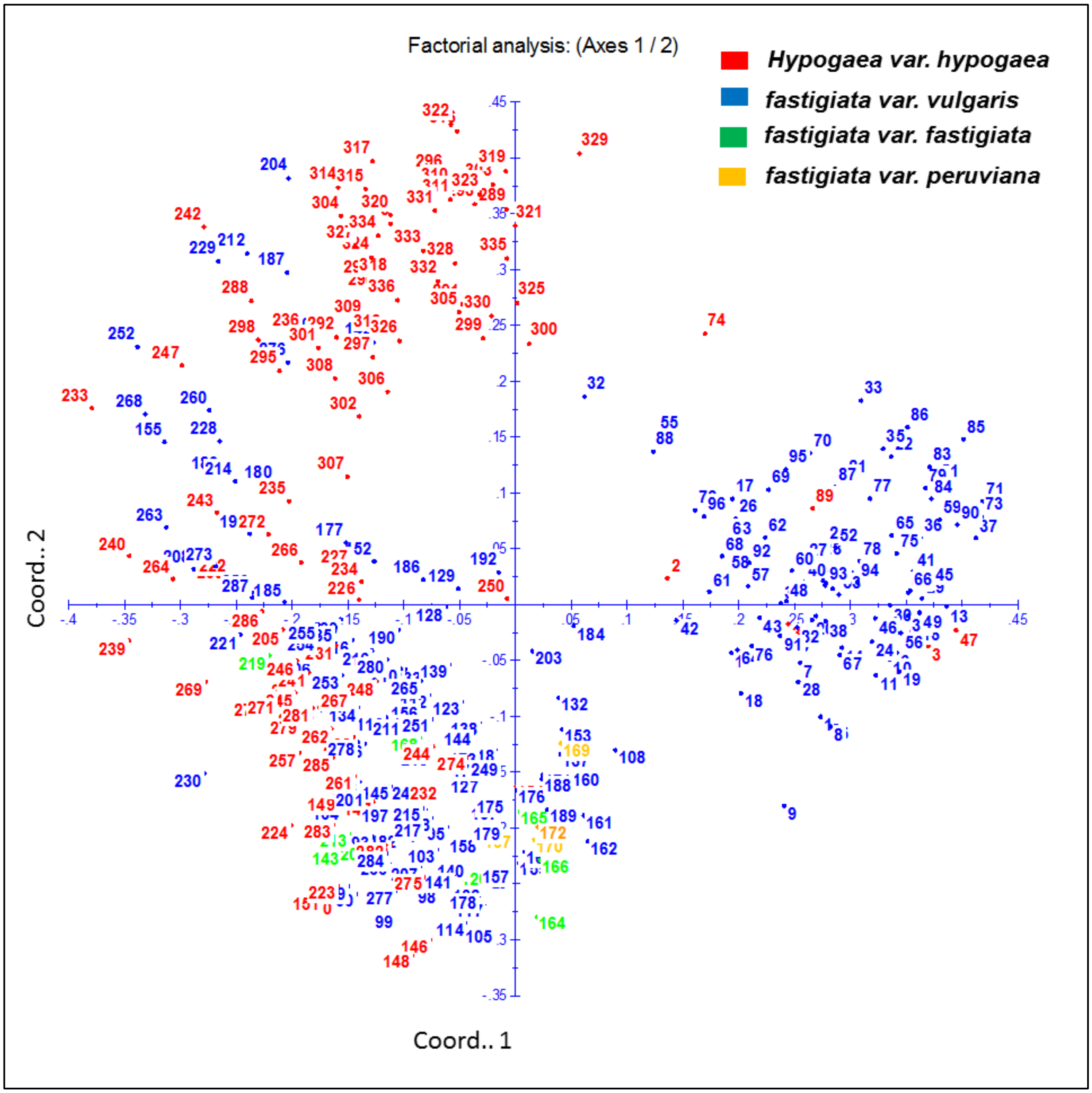

Figure 4.36 Principal Coordinate Analysis (PCoA) of Genomic Selection Panel based on trait linked SSRs. Genotypes represented in colors corresponding to the cluster observed in unweighted neighbor-joining tree

Table 4.41 Allelic range, unique, rare, common and most frequent alleles of the 14 SSR markers in Genomic Selection Panel of groundnut

S. No.	Markers	Range	Unique allele	Rare allele	Common allele	Major allele
1	GM2079	319-465	1	13	8	2
2	GM1954	98-196	3	17	18	0
3	GM1573	222-304	4	14	8	1
4	GM1009	321-498	2	14	8	2
5	GM1536	337-537	0	16	6	2
6	GM2301	101-225	20	16	10	1
7	PM36	158-254	4	27	8	2
8	TC1D02	201-273	5	13	9	2
9	TC1D12	153-233	7	18	15	0
10	TC3E02	264-332	0	16	12	1
11	TC6E01	115-189	5	12	13	1
12	TC6H03	160-254	3	14	19	0
13	IPAHM103	109-249	5	34	16	1
14	GM630	303-372	0	6	5	3
	Total		**59**	**230**	**155**	**18**
	Mean		**4.21**	**16.43**	**11.07**	**1.29**

Table 4.42 Detail of clusters identified by unweighted neighbor-joining tree based on the simple matching dissimilarity matrix of 14 SSR markers

Cluster	Sub-cluster	Number	Genotypes
C I	C Ia	37	24 × 37-2275, 24 × 39-31 MR, 26 × 37-IV- 9IR, 26 M- 119-1, 26× 27-164, 27 × 49- 27-1, 39 × 49 -77, 39 × 49 -8, 39× 49-81-1, 49 × 27-19, 49 × 27-37, 49 × 37- 99(b) tall, 49 × 37-134, 49 × 37-91, 49 × 39-21-1, 49 × 39-21-2(a), 49 × 39-74, 49 M-16, DTG 3, ICG 8517, ICGV 01328, ICGV 07273, M 110-14, M 28-2, MN1-35, SPS 1, SPS 10 , SPS 13, SPS 14, SPS 17, SPS 9, TAG 24, TDG 10, TDG 13, TDG 14, TG 42, TG LPS 7,
	C Ib	16	27 × 49- 14, 27 × 49- 16, 49 × 37-135, 49 × 37-97-1, ICGs 10036, 10053, 11088, 15419, 6022, 6646, 8751, M 28-2, Somnath, TG 41, TG 49, TG LPS 4,
	C Ic	26	24 M-86, 26 M 156-2, 27 × 49- 12, 49 × 27-13 (ii), ICGs 10701, 11651, 12625, 12991, 14985, 2031, 3102, 3140, 3343, 3421, 434, 4729, 9315, ICGVs 00371, 01232, 02022, 02189, 02286, 86011, 98432, JL 24, SunOleic 95R,
C II	C IIa	44	26 × M-223-1, 49 × 37-90, 49 M- 1-1, 49 M-2-2, BAU 13, Gangapuri, ICGs 1834, 1973, 2106, 3673, 3746, 442, 4955, 5221, 9507, ICGS 44, ICGVs 00440, 01478, 02251, 02298, 03136, 05198, 06234, 07168, 86352, 86564, 87378, 87921, 88145, 92267, 93216, 93470, 93920, 94169, 94361, 95377, 96466, 96468, 97128, 97182, ICR 48, TG 19, TG 39, TG LPS 3,
	C IIb	20	49 × 39-21-2, 49 × 39-8, GPBD 4, ICG 11337 , ICGV 00068, 00246, 00248, 01265, 02287, 02323, 04115, 05036, 05057, 05155, 06040, 06100, 86699, 90320, 98105, 98184, 98294,
C III	C IIIa	38	26 × M-95-1 RI, DTG 15, ICGs 12879, 14705, 15415, 3312, 3584, 4543, ICGVs 00346, 00362, 01361, 01464, 01495, 02038, 02271, 02317, 02434, 05032, 05141, 06042, 06110, 06175, 06188, 07023, 07359, 07368, 09112, 86590 , 87160, 87354, 87846, 88438, 97115, 97183, 98373, 99052, 99160, SPS 2,
	C IIIb	11	49 × 39-20-2, CS 39, ICGVs 01276, 02194, 02266, 02411, 04087, 06099, 97116, 97232, 99051,
C IV	C IVa	35	CSMG 84-1, ICGs 10185, 111, 11322, 12276, 12370, 12509, 12672, 13895, 14466, 14475, 14482, 14834, 15190, 156 , 1668, 2381, 2773, 2857, 3027, 3053, 4343, 4527, 532, 5662, 5663, 5745, 5891, 6766, 721, 8285, 875, 9961, ICGV 02290, ICGV 86325,
	C IVb	13	ICG 11426, ICGS 76, ICGV 02446, ICGV 03128, SPS 11, SPS 15, SPS 20, SPS 21, SPS 3, SPS 6, SPS 7, SPS 8, TMV 2 NLM,
C V	C Va	36	DH 86, ICGVs 00005, 00191, 00321, 00349, 00350, 01263, 02125, 03043, 03064, 03207, 04149, 05100, 06049, 06142, 06420, 07120, 07145, 07166, 07210, 07220, 07223, 91114, 91116, 94118, 95058, 95070, 97045, 99029, 99181, 99233, Mutant 3, TKG 19A, TMV 2, TPG 41,
	C Vb	25	ICGVs 00290, 00343, 00351, 01005, 01060, 01124, 01274, 01393, 02206, 03184, 03397, 03398, 04044, 06347, 06422, 06423, 07227, 07247, 07268, 86015, 86072, 93280, 95290, 95469, 99083,
	C Vc	25	Faizpur 1-5, ICGS 11 , ICGV 02144, 02321, 03042, 03056, 04124, 05161, 06424, 06431, 07148, 86143, 87187 , 89104, 92195, 93437, 97058, 97092, 97120, 97165, 97261, 97262, 98163, 99195, J 11,
	C Vd	10	ICGVs 00387, 01273, 02242, 04018, 05163, 05176, 07217, 07235, 07246, 99085,

Table 4.43a Cluster mean for different yield and its contributing traits of GSP evaluated across the four locations

Cluster	Sub-cluster	DFF	LLS 90	LLS 105	Rust 90	Rust 105	NPP	PYPP	SYPP	SH %	HSW	DM	PYH	HLM
C I	C Ia	32.14	4.74	6.68	4.73	6.60	13.86	9.09	5.28	58.16	33.60	118.73	1465.15	14.73
	C Ib	32.09	4.81	6.81	4.83	6.79	10.84	9.00	5.05	55.88	36.02	118.20	1326.10	17.43
	C Ic	31.47	5.47	7.22	5.60	7.19	13.66	8.92	5.24	59.06	31.19	118.24	1347.83	15.27
C II	C IIa	32.82	5.47	7.20	5.15	6.91	12.99	9.51	5.65	59.94	35.09	119.28	1453.14	17.69
	C IIb	33.80	3.75	5.62	3.23	5.00	15.37	11.11	6.42	57.24	35.09	124.74	1870.70	19.77
C III	C IIIa	33.33	4.68	6.44	4.17	5.81	13.63	9.57	5.53	57.87	34.16	121.58	1585.66	19.48
	C IIIb	33.39	4.52	6.39	3.91	5.82	16.59	11.83	7.02	59.44	34.11	124.39	1965.37	19.93
C IV	C IVa	35.72	4.67	6.58	4.70	6.21	9.63	6.46	3.75	57.36	30.72	121.54	896.96	18.77
	C IVb	33.87	3.95	5.62	3.44	5.13	14.66	9.95	6.00	60.06	30.75	123.09	1522.10	20.66
C V	C Va	32.16	4.80	6.55	4.44	6.09	15.76	10.69	6.37	59.73	32.00	122.29	1831.19	17.72
	C Vb	33.19	5.00	6.97	4.39	6.19	15.75	10.66	6.57	60.89	33.73	120.75	1873.44	18.68
	C Vc	32.45	5.24	6.96	4.83	6.57	14.74	9.69	5.80	60.15	30.22	117.17	1693.17	16.45
	C Vd	33.03	4.47	6.63	3.90	6.07	16.83	11.91	7.15	60.57	35.22	120.63	2163.31	18.15

Where; DFF= Days to 50% flowering, LLS90, LLS 105, Rust90 & Rust105= Disease severity score of late leaf spot and rust recorded at 90 and 105 days after sowing respectively, PH = Plant height (cm), NPP= Number of pods plant^{-1}, PYPP= Pod yield plant^{-1} (g), SH %= Shelling percent, DM= Days to physiological maturity, HSW= Hundred seed weight (g), PYH= Yield hectare^{-1} (kg), and HLM= Haulm weight plant^{-1} (g)

Table 4.43b Cluster mean for different nutritional quality traits of GSP evaluated across the four environments

Cluster	Sub-cluster	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
C I	C Ia	50.87	22.51	43.14	37.29	11.92	1.89	1.20
	C Ib	50.80	22.39	44.21	37.26	11.06	2.20	1.22
	C Ic	50.72	22.38	43.56	37.31	11.43	1.90	1.48
C II	C IIa	50.48	22.78	42.75	37.47	11.75	2.02	1.19
	C IIb	52.65	22.42	39.62	40.24	12.49	2.19	1.04
C III	C IIIa	50.67	22.96	41.30	38.24	12.04	2.10	1.12
	C IIIb	51.79	23.10	38.87	40.39	12.30	2.26	1.00
C IV	C IVa	50.36	22.44	44.27	35.86	11.66	1.96	1.29
	C IVb	53.17	22.46	44.95	36.19	12.27	1.87	1.30
C V	C Va	52.30	22.59	40.79	39.10	12.11	2.25	1.09
	C Vb	51.04	23.02	38.52	40.91	12.42	2.17	0.98
	C Vc	51.36	22.92	40.40	39.48	12.23	2.07	1.07
	C Vd	52.01	22.90	39.68	39.94	12.14	2.39	1.05

4.7 Population structure and Marker-Trait Association (MTA)

4.7.1 Population structure

STRUCTURE software was used to determine the relationship among the genotypes studied. The structure analysis distinguished 336 genotypes into three populations with a ΔK value of 740 (Fig 4.37 & Fig 4.38). Sub-population I consisted of 96 genotypes with nearly 94% (90/96) cultivars belongs to ssp. *fastigiata* whereas 191 genotypes were grouped into sub-population II (SP II) with a mixture of cultivars from both the subspecies. In SP II, nearly 70% (134/191) genotypes belong to ssp. *fastigiata* which includes genotypes from four botanical varieties of this subspecies *viz., vulgaris* (119/134), *fastigiata* (10/10), *peruviana* (4/4) and a single genotype from *aequatoriana* whereas 30% (57/191) were from ssp. *hypogaea*. However, sub-population III had 49 genotypes belong to ssp. *hypogaea* indicated that the genotypes with pure background of ssp. *hypogaea* were grouped in this sub-population. Pure or admixture genotypes were categorized through structure analysis. The genotype with score >0.80 was considered as pure and <0.80 as an admixture. Among the 96 genotypes, 93 genotypes were pure and 3 were admixed in sub-population I, while 185 pure and 6 admixed were reported in sub-population II whereas sub-population III contained all the pure genotypes with no admixture.

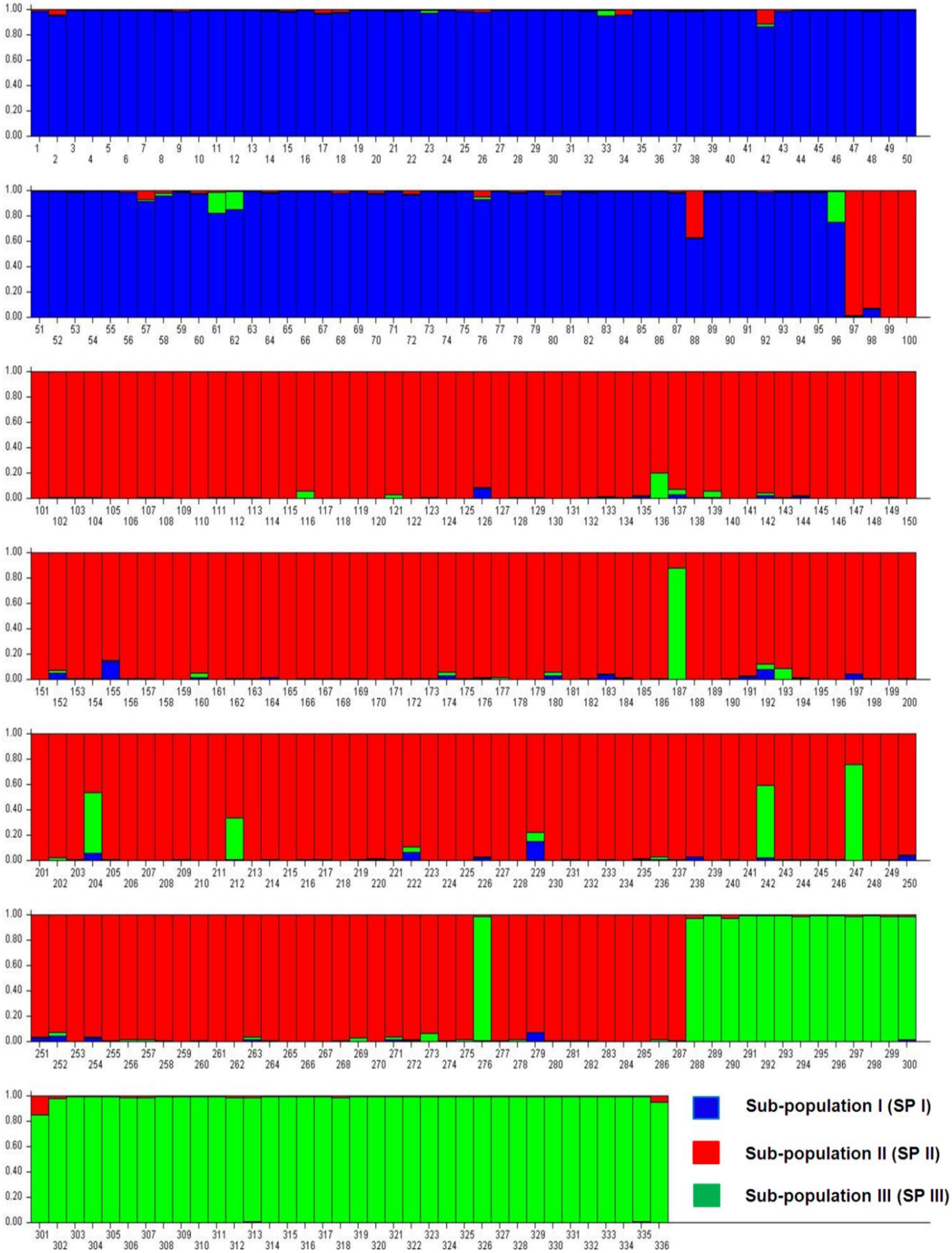

Figure 4.37 Population structure of Genomic Selection Panel of groundnut based on 14 SSR markers analysis

Note: Number on the y-axis show the subgroup membership and the number on the x-axis show the accession number

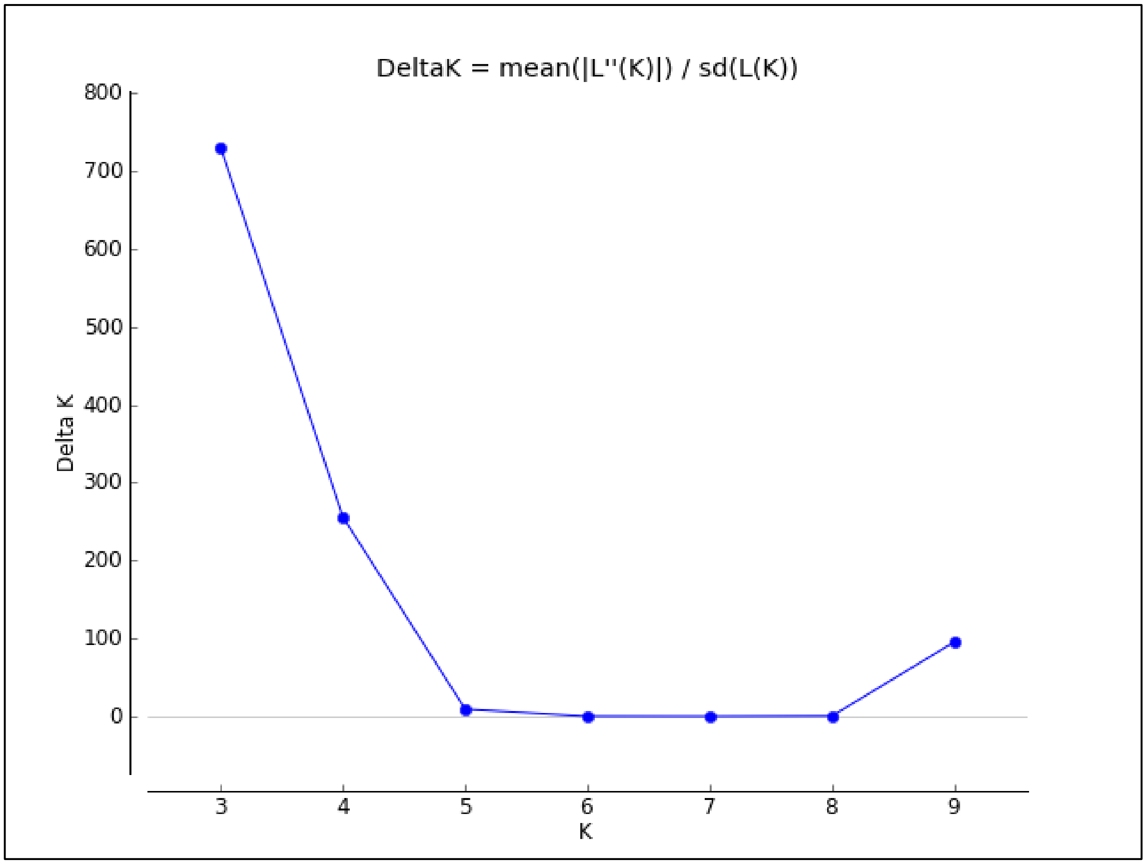

Figure 4.38 Estimation of the population using LnP (D) derived delta K for determining an optimum number of subpopulations

The admixture identified in the GSP for 14 SSR loci can be visualized in the graphical representation (Fig 4.37). The unweighted neighbor-joining tree clustered 336 genotypes into five clusters (Fig 4.35) based on 14 SSR marker data. Cluster V consisted of 96 genotypes corresponded to SP I whereas cluster IV had 48 genotypes represented SP III. However, cluster I, II and III had a total of 192 genotypes with comparatively narrow genetic distance together representing SP II. The results from neighbor-joining were generally consistent with the results from STRUCTURE analysis with a few exceptions.

4. 7.2 Marker-trait associations (MTAs)

Among all the traits resistant to both the disease (LLS and rust) at 90 and 105 DAS, seven yield traits and seven nutritional quality traits were used for their association with previously identified SSR markers. BLUPs for every trait of every genotype was calculated from the individual as well as across the environments and used for MTA analysis. A general linear mixed model (GLM) was used for association analysis using TASSEL 2.1 (Yu *et al.,* 2006). To identify the SSR markers associated with the quantitative traits, population structure (Q matrix) and BLUPs of different traits were used. The MTAs detected repeatedly in the individual as well as pooled across the environments were considered as better MTA. The identified MTAs were compared for the coefficient of determination (R^2) to select MTAs which explained more phenotypic variation (PV) for that trait. Details of MTAs detected in the individual as well as pooled across the environments are presented in Table 4.44 & 4.45.

A total of 311 significant MTAs for 18 traits including disease resistance, yield and nutritional quality traits were identified (Table 4.44). Of these, 73 MTAs were reported as significant ($P \leq 0.05$) across the environments. However, there were 60 MTAs reported in Aliyarnagar, 50 in Jalgaon and 89 in ICRISAT during rainy 2015 and 33 in ICRISAT during post-rainy 2015-16 (Fig 4.39). Phenotypic variance (PV) for these MTAs varied from low (8.38%) to very high (94.76%). Among these 311 MTAs, only 79 explained >30% phenotypic variance (PV) and were considered as potential MTAs (Table 4.45). The number of MTAs associated ($P \leq 0.05$) with the individual trait is described below.

4.7.2.1 MTA for disease resistance

Disease severity scores of both the diseases (rust and LLS) recorded at 90 and 105 DAS were considered for MTA analysis. The results revealed 29 MTAs for both the diseases with PV varied from 30.27 to 84.70%. Of these, 18 MTAs were associated with LLS (30.27 to 84.70% PV) whereas 11 with rust (30.45 to 63.14%). The SSR markers, GM 1009, GM 2301 and TC6H03 had a significant association with LLS resistance in pooled with PVE >30%. MTAs detected at individual environment also showed that marker GM 1009 was associated with LLS at Aliyarnagar and Jalgaon, GM 2301 and TC6H03 at Aliyarnagar and ICRISAT rainy 2015. Beside these GM 1954 involved in two MTAs with LLS at Aliyarnagar (30.95% PV) and ICRISAT during rainy 2015 (31.58%) was also a good SSR associated with this trait. However, GM 1573 (37.47%), TC1D12 (32.83%) and IPAHM 103 (84.7%) were found to be associated with single MTAs at Aliyarnagar, ICRISAT rainy 2015 and Jalgaon, respectively (Table 4.45).

Two markers GM 2301 (33.11%) and IPAHM 103 (43.49%) were reported to be associated with rust score across the environments. Among the 11 MTAs for rust, GM 2301 was involved in five MTAs (31.58 to 37.16% PV) whereas IPAHM 103 was involved in two MTAs (43.49 to 63.14% PV). GM 2301 was associated with rust at Aliyarnagar (31.64% PV), ICRISAT rainy 2015 (34.75% PV) and pooled (32.94% PV) at 90 DAS and ICRISAT rainy 2015 (37.16%) and pooled (33.11% PV) at 105 DAS whereas IPAHM 103 was associated with rust at Aliyarnagar (63.14% PV) and pooled (43.49%) at 105 DAS. Beside these GM 1009 (31.64% PV) at Aliyarnagar and GM 1954 (30.45% PV) at Jalgaon at 90 DAS, TC1D12 (35.88% PV) at Aliyarnagar and TC6E01 (30.60% PV) at Jalgaon at 105 DAS were also reported as significant MTAs at a particular location (Table 4.45).

4.7.2.2 Yield and its component traits

Total seven important yield component traits *viz.,* days to 50% flowering (DFF), days to maturity (DM), pod yield per plant (PYPP), shelling percent (SH), hundred seed weight (HSW), pod yield per hectare (PYH) and haulm yield per plant (HLM) were analyzed for MTA using 14 SSR markers. A total of 18 MTAs could be identified for these above mentioned seven yield and its component traits with PV > 30%. Two MTAs were identified for days to 50% flowering, among these two TC1D12 explained 32.10% phenotypic variation with pooled BLUPs whereas GM 2301 explained 30.0% PV at ICRISAT during rainy 2015. Five MTAs with >30% PV were reported for days to maturity, among these, TC1D12 showed good consistency and appeared thrice (total five MTAs) at Aliyarnagar, Jalgaon and ICRISAT during rainy 2015 with stable and high phenotypic variance of 32.01%, 41.34% and 32.33%, respectively and hence, is promising. IPAHM 103 (45.69% PV) and GM 1954 (34.22% PV) were associated with days to maturity only at Aliyarnagar and Jalgaon, respectively.

Two MTAs with a single marker (TC1D12) were reported for pod yield per plant at Jalgaon (31.12% PV) and with pooled BLUPs (30.27% PV) across the environments. Marker TC1D12 was found to be associated in both MTAs for shelling percent at Aliyarnagar (35.83% PV) and ICRISAT post-rainy 2015-16 (31.88% PV). Similarly, two MTAs were reported for hundred seed weight and pod yield per hectare with IPAHM 103 and TC1D12. Both the MTAs for hundred seed weight were reported at Aliyarnagar with a phenotypic variation of 45.69% (IPAHM 103) and 32.01% (TC1D12). Both the MTAs of pod yield per hectare were identified in pooled analysis, marker IPAHM 103 explained 35.19% PV whereas TC1D12 explained 34.74% PV across the environments. Three MTAs each one with TC6E01 (33.99% PV), TC1D12 (33.31% PV) and GM 1954 (30.96% PV) were identified for haulm weight per plant at ICRISAT during rainy 2015 (Table 4.45).

4.7.2.3 Nutritional quality traits

MTA analysis in present study included several oil and nutritional quality traits such as oil content (OC), oleic acid (OL), linoleic acid (LA), palmitic acid (PA), stearic acid (SA), oleic/linoleic acid ratio (O/L) and protein content (PC). Association analysis for seven nutritional quality traits with 14 SSR markers revealed 31 better MTAs with >30% phenotypic variation explained. Three MTAs were identified for oil content at Aliyarnagar, Jalgaon and pooled with 38.45%, 63.14% and 35.27% phenotypic variation, respectively. Marker IPAHM 103 was identified in all these three MTAs indicating that this marker was potential and significant for oil content (%). Of these 31 MTAs 6 were reported for protein content and among these six, four MTA involved IPAHM 103 whereas two MTAs had GM 1954 associated with protein content. Protein content had significant association with IPAHM 103 at Aliyarnagar (41.38% PV), ICRISAT rainy 2015 (38.80% PV), ICRISAT post-rainy 2015-16 (38.71% PV) and Jalgaon (43.68% PV) whereas GM 1954 was associated at ICRISAT rainy 2015 (31.17% PV) and Jalgaon (32.55% PV). Oleic acid is an important fatty acid responsible for longer self-life of groundnut oil and food products. MTA analysis for oleic acid content identified five MTAs with >30% PV, IPAHM 103 and GM 1954 were the marker involved in three (ICRISAT and Jalgaon during rainy 2015, and pooled across the environments) and two MTAs (ICRISAT and Jalgaon during rainy 2015). Marker IPAHM 103 was good and consistently associated with oleic acid at individual environments (39.53% PV at ICRISAT rainy 2015 and 45.95% PV at Jalgaon) as well as pooled (42.70% PV). Among the nutritional quality traits, highest number of MTAs (7 out 31) was reported for linoleic acid. Marker IPAHM 103 was identified only in single MTA with pooled BLUPs and largest phenotypic variation explained (43.49%) whereas TC6H03 was associated in two MTAs at Aliyarnagar (36.00%) and ICRISAT during post-rainy 2015-16 (40.03%). The marker TC6E01 was also associated in two MTAs with 33.71 and 31.51% phenotypic variation at ICRISAT during the rainy and post-rainy season, respectively (Table 4.45). PM 36 and TC1D12 were also associated with linoleic acid at ICRISAT during rainy 2015 explained 33.58% and 33.36% of the total phenotypic variation, respectively. Four MTAs were reported for palmitic acid with >30% PV at Aliyarnagar and ICRISAT post-rainy 2015-16. Two markers IPAHM 103 and GM 1954 were involved in these four MTAs each one in both the environments. Comparatively IPAHM 103 explained more phenotypic variation (91.86 and 91.80%) than GM 1954 (44.90% and 43.15%) at Aliyarnagar and ICRISAT post-rainy 2015-16, respectively. There were five MTAs reported for stearic acid, two of them involved IPAHM 103 explained greater phenotypic (87.10% and 94.76% at ICRISAT and Jalgaon during rainy 2015) variation than GM 1954 (46.23% and 37.94% at ICRISAT and Jalgaon during rainy 2015). However, marker TC6H03 was identified in pooled with 37.94% PV. For oleic linoleic acid ratio (O/L ratio), two MTAs with IPAHM 103 (86.74% PV) and GM 1954 (43.35% PV) were reported with pooled BLUPs. Among all the 31 MTAs for nutritional quality traits, 16 MTAs (nearly 50%) involved IPAHM 103 with higher phenotypic variation indicated its potential role in the expression of most of the nutritional quality traits (Table 4.45).

Table 4.44 Marker-trait association for disease resistance, yield and its contributing traits and nutritional quality traits in groundnut

S. No	Trait	MTAs	F value		p-value		PVE %	
			Min	Max	Min	Max	Min	Max
Foliar disease resistance								
1	LLS90	22	1.349	6.565	2.37E-23	0.046	8.60	37.99
2	LLS105	24	1.346	12.245	2.07E-53	0.042	10.93	84.70
3	Rust90	21	1.383	12.039	9E-53	0.045	8.43	63.14
4	Rust105	22	1.473	3.811	9.6E-11	0.021	8.94	35.88
Yield and its contributing traits								
5	Days to maturity	26	1.345	2.557	7.79E-08	0.043	11.51	45.69
6	Days to flowering	25	1.322	3.373	1.02E-05	0.051	8.44	37.17
7	Pod yield per plant (g)	18	1.332	2.225	0.000206	0.053	13.53	31.12
8	Shelling percent (%)	7	1.407	2.377	0.0013	0.027	9.25	35.83
9	Hundred seed yield (g)	17	1.365	2.316	0.00002	0.048	8.38	45.69
10	Yield per hectare (kg)	21	1.356	2.373	2.31E-05	0.049	14.47	35.19
11	Haulm weight per plant (g)	10	1.423	3.420	1.02E-05	0.050	10.45	33.99
Nutritional quality traits								
12	Oil content (%)	10	1.324	12.039	9E-53	0.048	15.24	63.14
13	Protein content (%)	9	1.453	1.788	0.00019	0.029	14.94	43.68
14	Oleic acid (%)	12	1.343	1.975	1.46E-05	0.037	17.01	45.95
15	Linoleic acid (%)	23	1.379	2.354	7.22E-06	0.049	11.49	43.49
16	Palmitic acid (%)	15	1.372	25.740	1.33E-83	0.046	10.41	91.86
17	Stearic acid (%)	17	1.383	40.566	1.3E-103	0.037	8.43	94.76
18	O/L Ratio	12	1.354	15.017	6.48E-63	0.049	9.32	86.74
	Total	**311**	**1.322**	**40.566**	**1.34E-103**	**0.053**	**8.38**	**94.76**

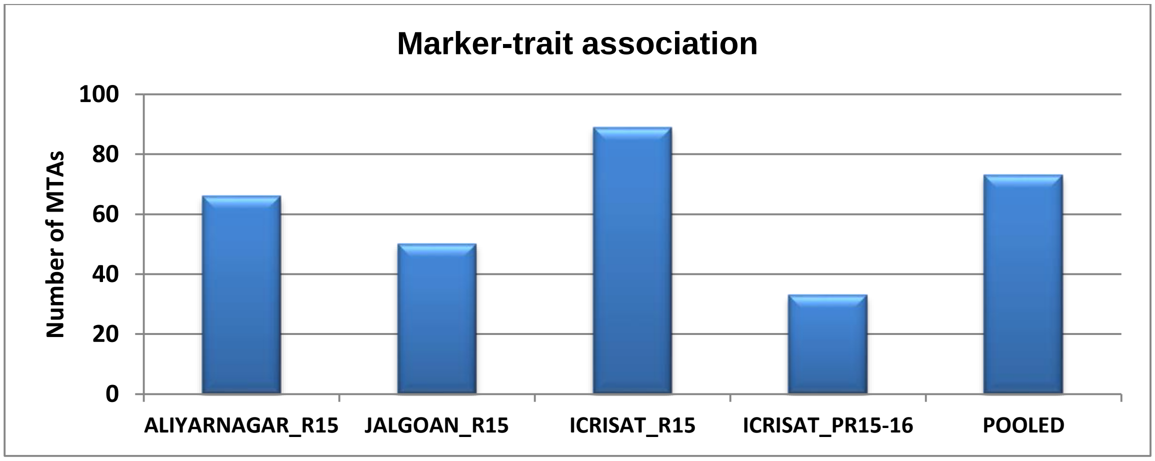

Figure 4.39 Number of marker-trait association reported between BLUPs of 18 important traits including foliar disease resistance, yield and nutritional quality traits of GSP evaluated across four environments

Table 4.45 Highly significant marker-trait associations for different traits explained >30 % phenotypic variation

S. No	Traits	Location/Season	Marker	F value	p-value	PVE %
Foliar disease resistance						
1	LLS score at 90 DAS	LLS90_AL_R15	TC6H03	1.575	0.0035	37.47
2		LLS90_AL_R15	GM1573	6.565	2.37E-23	36.82
3		LLS90_AL_R15	GM1009	2.412	2.97E-06	30.86
4		LLS90_AL_R15	GM2301	1.690	0.002	30.77
5		LLS90_ICR_R15	TC6H03	1.612	0.0023	37.99
6		LLS90_ICR_R15	GM2301	1.890	2.12E-04	33.18
7		LLS90_Pooled	TC6H03	1.492	0.0086	34.79
8		LLS90_Pooled	GM2301	1.879	2.11E-04	32.20
9	LLS score at 105 DAS	LLS105_AL_R15	GM2301	2.304	1.43E-06	37.76
10		LLS105_AL_R15	GM1954	1.475	0.0141	30.95
11		LLS105_ICR_R15	TC1D12	1.484	0.0115	32.83
12		LLS105_ICR_R15	GM2301	1.781	7.25E-04	31.86
13		LLS105_ICR_R15	GM1954	1.524	0.0086	31.58
14		LLS105_JL_R15	IPAHM103	12.245	2.07E-53	84.70
15		LLS105_JL_R15	GM1009	5.368	1.91E-20	49.89
16		LLS105_Pooled	TC6H03	1.665	0.0012	37.27
17		LLS105_Pooled	GM2301	2.040	3.09E-05	33.99
18		LLS105_Pooled	GM1009	2.481	1.28E-06	30.27
19	Rust score at 90 DAS	Rust90_AL_R15	IPAHM103	12.039	9.00E-53	63.14
20		Rust90_AL_R15	GM1009	2.487	1.32E-06	31.64
21		Rust90_AL_R15	GM2301	1.745	0.0011	31.58
22		Rust90_ICR_R15	GM2301	2.030	4.10E-05	34.75
23		Rust90_JL_R15	GM1954	1.544	0.007	30.45
24		Rust90_Pooled	GM2301	1.898	1.70E-04	32.94
25	Rust score at 105 DAS	Rust105_JL_R15	TC1D12	1.771	4.58E-04	35.88
26		Rust105_JL_R15	TC6E01	1.512	0.0097	30.60
27		Rust105_ICR_R15	GM2301	2.687	5.16E-07	37.16
28		Rust105_Pooled	IPAHM103	1.806	1.17E-04	43.49
29		Rust105_Pooled	GM2301	1.942	1.01E-04	33.11
Yield and its contributing traits						
30	Days to 50% flowering	DFF_ICR_R15	GM2301	1.640	0.0033	30.00
31		DFF_Pooled	TC1D12	1.905	7.22E-05	32.10
32	Days to maturity	DM_AL_R15	IPAHM103	1.946	2.20E-05	45.69
33		DM_AL_R15	TC1D12	1.483	0.0117	32.01
34		DM_ICR_R15	TC1D12	1.633	0.0023	32.33
35		DM_JL_R15	TC1D12	2.435	7.79E-08	41.34
36		DM_JL_R15	GM1954	1.925	8.87E-05	34.22
37	Pod yield per plant (g)	PYPP_JL_R15	TC1D12	1.582	0.0041	31.12
38		PYPP_Pooled	TC1D12	1.584	0.0036	30.27
39	Shelling percent (%)	SH_AL_R15	TC1D12	1.685	0.0013	35.83
40		SH_ICR_PR15	TC1D12	1.526	0.0075	31.88
41	Hundred seed weight (g)	HSW_AL_R15	IPAHM103	1.946	2.20E-05	45.69
42		HSW_AL_R15	TC1D12	1.483	0.0117	32.01
43	Pod yield per hectare (kg)	PYH_Pooled	IPAHM103	1.448	0.0111	35.19
44		PYH_Pooled	TC1D12	1.993	2.31E-05	34.74
45	Haulm yield per plant (g)	HLM_ICR_R15	TC6E01	1.744	7.68E-04	33.99
46		HLM_ICR_R15	TC1D12	1.555	0.0055	33.31
47		HLM_ICR_R15	GM1954	1.517	0.0092	30.96
Nutritional quality traits						
48	Oil Content (%)	OC_AL_R15	IPAHM103	1.457	0.011	38.45
49		OC_JL_R15	IPAHM103	12.039	9.00E-53	63.14
50		OC_Pooled	IPAHM103	2.550	1.75E-08	35.27

S. No	Traits	Location/Season	Marker	F value	p-value	PVE %
51	Protein content (%)	PC_AL_R15	IPAHM103	1.651	0.0011	41.38
52		PC_ICR_15	IPAHM103	1.460	0.0107	38.80
53		PC_ICR_15	GM1954	1.553	0.0063	31.17
54		PC_ICR_PR15	IPAHM103	1.453	0.0114	38.71
55		PC_JL_R15	IPAHM103	1.788	1.88E-04	43.68
56		PC_JL_R15	GM1954	1.652	0.0022	32.55
57	Oleic acid	OA_ICR_R16	IPAHM103	1.528	0.0049	39.53
58		OA_JL_R15	IPAHM103	1.975	1.46E-05	45.95
59		OA_JL_R15	GM1954	1.727	9.36E-04	33.42
60		OA_Pooled	IPAHM103	1.721	3.71E-04	42.70
61		OA_ICR_R15	GM1954	1.617	0.0032	31.74
62	Linoleic acid (%)	LA_AL_R15	TC6H03	1.515	0.007	36.00
63		LA_ICR_PR15	TC6H03	1.745	4.59E-04	40.03
64		LA_ICR_PR15	TC6E01	1.668	0.0018	33.71
65		LA_ICR_R15	PM36	2.236	7.22E-06	33.58
66		LA_ICR_R15	TC1D12	1.510	0.0088	33.36
67		LA_ICR_R15	TC6E01	1.509	0.01	31.51
68		LA_Pooled	IPAHM103	1.806	1.17E-04	43.49
69	Palmitic acid (%)	PA_AL_R15	IPAHM103	25.740	1.33E-83	91.86
70		PA_AL_R15	GM1954	2.687	4.16E-09	44.90
71		PA_ICR_PR15	IPAHM103	25.086	1.69E-82	91.80
72		PA_ICR_PR15	GM1954	2.495	5.45E-08	43.15
73	Stearic acid (%)	SA_ICR_R15	IPAHM103	15.418	2.35E-62	87.10
74		SA_ICR_R15	GM1954	2.847	4.77E-10	46.23
75		SA_JL_R15	IPAHM103	40.566	1.34E-103	94.76
76		SA_JL_R15	GM1954	3.020	4.54E-11	47.90
77		SA_Pooled	TC6H03	1.707	6.86E-04	37.94
78	O/L ratio	O/L_Pooled	IPAHM103	15.017	6.48E-63	86.74
79		O/L_Pooled	GM1954	2.550	1.75E-08	43.35

Where _AL_R15= Aliyarnagar rainy 2015; _JL_R15= Jalgaon rainy 2015; _ICR_R15= ICRISAT rainy 2015; _ICR_PR15= ICRISAT post-rainy 2015-16

4.8 Screening of GSP for mutant alleles of *ahFAD2* gene

Individuals of GSP were subjected to search mutant alleles of *ahFAD2A* and *ahFAD2B* in this diverse set of genotypes. The results of allele-specific PCR assay reported 87 (25.89%) out of 336 genotypes with a mutant allele of *ahFAD2A* whereas only one genotype (SunOleic 95R) had a mutant allele of *ahFAD2B* (Table 4.46 & Fig 4.40). The internal control used for assurance of successful PCR reaction revealed 88.99 (299 out of 336 genotypes) and 87.50% (294 out 336 genotypes) reactions were successful in the screening of genotypes for ah*FAD2A* and ah*FAD2B* gene, respectively. Out of 87 genotypes with a mutant allele of *ahFAD2A* (substitution of G:C→A:T) 68.97% (60) genotypes were from subspecies *fastigiata* var *vulgaris,* whereas 31.03% (27) genotypes were from subspecies *hypogaea* var *hypogaea*. However, only a single genotype in GSP had both the mutant allele (SunOleic 95R) belongs to subspecies *hypogaea* var *hypogaea* (Virginia runner)*.* The mean performance of genotypes for different major fatty acids with respect to presence or absence of mutant alleles revealed that genotype with both the mutant allele (SunOleic 95R) had higher oleic acid and lower linoleic and palmitic acid compared to all other genotypes across the four individual environment's and pooled. However, mean performance of genotypes with only single mutant allele (*ahFAD2A*) did not significantly differ from genotypes with its wild type allele. Hence, in order to enhance oleic acid content, both the mutant alleles are required. The Oleic acid of SunOleic 95R was 74.38% at Aliyarnagar, 80.47% at Jalgaon, 76.03% at ICRISAT rainy 2015, 76.06% during post rainy 2015-16 and 78.83% in pooled across location (Table 4.46). On the other hand this genotype had lowest linoleic and palmitic acid content across the location, 5.30 & 8.50 at Aliyarnagar, 5.12 & 6.98% at Jalgaon, 6.12 & 7.98% at ICRISAT during rainy 2015, 4.60 & 7.08% at ICRISAT during post rainy 2015 and 7.81 & 7.63% in pooled across the environments, respectively (Table 4.46).

Table 4.46 Mean performance of genotypes for major fatty acids with presence/absence of mutant alleles of *AhFAD2A* and *AhFAD2B* gene

Mutant allele	Genotypes	Location /season	Oleic acid	Linoleic acid	Palmitic Acid	Stearic acid	O/L ratio
AhFAD2A	87	Aliyarnagar	41.76	39.68	11.74	2.23	1.10
		Jalgaon	38.53	42.46	12.02	2.12	0.95
		ICRISAT_R	42.16	36.55	11.85	1.68	1.20
		ICRISAT_PR	43.64	34.58	12.63	2.44	1.31
		Pooled	41.53	38.32	12.06	2.12	1.14
Both *AhFAD2A* and *AhFAD2B*	1	Aliyarnagar	74.38	5.30	8.50	2.13	14.03
		Jalgaon	80.47	5.12	6.98	1.89	15.71
		ICRISAT_R	76.03	6.12	7.89	1.45	12.76
		ICRISAT_PR	76.06	4.60	7.08	2.02	16.53
		Pooled	78.83	5.61	7.63	1.86	14.09
Internal control no mutant allele	216	Aliyarnagar	41.78	40.06	11.64	2.19	1.08
		Jalgaon	38.74	42.40	11.90	2.10	0.94
		ICRISAT_R	42.93	36.23	11.66	1.67	1.23
		ICRISAT_PR	43.91	34.78	12.46	2.31	1.31
		Pooled	41.84	38.37	11.92	2.07	1.14
No Amplification	32	Aliyarnagar	42.60	38.94	11.67	2.09	1.13
		Jalgaon	39.24	41.85	12.04	2.03	0.97
		ICRISAT_R	43.37	35.38	11.84	1.57	1.28
		ICRISAT_PR	43.45	35.14	12.62	2.22	1.28
		Pooled	42.16	37.83	12.05	1.98	1.17

Where- ICRISAT_R= ICRISAT rainy 2015; ICRISAT_PR= ICRISAT post-rainy 2015-16

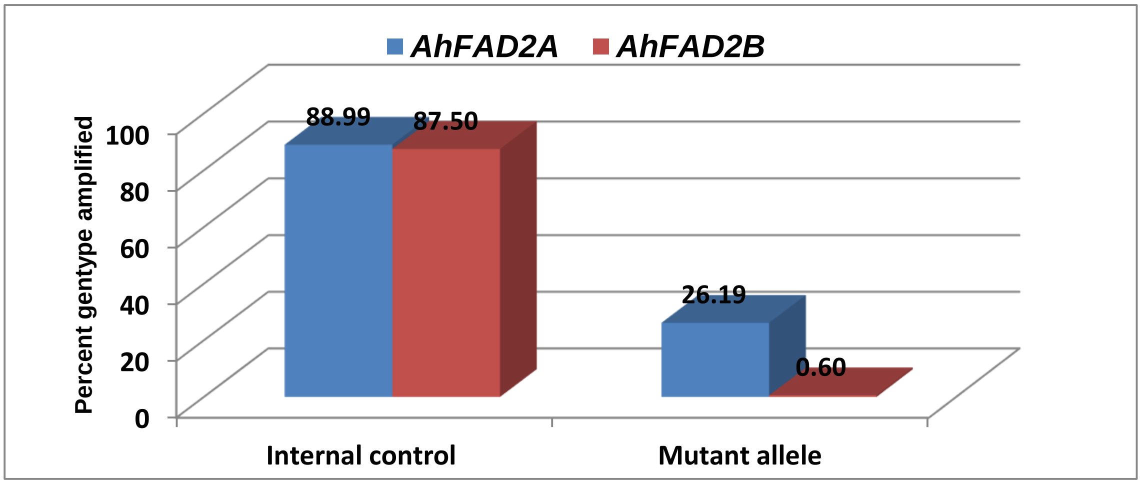

Figure 4.40 Graph showing frequency of genotypes of GSP amplified for internal control and mutant alleles of *AhFAD2A* and *AhFAD2B*

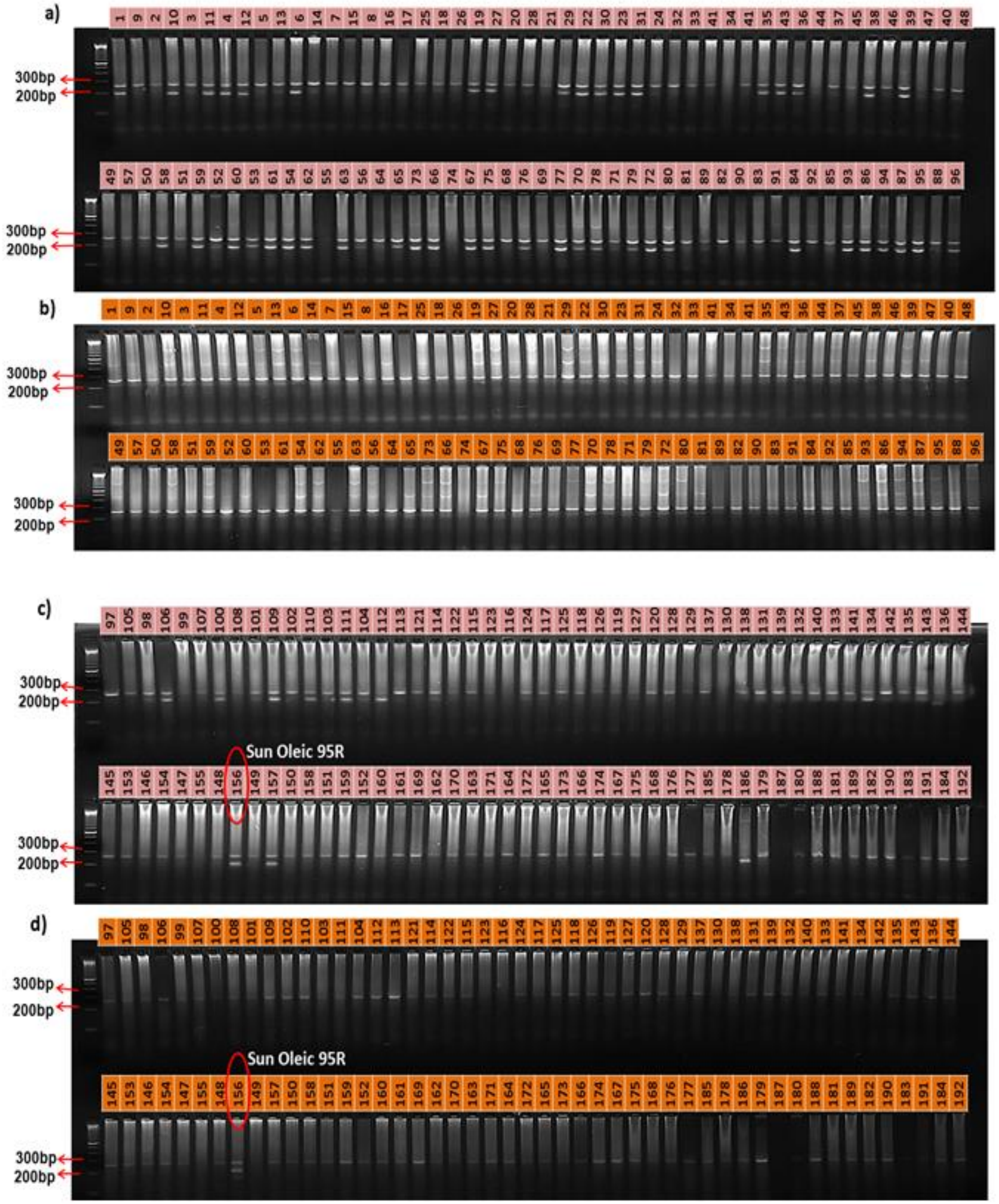

Figure 4.41a Screening of Genomic Selection Panel for mutant alleles of *ahFAD2* genes using allele-specific PCR assay. a) & c) Upper amplicons of panel a and c represents internal control (250bp) to verify successful PCR reaction and lower amplicon at 203 bp indicates presence of mutant allele of *ahFAD2A* on A-genome (substitution of G:C→A:T) (Genotype 1 to 192); b) & d) Upper amplicons of panel b and d represents internal control (250bp) to verify successful PCR reaction and lower amplicon (193 bp) indicates presence of mutant allele of *ahFAD2B* on B-genome (Insertion of A:T) (Genotype 1 to 192)

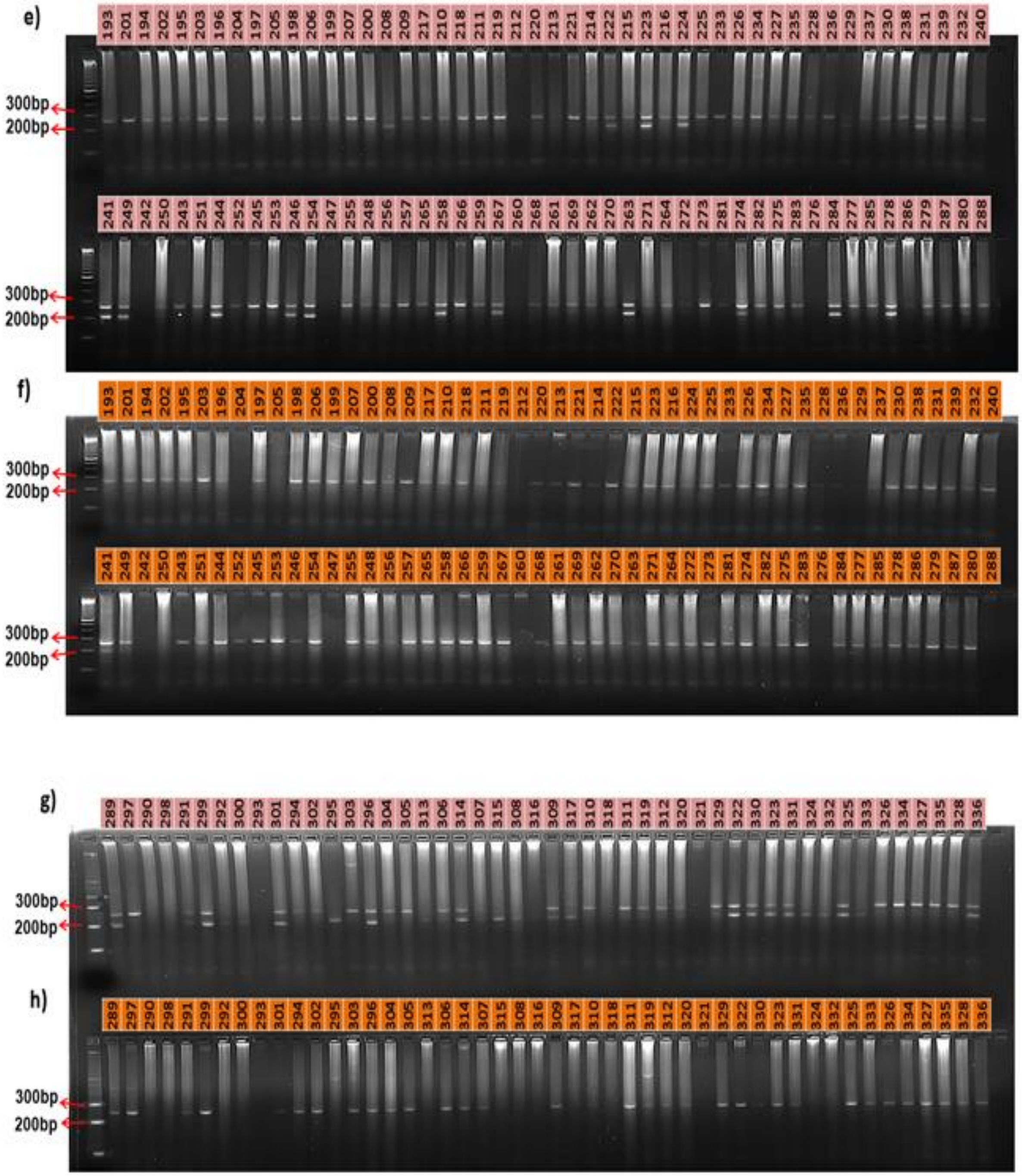

Figure 4.41b Screening of Genomic Selection Panel for mutant alleles of *ahFAD2* gene using allele-specific PCR assay. e) & g) Upper amplicons of panel e and g represents internal control (250bp) to verify successful PCR reaction and lower amplicon at 203 bp indicates presence of mutant allele of *ahFAD2A* on A-genome (substitution of G:C→A:T) (Genotype 196 to 336); f) & h) Upper amplicons of panel f and h represents internal control (250bp) to verify successful PCR reaction and lower amplicon (193 bp) indicates presence of mutant allele of *ahFAD2B* on B-genome (Insertion of A:T) (Genotype 193 to 336)

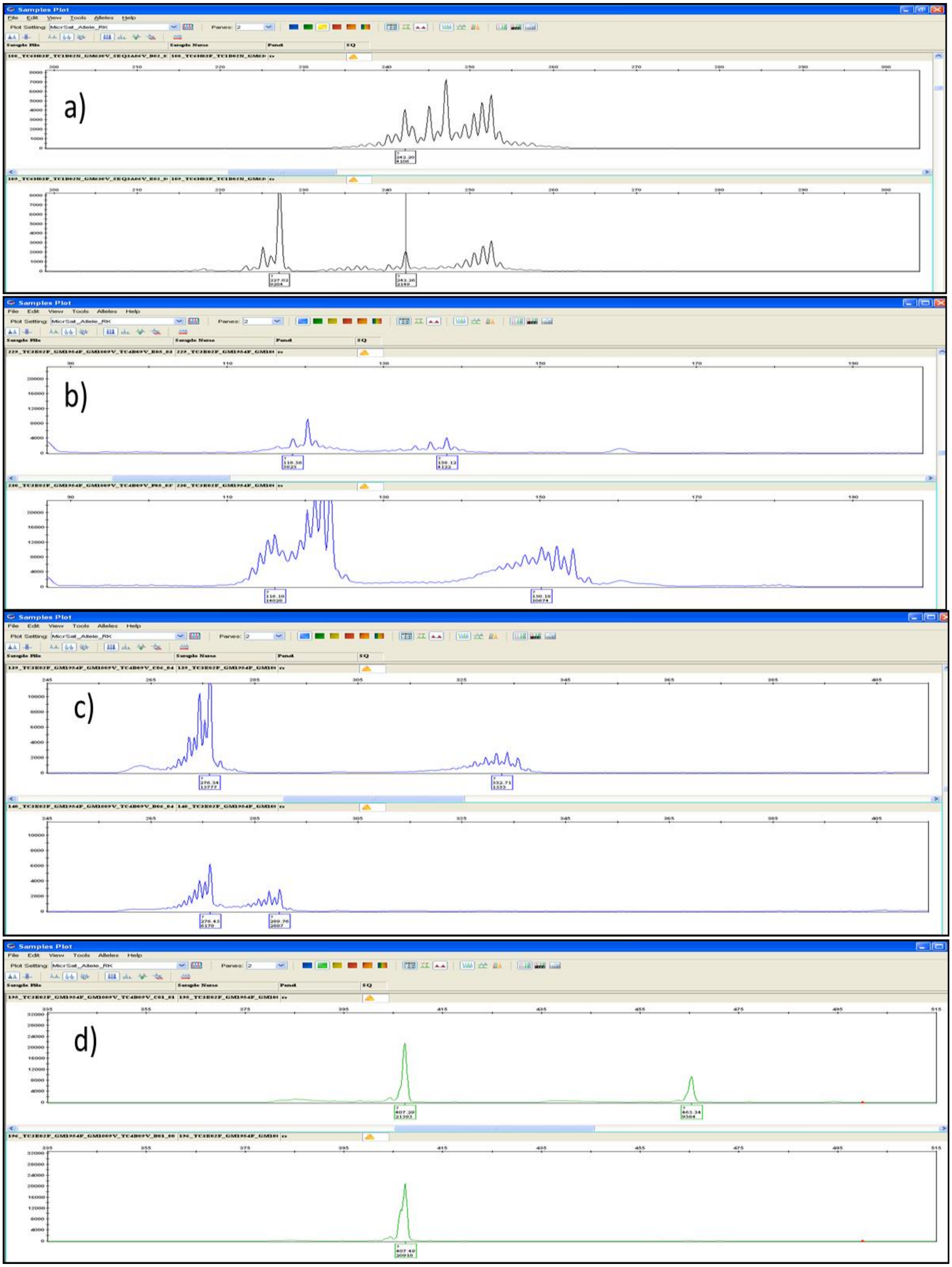

Figure 42 **Snapshot of separated PCR products by capillary electrophoresis (using ABI Prism 3700) showing polymorphism among genotypes for SSR locus a) TC1D02 (NED); b) GM 1954 (FEM); c) TC3E02 (FEM); d) GM 1009 (VIC)**

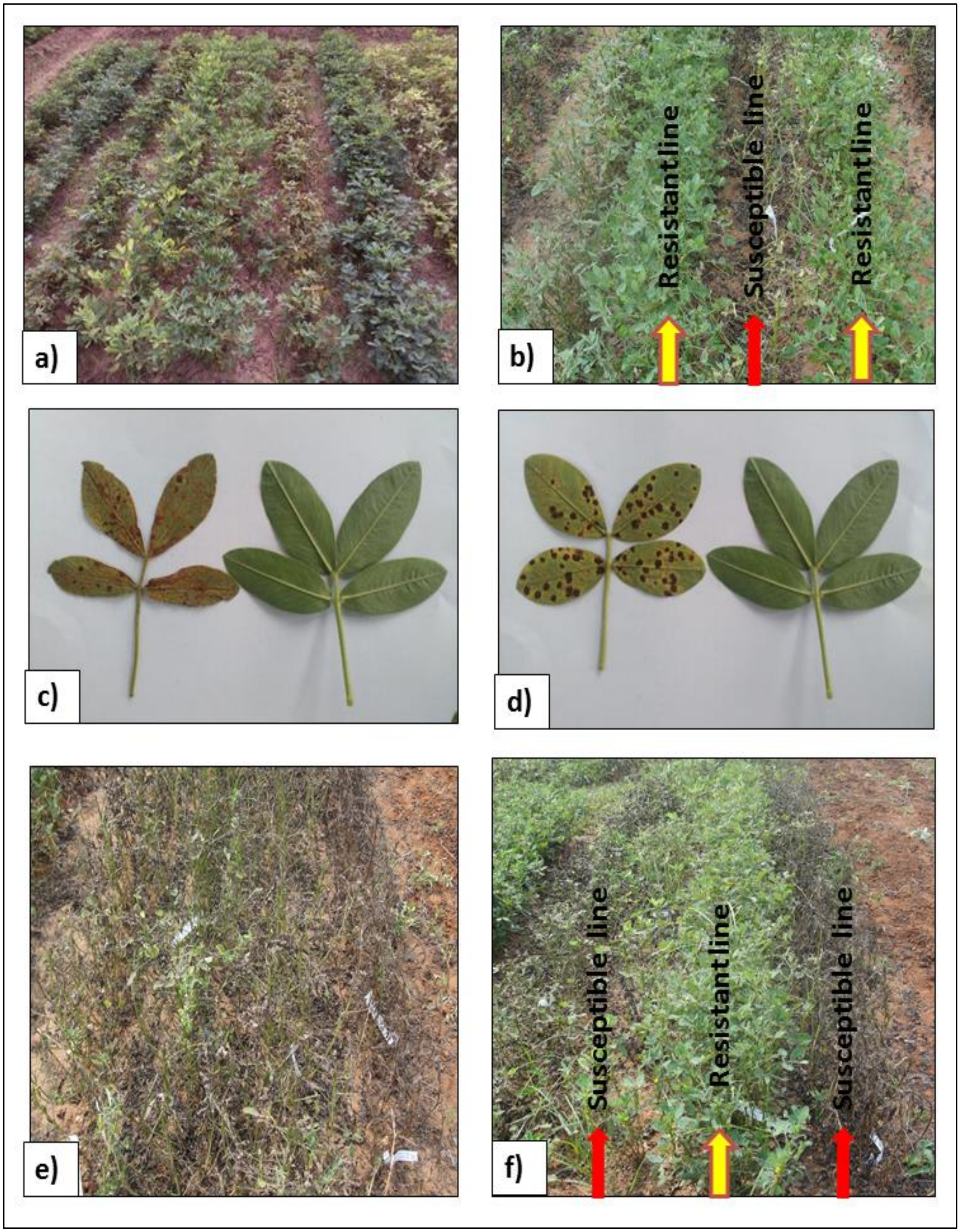

Figure 43 View of rust and LLS incidence occurred in experimental field. a) Initial disease incidence; b) Resistant lines (green foliage) with susceptible one; c) & d) symptoms of rust and late leaf spot; respectively; e) Complete defoliation in highly susceptible lines; f) Resistant line between susceptible lines

Chapter V
Discussion

Crop breeding programs have developed high yielding varieties through the accumulation of desirable alleles from vast plant genetic resources existing worldwide. Introgression of novel alleles from wild species to cultivated varieties has clearly demonstrated that certain novel alleles and their combinations potentially make dramatic changes in trait expression. Advancements in genomic sequence information have enabled us to identify and isolate novel and superior alleles of important genes governing expression of desirable traits from crop gene pools and deploy them for the development of improved cultivars (Varshney *et al.,* 2013). Tremendous efforts have been made by breeders to develop improved cultivars to feed the world but growing population pressure, urbanization of agricultural lands and adverse effects of changing climate scenario demand accelerated rate of genetic gain in breeding programs. Genomic Selection (GS) is one of the best approaches to accelerate genetic gain per unit of time and cost. GS helps to select genotypes with more number of desired alleles for complex traits through prediction model developed using whole genome marker and phenotypic data of traits of interest. GS enhances the selection efficiency and contributes to increasing selection intensity (i), and thus to enhanced genetic gain. Given the potential use of GS in crop breeding, a groundnut Genomic Selection Panel (GSP) was constituted at ICRISAT and in the present study multi-environment phenotyping of GSP for resistance to rust and LLS, yield and nutritional quality traits was conducted. The study assessed molecular diversity, allelic richness for rust, LLS and nutritional quality traits and marker-trait association to identify potential marker linked to important traits under study. The investigation was also aimed to screen GSP for mutant alleles of *ahFAD2A* and *ahFAD2B* genes responsible for the high oleic trait. The results reported in the present study are discussed below.

5.1 Analysis of variance and mean performance

Analysis of variance for disease resistance, yield traits and nutritional quality traits of GSP evaluated across the environments revealed significant genotypic difference for all the traits indicating a high degree of genetic variability within

GSP of groundnut. The observed genetic variability in part can be attributed to the divergent pedigree, origin and botanical types involved in the GSP. The high degree of variability for targeted traits in GSP is a prerequisite for constructing an accurate prediction model. The finding of present study revealed that the GSP of groundnut comprised of 340 genotypes is suitable for GS. Earlier studies reported significant genotypic variance based on their studies on either a limited population or groundnut mini-core collection for foliar fungal disease resistance (Upadhyaya *et al.,* 2005; Khedikar, 2008; Narasimhulu *et al.,* 2013; Ashish *et al.,* 2014; Sudini *et al.,* 2015), yield and its contributing traits (Korat *et al.,* 2009; Shoba *et al.,* 2009; Shridevi *et al.,* 2014) and nutritional quality traits (Sarvamangla *et al.,* 2010; Channayya *et al.,* 2011; Azharudheen *et al.,* 2013; Mukri *et al.,* 2014).

5.1.1 Sources for important traits in the GSP

Superior performing genotypes with a desirable combination of traits are important from breeder's perspective. Such genotypes can be released as a variety or used as a donor to introgress desirable genes into elite cultivars. It can also be used as a parent to create new variability and develop different population for gene/QTL identification. In the present study superior cultivars were identified in GS with disease resistance, high yield potential and nutritional quality traits.

5.1.1.1 Foliar fungal disease resistance

Out of 340 genotypes, a total of 31 and 66 genotypes showed resistance to LLS and rust, respectively across the environments at 90 days after sowing. Among these, 28 genotypes showed resistance against both the diseases with ≤3 disease severity score across the environments at 90 days after sowing (DAS). Genotypes, GPBD 4, ICGV's 06142, 02411, 00246, 00248, 00068, 86699, SPS 11 and SPS 20 had lowest scores for both the diseases across the environments. Genotypes with multiple disease resistance were earlier reported by Anderson *et al.* (1986a); Gowda *et al.* (2002a & b); Khedikar, (2008); Narasimhulu *et al.* (2013); Ashish *et al.* (2014) and Sudini *et al.* (2015). GBPD 4, a popular Spanish bunch cultivar is a national check for both the diseases

(Gowda *et al.,* 2002a) and widely used as a source of resistance genes in LLS and rust resistance breeding programs in India. Among the 28 identified resistant lines, 20 are advance breeding lines bred at ICRISAT, seven from Dharwad and a single line from mini core collection. Of these 20 lines, 17 lines share common donor of resistance from *A. cardenasii* whereas three other lines had other parents. Among the seven resistant lines from Dharwad, GPBD 4 was derived from *A. cardenasii*, four lines (SPS 2, SPS 8, SPS 11 and SPS 20) from *A. villosa* and two lines (49 M-16 and 49 M-1-1) had a mutant line M 28-2 as a source of resistant gene. Most of the groundnut breeding program derives resistance to foliar fungal diseases from *A. cardenasii*, for example, ICGV 86699 and GPBD 4 are often used as parents in breeding for resistance to LLS and rust in groundnut. The identification of lines with source of resistance from *A. villosa* and mutagenesis opens the possibility of widening the genetic base of resistance to both diseases in groundnut. Most of the resistant sources reported earlier belonged to late maturity group and had undesirable pod and kernel features, presumably due to the utilization of wild parent as the donor (Nigam, 2000). The present study identified genotypes resistant to both the diseases in early, medium and late maturity groups (103 to 128 days) (Table 5.1). The lines with early maturity (103 days) and a moderate level of resistance to LLS were identified by Padmaja *et al.* (2013). Nine superior performing genotypes in terms of combined disease resistance and yield >2500 kg/ha (SPS 11, ICGV’s 05163, 01274, 06142, 07235, 02323, 02411, 03043 and 49 M-16) were identified from advance breeding lines that can be recycled in hybridization to develop new lines with resistance to LLS and rust in groundnut (Table 5.1). The preferred pod and kernel feature of these genotypes and their superior pod yield performance offers an opportunity for breeders to recycle them in the breeding program to enhance the genetic gains.

5.1.1.2 Yield and its contributing traits

The genotypes in GSP were evaluated for different agronomic and yield related traits to identify trait specific genotypes which can be further used for development of trait specific cultivars or for combining the desirable traits into a single cultivar. The performance of genotypes across the environments was considered to identify trait specific genotypes. In the present study, genotypes, ICGV’s 06431, 99181, 06049, 91116, 04149, 02189, 26 × M-95-1R1, DTG 15, TAG24, and ICG 3102 had taken minimum number of days to 50% flowering (<29 days) across the environments. However, studies have shown that early flowering in groundnut is not associated with early maturity because maturity duration is largely determined by the length of pod development period of the cultivars. Hence identifying groundnut lines with early maturity based on days to first flowering and/or days to 50% flowering would be ineffective (N’Doye and Smith, 1992). Early maturity is a desirable trait in groundnut to make it fit for an intensive cropping system where more than three crops are cultivated in a year on the same field (Gibbons, 1980) and also to escape drought in drought-prone areas (Serraj *et al.,* 2003).

In the present study, number of days to 50% flowering and maturity were high among the genotypes during post-rainy season compared to rainy season across the environments indicating that maturity is influenced by environmental factors. The delay in flowering and maturity could be attributed to low temperature during the month of December and January leads to delay in emergence and slow vegetative growth during post-rainy season compared to rainy season. The cool temperature considerably increases emergence time and reduces the rate of vegetative growth (Awal and Ikeda, 2002; Banterng *et al.,* 2003). On the other hand, high temperature and sunshine radiation during reproductive stage (February to April) had a negative effect on flowering and the pod filling period in groundnut (Prasad *et al.,* 2001; Canavar and Kaynak, 2010) could also be a reason for delay in maturity during post-rainy season. Genotypes, ICGV’s 92195, 13242, 86011, 93470, 02266 and 02125, 49 × 39-74, 26 × M-95-1R1, 39 × 49-81-1 and ICG 2031 reported early maturing (97 to 107 days during rainy season) genotypes across the environments. The genotypes identified in the study can be used in breeding programs aimed at developing early maturing genotypes with high yield. Potential sources of early maturity are also available in the groundnut mini-core collection (Upadhyaya, 2003; Upadhyaya *et al.,* 2006). Recycling of agronomically superior and early maturing lines in the breeding program resulted in enhanced genetic gain for pod yield with early maturity (Janila *et al.,* 2013a).

Table 5.1 Performance of resistant genotypes for disease severity scores to LLS and rust, and other yield traits across the environments

S. No.	Genotype	Botanical variety	LLS 90	Rust 90	SH%	HSW	DM	PYH	HLM
1	SPS 20	*hypogaea*	2.33	2.00	59.1	28.0	127	923	24.2
2	ICGV 99052	*hypogaea*	3.00	2.00	56.0	31.5	126	1822	25.7
3	ICGV 86699	*hypogaea*	2.00	2.33	57.6	27.0	103	1010	20.4
4	GPBD 4	*vulgaris*	2.33	2.33	62.0	27.3	127	1647	22.0
5	ICGV 00248	*hypogaea*	2.33	2.33	57.8	31.0	127	1819	20.7
6	ICGV 06142	*vulgaris*	2.67	2.33	61.9	29.6	128	2677	18.5
7	ICGV 02411	*vulgaris*	2.67	2.33	58.5	37.1	125	2562	23.0
8	ICGV 99051	*hypogaea*	2.67	2.33	57.5	34.3	126	1839	25.7
9	ICGV 00246	*hypogaea*	2.67	2.33	57.1	34.4	127	1316	21.8
10	SPS 2	*hypogaea*	2.67	2.33	57.2	31.6	112	1394	27.4
11	SPS 11	*hypogaea*	2.67	2.33	62.4	30.7	127	3129	16.2
12	ICGV 07235	*vulgaris*	3.00	2.33	63.3	35.5	119	2668	15.3
13	ICGV 05100	*vulgaris*	3.00	2.33	59.0	33.0	126	1784	20.0
14	49 M-16	*vulgaris*	3.00	2.33	62.6	31.5	126	2526	19.4
15	ICGV 00362	*vulgaris*	3.00	2.33	54.3	26.7	111	1470	23.7
16	ICGV 99160	*vulgaris*	3.00	2.33	55.8	35.2	126	2075	24.0
17	ICGV 02323	*vulgaris*	3.00	2.33	64.9	39.5	128	2620	17.6
18	ICGV 02446	*hypogaea*	3.00	2.33	55.5	32.9	125	1406	24.0
19	ICGV 00068	*hypogaea*	2.67	2.67	53.5	28.6	126	1713	19.3
20	ICGV 05036	*vulgaris*	2.67	2.67	55.6	36.6	126	2277	27.6
21	ICGV 05141	*hypogaea*	2.67	2.67	61.7	38.7	125	2163	24.9
22	ICG 11337	*vulgaris*	2.67	2.67	52.3	30.9	126	816	23.5
23	SPS 8	*hypogaea*	2.67	2.67	58.8	28.7	110	1433	25.3
24	ICGV 01274	*vulgaris*	3.00	2.67	61.1	32.7	108	2678	14.5
25	ICGV 03043	*vulgaris*	3.00	2.67	59.7	36.4	126	2547	15.8
26	ICGV 04087	*hypogaea*	3.00	2.67	56.3	29.9	126	2146	27.5
27	49 M- 1-1	*hypogaea*	3.00	2.67	60.3	45.8	125	1150	19.4
28	ICGV 05163	*vulgaris*	3.00	3.00	57.0	35.5	112	2978	18.2
29	TMV 2 (SC)	*vulgaris*	7.00	6.67	53.1	30.1	106	1421	12.1

Where LLS90 & Rust90= Disease severity score of late leaf spot and rust across the environments at 90 days after sowing, respectively; SH%= Shelling percent; HSW= Hundred seed weight; DM= Days to maturity; PYH=Pod yield per hectare (kg); HLM= Haulm yield per plant (g); SC= Susceptible check

Number of primary branches per plant with short internode length directly contributes for pod and haulm yield, therefore, genotypes with more number of primary branches are preferred. Genotypes belonging to Virginia bunch or runner type usually have higher number of primary branches with alternate flowering whereas genotypes of Spanish bunch have lower number of primary branches with sequential flowering (flower present on every leaf axil) (Krapovickas and Gregory, 1994). In the study, genotypes, 49 M-2-2, ICGV's 07246, 01361, 07247, 07235 and 07227 had high number of primary branches per plant. The genotypes, ICG's 15419, 6022, 6646, 8751 and ICGV 03184 reported higher plant height across the environments.

Genotypes ICGV's 07247, 01276, 05163, 02323, 06099, 06100, 01495, 06142, 03128 and 07246, SPS 11 and 49 M-16 recorded higher number of mature pods per plant (>22), pod yield per plant (>16 g), seed yield per plant (> 10 g) and pod yield per hectare (>2800 kg); while genotypes ICGV's 95469, 07268, 02038, 03184, 03128 and 95290, ICG 2106, ICG 4955, 26 × 27-164 and 26 M-119-1 had higher shelling percent across the environments. The identified superior genotypes can be used as a parent to develop further high yielding lines in groundnut. Genotypes with high yield and shelling percent were earlier reported by Upadhyaya *et al.* (2005). High hundred seed weight (>48 g) was observed for the genotypes ICGV's 05198, 06188, 00440, 05176, 06234, 07368 and 01478, TG 42, TG 41 and 49 × 37-97-1 across of the environment can be recycled into breeding program to develop lines with a greater seed mass coupled with low oil and higher protein content for confectionery purpose.

5.1.1.3 Nutritional quality traits

Groundnut is one of the major oilseed crops grown in India. Groundnut kernels are rich source of oil, protein and fatty acids, especially mono- and poly-unsaturated fatty acids which helps to reduce fat in the human body. In India, nearly 80% of the seed is crushed for extraction of edible oil and it constitutes 34% of the total oil produced in the country (Brithal *et al.,* 2010). To improve its dominance vis-à-vis other oilseeds there is an urgent need to increase the oil content among the cultivated types. High oil containing groundnuts are more preferred by the oil mills and fetch higher market price. Among the oil quality traits, high oleic groundnuts are in wide demand due to their health benefits to consumers and extended shelf-life of oil and other groundnut based food products. Apart from these, high oleic groundnuts with low oil content, higher protein and large seed size are preferred for confectionery or table purpose groundnut (Janila *et al.,* 2016b). Hence, improvement in nutritional quality of groundnut is gaining more importance along with yield components to meet the market, industry and consumer's needs.

The genotype ICG's 15419, 2381, 5221, 14482, 12625 and 6022, ICGV's 99085, 05155 and 97128 recorded high oil content (58 to 60%) whereas genotypes, Faizpur 1-5, ICGV's 02038, 00321, 03398, 05176, 06110, 98294 and ICG 9507 recorded higher protein content (27 to 29%) across the environments. Evaluation of the genotypes for three major fatty acids palmitic acid, oleic acid and linoleic acid revealed that SunOleic 95R had high oleic acid (>70%), O/L ratio (>12) and low linoleic acid (<7%) and palmitic acid content (<7%) at individual as well as across the environments. SunOleic 95R is the potential donor that can be used as a parent to develop lines with improved oleic acid content. Genotypes, ICG's 15419, 2381, 5221, 6022 and 12625 recorded lower palmitic acid (<9%) across the environments in comparison with normal range 8 to 15%, whereas ICG's 4955, 3673, 422, 12672 and DTG 3 had lower stearic acid (≤1%) in comparison with normal range 0.2 to 5% across the environments. Similarly, potential trait specific genotypes for oil and protein content were earlier reported by Gautami *et al.* (2009); Sarvamangla *et al.* (2010) and for oleic acid by Mukri *et al.* (2014) from screening of mini-core collection.

5.2 Genetic variability

5.2.1 Genetic variability parameters

5.2.1.1 Foliar disease resistance

High genotypic and phenotypic coefficient of variation (GCV and PCV) was observed for disease severity scores to LLS and rust at 75 DAS whereas moderate at 90 DAS and low at 105 DAS across the environments. The differences in GCV and PCV at different stages of evaluation could be attributed to progress in disease incidence and their strong interaction with environmental conditions (Sudini *et al.,* 2015). Besides moderate GCV and PCV for LLS and rust disease scores at 90 DAS, heritability estimates were high along with high genetic advance as percent of mean (GAM) which indicated a strong response to selection and opportunity for direct phenotypic selection of resistant lines. High heritability and GAM further indicates that resistance to both the diseases is governed by additive genetic components and involvements of polygenes in the inheritance of these two diseases. High heritability and GAM for both the disease were earlier reported by Kavani *et al.* (2004); Venkataravana and Kumar, (2008); Vishnuvardhan *et al.* (2012); Padmaja *et al.* (2013); Narasimhulu *et al.* (2013) and Ashis *et al.* (2014). The inheritance studies also showed presence of complex inheritance and involvement of several genetic factors in inheritance of LLS and rust in groundnut (Nevill, 1982; Singh *et al.,* 1984; Tiwari *et al.,* 1984; Anderson *et al.,* 1986b; Reddy *et al.,* 1987; Varman *et al.,* 1991; Jogloy *et al.,* 1999; Janila *et al.,* 2013b; Wambi *et al.,* 2014).

5.2.1.2 Yield and its contributing traits

Among the yield traits, high GCV and PCV values were reported for number of pods per plant, pod yield per plant, seed yield per plant, hundred seed weight, pod yield per hectare and haulm yield per plant indicating higher genetic variability for these traits in GSP. Moderate heritability with high GAM for some traits such as number of pods per plant, pod yield per plant, seed yield per plant and haulm yield per plant revealed that these traits are governed by additive gene effects and hence direct phenotypic selection will be fruitful for improvement in these traits. Moderate heritability can mainly be attributed to the large genotype × environment interactions for most of the traits. High GCV and PCV coupled with moderate to high heritability and GAM for yield and its associated traits was earlier reported by Islam and Rasul (1998); Reddy *et al.* (2001); Makhanlal *et al.* (2003); Kavani *et al.* (2004); Suneetha *et al.* (2004); John *et al.* (2005a); Upadhyaya *et al.* (2005); Hariprasanna *et al.* (2008); Korat *et al.* (2009); Shoba *et al.* (2009) and Shridevi, (2014).

Days to 50% flowering, number of primary branches per plant, shelling percent and days to maturity had lower GCV and PCV values, high heritability and low to moderate GAM across the environments. The low GCV, PCV with high heritability indicated that a large proportion of total variance is due to genes that are least affected by the environments. Despite the wide range in phenotypic performance, low GCV and PCV values could be due to the narrow dispersion of the values of genotypes around the mean. Inclusion of genotypes with extremely low and high values could be useful for a better estimation of the genetic parameters in such cases. Despite the low GCV and PCV values, the range of variation observed among the genotypes offers an opportunity to use them in breeding programs for trait improvement. High heritability coupled with low GAM was reported for shelling percent and days to maturity which is in accordance with the findings of Uddin *et al.* (1995); Kavera, (2009) and Channayya *et al.* (2011).

5.2.1.3 Nutritional quality traits

Low GCV and PCV values were observed for oil and protein content, and fatty acid composition at individual as well as across the environments indicated narrow variability for these traits. High heritability coupled with low GAM was reported for these traits indicating that non-additive gene action could be involved in the inheritance of these traits. Thus, delaying selection to later generations could be useful to improve these traits (Uddin *et al.,* 1995; Kavera, 2009; Channayya *et al.,* 2011). The improvements in these traits can be achieved through increase in selection intensity and accuracy. Low GCV and PCV values for nutritional quality traits could be due to narrow distribution of values around the mean. Besides the narrow genetic variability, wide range of performance of genotypes offers opportunities for direct phenotypic selection and to create variability by crossing of inferior and superior genotypes for nutritional quality traits. Narrow genetic variability for nutritional quality traits in groundnut was earlier reported by Dwivedi *et al.* (1993); Azharudheen, (2010); Sarvamangala *et al.* (2010) and Channayya *et al.* (2011). It was suggested from their studies that there is a need to increase genetic variability for nutritional quality traits in the cultivated groundnut.

5.2.2 Variability among subspecies and botanical varieties of groundnut

5.2.2.1 Foliar disease resistance

In the present study, 28 genotypes showed resistance to rust and LLS. Of these 14 (50%) belongs to the subspecies *fastigiata* var. *vulgaris* (Spanish bunch) whereas remaining 14 are from subspecies *hypogaea* var. *hypogaea* (Virginia bunch). This indicated that sources of resistance to both the disease are available in both the subspecies of cultivated groundnut. Similarly, sources of resistance to LLS and rust in different botanical varieties were earlier identified (Chiteka *et al.,* 1988; Anderson *et al.,* 1993; Holbrook and Islebi, 2001), and used to develop resistant breeding lines (Melouk *et al.,* 1984; Wells *et al.,* 1994; Xue and Holbrook, 1998, 1999). Extensive screening of 13000 accessions at ICRISAT led to the identification of 49 landraces and 20 genotypes of var. *peruviana* with LLS resistance (Subrahmanyam *et al.,* 1995; Mehan *et al.,* 1996).

5.2.2.2 Yield and its contributing traits

The mean performance of different botanical varieties revealed that cultivars belonging to sub-species *fastigiata* var. *vulgaris* (Spanish Bunch) had higher number of mature pods per plant, pod and seed yield per plant, shelling percent and pod yield per hectare at individual as well as across the environments. The results suggested that cultivars of sub-species *fastigiata* var. *vulgaris* had high yield potential compared to other botanical varieties. The superior performance of sub-species *fastigiata* var. *vulgaris* cultivars was also reported by Bansal *et al.* (1993) and Upadhyaya (2003). Genotypes of subspecies *hypogaea* var. *hirsuta* followed by var. *hypogaea* (Virginia runner and bunch) had higher hundred seed weight across the environments, which suggested that most of the genotypes with large seed size in GSP are Virginia type. For days to maturity, genotypes belonging to sub-species *fastigiata* var. *peruviana* took less number of days to mature. Hence, such genotypes can be used to breed early maturing varieties. A single cultivar from var. *hirsuta* followed by Virginia bunch cultivars recorded higher haulm yield per plant in individual and pooled across seasons at ICRISAT (Table 5.2). The present findings are in agreement with the findings of Upadhyaya (2003).

5.2.2.3 Nutritional quality traits

Among the nutritional quality traits, high oil containing genotypes were identified in sub-species *fastigiata* var. *aequatoriana* followed by subspecies *hypogaea* var. *hirsuta.* Estimates of protein content of cultivars of different botanical varieties suggested that Virginia runner type cultivars had higher protein content across the environments. The mean performance of genotypes of different botanical varieties for four fatty acids revealed that genotypes of

Table 5.2 Mean performance of genotypes belongs to different subspecies and botanical varieties for disease resistance and important yield traits

Subspecies	*Botanical variety*	*Market type*	LLS90	Rust90	DFF	NPP	PYPP	SYPP	SH %	HSW	DM	PYH	HLM
Aliyarnagar													
fastigiata	*aequatoriana*	*UNK*	3.0	5.0	30	10	6.4	3.4	53.1	29.9	120	661.8	-
	fastigiata	*Valencia*	4.3	5.5	29	11	9.5	5.2	55.8	30.6	107	929.6	-
	peruviana	*UNK*	4.5	3.8	29	13	11.9	7.0	57.5	29.4	105	1407.0	-
	vulgaris	*Spanish Bunch*	4.9	5.1	29	18	12.7	8.6	63.2	31.9	108	1510.6	-
hypogaea	*hirsuta*	*UNK*	4.0	4.0	28	3	4.8	2.6	53.4	36.7	107	1257.8	
	hypogaea	*Virginia Bunch*	4.2	4.5	32	15	11.6	7.0	60.2	34.5	110	1475.6	-
		Virginia Runner	4.7	5.0	31	13	9.0	5.4	61.6	30.6	106	956.4	-
Jalgaon													
fastigiata	*aequatoriana*	*UNK*	3.0	3.0	32	9	6.3	3.2	53.5	26.5	140	1175.7	-
	fastigiata	*Valencia*	3.3	3.5	30	11	9.0	5.1	55.7	32.8	120	1173.5	-
	peruviana	*UNK*	3.5	3.5	32	10	8.0	4.5	53.2	29.7	117	1119.0	-
	vulgaris	*Spanish Bunch*	3.5	3.2	30	17	11.4	6.7	59.1	33.7	121	1765.1	-
hypogaea	*hirsuta*	*UNK*	3.0	3.0	28	8	10.5	5.2	47.8	35.4	121	1377.4	-
	hypogaea	*Virginia Bunch*	2.9	2.6	31	14	9.4	5.4	56.8	34.5	125	1351.5	-
		Virginia Runner	2.4	2.8	30	12	7.4	4.3	56.4	29.1	119	1107.5	-
ICRISAT rainy 2015													
fastigiata	*aequatoriana*	*UNK*	5.0	3.0	28	9	7.3	3.8	53.9	34.3	126	1222.4	17.0
	fastigiata	*Valencia*	6.2	5.8	28	11	7.7	4.5	57.4	30.3	108	1061.0	17.4
	peruviana	*UNK*	6.3	4.8	28	11	11.5	6.3	56.2	31.2	104	1503.7	16.7
	vulgaris	*Spanish Bunch*	6.9	6.1	28	16	10.5	6.0	57.7	31.6	108	1661.4	15.2
hypogaea	*hirsuta*	*UNK*	6.0	5.0	26	7	8.5	4.7	54.2	35.6	109	1268.0	20.3
	hypogaea	*Virginia Bunch*	6.2	5.3	31	13	10.3	5.9	57.4	34.8	112	1495.4	18.0
		Virginia Runner	7.0	6.2	31	10	6.8	3.8	56.4	27.6	105	1050.2	15.1
ICRISAT post-rainy 2015-16													
fastigiata	*aequatoriana*	*UNK*	-	-	41	10	7.6	4.1	53.9	35.4	136	2013.2	14.6
	fastigiata	*Valencia*	-	-	42	9	6.1	3.4	54.3	28.2	141	1492.8	17.9

Subspecies	Botanical variety	Market type	LLS90	Rust90	DFF	NPP	PYPP	SYPP	SH %	HSW	DM	PYH	HLM
	peruviana	*UNK*	-	-	40	8	6.1	3.2	52.7	34.0	140	1576.9	17.6
	vulgaris	*Spanish Bunch*	-	-	41	12	7.1	4.4	60.9	34.3	140	1797.2	18.1
hypogaea	*hirsuta*	*UNK*	-	-	38	5	5.2	2.8	55.3	49.9	124	1299.4	33.3
	hypogaea	*Virginia Bunch*	-	-	44	9	5.8	3.4	57.8	33.8	146	1387.1	22.5
		Virginia Runner	-	-	45	7	4.9	2.6	52.7	28.0	143	1152.3	17.9
Pooled across the environments													
fastigiata	*aequatoriana*	*UNK*	3.7	3.7	33	10	7.0	3.7	53.6	31.5	131	1273.3	15.8
	fastigiata	*Valencia*	4.6	4.9	32	11	8.1	4.6	55.7	30.4	119	1164.7	17.6
	peruviana	*UNK*	4.8	4.0	32	11	9.4	5.3	54.8	31.1	116	1405.5	17.2
	vulgaris	*Spanish Bunch*	5.1	4.8	32	15	9.9	5.9	59.7	32.9	119	1659.1	16.6
hypogaea	*hirsuta*	*UNK*	4.3	4.0	30	6	7.3	3.8	52.9	39.3	115	1308.5	26.6
	hypogaea	*Virginia Bunch*	4.5	4.1	35	13	9.3	5.4	58.1	34.4	123	1425.9	20.3
		Virginia Runner	4.7	4.6	34	11	7.0	4.1	56.7	28.8	118	1066.0	16.5

Where- LLS90 & Rust90= Disease severity score of late leaf spot and rust across the environments at 90 days after sowing, respectively; DFF= Days to 50% flowering; PYPP= Pod yield per plant (g); SYPP= Seed yield per plant (g); SH%= Shelling percent; HSW= Hundred seed weight; DM= Days to maturity; PYH=Pod yield per hectare (kg); HLM= Haulm yield per plant (g); UNK = Unknown

Table 5.3 Mean performance of genotypes belongs to different subspecies and botanical varieties for nutritional quality traits

Subspecies	Botanical variety	Market type	OC%$^{\#}$	PC%$^{\#}$	OA%$^{\#}$	LA%$^{\#}$	PA%$^{\#}$	SA%$^{\#}$	O/L ratio
Aliyarnagar									
fastigiata	*aequatoriana*	*UNK*	63.5	17.5	46.1	44.7	8.2	2.9	1.0
	fastigiata	*Valencia*	55.0	19.8	42.8	40.8	11.4	2.3	1.1
	peruviana	*UNK*	53.2	18.8	41.2	41.0	11.4	2.3	1.0
	vulgaris	*Spanish Bunch*	53.4	20.0	41.3	40.2	11.7	2.2	1.1
hypogaea	*hirsuta*	*UNK*	62.1	19.0	48.5	42.2	7.5	3.5	1.2
	hypogaea	*Virginia Bunch*	53.6	20.7	43.0	38.8	11.7	2.2	1.2
		Virginia Runner	51.1	21.1	43.8	37.2	11.1	2.2	2.1
Jalgaon									
fastigiata	*aequatoriana*	*UNK*	58.9	17.9	49.1	42.7	7.0	2.6	1.2
	fastigiata	*Valencia*	55.3	19.4	41.2	41.8	11.6	2.4	1.0
	peruviana	*UNK*	50.6	18.8	42.4	39.7	10.8	2.1	1.1
	vulgaris	*Spanish Bunch*	53.7	19.7	38.1	42.9	12.0	2.1	0.9
hypogaea	*hirsuta*	*UNK*	59.4	21.5	46.4	44.0	6.5	3.9	1.1
	hypogaea	*Virginia Bunch*	53.6	19.5	39.5	41.4	12.1	2.1	1.0
		Virginia Runner	52.1	19.8	42.9	38.6	11.0	2.1	2.2
ICRISAT rainy 2015									
fastigiata	*aequatoriana*	*UNK*	55.6	21.7	57.3	30.8	8.9	2.4	1.9
	fastigiata	*Valencia*	52.1	22.4	44.4	36.3	11.9	1.9	1.2
	peruviana	*UNK*	47.4	24.1	44.2	36.0	11.2	2.0	1.3
	vulgaris	*Spanish Bunch*	48.6	24.1	42.2	36.8	11.7	1.6	1.2
hypogaea	*hirsuta*	*UNK*	59.9	21.2	51.6	36.6	8.1	3.1	1.4
	hypogaea	*Virginia Bunch*	48.2	24.2	43.6	35.1	11.9	1.7	1.3
		Virginia Runner	46.0	24.3	45.8	33.3	10.9	1.6	2.2
ICRISAT post-rainy 2015-16									
fastigiata	*aequatoriana*	*UNK*	55.9	21.8	51.3	34.8	10.2	2.3	1.5
	fastigiata	*Valencia*	50.6	26.5	45.5	34.7	12.4	2.3	1.4
	peruviana	*UNK*	46.8	27.3	45.8	34.2	11.5	2.4	1.4
	vulgaris	*Spanish Bunch*	48.8	26.9	43.0	35.4	12.5	2.3	1.3
hypogaea	*hirsuta*	*UNK*	54.9	24.1	50.3	34.9	9.8	2.8	1.5

Subspecies	**Botanical variety**	**Market type**	**OC%[#]**	**PC%[#]**	**OA%[#]**	**LA%[#]**	**PA%[#]**	**SA%[#]**	**O/L ratio**
	hypogaea	*Virginia Bunch*	49.5	26.4	44.9	33.7	12.7	2.4	1.4
		Virginia Runner	48.7	27.3	47.2	31.3	11.6	2.6	2.6
Pooled across the environments									
fastigiata	*aequatoriana*	*UNK*	58.3	19.9	51.0	38.2	8.6	2.6	1.4
	fastigiata	*Valencia*	53.3	22.0	43.4	38.4	11.8	2.2	1.2
	peruviana	*UNK*	49.6	22.2	43.4	37.7	11.2	2.2	1.2
	vulgaris	*Spanish Bunch*	51.1	22.7	41.2	38.8	12.0	2.1	1.1
hypogaea	*hirsuta*	*UNK*	59.2	21.4	49.1	39.6	8.0	3.4	1.3
	hypogaea	*Virginia Bunch*	51.2	22.7	42.7	37.2	12.1	2.1	1.2
		Virginia Runner	49.5	23.1	45.1	35.1	11.1	2.1	2.2

Where- OC%= Oil content (%); PC%= Protein content (%); OA%= Oleic acid (%); LA% = Linoleic acid (%); PA%= Palmitic acid (%); SA%= Stearic acid (%); O/L ratio= Oleic/ Linoleic acid ratio; UNK= Unknown; # = Nutritional quality traits were estimated by NIRS and could deviate by ±2.5.

Virginia runner had high oleic acid, low linoleic acid and high O/L ratio compared to other botanical varieties across the environments. Significant variability within and among the different botanical varieties for oil and protein content along with fatty acid was also observed by Bansal *et al.* (1993); Nagaraj *et al.* (1989) and Mukri *et al.* (2014). They reported that the oleic acid concentration was high in V*irginia* runner genotypes followed by Virginia bunch and a minimum in the Spanish bunch type. This trend was reversed with respect to linoleic acid concentration (Bansal, *et al.,* 1993).

5.3 Traits association

Yield is a complex polygenic trait governed by a large number of genes and is greatly influenced by environmental factors. Yield can be improved by effecting indirect selection for its contributing traits, which have high heritability and strong association with yield (Nunes *et al.,* 2011). The information on the interrelationship among nutritional quality traits is also useful to decide breeding procedure for improvement in these traits and to achieve desired modification in fatty acid composition. The findings of association among different traits have been discussed below.

5.3.1 Association among yield and its contributing traits

In general genotypic correlation coefficient was slightly higher than their corresponding phenotypic correlation coefficient for the majority of the traits indicating an inherent association between traits. It also indicated that the environmental component had less influence on the association of the traits and the reported associations could be the result of pleiotropic effect or linkage between the genes governing respective traits. Pod yield per hectare had significant positive associations (>0.7) with a number of mature pods per plant, pod and seed yield per plant at individual as well as across the environments which indicated that these traits are important yield components and an effective improvement in yield can be achieved through selection based on these traits. The number of mature pods per plant and hundred seed weight had a significant negative association but the extent of association is low suggesting that simultaneous selection for both the trait is possible. The present findings are in accordance with those of John *et al.* (2009); Channayya *et al.* (2011); Vekariya *et al.* (2011); Alam, (2014); Prabhu *et al.* (2014); Patil *et al.* (2014); Gupta *et al.* (2015); Rasheed *et al.* (2015) and Vasanthi *et al.* (2015).

5.3.2 Association among disease resistance and yield traits

Disease severity scores of both rust and LLS had a significant negative genotypic association (-0.40 to -0.65) with yield and its contributing traits across the environments. It revealed that both the diseases pose a negative impact on yield and responsible for yield reduction in groundnut especially under disease favouring conditions. The negative association also indicated the absence of linkage drag between resistance and pod yield and opens up the possibility to develop high yielding resistance cultivars for both the diseases. Yield penalty due to the incidence of rust and LLS is common for rainy season groundnut, and the extent of loss is determined by the severity of the disease. Significant negative effect of disease severity of LLS and rust on yield and its contributing traits was also evident from earlier reports (Subrahmanyam *et al.,* 1984; McDonald *et al.,* 1985; Anderson *et al.,* 1990; Vishnuvardhan *et al.,* 2012; Narasimhulu *et al.,* 2013 and Sudini *et al.,* 2015). The disease severity to LLS and rust had a strong positive association (>0.80) with each other. This could be due to the similarity in genes/QTLs governing resistance to both the diseases. Quantitative trait locus (QTL) mapping studies have confirmed this association wherein a major QTL explaining >80% phenotypic variation (PV) for rust resistance on linkage group AhXV, recently assigned to chromosome A03, also explained 68 % PV for LLS in groundnut (Sujay *et al.,* 2012; Pandey *et al.,* 2017). A significant positive relationship among LLS and rust severity scores along with their negative effect of pod and seed yield was reported by Anderson *et al.* (1990); Vasanthi and Naidu, (1998); Narasimhulu *et al.* *(*2013) and Prabhu *et al.* (2014 & 2015). The positive association among LLS and rust suggested that resistance to both diseases can be incorporated into a single background by a single breeding effort.

Disease severity scores of both rust and LLS had a significant negative association with days to maturity, but the extent of association was low (~-0.4) indicating that under severe conditions the plants begin to senescence early resulting in advanced harvesting (Subrahmanyam *et al.,* 1984; McDonald *et al.,* 1985). High level of resistance to foliar fungal diseases is required in groundnut varieties belonging to all maturity groups. The significant negative association of disease severity scores with haulm yield per plant at ICRISAT during rainy 2015 revealed that both the diseases had significant impact on reduction in haulm yield and quality. Similar findings were earlier reported by Subrahmanyam *et al.* (1984); Narasimhulu *et al.* (2013) and Sudini *et al.* (2015).

Strong positive genotypic association (r_g=~0.90) was also observed between disease severity scores for rust and LLS recorded at different stages (75, 90 and 105 DAS). Severe disease during pod development stage results in acute pod yield losses. Infection of LLS and rust starts from 60 DAS, therefore disease scores recorded at 75 DAS are usually low. On the other hand, the scores at 105 DAS were high when most of the genotypes of medium maturity duration complete their pod development stage and are close to physiological maturity. A significant portion of pod growth and development in groundnut occurs during 60 to 100 DAS (Prasad *et al.,* 2010). Hence, disease severity scores recorded at 90 DAS would be more informative to identify resistant cultivars. The strong positive association among disease scores of different stages further indicated that selection decision based on scores at 90 DAS would optimize resources rather than taking observations at 75, 90 and 105 DAS.

5.3.3 Association among nutritional quality traits

Nutritional quality of groundnut is largely determined by oil content, protein content and fatty acid composition. Improvement in nutritional quality traits can only be possible when the knowledge of direction and magnitude of interrelationships among these traits is available. The interrelationship among different nutritional quality parameters helps to decide effective selection procedure to simultaneously improve desirable traits. All the fatty acids are linked in the biosynthetic pathway through modifications such as elongation and desaturation. Hence, any alteration in the biosynthetic steps influences the whole fatty acid profile and the relationships among different fatty acids. These correlations may reflect precursor product relations in some instances, but probably also reflect genetic linkages of various enzymes involved in the conversions (Anderson *et al.,* 1998).

Oil content had a negative association with protein content in the population studied at individual as well as pooled across the environments. This indicated that an increase in oil content would be at the cost of reduction in protein content and *vice versa* (Dwivedi *et al.,* 1990; Kale *et al.,* 1998; Parmar *et al.,* 2002; Sarvamangla *et al.,* 2010; Ajay *et al.,* 2012). The negative association among two desirable traits always creates difficulties to develop cultivars with higher value of both the traits (Parmar *et al.,* 2000; Sarvamangala, *et al.,* 2010; Mukri *et al.,* 2012). Among oil quality traits O/L is more important and is desired to be high in the cultivars. A strong negative genetic association of oleic acid was observed with linoleic acid (>0.90), and palmitic acid (>0.60) indicated that an increase in oleic acid will lead to decrease in linoleic and palmitic acid. The inverse relationship of oleic acid with linoleic acid is due to changes in the fatty acid biosynthetic pathway arising from a mutation involving the fatty acid desaturase gene (FAD). The FAD enzyme is responsible for converting oleic to linoleic acid and mutation in FAD gene results in accumulation of high level of oleic acid. Inverse relationships between a desirable (oleic acid) and undesirable (linoleic acid) trait are useful for the breeders to achieve targeted trait improvement. The inverse relationship of oleic acid with palmitic and linoleic acid was also evident from the earlier studies (Bovi, 1983; Sekhon *et al.,* 1980; Sarvamangala *et al.,* 2010; Shoba *et al.,* 2012a).

The strong negative relationship between palmitic acid and oleic acid most likely represents an increased rate of palmitic acid elongation to stearic acid, with rapid desaturation to oleic acid through Δ9 desaturase enzyme (Groff *et al.,* 1996). The strong negative correlation between oleic and linoleic acids (r >0.90) results from their being the chief acyl groups in the oil so that one cannot increase much without a decrease in the other. Fatty acid composition in any oilseed crop largely depends on the relative activity of the enzymes involved in the fatty acid biosynthetic pathway (Guy *et al.,* 2007). Therefore, by understanding the biochemical pathway one can manipulate the composition of fatty acids in oil (Marketta *et al.,* 1989; Ohlrogge, 1994; Alt *et al.,* 2005; Bachlava *et al.,* 2008).

5.3.4 Association among disease resistance and nutritional quality traits

A significant negative association of oil content with disease severity of LLS and rust (≥0.50) at 90 DAS indicated that the severity of both the diseases can lead to a reduction in oil content in the kernels. Reduction in oil recovery and quality due to disease severity of LLS and rust in groundnut was earlier reported by Motagi *et al.* (2000b) and Dwivedi *et al.* (1993). There was no such direct effect of rust and LLS pathogen on nutritional quality has been reported so far. The reduction in oil content might be due to advanced harvesting of susceptible cultivars, leading to more number of immature pods and insufficient partitioning of photosynthates from leaves to pods under disease pressure.

5.3.5 Association among yield and nutritional quality traits

Pod yield per plant had a positive association with oil content whereas the association is non-significant with protein content indicating that improvement in oil or protein content can be achieved together with improvement in yield potential. Hundred seed weight had a significant negative association with oil content (rg=-0.22 to -0.35), and significant positive association with protein content (rg=0.29 to 0.44) across the environments. However, the magnitude of association is low which offers an opportunity to develop cultivars that combine high hundred kernel mass with either high oil or high protein content for targeted end uses. The cultivars with large seed size, high protein and low oil content are preferred for confectionery purpose, whereas cultivars with small to medium seed size and high oil content are suitable for oil extraction (Janila *et al.,* 2016b).

5.4 Principal component analysis (PCA)

Diversity among genotypes for economically important traits provides an opportunity for breeders to develop improved cultivars with a desirable combination of characteristics. Therefore, understanding the level of diversity among the genotypes being utilized in breeding is crucial to the success of the breeding program. Genetic diversity and relationship among genotypes can be measured by calculating similarity or dissimilarity among the genotypes for different qualitative/quantitative traits, assuming that the difference between genotypes is due to genotype or genotype × environment interactions. Within a reasonable range, diversity among parents for the target trait offers the best chance for trait improvement in the resulting offspring. Ward (1963) clustering is a very reliable tool for measuring genetic divergence based on quantitative traits and is widely used by many geneticists and breeders for selecting diverse parents for hybridization.

Principal component analysis is a descriptive method that describes the pattern of variation of characters among individuals. It tends to reduce the dimension of multivariate data by removing inter-correlation among variables and allows a multi-dimensional relationship to be plotted on 2 or 3 principal axes. Cluster analysis is commonly performed to study genetic diversity and for forming core subset for grouping accessions with similar characteristics into one group using the values of major principal components that accounted most of the variability present in the population (Upadhyaya *et al.,* 2009). In the present study, 70.62 to 79.41% of total genetic variability was explained by the first six principal components (PCs) whose Eigenvalues were greater than one across the environments. PCA was earlier used for cluster analysis using first seven PCs, which explained ≥75.00% of total genetic variation (Makinde and Ariyo, 2010); first five PCs explained 76% of variation (Kumar *et al.,* 2010) and first nine PCs accounted 79% of the total genetic variation (Upadhyaya *et al.,* 2009). The first and second PCs are more important because they contribute >40% of the total variation present in GSP with disease score of rust and LLS at 90 and 105 DAS, pod yield per plant, number of pods per plant, and pod yield per hectare being the major contributors. In contrast, the nutritional quality traits such as oil content, protein content and fatty acid composition showed less variability as they contributed towards variability explained by fourth and fifth PCs rather than first two PCs. Similarly, Upadhyaya, (2003); Upadhyaya *et al.*

(2006 & 2012) and Amarasinghe *et al.* (2016) concluded that first two PCs had a greater contribution towards total genetic diversity.

5.4.1 Clustering

Cluster analysis has grouped the 340 genotypes of GSP and the number of clusters varied from six to eight across the environments. Seven clusters were formed at Aliyarnagar and ICRISAT and eight clusters at Jalgaon during rainy 2015 whereas six clusters were formed at ICRISAT during post-rainy season 2015-16 and pooled across the environments. Several studies in the past have reported 3 to 15 clusters and concluded high genetic diversity for yield traits compared to nutritional quality traits (Vaddoria and Patel, 1990; Reddy and Gupta, 1992; Pathirana, 1993; Senapati and Roy, 1998; Singh and Chaubey, 2003; Upadhyaya *et al.,* 2003; John *et al.,* 2005; Upadhyaya *et al.,* 2005; Upadhyaya *et al.,* 2006; Kotzamanidis *et al.,* 2006; Sumathi and Muralidharan, 2007; Korat *et al.,* 2009; Sumathi *et al.,* 2009; Sadeghi *et al.,* 2011; Vekariya *et al.,* 2011; Nautiyal *et al.,* 2012; Suneetha *et al.,* 2013).

The stable genotypes in these clusters can be used as a parent in breeding program to develop high yielding cultivars. The genotypes of clusters that has high cluster mean for hundred seed weight and protein content can be recycled in breeding program to develop cultivars for confectionery or table purposes. Among the genotypes, SunOleic 95R maintained a separate identity as high oleic genotype with an oleic acid content of >75%, O/L ratio of >12, linoleic acid content of <7% and palmitic acid content of <9% in all the environment. Hence, it is suggested that this genotype could be one of the best parents to develop high oleic lines in groundnut. SunOleic 95R has been used at ICRISAT's breeding program to develop high oleic lines in Spanish and Virginia botanical types (Janila *et al.,* 2016b). Mukri *et al.* (2014) reported ICG 2381 with high oleic acid and low linoleic acid content which formed a separate cluster across growing regions. Based on the information generated from Wards cluster analysis, genotypes grouped in different clusters with desirable traits such as resistance to LLS and rust, yield and nutritional quality traits can be selected and used in groundnut improvement program to further development of new cultivars and to enrich the groundnut breeding populations with new recombinants. The present study also suggests that sufficient amount of diversity is available in GSP which is a prerequisite to construct prediction model based on phenotypic and genotype by sequencing data generated on the population.

The genotypes of common eco-geographic origin or location grouped into different clusters which indicated that geographic diversity was not related to genetic diversity (Makinde and Ariyo, 2010; Zaman *et al.,* 2011). Many of the genotypes belong to different clusters exhibited superior performance for one or more economically important traits.

5.5 Stability analysis using GGE biplot

Multi-environment testing helps to identify cultivars that perform consistently from year to year (small temporal variability) and those that perform consistently from location to location (small spatial variability). Temporal stability is desirable and beneficial to growers, whereas spatial stability is beneficial to seed companies and breeders. There are two concepts of stability*, i.e.* static and dynamic. The static concept means that a genotype has a stable performance across the environments and there is no variation among the environment. This would mean that a genotype would not respond to high levels of inputs, such as fertilizer and better agronomic practices. This type of stability would not be beneficial for the farmer, and it has been referred to as the biological concept of stability (Becker, 1981). The dynamic concept means that a genotype has a stable performance, but, for each environment, its performance corresponds to the estimated level or predicted level. There would be an agreement between the estimated or predicted level and the level of actual performance (Becker and Leon, 1988). This concept has been referred to as the agronomic concept (Becker, 1981). The static stability would be most desirable and advantageous for the traits like disease resistance, whereas dynamic stability is desirable for yield and nutritional quality traits.

Pooled analysis of variance revealed significant genotypic, environment and genotype × environment interaction (G×E) variances for all the traits studied. The highly significant environmental variance for most of traits indicated the influence of environmental factors on the expression of disease resistance, yield and nutritional quality traits. However, the significance of G×E interaction indicated that the performance of genotypes is conditioned by the environments. Thus, stability analysis was performed to identify stable genotypes across the environments. The significant genotype, environment and G×E interaction variances for disease resistance (Sing *et al.,* 1997; Iwo and Olorunju, 2009; Mothilal *et al.,* 2010b), yield and nutritional quality traits were earlier reported (Viswanathan *et al.,* 2001; Thaware *et al.,* 2009; Makinde and Ariyo, 2010; Upadhyaya *et al.,* 2012; Patil *et al.,* 2014; Upadhyaya *et al.,* 2014).

5.5.1 Stability of disease resistance

The results of GGE biplot analysis for disease severity to LLS and rust at 90 DAS revealed that first two PCs explained 87.51 and 89.94% of the total variation due to G×E interaction (De-lacy *et al.,* 1996). The ranking of 109 genotypes of GSP based on their disease severity score and stability performance identified eight genotypes stable for resistance to LLS whereas 24 as stable for resistance to rust across the environments with low disease score and shortest vector length from average environment axis (AEA) in the biplot. The stable sources of resistance to LLS and rust were earlier reported by Singh *et al.* (1997); Mothilal *et al.* (2010b) and Sudini *et al.* (2015). Significant differences in cultivar stability for yield and resistance to LLS were reported by Iwo and Olorunju, (2009).

The position of environments on biplot revealed positive correlation among the environments. Environment ICRISAT_R15 (ICRISAT rainy season 2015) was farthest on right side of the perpendicular line indicating that it was the best environment for disease screening where genotypes got high diseases scores followed by Aliyarnagar and Jalgaon. It could be attributed to the best foliar disease screening nursery available at ICRISAT with better resources to put artificial disease pressure and to maintain favourable condition for disease development and spread. Jalgaon which plotted near to the biplot origin was the poorest environment in terms of disease scores of the genotypes. This might be attributed to unfavourable environmental components such as low humidity (<85%) and lack of rains for disease infection, establishment and spread. Environmental factors especially humidity, temperature, and rainfall plays an important role in disease infection and establishment of rust and LLS (Nigam *et al.,* 1991). Besides these, sowing at Jalgaon (23rd June 2015) was nearly 15 days earlier compared to Aliyarnagar (07th July 2015) and ICRISAT (10th July 2015) which could be another reason for low disease pressure at Jalgaon. Significant influence of sowing time on disease severity of rust and LLS was earlier reported by Naidu and Vasanthi, (1995). The ranking of environments with respect to ideal test environment revealed that the ICRISAT_R15 (ICRISAT rainy season 2015) and Aliyarnagar plotted on border of inner circle in the biplot indicating that both the environments are ideal for screening of genotypes for resistance to rust and LLS.

5.5.2 Stability for yield and its contributing traits

Development of genotypes with high and stable yield performance is an important breeding objective in groundnut. For this, suitable parents need to be identified for use in crossing programs. Principal component of the biplot explained 71.92 to 81.65% of total variation due G×E interaction for different yield traits. In the present study, biplot analysis identified stable, environment and location specific genotypes showing consistent performance for different target traits. Finding location specific adaptability is also important to develop cultivars for a targeted region with region specific adapted traits. The genotypes, ICGV's 07247, 01276, 01495 and 49 M-16 are plotted nearer to environment Aliyarnagar and Jalgaon whereas ICGVs 03064, 06142, 01274, 03042 and SPS 11 plotted towards ICRISAT_PR15 indicating that these genotypes had location specific adaptability. The stable genotypes across the environments can be released after evaluation and comparison with popular national checks or recycled in breeding program as a parent. Genotypes with stable yield performance were earlier reported by Mothilal *et al.* (2010a); Thaware, (2009); Chunilal *et al.* (2006); Hariprasana *et al.* (2008) and Pradhan *et al.* (2010). Mathur *et al.* (1997) reported that genotypes stable for shelling percent are also stable for seed yield per plant across the environments. The genotypes with stable hundred seed weight were earlier reported by Chavan *et al.* (2009) and Mothilal *et al.* (2010a).

The polygon view of MET data of four environments *viz.,* Aliyarnagar, Jalgoan, ICRISAT during rainy 2015 and ICRISAT during post-rainy 2015-16 in the biplot showed that genotypes were distributed in four sections, whereas the environments in two sections. Among the four environments, ICRISAT post-rainy discriminating itself from other environments indicated that the performance of genotypes differed during post-rainy season compared to three rainy season environments. The superior performance of genotypes during post-rainy season could be due to disease-free condition.

In the present study, most of the stable genotypes for yield and its contributing traits are improved breeding lines. The genotypes from mini-core and reference set collection do not possess high yield, but they may have desirable genes or QTLs for other traits like disease resistance and nutritional quality traits (Upadhyaya *et al.,* 2012 & 2014 and Patil *et al.,* 2014) which need to be explored. Different germplasm lines with disease resistance and nutritional quality traits were identified in mini-core collection (Upadhyaya *et al.,* 2005 & 2006).

5.5.3 Stability for nutritional quality traits

The environment variance was highly significant for all the nutritional quality traits indicating that these traits were significantly influenced by environmental factors such as growing location/season, soil type and production practices. Burkey *et al.* (2007) and Upadhyaya *et al.* (2012) also reported significant variation in performance of groundnut genotypes for oil, protein and fatty acid composition grown under different seasons. Linoleic acid, a polyunsaturated fatty acid is unstable at a higher temperature and has an inverse relationship with oil stability (Braddock *et al.,* 1995 and O'Keefe *et al.,* 1993). Growing conditions also play an important role in deciding fatty acid profile (Oliva *et al.,* 2006). Significant genotypic interactions with growing season and geographic location have been earlier reported for fatty acid profiles in groundnut (Holaday and Pearson, 1974; Norden *et al,* 1987).

The position of environments on the biplot revealed that genotypes had higher oil content during rainy season across the environments compared to post-rainy season at ICRISAT whereas reverse trend was observed for protein content. Wide changes in environmental conditions especially high temperature during post-rainy season could be one of the reasons for the low oil content during post-rainy season. The accumulation of oil and other nutrients in the seed begins after the seed has fully developed. Under conditions of high temperature and moisture stress, seed development gets affected which also impacts the accumulation of nutrients in the seed. The location temperatures after pegging appeared to have an adverse effect on the oil composition and oil content, whereas protein content on the other hand was unaffected by temperature but affected by location and soil type (Canvin, 1965, Bovi, 1983; Sanders, 1982; Slack and Browse, 1984; Dwivedi *et al.,* 1993 & 1996).

Stable genotypes for protein content, oleic and linoleic acid content were also identified in GSP and can be used in the further breeding program for quality improvement in groundnut. High temperature favours the production of high oleic acid, which is prevailed during summer season (Jeong-Dong *et al.,* 2009). Expression of traits in different seasons suggested the requirement of specific environment for the better expression of a particular trait (Venkataraman *et al.,* 2001; Singh and Singh, 2001; Mohan *et al.,* 2004). Hence, to get the desired level of expression for nutritional quality traits, genotypes should be grown under specific environment and better agronomic management (Singh and Sinha, 1993; Moinuddin *et al.,* 1998; Minimol *et al.,* 2000; Patil *et al.,* 2014).

5.6 Molecular diversity

Assessment of molecular diversity facilitates the identification of agronomically valuable and diverse germplasm that can be used to develop different mapping populations and genetic enhancement of specific traits in groundnut. DNA markers have been used to evaluate genetic diversity in different crops (Cooke, 1995; Azzam *et al.,* 2007). Availability of co-dominant markers, such as SSR and EST-SSR in groundnut has greatly aided in diversity and other genomic studies in this crop. The primers used in the present study were highly polymorphic and produced a higher number of alleles per locus. Primers detected more than one locus indicating the presence of duplicate loci. This may be attributed to the presence of A-genome as well as B-genome in the allotetraploid cultivated groundnut. Amplification of more than one fragment by single primer pair tetraploid groundnut accessions is also evident from earlier studies (Hopkins *et al.,* 1999; Gimenes *et al.,* 2007; Varshney *et al.,* 2009a).

The majority of the primers used in the study had higher polymorphic information content (PIC) value (>0.6) indicating greater polymorphism in GSP for all the tested loci. Such higher PIC value could be due to the presence of a large number of diverse genotype and represent 21 countries. Similarly, high PIC values for polymorphic markers (0.10 to 0.89) with an average of 0.31 to 0.61 per marker were reported in earlier genetic diversity studies (Mace *et al.,* 2008; Cuc *et al.,* 2008; Gautami *et al.,* 2009; Varshney *et al.,* 2009b; Pandey *et al.,* 2012; Pandey *et al.,* 2014a). Diversity revealed by PIC values of markers needs to be verified by number of alleles amplified per locus (allelic richness) prior to assessing their informativeness. All the primers except GM 630 used in the study were highly informative in revealing the genetic diversity and partitioning of genetic variation due to their higher number of alleles per locus (>20) as well as higher PIC values. Similarly, several previous studies reported higher number of alleles per locus in groundnut indicated sufficient amount of molecular diversity for various traits (Krishna *et al.,* 2004; Barkley *et al.,* 2006; Varshney *et al.,* 2009a; Pandey *et al.,* 2014a). The higher number of alleles identified per marker could be attributed to a large set of genotypes (336) representing different botanical varieties and geographical locations.

In the study, heterozygosity among genotypes was varied from 0.00 (GM 630, GM 1536 and TC3E02) to 0.42 (GM 2301) for the different markers which could be due to its tetraploid nature and differences in genomic regions of both the progenitor's *viz. A. duranansis* and *A. ipensis* (Bertioli *et al.,* 2016). Heterozygosity in cultivated groundnut due to differences in genomic regions of its diploid progenitors was reported by Hopkins *et al.* (1999) and Tang *et al.* (2007).

Out of 462 alleles detected in the 336 genotypes of GSP for 14 SSR loci, 230 alleles were rare, 155 common, 18 most frequent alleles and 59 unique alleles. The present findings are in accordance with the findings of Varshney *et al.* (2009a) who reported 59 unique alleles and 127 rare alleles for 25 SSR loci in 189 genotypes of groundnut. The higher number of unique and rare alleles in groundnut was also reported by Mondal and Badigannavar (2010); Pandey *et al.* (2012); Ren *et al.* (2014) and Pandey *et al.* (2014a). The unique alleles reported for different SSR regions can be used in DNA fingerprinting to protect intellectual property rights whereas the rare alleles can be used for broadening the genetic base of associated trait in the breeding material. The high number of unique, rare and common alleles detected in the study was indicative of the existence of sufficient molecular diversity and allelic richness among the genotypes of GSP and can be used to construct prediction models to predict breeding values of the genotypes.

The PIC values, heterozygosity, gene diversity and number of alleles reported for both the subspecies *hypogaea* and *fastigiata* for 14 SSR loci revealed that both the sub-species exhibit sufficient molecular diversity for testing loci. Molecular variation in both the subspecies was earlier reported by Barkley *et al.* (2007); Kameswara *et al.* (2007); Mace *et al.* (2006); Tang *et al.* (2007); Varshney *et al.* (2009b); Mondal and Badigannavar (2010) and Pandey *et al.* (2012 & 2014a).

The neighbor-joining tree based on simple matching dissimilarity matrix between 336 genotypes of GSP grouped genotypes into five major clusters. Cluster I (C1) contained 79 of which 69 genotypes (88.4%) were from subspecies *fastigiata*. Genotypes of cluster CI were grouped into three sub-clusters, *i.e.,* CIa, CIb and CIc comprising of 37, 16 and 26 genotypes, respectively. Among these three sub-clusters, CIa comprised 91.6% genotypes developed at UAS, Dharwad Cluster II (CII) consisted of 64 genotypes grouped into two sub-clusters- CIIa and CIIb, of which CIIb comprised mostly of genotypes showing resistance to rust and LLS at 90DAS. The grouping of resistant genotypes into the same cluster could be due to the use of same or closely related wild donor in the pedigree. Apart from this, all the 48 genotypes included in CIVa and CIVb belongs to subspecies *hypogaea*. Cluster V comprised of four sub-clusters- CVa, CVb, CVc, CVd and 93.75% genotypes in this cluster were of subspecies *fastigiata* var. *vulgaris*. The results indicated that molecular markers could clearly differentiate the genotypes based on subspecies and botanical varieties and/or place of breeding. This could be attributed to availability and use of limited set of groundnut genotypes in breeding programs for traits like disease resistance and nutritional quality. For example, GPBD 4 is the most common source for incorporating LLS and rust resistance in groundnut. Similarly, SunOleic 95R is the potential donor for incorporating the high oleic trait into elite lines. In the study, the grouping of genotypes based on 14 SSR markers corresponded well with the classification based on biological diversity (sub-species level) and expression of specific traits such as resistance to LLS and rust, nutritional quality traits and agronomic performance across the environments. The principal coordinate analysis also reported grouping of genotypes corresponded with a neighbor-joining tree. The results indicated that there is a sufficient level of molecular diversity present in GSP. Diversity for disease resistance in groundnut at the molecular level was earlier reported by Mondal and Badigannavar (2010) and Shoba *et al.* (2010).

5.7 Population structure

Population structure grouped GSP into three sub-populations corresponded with clustering based on a neighbor-joining tree with some exception. Nearly 94% (90/96) cultivars of sub-population I (SPI) belong to subspecies *fastigiata,* whereas sub-population III had 49 genotypes from subspecies *hypogaea.* The results indicated that the genotypes with a pure background of subspecies *fastigiata* and *hypogaea* were grouped in these sub-populations. Structure analysis in groundnut with relatively low level of admixture was earlier reported by Wang *et al.* (2011) and Pandey *et al.* (2014a).

5.8 Marker-trait association (MTA)

The present study reported 311 (24.6%) significant MTAs for 18 traits, including disease resistance, yield and its contributing traits and nutritional quality traits. A strong correlation between phenotypic variance (PV), p values, and F values was observed. MTAs detected with high PV for desired agronomically important traits such as disease resistance, yield, and nutritional quality traits will be helpful to accelerate genetic gain in groundnut through molecular breeding (Pandey *et al.,* 2014). In the present study out of 311 MTAs, only 79 had explained >30% PV and were considered as potential MTAs. MTAs with >20% PV for disease resistance, yield, and nutritional quality traits were reported by Pandey *et al.* (2014a).

5.8.1 MTA for resistance to LLS and rust

Association analysis identified 29 MTAs for both the diseases with PV ranged from 30.27 to 63.14%. Of these 29 MTAs, 18 MTAs were identified for LLS (30.27 to 49.89% PV) and 11 MTAs for rust (30.45 to 63.14%) at 90 and 105 DAS. The SSR markers GM 1009, GM 2301 and TC6H03 had a significant association with LLS resistance in pooled across the environments with PV >30%. The identified MTA can be deployed in the marker-assisted breeding program for forward selection. The significant marker-trait associations for LLS and rust with PV varied from 10.2 to 82.96% were earlier reported by Khedikar *et al.* (2010); Mondal *et al.* (2012); Sujay *et al.* (2012); Shoba *et al. (*2012b) and Kolekar *et al.* (2016).

Two markers GM 2301 (33.11%) and IPAHM 103 (43.49%) were reported to be associated with rust score across the environments. Among the 11 MTAs for rust, GM 2301 was involved in 5 MTAs (31.58 to 37.16% PV) whereas IPAHM 103 was involved in two MTAs (43.49 to 63.14% PV). The results suggested that GM 2301 and IPAHM 103 were the best markers associated with rust resistance can be used in the forward breeding program to select resistant genotypes with desired alleles. A major QTL for rust (QTLrust01) potentially associated with candidate marker IPAHM 103 was earlier identified and validated using a wide range of resistant/susceptible breeding lines by Khedikar *et al.* (2010). In addition to marker IPAHM 103, four new markers (GM 2009, GM 1536, GM 2301 and GM 2079) were reported to be associated with the major QTL for rust with PV of 82.96% (Sujay *et al.,* 2012) and another QTL region flanked by GM1839-GM1009 on linkage group AhXII explained PV of 14.1–35.2% for LLS resistance (Kolekar *et al.,* 2016). These markers were successfully used for introgression of major QTL region for rust resistance from GPBD 4 into three elite cultivars (ICGV 91114, JL 24 and TAG 24) through marker-assisted backcrossing (Varshney *et al.,* 2014). Similarly, significant marker-trait association for resistance to LLS and rust were earlier reported by Shoba *et al.* (2012b); Gajjar *et al.* (2014); Jakkeral *et al.* (2014) and Sukruth *et al.* (2015).

5.8.2 Yield and yield component traits

Yield and its component traits are the prime target of improvement in all the breeding programs. A total of 18 MTAs could be identified for seven yield and its component traits with PV >30%. Two MTAs were identified for days to 50% flowering, of which TC1D12 explained 32.10% PV with pooled BLUPs, whereas GM 2301 explained 30.0% PV at ICRISAT during rainy 2015. Five MTAs with >30% PV were reported for days to maturity, of which TC1D12 showed good consistency and appeared thrice at Aliyarnagar, Jalgaon and ICRISAT during rainy season 2015 with stable and high phenotypic variance (>32%) could be a promising marker associated with days to maturity. Two MTAs with a single marker (TC1D12) were reported for pod yield per plant at Jalgaon (31.12% PV) and with pooled BLUPs (30.27% PV) across the environments. Marker TC1D12 was also found to be associated in both MTAs for shelling percent at Aliyarnagar (35.83% PV) and ICRISAT post-rainy 2015-16 (31.88% PV). Similarly, two MTAs with >30% PV were reported for hundred seed weight and pod yield per hectare involving the markers IPAHM 103 and TC1D12. In the results, the marker TC1D12 was found associated with most of the important yield traits which might be due to the positive genetic correlation among these yield traits or it could be attributed to the association of this marker with major QTL governing yield and other traits. Five QTLs were earlier identified through family-based mapping approach for seed weight with PV varied from 4.18-19.80% (Varshney *et al.,* 2009b; Ravi *et al.,* 2011). Marker-trait association analysis identified significant association of five SSRs with kernel mass which together accounted up to 28% PV (Goswami *et al.,* 2013). Three MTAs each one with TC6E01 (33.99% PV); TC1D12 (33.31% PV) and GM 1954 (30.96% PV) were identified for haulm yield per plant at ICRISAT during rainy 2015. Similarly, the MTAs for various traits through association mapping in groundnut were also reported by Pandey *et al.* (2014a). The QTLs for pod and seed related traits such as pod length, pod width, pod yield per plant, hundred seed weight and haulm yield per plant with PV ranged from 3.68 to 27.84% were also reported in earlier studies (Fonceka *et al.*, 2012; Chen *et al.,* 2016; Luo *et al.,* 2017). The results of the study suggest that these markers can be used after validation for improving yield and its component traits.

5.8.3 Nutritional quality traits

High oleic groundnut offers remarkable health benefits to consumers; longer shelf life of oil and food products to processing industries and enhances profitability to groundnut farmers. Increase in genetic gain for nutritional quality traits in groundnut through conventional breeding efforts would be tedious, less effective and time and resource consuming. Marker-assisted breeding coupled with robust phenotyping and rapid generation advancement can overcome these and offers high genetic gain per unit of time and cost. A total of 31 significant MTAs with >30% PV were observed for seven nutritional quality traits. Marker IPAHM 103 was involved in three MTAs identified for oil content and four for protein content with high PV, indicating that this marker was potentially associated with oil and protein content in groundnut. The significant MTAs for oil and protein content were earlier reported by Pandey *et al.* (2014b). The association of IPAHM 103 with oil and protein in groundnut is in accordance with the findings of Sarvamangala *et al.* (2011). Seven QTLs and MTAs for oil content in groundnut with low PV (1.5-9.5%) was reported by Selvaraj *et al.* (2009); Liang *et al.* (2009); and Wang *et al.* (2011).

Marker IPAHM 103 was found consistently associated with oleic acid at the individual as well as across the environments with high PV ranged from (>35%). Among all the 31 MTAs for nutritional quality traits, 16 MTAs (nearly 50%) involved IPAHM 103 with higher phenotypic variation indicating its close association with these traits. The present findings are in accordance with the findings of Pandey *et al.* (2014) where they have reported a total of 25 MTAs for oil and nutritional quality traits with PV varied from 5.84% to 40.37%. The MTAs identified for different traits in the present study explained higher PV compared to MTA identified by Pandey *et al.* (2014a) for disease resistance, yield and nutritional traits and by Wang *et al.* (2011) for fatty acids.

5.9 Screening of GSP for mutant alleles of *ahFAD2A* and *ahFAD2B* gene

High oleic groundnut varieties are preferred by both consumers and food processing industries due to their multiple health benefits and enhanced shelf-life of oil and groundnut based food products. Thus, breeding of high oleic groundnuts is an important aspect of groundnut improvement programs worldwide (Janila *et al.,* 2016b). The enzyme, fatty acid desaturase (*ahFAD2*) catalyzes the conversion of oleic to linoleic acid, and is encoded by two homeologous genes, *ahFAD2A* and *ahFAD2B*, located on the A and B genome, respectively (Jung *et al.,* 2000a & b; Yu *et al.,* 2008). Both the *ahFAD2* genes have 99% sequence homology and inactivation of both the genes is required for accumulation of high oleic acid in groundnut kernels. The identification of molecular markers linked to both *ahFAD2* genes in groundnut has made it possible to target this trait in groundnut improvement programs through screening of breeding material using a molecular marker (Janila *et al.,* 2016b).

In the present study, 87 genotypes were detected having *ahFAD2A* mutation, while only SunOleic 95R had mutation in both A and B genome with high oleic acid (≥75%) and low linoleic acid content (<7%) at individual as well as across the environments. The oleic and linoleic acid content in the genotypes with *ahFAD2A* mutation ranged from 32.64 to 54.19% and from 26.11 to 47.06%, respectively which was similar to the range observed in the wild-type genotypes (32.09 to 54.22% for oleic acid and 31.05 to 46.76% for linoleic acid). This is in contrast to the findings by other authors (Chen *et al.,* 2010; Nawade *et al.,* 2016) who reported moderate levels of oleic acid (>50%) in the presence of *ahFAD2A* mutation. Being an allotetraploid crop with 97% sequence homology between the genomes of diploid progenitors, a single mutant allele of the gene in groundnut could not make a significant impact on phenotype of a trait unless and until its homeologous gene got mutated. In the presence of both mutant alleles, the activity of fatty acid desaturase is completely inhibited leading to high oleic acid content in the seeds. Another reason for this variation among the genotypes could be due to the presence of some modifier genes or due to genotype x environment interactions. Modifying genes were reported to be responsible for modification of oleic acid content in other oilseed crops like safflower (Hamdan *et al.,* 2009) and sunflower (Hamdan *et al.,* 2012). Besides genes, linoleic acid content in developing seeds is also widely influenced by the temperature (Slack and Browse, 1984; Graces *et al.,* 1992; Bansal, *et al.,* 1993; Martinez-Rivas *et al.,* 2000). High temperature during seed development could have decreased the linoleic acid content in the oil (Rebiei *et al.,* 2007).

Studies concerning high oleic acid content have mostly focused on the levels of oleic acid and linoleic acid in the improved lines. Very often it is observed that a change in one metabolite brought about by a change in the corresponding enzyme in a biosynthetic pathway, can affect the levels of all subsequent metabolites in the pathway. Recent studies by Pandey *et al.* (2014) and Wang *et al.* (2011) showed that *ahFAD2* mutant alleles also had effect on palmitic acid levels. In the present study, the genotype with both mutant alleles (SunOleic 95R) had low palmitic acid across the environments. Significant phenotypic variability in oleic and linoleic acid content was found in the genotypes that were identified positive for the target allele using molecular markers. Therefore, phenotypic confirmation of marker-assisted selected lines is essential to advance the selected lines for further evaluations (Janila *et al.,* 2016b). Eighty-seven genotypes reported with a mutant allele of *ahFAD2A* can be used to as a parent to cross with SunOleic 95R to further introgress mutant allele of *ahFAD2B* gene. The presence of at least one mutant allele in female parent would make the introgression of another allele easy because the probability of getting individuals with favourable combination of alleles in F_2 generation is reduced with an increase in the number of targeted alleles.

5.10 Significant MTAs for molecular breeding

Out of 14 SSR markers used in the study, three markers GM 1009, GM 1954 and GM 2301 were potentially associated with resistance to LLS, whereas two markers GM 2301 and IPAHM 103 were associated with resistance rust across the environments. A single marker TC1D12 had a significant association with all seven yield and its contributing traits indicating its association with multiple yield traits. The marker IPAHM 103 was potentially associated with multiple nutritional quality traits such as oil and protein content along with oleic, linoleic and stearic acid with high PVE. Several other significant and validated markers earlier identified for LLS and rust (Kediker *et al.,* 2010; Sujay *et al.,* 2012; Shoba *et al.,* 2012b; Gajjar *et al.,* 2014 and Sukruth *et al.,* 2015) are being used in marker-assisted breeding (Varshney *et al.,* 2014 and Janila *et al.,* 2016a). Recently, SNPs were developed for rust and LLS and validation is in progress to identify best SNPs (Pandey *et al.,* 2017) for use in genomic assisted breeding.

In the absence of linked markers, the phenotypic selection was used to breed high oleic groundnut lines such as SunOleic 95R (Gorbet and Knauft, 1997), Tamrun OL01 (Simpson *et al.,* 2003) etc. The first instance of using MABC targeting the high oleic trait in groundnut was reported by Chu *et al.* (2011). The use of linked molecular markers to improve such traits would considerably help to optimize time and resources by rejecting a large number of unwanted plants even at seedling stage (Janila *et al.,* 2016b). All these associated markers and identified genotypes with favourable alleles can be deployed for improving different traits through molecular breeding.

Chapter VI

Summary, Conclusions and Suggestions for further work

The investigation entitled “Phenotyping of Genomic Selection Panel (GSP) for foliar fungal diseases and nutritional quality traits” was conducted to evaluate the GSP comprising of 340 diverse genotypes for reaction to two major foliar fungal diseases *i.e.,* late leaf spot (LLS) and rust, yield and nutritional quality traits based on multi-location trials. The study also involved preliminary evaluation of GSP for the level of genetic and molecular diversity and allelic richness for the targeted traits as a prerequisite for Genomic Selection (GS). Marker-trait Association (MTA) for disease resistance and nutritional quality traits was performed to validate markers on a diverse set of genotypes and find significant markers linked to the traits of interest for potential deployment in marker-assisted breeding. The 340 genotypes representing 21 geographically diverse countries were evaluated in three states *viz.,* Tamil Nadu (Aliyarnagar), Maharashtra (Jalgaon) and Telangana (ICRISAT, Patancheru) of India for foliar fungal disease resistance, yield and nutritional quality traits during rainy season 2015. A post-rainy trial was planted at ICRISAT, Patancheru during 2015-16 for evaluation of yield and nutritional quality traits under disease-free conditions. Aliyarnagar and Jalgaon are the disease hot-spot locations, while artificial disease pressure through inoculation on infector rows at 45 days after sowing (DAS) complemented the natural disease incidence at ICRISAT, Patancheru. The trial was planted in Alpha Lattice Design (incomplete block design) with two replications; each replication is divided into 20 equal sized blocks with 17 genotypes in each block to reduce inter-block variation and to maintain homogeneity. The genotypes were planted in single rows of 4 m length, with a spacing of 30 and 10 cm between the rows and plants, respectively. Observations were recorded on disease severity score of LLS and rust at 75, 90 and 105 DAS, yield and its contributing traits (10) and nutritional quality traits (7). Standard procedures were adopted for data analysis using different softwares. Box plots were generated using GenStat 15th Edition to find out outliers in the data set and Cooks statistics used for finding genotypes with higher residuals. Analysis of variance (ANOVA) was done using general linear mixed model (GLM) through proc glm function of SAS version 9.2, and genetic parameters were estimated using partitioned variance components from ANOVA in MS Excel. Principal component analysis (PCA) was done using Best Linear Unbiased Prediction of means by GenStat 15th Edition. Cluster analysis (Ward, 1963) was performed using scores of the first six principal components that together explained >75% towards total variability. Graphical representation of stability based on PCA, called as GGE biplot method (Yan *et al.,* 2000), was used to find stable sources of disease resistance, yield and nutritional quality traits. STRUCTURE was used to generate population structure and Q matrix, and TASSEL 2.1 was used for marker-trait association. Findings of the present study are summarized here:

6.1 Summary

6.1.1 Genetic variability

- Analysis of variance showed significant genotypic differences for disease resistance and yield traits, and nutritional quality traits indicating a high degree of genetic variability within GSP.
- GCV and PCV values were high for disease severity scores to rust and LLS at 75 DAS, moderate for both at 90 DAS; and low at 105 DAS. The estimated of heritability and genetic advance as percent of mean (GAM) were high for disease severity scores of both LLS and rust across environments and different stage of observations.
- High GCV and PCV values for number of matured pods per plant, pod yield per plant, seed yield per plant, hundred seed weight, pod yield per hectare and haulm yield per plant indicate higher genetic variability for these traits in GSP.
- Heritability and GAM were high for plant height, hundred seed weight, pod yield per hectare; and moderate heritability with high GAM for number of matured pod per plant, pod yield per plant, seed yield per plant and haulm yield per plant revealed that these traits are governed by additive gene effects.

- Very low GCV and PCV values were observed for oil and protein content and three major fatty acids *i.e.,* oleic, linoleic and palmitic acid at individual as well as across environments indicate narrow variability and least opportunities for direct phenotypic selection.
- High estimates of heritability coupled with low GAM were reported for oil, protein and fatty acid content indicated the involvement of non-additive gene action.

6.1.2 Association among traits

- Significant positive association of pod yield per hectare with number of matured pods per plant, pod yield per plant, seed yield per plant, number of primary branches per plant, hundred seed weight and days to maturity at individual and across environment indicate that effective improvement in yield can be achieved through selection based on these characteristics.
- Significant negative association of disease severity scores of LLS and rust with number of primary branches per plant, number of pods per plant, seed yield per plant, hundred seed weight, days to maturity, pod yield per hectare and haulm yield per plant at individual as well as across environment revealed that both the diseases responsible for yield reduction in groundnut.
- Disease severity to LLS and rust had a strong positive association with each other due to the similarity in genes/QTLs governing resistance to both the diseases.
- Negative association of oil content with protein content at individual as well as across environment indicate that development of cultivars with an elevated level of oil will have trade-offs with protein content. Combining high oil and protein content would, therefore, be difficult.
- Oil content had a positive association with linoleic, palmitic and stearic acid content at individual as well as across environment. A strong negative association between oleic acid and three other fatty acids *viz.,* linoleic, palmitic and stearic acid indicate that an increase in oleic acid will lead to decrease in other fatty acids.

- A significant negative association of oil content, protein content and three fatty acids (linoleic, palmitic and stearic acid) with disease severity scores of LLS and rust indicate that the severity of both the diseases greatly responsible for the reduction in oil and protein content along with a reduction in undesirable fatty acids.
- Positive association of pod yield per plant with oil content indicates that genetic improvement in pod and oil yield is possible through single breeding strategy.
- Significant negative association of oil content with hundred seed weight and positive with protein content indicate that the cultivars had high seed mass had lower oil and high protein content and vice-versa for low seed mass.

6.1.3 Principal component analysis

- Principal component analysis (PCA) explained 70.62 to 79.41% of total genetic variability by the first six principal components (PCs) for which Eigenvalues were greater than one across the four environments and pooled.
- Disease severity score of LLS and rust at 90 and 105 DAS, pod yield per plant, number of matured pods per plant, and pod yield per hectare contributed more towards total variability explained by first PC in all the environments and pooled. However, nutritional quality traits had larger contribution towards fourth and fifth PCs rather than first two PCs indicating least contribution of nutritional quality traits compared to disease resistance and yield traits toward total genetic diversity present in GSP.
- A hierarchical cluster analysis (Wards, 1963) for individual environment separately and for pooled data grouped GSP into different clusters ranged from six to eight. Seven clusters were formed at Aliyarnagar and ICRISAT during rainy 2015 whereas eight at Jalgaon and six at ICRISAT during post-rainy and pooled across the environment.
- The genotypes of the common geographical origin or same location grouped into different clusters without forming any separate cluster indicated that geographic diversity was not related to genetic diversity in groundnut.

- High cluster mean for number of pods per plant, pod yield per plant, haulm weight per plant and yield per hectare with lowest disease severity score to LLS and rust in Cluster I comprised of 49 out 340 genotypes of GSP indicate that most of the high yielding cultivars with resistance to both the diseases across the environment were grouped together in this cluster.
- Cluster IV grouped 90 genotypes identified for high cluster mean for hundred seed weight and protein content along with low cluster mean for oil content indicate that most of the genotypes of this cluster had higher seed mass with high protein and low oil content across the environments. These genotypes can be used to develop cultivars with larger seed size, high protein and low oil content especially preferred for confectionery or table purposes.
- In contrast to other genotypes of GSP, a single genotype SunOleic 95 R recorded higher mean performances for oleic acid (>75%) and O/L ratio (>12) whereas lower linoleic acid (<6 %) and palmitic acid (<9%) maintained a separate identity as high oleic genotype and clusters separately at individual as well as across locations.
- Cluster VI comprised of 22 genotypes had high cluster mean for oil content and haulm yield per plant whereas low cluster mean for protein content indicated that genotypes of this cluster could be used to develop cultivars with high oil content.
- Genotypes grouped in different clusters with desired traits such as disease resistance to LLS and rust, yield and nutritional quality traits based on Wards cluster analysis can be selected and used in future groundnut improvement programs to develop new cultivars and to enrich the groundnut breeding material with new recombinants.

6.1.4 Stability analysis

- Pooled analysis of variance revealed significant genotypic, environment and genotype × environment (G × E) interactions for all the studied traits.
- Stability analysis of 109 out of 340 genotypes of GSP using GGE biplot technique reported GPBD 4, ICGV’s 00248, 06142, 02411, 00246 and

00068, SPS 11 and ICG 11426 as stable for LLS across the environment with lower disease score and shortest vector length from AEA.

- Low disease score with shortest vector length from AEA for the genotype GPBD 4, ICGV’s 99052, 99051, 86699, , 06422, 07223, 07235, 05100, 06142, 02411, 05155, 00362, 00362, 00248, 01361, 99160, 02323, 87846 and 02446, SPS2, SPS 7, SPS 11, SPS 21 and ICG 11426 indicate their superiority and stability for resistance to rust across environment.
- Environments Aliyarnagar, Jalgaon and ICRISAT have a positive correlation with each other. The position of the environment on biplot revealed that ICRISAT_R15 (ICRISAT rainy 2015) was the best environments where genotypes got higher diseases scores followed by Aliyarnagar and Jalgaon. This also indicated that ICRISAT has best foliar disease screening nursery with better resources to put artificial disease pressure and to maintain favorable condition for disease development and spread.
- Genotypes ICGV 06100 followed by ICGV’s 05163, 05155, 07223, 07235, 02323, 06099, 07120, 02411, 05161, 03043, 06423, 01273 and 06422 had high and stable pod yield across environments.
- The polygon view of biplot of MET data of four environments showed that genotypes fell in four sections whereas the test environments fell in two sections for all nutritional quality traits.
- Genotypes ICGV’s 05155, 97128, 00248, 06142, 03042, 07220, 02411, 06424, 06100, 05163 and 06040, GPBD 4, SPS 21, SPS 11, SPS 9 and 49 M-16, had high and stable performance for oil content across the environment.
- Genotypes ICGV’s 01276 00362, 02287,02323, 02266, 02321 and 01274, ICG 10053, 49 M-16, SPS 11 and 24 M-86 were superiority and stable for protein content across the environment.

6.1.5 Molecular diversity

- All the primers except GM 630 used in the study, were highly informative in revealing the genetic diversity and partitioning of genetic variation due to their high number of alleles per locus (>20) as well as higher PIC values (>0.6).

- The neighbor-joining tree based on simple matching dissimilarity matrix grouped genotypes into five clusters with lowest cluster mean for severity to LLS and rust across the environments and majority of resistance genotypes in sub-cluster CIIb.
- Cluster I with three sub-clusters contained 79 genotypes, of which 69 (88.4%) were from subspecies *fastigiata*. Whereas, CIa comprised of 91.6% genotypes developed at UAS Dharwad and CIb had all the genotypes of var *peruviana*. Cluster IV comprised of 48 genotypes all of the subspecies *hypogaea* whereas cluster V had 96 genotypes with 93.75% genotypes of subspecies *fastigiata* var *vulgaris*.
- The grouping of genotypes based on 14 SSR molecular markers corresponded well with the classification based on biological diversity (sub-species level), place of breeding and expression of specific traits such as resistance to LLS and rust, nutritional quality traits and agronomic performance across the environments.
- 14 SSR markers detected a total of 462 alleles in 336 genotypes ranged from 14 (GM 630) to 56 (IPAHM 103) with an average 33 alleles per locus indicated a wide range of allelic diversity present in GSP for these 14 loci.
- Allelic richness available for each locus is attributed by high polymorphic expression of all the markers with PIC values more than 0.60, very high gene diversity (>0.65) and 0.00 (GM 630, GM 1536 and TC3E02) to 0.42 (GM 2301) heterozygosity.
- Out of 462 detected alleles in the 336 genotypes for 14 SSR loci, 230 were rare, 155 common, 18 most frequent alleles and 59 unique alleles. It indicates sufficient level of molecular diversity and allelic richness present in GSP.
- The highest number of unique alleles were recorded for GM 2301 (20) followed by TC1D12 (7), TC6E01 (5), IPAHM 103 (5) whereas no unique alleles reported on GM 1536, GM 630, and TC3E02.

- Out of 462 alleles, a total of 365 (79.00%) alleles were detected in ssp. *fastigiata* whereas 332 (71.86%) in ssp. *hypogaea*. The PIC values and gene diversity in both the subspecies for 14 SSR markers revealed that both the subspecies has a great amount of molecular diversity for studied loci.

6.1.6 Marker-trait association (MTAs)

- Out of 311 (24.6%) significant MTAs observed for 18 traits, only 79 were explained >30% phenotypic variance (PV) and considered as potential MTAs.
- Association analysis identified 29 MTAs for both the diseases with PV from 30.27 to 63.14%. Of these, 18 MTAs were identified for LLS (30.27 to 49.89% PV) and 11 for rust (30.45 to 63.14%) together at 90 and 105 DAS. The SSR markers GM 1009, GM 2301 and TC6H03 had a significant association with LLS resistance whereas two markers GM 2301 (33.11%) and IPAHM 103 (43.49%) were reported to be associated with rust score across the environments.
- 18 MTAs were identified for yield and its components with PV >30% *viz.,* two for days to 50 % flowering; five for days to maturity; two for hundred seed weight and pod yield per hectare; two for pod yield per plant. Marker TC1d12 is potentially associated with yield and its contributing traits.
- Out of 31 MTAs with >30% PV for nutritional quality traits, three were for oil content; six for protein content; five for oleic acid; seven for linoleic acid; four for palmitic acid; five for stearic acid and two for oleic/linoleic acid ratio. Markers IPAHM 103 and GM 1954 explained highest PV for all the observed nutritional quality traits.
- 87 (25.89%) out of 336 genotypes had a mutant allele of *ahFAD2A* whereas only one (SunOleic 95R) had mutant allele of *ahFAD2B*. Out of 87 genotypes with mutant allele of *ahFAD2A* 68.97% (60) genotypes were from subspecies *fastigiata* var *vulgaris;* whereas 31.03% (27) from subspecies *hypogaea* var *hypogaea* and only a single genotype with both the mutant allele belongs to subspecies *hypogaea* var *hypogaea* (Virginia runner).

- A considerable variation for oleic acid (32.64 to 54.19%) and for linoleic acid (26.11 to 47.06%) content was observed among the genotypes with only a single mutant allele of a*hFAD2A*.
- SunOleic 95R had high oleic acid content of ≥75% and low linoleic acid content <6% in the individual as well as across the environments with mutant alleles of both the genes *ahFAD2A* and *ahFAD2B* gene.

6.2 Conclusions

In order to deploy genomic selection for improvement of complex polygenic traits in groundnut breeding program, multi-environment phenotypic data on targeted traits and assessment of genomic selection panel for phenotypic and molecular diversity is important to construct a prediction model with higher accuracy. The present study is most comprehensive and first preliminary evaluation of GSP for the level of genetic and molecular diversity, allelic richness, marker-trait association and trait heritability conducted so far in groundnut. The conclusions from the present investigation are mentioned below.

- The results revealed high genetic variability among the genotypes for resistance to LLS and rust along with yield traits that will be useful to develop resistant varieties through breeding.
- Sufficient level of phenotypic and molecular diversity and allelic richness (33 alleles per locus) was observed in GSP for both the diseases with a higher number of unique and rare alleles per locus.
- Nine superior genotypes in terms of combined disease resistance and yield >2500 kg/ha (SPS 11, ICGV's 05163, 01274, 06142, 07235, 02323, 02411, 03043 and 49 M-16) along with acceptable pod and seed features were identified from advanced breeding lines that can be recycled in breeding program to develop new lines with resistance to LLS and rust in groundnut.
- The resistant genotypes derived from *A. villosa* and mutagenesis would be useful for widening the genetic base of resistance to both the diseases as most of the resistance breeding programs are dependent on *A. cardenassii* for source of resistance.

- Deployment of potential marker-trait association with high PV for LLS (GM 1009, GM 2301 and TC6H03) and rust (GM 2301 and IPAHM 103) in marker-assisted breeding would enhance intensity and accuracy of selection.
- There was high frequency (25.9%) of mutant allele of *ahFAD2A* reported in GSP whereas, mutant allele of *ahFAD2B* gene was not detected, except for SunOleic 95R a high oleic genotype released by the USA.
- There was no significant difference in the mean oleic acid observed for individuals carrying mutant allele on A genome (*ahFAD2A*) with individual carrying wild-type allele. Therefore, it is concluded that presence of both the mutant alleles is required for the expression high oleic trait.

6.3 Suggestions for further work

On the basis of finding of present investigation, breeding repercussions and suggestions have been made for further works are given below

- The identified resistant advance breeding lines with acceptable pod and seed features will be recycled in breeding program to develop new lines with resistance to both the diseases.
- Unique alleles reported for targeted SSR regions can be used for cultivar identification at molecular level and used as DNA fingerprint to protect intellectual property rights (IPR).
- Potential MTAs identified explaining higher phenotypic variation for different traits will be deployed in marker-assisted breeding to improve selection accuracy and intensity for complex traits.
- The multi-environment phenotypic data on different traits of GSP generated in the present study will further be used along with genotype by sequencing data to construct first genomic selection prediction model in groundnut that can accelerate genetic gain in the breeding program per unit of time and cost.
- The available germplasm of groundnut lacking high oleic genotypes indicates strong need to breed high oleic groundnut varieties.

References

Ajay BC, Gowda MVC, Rathnakumar AL, Kusuma VP, Abdul Fiyaz R, Prasanna Holajjer Ramya KT, Govindaraj G, Prashanth and Babu H. 2012. Improving genetic attributes of confectionary traits in peanut (*Arachis hypogaea* L.) using multivariate analytical tools. J. Agric. Sci., 4(3):30-37.

Alam MK. 2014. Genetic correlation and path analysis in groundnut. SAARC J. Agric., 12(1):96-105.

Alam MS, Begum D and Khair AB. 1985. Study of genetic parameters and character inter-relationship in groundnut in groundnut. Bangladesh J. Agric. Res., 10:111-117.

Alt JL Fehr WR, Welke GA and Sandhu D. 2005. Phenotypic and molecular analysis of oleate content in the mutant soybean line M23. Crop Sci., 45:1997-2000.

Amarasinghe YP, Wijesinghe G, Pushpakumara RW. 2016. Multivariate analysis, genetic diversity and phenotypic correlation of nineteen exotic groundnut accessions. Journal of AgriSearch. 3(1):167-176.

Anderson WF, Wynne JC and Green CC. 1986a. Potential for incorporation of early and late leaf spot resistance in peanut. Plant Breed., 97:163-170.

Anderson WF, Wynne JC, Green CC and Beute MK. 1986b. Combining ability and heritability of resistance to early and late leaf spot of peanut. Peanut Sci., 13:13-14.

Anderson WF, Beute MK, Wynne JC and Wongkaew S. 1990. Statistical procedures for assessment of resistance in a multiple foliar disease complex of peanut. Phytopathology 80:1451-1459.

Anderson WF, Holbrook CC and Brenneman TB. 1993. Resistance to *Cercosporidium personatum* within peanut germplasm. Peanut Sci., 20:53-57.

Anderson PC, Hill K, Gorbet DW and Brodbeck BV. 1998. Fatty acid and amino acid profiles of selected peanut cultivars and breeding lines. J. Food Comp. Anal., 11:100-111.

Ariyo OJ. 1992. Factor analysis of vegetative and yield traits in okra (*Hibiscus esculentus*). Indian J. Agric. Sci., 60(12):793-795.

Ashish J, Nadaf HL and Gangadhara K. 2014.Genetic Analysis of Rust and Late Leaf Spot in Advanced Generation Recombinant Inbred Lines of Groundnut (*Arachis hypogaea* L.) Int J Genet Eng and Biotech. 5(2):109-114.

Awal MA and Ikeda KT. 2002. Effects of changes in soil temperature on seedling emergence and phenological development in field-grown stands of peanut (*Arachis hypogaea* L.). Environ. Exp. Bot. 47:101-113.

Azharudheen MTP. 2010. Evaluation of RILs for nutritional traits in groundnut. M.Sc. Thesis Submitted to UAS Dharwad. p 89.

Azharudheen MTP and Gowda MVC. 2013. An assessment of the prospects of developing confectionery grade genotypes with multiple disease resistance in groundnut. Int J Biotech and Bioeng Res., 4:347-354

Azharudheen TPM, Gowda MVC, Lingaraju S, Bhat RS, Bhat R and Motagi BN. 2013. Evaluation of sister homozygous lines for oil content and oil quality in groundnut. Karnataka J. Agric. Sci., 26(1):1-5

Azzam CR, Azer SA, Khaleifa MMA, Abol-Ela MF. 2007. Characterization of peanut genotypes and molecular markers associated with resistance to pod rot diseases and aflatoxin contamination by RAPD and ISSR. Arab. J. Biotech. 10:301-320.

Bachlava E, Joseph WB, Cavell B, Sanbao W, Jerome A and Andera JC. 2008. Heritability of oleic acid content in soybean seed oil and its genetic correlation with fatty acid and agronomic traits. Crop Sci., 48:1764-1772.

Badigannavar AM, Kale DM and Murty GSS. 2002. Genetic base and diversity in groundnut genotypes. Plant Breed., 121:348-353.

Bandyopadhyay A and Desai S. 2000. Groundnut as a source of oil and food-the facts and national perspective. In: Nat. Sem. Oilseeds and oils-Res. Develop. Needs in the Millennium, Directorate of oilseed Research, Hyderabad, 2-4, Feb., 72-87.

Bansal UK, Satija DR and Gupta VP. 1992. Variability and Genotype × Environment interaction in relation to growth habits in groundnut. Crop Improvement. 19(1):42-47.

Bansal UK, Satija DR and Ahuja KL. 1993. Oil composition of diverse groundnut (*Arachis hypogaea* L.) genotypes in relation to different environments. J. Sci. Food Agric., 63:17-19.

Banterng P, Patanothai A, Pannangpetch, Jogloy S, Hoogenboom G. 2003. Seasonal variation in the dynamic growth and development traits of peanut lines. J. Agric. Sci., (Camb) 141(1):51-62.

Barkley NA, Dean RE, Pittman RN, Wang ML, Holbrook CC and Pederson GA. 2007. Genetic diversity of cultivated and wild-type peanuts evaluated with M13-tailed SSR markers and sequencing. Genet Res. Camb., 89:93-106.

Barkley NL, Dean R, Pittman RN, Wang ML, Holbrook CC and Pederson GA. 2006. Genetic diversity of the peanut mini-core. American Peanut Res. Education Society Proceedings. pp 14.

Becker HC and Leon J. 1988. Stability analysis in plant breeding. Plant Breed., 101:1-23.

Becker HC. 1981. Correlations among some statistical measures of phenotypic stability. Euphytica, 30(3):835-840.

Bera SK, Kumar V, Radhakrishnan T, Sojitra VK and Gedia MV. 2010. Interspecific derivatives for widening the genetic base of groundnut. Indian J. Plant Genet. Resour., 23(2):160-163.

Bertioli DJ, Cannon SB, Froenicke L, Huang G, Farmer AD, Cannon EK, Liu X, Gao D, Clevenger J, Dash S and Ren L. 2016. The genome sequences of *Arachis duranensis* and *Arachis ipaensis*, the diploid ancestors of cultivated peanut. Nature genetics. 48:438-446

Bhagat NR, Lalwani HB, Taslim Ahmad, Dhapwal GS and Nagaraj G. 1984. Evaluation of groundnut collections from Zambia. Indian J Genet Plant Breed., 44:406-410.

Bhagat NR, Ahmed T, Lalwani HB and Nagaraj G. 1986. Character association and pathanalysis in improved groundnut varieties. Indian J Agric Sci., 56(4):300-302.

Bhakal M and Lal GM. 2015. Studies on Genetic Diversity in Groundnut (*Arachis hypogaea* L.) Germplasm. J. Plant Sci. Res., 2(2):128

Birthal PS, Rao PP, Nigam SN, Bantilan CS, and Bhagavatulu S. 2010. Groundnut and Soybean Economies in Asia: Facts, Trends, and Outlook. Patancheru: International Crops Research Institute for the Semi-Arid Tropics. pp 11.

Botstein D, White RL, Skolnick M and Davis RW. 1980. Construction of a genetic linkage map in man using restriction fragment length polymorphisms. Am. J. Hum. Genet., 32(3):314.

Bovi MLA. 1983. Genotype and environmental effects on fatty acid composition, iodine value and oil content of peanut (*Arachis hypogaea* L.). Abstract Diss. Abst. Internat., 44:406.

Braddock JC, Sims CA andO'keefe SF. 1995. Flavor and oxidative stability of roasted high oleic acid peanuts. J. Food Sci. 60(3):489-493.

Branch WD and Culbreath AK. 1995. Combination of early maturity and leaf spot tolerance within an advanced Georgia peanut breeding line. Peanut Sci., 22:106-108

Bromfield KR and Bailey WK. 1972. Inheritance of resistance to *Puccinia arachidis* in peanut. Phytopathology. 62:748.

Bruner AC, Jung S, Abbot AG and Powell GL. 2001. The naturally occurring high oleate oil character in some peanut varieties results from reduced oleoyl-PC desaturase activity from mutation of aspirate 150 to asparagines. Crop Sci., 41:522-526.

Bucheyeki TL, Shenkalwa EM, Mapunda TX and Matata LW. 2008. On-farm evaluation of promising groundnut varieties for adaptation and adoption in Tanzania. Afr. J. Agric. Res., 3(8):531-536.

Budiman MA, Jones JIT, Citek RW, Warek U, Bedell JA and Knapp SJ. 2006. Methylation-filtered and shotgun genomic sequences for diploid and tetraploid peanut taxa. http://www.ncbi.nlm.nih.gov/nucgss.

Burkey KO, Booker FL, Pursley WA and Heagle AS. 2007. Elevated carbon dioxide and ozone effects on peanut: II. Seed yield and quality. Crop sci., 47(4):1488-1497.

Byrum JR, Kinney AJ, Stecca KL, Grace DJ and Diers BW. 1997. Alteration of the omega-3 fatty acid desaturase gene is associated with reduced linoleic acid in the A5 soybean genotype. Theor. Appl. Genet., 94:356-359.

Canavar O. and Kaynak MA. 2010. Growing degree day and sunshine radiation effects on peanut pod yield and growth. African Journal of Biotechnology. 9(15):2234-2241.

Canvin DT. 1965. The effect of temperature on the oil content and fatty acid composition of the oils from several oil seed crops. Can. J. Bot., 43(1):63-69.

Channayya P, Hiremath, Nadaf HL and Keerthi CM. 2011. Induced genetic variability and correlation studies for yield and its component traits in Groundnut (*Arachis hypogaea* L.). Electronic J. Plant Breed., 2(1):135-142

Chavan RD, Toprope VN, Jagtap PK and Aglave BN. 2009. Stability analysis in groundnut for pod yield and its component traits. Int. J. Plant Sci., 4(2):531-534

Chen W, Jiao Y, Cheng L, Huang L, Liao B, Tang M, Ren X, Zhou X, Chen Y and Jiang H. 2016. Quantitative trait locus analysis for podand kernel-related traits in the cultivated peanut (*Arachis hypogaea* L.). BMC Genetics. 17(1) p.25.

Chen Z, Wang ML, Barkley NA and Pittman RN. 2010. A simple allele-specific PCR assay for detecting FAD2 alleles in both A and B genomes of the cultivated peanut for higholeate trait selection. Plant Mol. Biol. Rep., 28:542-548.

Chiteka ZA, Gorbet DW, Knauf DA, Shokes, FM and Kucharek TA. 1988. Components of resistance to late leaf spot in peanut II Correlations among components and their significance in breeding for resistance. Peanut Sci.,15:25-30.

Choudhary M, Sharma SP, Dashora A and Maloo SR. 2013. Assessment of genetic variability, correlation and path analysis for yield and its components in groundnut (*Arachis hypogaea* L.). J. Oilseeds Res., 30(2):163-166.

Chu Y, Ramos ML, Holbrook CC and Ozias-Akins P. 2009. Two alleles of *ahFAD2B* control the higholeic acid trait in cultivated peanut. Crop Sci., 49:2029-2036.

Chu YY, Wu CL, Holbrook CC, Tillman BL, Person G andOzias-Akins P. 2011. Marker-assisted selection to pyramid nematode resistance and the high oleic trait in peanut. Plant Genome. 4:110-117

Chunilal R, Rathnakumar AL, Hariprasanna K, Gor HK and Chikani BM. 2006. Early maturing groundnut advanced breeding lines with high day-1 productivity under rainfed situations. e-journal. icrisat.org 5(1):4.

Cobb WY and Johnson BR. 1973. Physico-chemical properties of peanuts. In: Peanut- Culture and Uses, American Peanut Research and Education Society, Stone Printing Co., Raonoke, USA. pp 209-261.

Cocharan WG and Cox GM. 1957. Experimental designs. John Wiley and sons, New York. pp 611.

Coffelt TA and Porter DM. 1986. Field screening of reciprocal Chico 9 Florigiant peanut populations for resistance to leaf spot in Virginia. Peanut Sci., 13:57-60.

Cooke RJ. 1995. Gel electrophoresis for the identification of plant varieties. J. Chromatography. 698:281-299.

Crossa J, Cornelius PL and Seyedsadr MS. 1996. Using the shifted multiplicative model cluster methods for crossover GE interaction. In: Kang, M.S. and Gauch, H.G., Jr (eds) Genotype-by-Environment Interaction. CRC Press, Boca Raton, Florida: 175–198.

Cuc LM, Mace ES, Crouch JH, Quang VD, Long TD and Varshney RK. 2008. Isolation and characterization of novel microsatellite markers and their application for diversity assessment in cultivated groundnut (*Arachis hypogaea* L.). BMC Plant Biol., 8:55.

Daetwyler HD, Pong-Wong R, Villanueva B andWoolliams JA. 2010. The impact of genetic architecture on genome-wide evaluation methods. Genetics. 185:1021-31.

DeLacy IH, Cooper M and Basford KE. 1996. Relationships among analytical methods used to study genotype-by-environment interactions and evaluation of their impact on response to selection. In: Kang, M.S. and Gauch, H.G., Jr (eds) Genotype-by-Environment Interaction. CRC Press, Boca Raton, Florida, pp 51-84.

Dellaporta SL, Wood J and Hicks JB. 1983. A plant DNA minipreparation: version II. Plant molecular biology reporter. 1(4):19-21.

Deshmukh SN, Basu MS and Reddy PS. 1986. Genetic variability character association and path coefficient of quantitative traits in Virginia bunch varieties of groundnut. Indian J. Agric Sci., 56:816-821.

Dolinassou S, Noubissié TJB, Djiranta AK and Njintang YN. 2016. Genotype × environment interaction and kernel yieldstability of groundnut (*Arachis hypogaea* L.) in Northern Cameroon. J App Biol Biotech. 4(01):001-007.

Dutton HJ, Lancaster CR, Evans CD and Cowan JC. 1951. The flavour problem of soybean oil: VII. Linoleic acid. J. American Oil Chem. Soc., 28:115-118.

Dwivedi SL, Jambunathan R, Nigam SN, Ragunath K, Ravishankar K and Nagabhushanam GVS. 1990. Relationship of seed mass to oil and protein content in *Arachis hypogaea* L. Peanut Sci., 17:48-52.

Dwivedi SL, Nigam SN, Jambunathan R, Sahrawat KL, Nagabhushanam GVS and Ragunath K. 1993. Effect of genotypes and environment on oil content (quality parameters and their correlation in peanut (*Arachis hypogaea* L.). Peanut Sci., 20:84-89

Dwivedi SL, Nagabhushanam GVS, Nigam SN, Ragunath K and Kambunathan R. 1994. Germplasm enhancement for seed quality traits in groundnut.Internat. Arch. News Lett., 14:14-15.

Dwivedi SL, Nigam SN, Nageswara Rao RC, Singh U and Rao KVS. 1996. Effect of drought on oil, fatty acids and protein contents if groundnut (*Arachis hypogaea* L.) Seeds. Field Crop Res., 48:125-133.

Dwivedi SL, Gurtu S, Chandra S, Yuejin W and Nigam SN. 2001. Assessment of genetic diversity among selected groundnut germplasm- I: RAPD analysis. Plant Breed., 120:345-349.

Dwivedi SL, Pande S, Rao JN and Nigam SN. 2002. Components of resistance to late leaf spot and rust among interspecific derivatives and their significance in a foliar disease resistance breeding in groundnut (*Arachis hypogaea* L.). Euphytica. 125:81-88.

Dwivedi SL and Nigam SN. 2005. Confectionery groundnuts: issues and opportunities to promote export and food uses in India. J. Oilseeds Res., 22:1-4.

East EM. 1916. Studies on flower size inheritance in Nicotiana. Genetica. 1:164-176.

Eberhart SA and Russell WA 1966. Stability parameters for comparing varieties. Crop Science. 6:36–40.

Emeroglu SH and Mortuary R. 1984. Productivity and quality properties of Turkish peanut selections in comparison to international varieties. Fette Seifen Anstrichm. 86:103-107.

Eskridge KM. 1996. Analysis of multiple environment trials using the probability of outperforming a check. In: Kang, M.S. and Gauch, H.G., Jr (eds) Genotype-by-Environment Interaction. CRC Press, Boca Raton, Florida, pp 273–307.

Evanno G, Regnaut S and Goudet J. 2005. Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. Molecular ecology. 14(8):2611-2620.

Falconer DS. 1981. Introduction to Quantitative Genetics, 2nd edition, Longman Group Limited, Longman Burnt Mills, Harlow, Essesc, England.

Falush D, Stephens M and Pritchard JK. 2003. Inference of population structure using multilocus genotype data: linked loci and correlated allele frequencies. Genetics. 164:1567-1587.

Falush D, Stephens M and Pritchard JK. 2007. Inference of population structure using multilocus genotype data: dominant markers and null alleles. Mol. Ecol. Notes 7:574-578.

FAOSTAT. 2014. Online Agriculture Statistics http/www.faostat.org.

Ferguson ME, Burow MD, Schulze SR, Bramel PJ, Paterson AH, Kresovich S and Mitchell S. 2004. Microsatellite identification and characterization in peanut (*A hypogaea* L.). Theor. Appl. Genet., 108:1064-1070.

Finlay KW and Wilkinson GN. 1963. The analysis of adaptation in a plant breeding program. Austr. J. Agric. Res., 14:742-754.

Fonceka D, Tossim HA, Rivallan R, Vignes H, Lacut E, De Bellis F, Faye I, Ndoye O, Leal-Bertioli SC, Valls JF, Bertioli DJ. 2012. Construction of chromosome segment substitution lines in peanut (*Arachis hypogaea* L.) using a wild synthetic and QTL mapping for plant morphology. PLoS One. 7(11):e48642.

Fore SP, Morris NJ, Mack CH, Freeman AF and Bickford WG. 1953. Factors affecting the stability of crude oils of 16 varieties of peanuts. J. Amer. Oilseed Chem. Soc., 30:298-301.

Gajjar KN, Mishra GP, Radhakrishnan T, Dodia SM, Rathnakumar AL, Kumar N, Kumar S, Dobaria JR and Kumar A. 2014. Validation of SSR markers linked to the rust and late leaf spot diseases resistance in diverse peanut genotypes. Aust. J. Plant Sci., 8(6):927-936.

Ganeshan K and Sudhakar D. 1995. Variability studies in Spanish bunch groundnut. Madras Agric. J., 82(5):395-397.

Gauch HG Jr and Zobel RW. 1996. AMMI analysis of yield trials. In: Kang, M.S. and Gauch, H.G., Jr (eds) Genotype-by Environment Interaction. CRC Press, Boca Raton, Florida, pp 85–122.

Gautami B, Fonceka D, Pandey MK, Moretzsohn MC, Sujay V, Qin H, Hong Y, Faye I, Chen X, Prakash AB, Shah TM, Gowda MVC, Nigam SN, Liang X, Hoisington DA, Guo B, Bertioli DJ, Rami JF and Varshney RK. 2012. An international reference consensus genetic map with 897 marker loci based on 11 mapping populations for tetraploid groundnut (*Arachis hypogaea* L.) PLoS ONE 7(7), e41213.

Gautami B, Ravi K, Narasu ML, Hoisington DA and Varshney RK. 2009. Novel set of groundnut SSR markers for germplasm analysis and interspecific transferability. Int. J. Integrative Biol., 7(2):100-106.

Ghosh AK and Biswas AK. 1995. Regulation of Correlative Senescence in *Arachis hypogaea* L. by source-sink alteration through physical and hormonal means. J. Agron. Crop Sci.,175(3):195-202.

Ghuge SS, Mayee CD, and Ghodbole GM. 1981. Assessment of losses in groundnut yield due to rust and Tikka leaf spots. Indian Phytopath., 34(2):179-182.

Gibbons RW. 1980. The ICRISAT Groundnut Program. In: Proceedings of International Workshop on Groundnuts, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Andhra Pradesh, India, October 13-17, pp 12-16.

Gimenes MA, Hosino AA, Barbosa AVG, Palmieri DA and Lopes CR. 2007. Characterization and transferability of microsatellite markers of cultivated peanut (*Arachis hypogaea*). BMC Plant Biol. 7(1):9.

Glaz B, Miller JD and Kang MS. 1985. Evaluation of cultivar-testing locations in sugarcane. Theoretical and Applied Genetics. 71:22–25.

Godfrey AI and Olorunju PE. 2009. Yield stability and resistance to leaf spot disease and rosette in Groundnut. Czech J Genet Plant Breed. 45(1):18-25.

Golakia PR, MakneVG and Monpara BA. 2005. Heritable variation and association in virginia runner and Spanish bunch group of groundnut. Nat. J. Plant Improv., 7(1):50-53.

Gorbet DW and Knauft DA. 1997. Registration of ‘SunOleic 95R’ peanut. Crop Sci., 37:1392.

Gorbet DW, Knauft DA and Shokes FM. 1990. Response of peanut genotypes with different levels of leaf spot resistance to fungicide treatments. Crop Sci., 30:529-533.

Gorbet DW, Stokes FM, Culbreath AK, Todd JM and Whitty ED. 1999. C-99R- a new multiple disease-resistant peanut cultivar Marianna, North Florida Res Ext Ctr Rept, pp 99.

Goswami BR, Kamdar JH and Bera SK. 2013. Molecular diversity and association of simple sequence repeat markers with kernel mass in cultivated groundnut (*Arachis hypogaea* L.). Aust J. Crop Sci., 7(8):1152-1159.

Gowda MVC, Motagi BN, Naidu GK, Diddimani SN and Sheshagiri R. 2002a. GPBD-4: a Spanish bunch groundnut genotype resistant to rust and late leaf spot. International *Arachis* Newsletters. 22:29-32

Gowda MVC, Motagi BN, Sheshagiri R, Naidu GK and Rajendraprasad MN. 2002b. Mutant 28-2: A bold seeded disease and pest resistant groundnut genotypes for Karnataka, India. International *Arachis* Newsletter, 22:16-17

Gowda MVC, Prabhu TG and Bhat RS. 1996. Variability and association of late leaf spot resistance and productivity in two crosses of groundnuts. Crop Improvement. 23(1):44-48.

Graces R, Sarmiento C, Mancha M. 1992. Temperature regulation of Oleate desaturase in sunflower (Helianthus annuus L.) seeds, Planta 186:461-465.

Gremillion SK, Culbreath AK and Gorbet DW. 2011. Field evaluation of leaf spot resistance and yield in peanut genotypes in the United States and Bolivia. Plant Disease, 95(3):263-268.

Groff JL, Gropper SS and Hunt SM. 1996. Lipid: In Advanced Nutrition and Human Metabolism, West Publishing Minneapolis/st. Paul M. N., pp 113-146.

Gupta PK, and Varshney RK. 2000. The development and use of microsatellite markers for genetic analysis and plant breeding with emphasis on bread wheat. Euphytica. 113:163-185.

Gupta SK, Gupta PO, Parashar RD and Sindhan GS. 1987. Fungicidal control of leaf spots and influence on quality of peanut. Indian Phytopathol. 40:360-364.

Gupta RP, Vachhani JH, Kachhadia VH, Vaddoria MA and Barad HR. 2015a.Correlation and path analysis in Virginia groundnut (*Arachis hypogaea* L.). Electronic J Plant Breed., 6(1):248-252.

Gupta RP, Vachhani JH, Kachhadia VH, Vaddoria MA and Bhatiya VJ. 2015b. Genetic divergence in Virginia groundnut (*Arachis hypogaea* L.). Electronic J. Plant Breed., 6(2):566-569.

Guy CB, Tony RL, Lan AG, James RL and Graham JK. 2007. Novel insights into seed fatty acid synthesis and modification pathways from genetic diversity and quantitative trait Loci analysis of the Brassica C Genome. Plant Physiol., 144:1827-1842.

Haldane JBS. 1947. The interaction of nature and nurture. Annals of Eugenics. 13:197–205.

Halward T and Stalker HT. 1987. Incompatibility mechanism in interspecific peanut hybrids. Crop Sci., 27:456-460.

Halward TM, Stalker HT, Larue EA, Kochert G. 1991. Genetic variation detectable with molecular markers among unadapted germ-plasm resources of cultivated peanut and related wild species. Genome.34(6):1013-1020.

Hamdan YA, Pérez-Vich B, Velasco L and Fernández-Martínez JM. 2009. Inheritance of high oleic acid content in safflower. Euphytica. 168(1):61-69.

Hamdan YA, García-Moreno MJ, Fernández-Martínez JM, Velasco L and Pérez-Vich B. 2012. Mapping of major and modifying genes for high oleic acid content in safflower. Molecular Breeding. 30(3):1279-1293.

Hammonds EG, Duvick D, Wang D, Dodo DH and Pittman RN. 1997. Survey of the fatty acid composition of peanut (*Arachis hypogaea* L.) germplasm and characterization of their epoxy and eicosenoin acids. J. Am. Oil Chem. Soc., 74:1235-1239.

Hanson GH, Robinson HF and Comstock RE. 1956. Biochemical studies of yield in segregating population of Korean Lespodzoa. Agron. J., 48:267-282.

Hardwick RC and Wood JT. 1972. Regression methods for studying genotype-environment interactions. Heredity 28:209-222.

Hariprasanna K, Chunilal and Radhakrishnan T. 2008. Genotype x environmental interaction and stability analysis in large seeded genotypes of groundnut, *Arachis hypogaea* L. J. Oilseeds Res., 25(2):126-131.

Harman HH. 1967. Modern factor analysis.2nd edition. University of Chicago Press.Chicago:124.

Harrison AL. 1973. Control of peanut leaf rust alone or in combination with *Cercospora* leaf spot. Phytopathology. 63 (6):668-673.

Hashim IB, Koehler PE, Eitenmiller RR and Kevin CK. 1993. Fatty acid composition and tocopherol content of drought-stressed Florunner peanuts. Peanut Sci., 20:21-24.

Hassan FU and Ahmed M. 2012. Oil and fatty acid composition of peanut cultivars grown in Pakistan, Pak. J. Bot., 44(2):627-630.

Hassan RM, and Beute MK. 1977. Evaluation of resistance to *Cercospora* leaf spot in peanut germplasm potentially useful in a breeding program. Peanut Sci., 4:78-83.

He G, Meng R, Newman M, Gao G, Pittman RN and Prakash CS. 2003. Microsatellites as DNA markers in cultivated peanut (*Arachis hypogaea* L.). BMC Plant Biol., 3:3-9.

Henderson MM. 1991. Correlations between fatty acid intake and cancer incidence. Health effects of dietary fatty acids. American Oil Chemist's Society, pp.136-149.

Henderson CR. 1975. Best linear unbiased estimation and prediction under a selection model. Biometrics. 31:423-447.

Herselman L. 2003. Genetic variation among Southern African cultivated peanut (A *hypogaea* L.) genotypes as revealed by AFLP analysis. Euphytica. 133:319-327.

Hinds ML. 1995.Fatty acid composition of Caribbean-grown peanuts (*Arachis hypogaea* L.) at three maturity stages. Food Chem., 55:7-14.

Holaday PE and Pearson JL. 1974. Effects of genotype and production area on the fatty acid composition, total oil, and protein in peanuts. J. Food Sci., 39:1206-1209.

Holbrook CC and Anderson WF. 1995. Evaluation of a core collection to identify resistant late leaf spot in peanut Crop Sci., 35:1700-1702.

Holbrook CC. and Isleib TG. 2001. Geographical distribution of genetic diversity in *Arachis hypogaea.* Peanut Sci., 28:80-84.

Holbrook CC and Dong W. 2005. Development and evaluation of mini core collection or US peanut germplasm collection. Crop Sci., 45:1540-1544.

Hopkins MS, Casa AM, Wang T, Mitchell SE, Dean RE, Kochert GD and Kresovich S. 1999. Discovery and characterization of polymorphic simple sequence repeats (SSRs) in peanut. Crop Sci., 39:1243-1247.

Iroume RN and Knauft DF. 1987. Heritability and correlations for pod yield and leaf spot resistance in peanut (*Arachis hypogaea* L.) implications for early generation selection. Peanut Sci., 14:46-50.

Islam MS and Rasul MG. 1998. Genetic parameters, correlations and path coefficient analysis in groundnut (*Arachis hypogaea* L.). Bangladesh. J. Scientific and Industrial Res., 33(2):250-254.

Iwo GA and Olorunju PE. 2009. Yield Stability and resistance to late leaf spot disease and Rosette in groundnut. Czech J. Genet. Plant Breed., 45(1):18-25.

Iwo GA, Idowu AA and Olorunji PE. 2002. Genotype × environment interaction for pod yield of groundnut varieties in southern Guinea savannah of Nigeria. Nigerian Journal of Genetics. 16 & 17:48-51.

Jakkeral SA, Nadaf HL, Gowda MVC and Bhat RS. 2013. Inheritance of rust resistance in cultivated groundnut (*Arachis hypogaea* L.). Indian J. Genet., 73(4):450-453.

Jakkeral SA, Nadaf HL, Gowda MVC, and Bhat RS. 2014. Marker detection and genetic analysis for rust resistance of recombinant and backcross inbred lines in groundnut. Indian J. of Genet. Pl. Breed., 74 (2):213-221.

Jambunathan RS, Madhusudana R and Shubhada PB. 1985. Analysis of oil content of groundnut by nuclear magnetic resonance spectrometry. J. Sci. Food Agric., 36:162-166.

Janila P, Nigam SN, Pandey MK, Nagesh P and Varshney RK. 2013a. Groundnut improvement: use of genetic and genomic tools. Frontiers in Plant Science. February 25; 4(a):23.

Janila P, Ramaiah VP, Rathore A, Rupakula A, Reddy KR, Waliyar F and Nigam SN. 2013b. Genetic analysis of resistance to late leaf spot in interspecific groundnuts. Euphytica.193:13-25.

Janila P, Pandey MK, Manohar SS, Murali TV, Premalatha NT, Nadaf HL and Varshney RK. 2016a. Foliar fungal disease-resistant introgression lines of groundnut (*Arachis hypogaea* L.) record higher pod and haulm yield in multi-location testing. Plant Breed. 135(3):355-366.

Janila P, Pandey MK, Yaduru Shasidhar, Murali T V, Mand Sriswathia, Khera P, Singh SM, Patne N, Vishwakarma MK, Mishra GP, Radhakrishnan T, Manivannan N, Dobariya KL, Vasanthi RP and Varshney RK. 2016b. Molecular breeding for introgression of fatty acid desaturase mutantalleles (*ahFAD2A* and *ahFAD2B*) enhances oil quality in high and low oil containing peanut genotypes. Plant Science. 242:203-213.

Jeong-Dong L, Melissa W, David AS, James RS, Vincent RP, Catherine NN and Grover S. 2009. Environmental effects on oleic acid in soybean seed oil of plant introductions with elevated oleic concentration. Crop Sci., 49:1762-1768.

Jogloy S, Wynne JC, Beute MK. 1987. Inheritance of late leaf spot resistance and agronomic traits in peanut. Peanut Sci., 14:86-90.

Jogloy S, Pensuk V, Patanothai A and Wongkaew S. 1999. Generation mean analyses of late leaf spot and rust resistance in peanut (*Arachis hypogaea* L.). Thai. J. Agric. Sci., 32:423-433.

Johansen WL. 1909. ElementadorexaktenErbik. Int. Jena :Gustav Tisher. pp 515.

John K, Vasanthi RP, Venkateswarlu O and Naidu PH. 2005a. Variability and correlation studies for quantitative traits in Spanish bunch groundnut (*Arachis hypogaea* L.) genotypes. Legume Res., 28:189-193.

John K, Vasanthi RP, Venkateswarlu O and Sudhakar P. 2005b.Genetic variability and correlation studies among F_1 and parents in groundnut (*Arachis hypogaea* L.). Legume Res., 28(4):262-267.

John K, Murali Krishna T, Vasanthi RP, Ramaiah M, Venkateswarlu O and Naidu HP. 2006. Variability studies in groundnut germplasm. Legume Res., 29 (3):219-220.

John K, Vasanthi RP and Venkateswarlu O. 2009.Studies on variability and association in Spanish bunch groundnut (*Arachis hypogaea* L.). Legume Res., 32(1):65-69.

Johnson HW, Robinson HF and Comstock RF. 1955. Estimation of genetic and environmental variability of soybean. Agron. J., 47:314-318.

Jung S, Swift D, Sengoku E, Patel M, Teule F, Powell G, Moore K, Abbott A. 2000a. The high oleate trait in the cultivated peanut [*Arachis hypogaea* L]. I. Isolation and characterization of two genes encoding microsomal oleoyl-PC desaturases. Mol. Gen. Genet., 263 (5):796-805.

Jung S, Powell G, Moore K and Abbott A. 2000b.The high oleate trait in the cultivated peanut [*Arachis hypogaea* L.]. II. Molecular basis and genetics of the trait, Mol.Gen. Genet., 263(5):806-811.

Jung S, Tate PL, Horn R, Kochert G, Moore K and Abbott AG. 2003. The phylogenetic relationship of possible progenitors of the cultivated peanut. J. Hered., 94:334-340.

Kale DM, Gadgil JD and Murthy GSS. 1998. Relationship between seed size, oil and protein contents in groundnut. J. Oilseeds Res., 5:170-175.

Kale DM, Badigannavar AM and Murthy GSS. 2000. Development of new large pod Trombay groundnut (*Arachis hypogaea*) selections. Ind. J. Agric. Sci., 70(6):365-369.

Kalmeshwar GP, Kenchangoudar PV, Parmshwarappa KG and Salimath PM. 2006. A study of correlation and path analysis in groundnut. Karnataka J. Agric Sci., 19:272-277.

Kameshwara RK, Burow MD, Gloria Burow, John Burke, and Naveen P. 2007. Molecular characterization of the U.S. Peanut Mini-Core collection using microsatellite markers. Crop Sci., 47:1718-1727.

Kang MS and Miller JD. 1984. Genotype × environment interactions for cane and sugar yield and their implications in sugarcane breeding. Crop Science. 24:435–440.

Kang MS. Miller JD and Darrah LL. 1987. A note on relationship between stability variance and ecovalence. Journal of Heredity. 78:107.

Kang MS. 1988. A rank-sum method for selecting high-yielding, stable corn genotypes. Cereal Research Communications. 16:113–115.

Kang MS. 1990. Genotype-by-Environment Interaction and Plant Breeding. Louisiana State University Agricultural Center, Baton Rouge, Louisiana.

Kang MS. 1993. Simultaneous selection for yield and stability in crop performance trials: consequences for growers. Agronomy Journal. 85:754–757.

Kang MS and Gauch HG Jr. 1996. Genotype-by-Environment Interaction. CRC Press, Boca Raton, Florida.

Kavani RH, Golakia PR, Makne VG and Madaria RB. 2004. Genetic variation and trait associations in Valencia groundnut (*Arachis hypogaea* L.). In: Proceedings of National symposium on enhancing productivity of groundnut for sustaining food and nutritional security, NRCG, Junagadh.

Kavera 2009. Oil quality improvement in groundnut (*Arachis hypogaea* L.) through induced mutagenesis. Ph.D. Thesis, Univ. Agric. Sci., Dharwad (India).

Kaveri SB, Nadaf HL, Vijayakumar AG and Salimath PM. 2008. Fatty acid profile of groundnut (*Arachis hypogaea* L.) cultivars. Crop Improvement. 35(1):61-65.

Khan A, Bano A, Bakht J, Khan SA, Malik NJ and Naz I. 2009. Response of exotic groundnut genotypes to environmental diversities at higher altitude of northern. Pakistan. Sarhad J. Agric., 25(4):545-550.

Khedikar YP, Gowda MVC, Sarvamangala C, Patgar KV, Upadhyaya HD and Varshney RK. 2010. A QTL study on late leaf spot and rust revealed one major QTL for molecular breeding for rust resistance in groundnut (*Arachis hypogaea* L.). Theor. Appl. Genet., 121:971-984.

Khedikar YP. 2008. Molecular tagging and Mapping of resistance to late leaf spot and rust in Groundnut (*Arachis hypogaea* L.). Ph. D. Thesis, Uni. Agric. Sci. Dharwad (India).

Khera P, Upadhyaya HD, Pandey MK, Roorkiwal M, Sriswathi M and Janila P. 2013. Single nucleotide polymorphism-based genetic diversity in the reference set of peanut (*Arachis* spp.) by developing and applying cost-effective competitiveallele-specific polymerase chain reaction genotyping assays. Plant Genome 6, 3 10.3835/plantgenome2013.06.0019.

Knauft DA and Norden AJ. 1983. Inheritance of rust resistance in peanuts. Proc Am Peanut Res Educ Soc 15:76.

Knauft DA, Norden AJ, Gorbet DW and Martin FG. 1987. Stability of market quality factors in peanut (*Arachis hypogaea* L.). Proc. Soil Crop Sci. Soc. Florida, 46:72-74.

Knauft DA. 1987. Inheritance of rust resistance in groundnut. In: Groundnut Rust Disease: Proc Discuss Group Meet. 24-28 September 1984, ICRISAT, Patancheru, AP 502324, India. pp 183-187.

Knauft DA, More K and Gorbet DW. 1993. Further studies on inheritance of fatty acid composition in peanut. Peanut Sci., 20:74-76.

Kocher G, Halward T, Branch WDand Simpson CE. 1991. RFLP variability in peanut (*Arachis hypogaea* L.) cultivars and wild species. Theor. Appl. Genet., 81:565-570.

Kochert GA, Stalker T, Gimenes M, Galgaro L, Lopes CR and Moore K. 1996. RFLP and cytogenic evidence on the origin and evolution of allotetraploid domesticated peanut *Arachis hypogaea* (*Leguminosae*). American. J. Botany., 83:1282-1291.

Kolekar RM, Sujay V, Kenta S, Sukruth M, Khedikar Y P, Gowda MVC, Pandey MK, Varshney RK and Bhat RS. 2016. QTL mapping for late leaf spot and rust resistance using an improved genetic map and extensive phenotypic data on a recombinant inbred line population in peanut (*Arachis hypogaea* L.). Euphytica. 209:147-156.

Korat VP, Pithia MM, Savaliya JJ, Pansuriya AG and Sodavadiya PR. 2009. Studies on genetic variability in different genotypes of groundnut (*Arachis hypogaea* L.). Legume Res., 32(3): 224-226.

Korat VP, Pithia MS, Savaliya JJ, Pansuriya AG and Sodavadiya PR. 2010. Studies on characters association and path analysis for Seed yield and its components in groundnut (*Arachis hypogaea* L.). Leg. Res., 33 (3):211-216.

Kornegay JL, Beute MK and Wynne JC. 1980. Inheritance of resistance to *Cercospora arachidicola* and *Cercosporidium personatum* in six Virginia-type peanut lines. Peanut Sci., 7:4-9.

Kotzamanidis ST, Stavropoulos N and Ipsilandis CG. 2006. A systematic analysis for grouping Greek peanut (*Arachis hypogaea* L.) germplasm based on eight important phenotypic traits. Asian J. Plant Sci., 5:481-486.

Krapovickas A. 1969. The origin, variability and spread of groundnut (*Arachis hypogaea* L.) In: Ucko PJ, Dimbley G (eds) The Domestication and Exploitation of Plants and Animals Duckworth, London, UK, pp 135-151.

Krapovickas A. 1973. Evolution of the genus *Arachis*.(In) Agricultural Genetics-Selected Topics, Edited by R. Moav. John Wiley & Sons, New York, USA. pp 135-151.

Krapovickas A and Gregory WC. 1994. Taxonomaadelgeneva *Arachis* (*Leguminosae*). Bon Plandia. 8:1-86.

Krapovickas A, Gregory WC. 2007. Taxonomy of the genus *Arachis* (*Leguminosae*) (Translated by DE Williams and CE Simpson). Bonplandia. 16:1205.

Krishna GK, Jinta Zhang, Mark Burow, Roy N, Pitman Stanko G, Delikostadinov Nazhilu YI and Puppala N. 2004. Genetic diversity analysis in Valencia peanut (*Arachis hypogaea* L.) using microsatellite markers. Cellular and Molecular Biology Letter. 9:685-697.

Kumar IS, Govindaraj M and Kumar VK. 2010. Estimation of genetic diversity of new breeding lines of groundnut (*Arachis hypogaea* L.). World J. Agril. Sci., 6(5):547-54.

Kusuma VP, Yugandhar G, Ajay BC, Gowda MVC and Upadhyaya HD. 2007. Identification of sources of multiple disease resistance in groundnut mini-core. In: Proceedings of the National Seminar on Challenges before India, Hyderabad, India. 29-31 Jan. 2007. Indian Society of Oilseeds Research, Rajendranagar, Hyderabad, India. P. 31-32.

Lakshmidevamma TN, Byre gowda M and Mahadevu P. 2004. Character association and path analysis in groundnut (*Arachis hypogaea* L.). Mysore Journal of Agricultural Sciences. 38(2):221-226.

Leal-Bertioli SCM, Jose ACVF, Alves-Freitas DMT, Moretzsohn MC, Guimaraes PM, Nielen S, Vidigal BS, Pereira RW, Pike J, Favero AP, Parniske M, Varshney RK and Bertioli DJ. 2009. Identification of candidate genome regions controlling disease resistance in *Arachis*. BMC Plant Biol. 9:112-123.

Liang X, Zhou G, Hong Y, Chen X, Liu H, Zhou G, Li S and Guo B. 2009. Utility of EST-derived SSR in cultivated peanut (*Arachis hypogaea* L.) and *Arachis* wild species. BMC Plant Biol., 9:35.

Liao B and Lei Y. 2004. A black seed coat groundnut cultivar Zhonghua 9 Released in china. Inter *Arachis* Newsletter. 24:29.

Liu K and Muse SV. 2005. PowerMarker: integrated analysis environment for genetic marker data. Bioinformatics. 21:2128-2129.

Lopez Y, Smith DD, Senseman SA and Rooney WL. 2001. Genetic factor influencing high oleic acid content in Spanish market type peanut varieties. Crop Sci., 41:51-56.

Lukange E, Labus Chang MT and Hugo A. 2007.The evaluation of oil and fatty acid composition in seed of cotton accession from various countries. J. Sci. Food Agri., 87:340-347.

Luo H, Ren X, Li Z, Xu Z, Li X, Huang L, Zhou X, Chen Y, Chen W, Lei Y and Liao B. 2017. Co-localization of major quantitative trait loci for pod size and weight to a 3.7 cM interval on chromosome A05 in cultivated peanut (*Arachis hypogaea* L.). BMC genomics. Jan 9;18(1):58.

Lush JL. 1945. Heritability of quantitative characters in farm animals. Proc. 8th Cong. Genet.Heriditas. 35:356-375.

Lynd JQ and Ansman TR. 1989. Effects of P, Ca with 4 K levels on nodule histology, nitrogenase activity, and improved Spanish peanut yields. J. Pl. Nutr., 12:65-84.

Mace ES, Buhariwalla KK, Buhariwalla HK and Crouch JH. 2003. A high-throughput DNA extraction protocol for tropical molecular breeding programs. Plant Molecular Biology Reporter, 21(4):459-460.

Mace ES, Phong DT, Upadhyaya HD, Chandra S and Crouch JH. 2006. SSR analysis of cultivated groundnut (*Arachis hypogaea* L.) germplasm resistant to rust and late leaf spot diseases. Euphytica. 152:317-330.

Mace ES, Varshney RK, Mahalakshmi V, Seetha K, Gafoor A, Leeladevi Y and Crouch JH. 2008. In silico development of simple sequence repeat markers within the aeschynomenoid/dalbergoid and genistoid clades of the Leguminosae family and their transferability to *Arachis hypogaea*, groundnut. Plant Science. 174(1):51-60.

Madhura C, Kenchanagoudar, Basamma PV, Sujay V. 2011. Morphological characterization of a mini-core subset in different botanical types of groundnut (*Arachis hypogaea* L.). Int. J. Plant Sci., 6:280-284.

Makhanlal, Roy D and Ojha OP. 2003. Genetic variability and selection response for root and other characters in groundnut (*Arachis hypogaea* L.). Legume Res., 26(2):128-130.

Makinde SCO and Ariyo OJ. 2010. Analysis of genotype × environment interaction of groundnut (*Arachis hypogaea* L.). Malays. J. Appl. Biol., 40(2):19-26.

Manivel P, Mathur RK, Bandyopadhyaya A, Samdur MY and Misra JB. 2000. Evaluation of some confectionary types advanced breeding lines of groundnut. Int. *Arachis* Newsletter., 20:20 – 21.

Manoharan V, Vindhiyavarman P and Ramalingam RS. 1990. Variability and correlation studies of kernel weight and related attributes in groundnut. Madras Agril. J., 77:9-12.

Marketta S, Joram K and Seppo N. 1989.Genetic and environmental variation in oil content and fatty acid composition of oats. Cereal Chem., 66 (4):296-300.

Martinez-Rivas LM, Gracia-Diaz MT and Mancha M. 2000. Temperature and oxygen regulation of microsomal oleate desaturase (FAD2) from sunflower. Biochem. Society., 28:890–892.

Mathur RK, ManivelP, KumarRV, KhanMA, Gor HK and Chikani BM. 1997. G x E interaction in certain Virginia and Spanish genotypes of groundnut. Ann. Agric. Res., 18:523-525.

Mayee CD. 1987. Diseases of groundnut and their management. In: Plant protection in field crops, (Eds.): M.V.N. Rao and S. Sitanantham, PPSI, Hyderabad. pp 235-243.

McDonald D, Subrahmanyam P, Gibbons RW and Smith DH. 1985. Early and late leaf spot of groundnut Information Bulletin No 21, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, AP, India.

Mehan VK, Reddy PM, Rao VK and McDonald D. 1994.Components of rust resistance in peanut genotypes. Phytopathology. 84:1421-1426.

Mehan VK, Reddy PM, Subrahmanyam P, McDonald D and Singh AK. 1996. Identification of new sources of resistance to rust and late leaf spot in peanut. Int. J. Pest Manag., 42:267-271.

Mekontchou T, Ngueguim M and Fobasso M. 2006. Stability analysis for yield and yield components of selected peanut breeding lines (*Arachis hypogaea* L.) in the North province of Cameroon. Tropicultura. 24(2):90-94.

Melouk HA, Banks DJ and Fanous MA. 1984. Assessment of resistance to *Cercospora arachidicola* in peanut genotypes in field plots. Plant Disease. 68:395-397.

Meuwissen THE, Hayes BJ, Goddard ME. 2001. Prediction of total genetic value using genome-wide dense marker maps. Genetics. 157:1819-1829.

Middleton K and Shorter R. 1987. Occurrence and management of groundnut rust in Australia. In Groundnut rust disease. Proceedings of a Discussion Group Meeting, 24-28 September 1984, ICRISAT, India. pp 73-75.

Minimol JS, Datke SB, Deshmukh SN and Satpute GN. 2000. Genotype x environment interaction in groundnut (*Arachis hypogaea* L.). Ann. Plant Physiol., 14 (1):74-79.

Mishra JB, Chauhan S and Mathur RS. 1992. variation in oil and protein contents in groundnut gerplasm. Groundnut News. 4:2-3.

Mohamed-Som, HZ. 1974. Chemical composition and flavour of Virginia-type peanuts. M.Sc. Thesis Department of Food Sci..N. C. State University, Raleigh.

Mohan B. 2002. Stability analysis for yield and confectionary characteristics in large seeded groundnut (*Arachis hypogaea* L.) genotypes M Sc (Agri) thesis submitted to Univ Agric Sci, Dharwad.

Mohan GB, Parameshwarappa KG and Malligwad LH. 2004. Stability analysis in large seeded groundnut genotypes for yield and its component traits. J. Oilseeds Res., 21 (1):17-20.

Moinuddin HH. 1997. Evaluation of Genotype × Environment interaction in Groundnut (*Arachis hypogaea* L.) genotypes MSc (Agri) thesis submitted to Univ Agric Sci, Bangalore.

Moinuddin HH, Reddy BGS, Lohithaswa HC, Sheriff RA, Kulkarni RS and Patil BR. 1998. Stability for yield and its components in groundnut (*Arachis hypogaea* L.). J. Oilseed Res., 15:238-241.

Mondal S, Anand, Badigannavar M and Murty GSS. 2007. RAPD markers linked to a rust resistance gene in cultivatedgroundnut (*Arachis hypogaea* L.). Euphytica. 159:233-239.

Mondal S and Badigannavar AM. 2010. Molecular diversity and association of SSR markers to rust and late leaf spot resistance in cultivated groundnut (*Arachis hypogaea*L.). Plant Breed. 129:68-71

Mondal S, Badigannavar AM and D'Souza SF. 2012. Development of genic molecular markers linked to a rust resistance gene in cultivated groundnut (*Arachis hypogaea* L.). Euphytica. 188:163-173.

Moore KM and Knauft DH. 1989. The inheritance of high oleic acid in Peanut. J. Hered., 80:252-253.

Moore LN, Moore KM, Sims CA, and Knauft DA. 1989. Characterization of a high oleic acid peanut. Inst. Food Tech. Abstr., 50:193.

Moretzsohn MC, Hopkins, MS Mitchell SE, Kresovich S, Valls JFM and Ferreira ME. 2004. Genetic diversity of peanut (*Arachis hypogaea* L.) and its wild relatives based on the analysis of hypervariable regions of the genome. BMC Plant Biol., 4:11-20.

Moretzsohn MC, Leoi L, Proite K, Guimara PM, Leal-Bertioli SCM, Gimenes MA, Martins WS, Valls JFM, Grattapaglia D and Bertioli DAJ. 2005. Microsatellite-based, gene-rich linkage map for the AA genome of *Arachis* (*Fabaceae*). Theor. Appl. Genet., 111:1060-1071.

Motagi BN, Gowda MVC and Sheshagiri. 1996. Mutants resistant to foliar diseases in groundnut (*Arachis hypogaea* L.). Current Science. 71(7):10.

Motagi BN, Gowda MVC and Nigam SN. 2000a. Oil recovery and quality influenced by foliar diseases in groundnut. International *Arachis* Newsletters. 20:582-584

Motagi BN, Gowda MVC and Naidu GK. 2000b. Inheritance of late leafspot resistance in groundnut mutants. Indian J. Genet., 60:347-352.

Motagi BN, Gowda MVC and Nigam SN. 2005. Fatty acid composition, oil quality and oil yield in foliar disease resistant groundnut genotypes. Karnataka J. Agri. Sci., 18:660-663.

Mothilal A, Vindhiya VP, Manivannan N. 2010a. Genotype × environment for kernel yield in groundnut (*Arachis hypogaea* L.). Electronic J. Plant Breed., 1(5):1306-1308.

Mothilal A, Vindhiyavarman P and Manivannan N. 2010b. Stability analysis of foliar disease resistant groundnut genotypes (*Arachis hypogaea* L.). Elect J. Pl. Breed., 1(4):1021-1023.

Mounts TL, Warner K, List GR, Kleiman R, Fehr WR, Hammond EG and Wilcox JR. 1988. Effect of altered fatty acid composition on soybean oil stability. J. American Oil Chem. Soc., 65:624-628.

Mozingo RW and Steele JL. 1982. Fatty acid composition of peanut genotypes in the Virginia-Carolina production area. Proc. Am. Peanut Res. Soc., 14:7-11.

Mukri G, Nadaf HL, Ramesh SB, Gowda MVC, Upadhyaya HD and Sujay V. 2012. Phenotypic and molecular dissection of ICRISAT mini core collection of peanut (*Arachis hypogaea* L.) for high oleic acid. Plant Breed.Doi:10.1111/j.1439-0523.2012.01970.x.

Mukri G, Nadaf HL, Gowda MVC, Bhat RS and Upadhyaya HD. 2014. Genetic diversity analysis based on nutritional, oil quality and yield component traits in mini core collection of groundnut. Karnataka Journal of Agricultural Sciences. 27(02):219-221.

Murray MG and Thompson WF. 1980. Rapid isolation of high molecular weight plant DNA. Nucleic acids research. 8(19):4321-4326.

Nadaf HL and Habib AF. 1987. Studies on genetic variability in bunch groundnut. Mysore J. Agril. Sci., 21 (3):297-301.

Nadaf HL, Gowda MVC, Bhat RS and Upadhyaya HD. 2014. Genetic diversity analysis based on nutritional, oil quality and yield component traits in mini core collection of groundnut. Karnataka J. Agric. Sci., 27(2):219-221.

Nagaraj G, Chauhan S and Ravinada V. 1989. Peanut composition and oil quality as influenced by genotype and harvest stages. Journal of the Oil Technologists' Association of India. 21(3):60-63.

Nagy ED, Chu Y, Guo YF, Khanal S, Tang S, Li Y, Dong WB, Timper P, Taylor C, Ozias-Akins P, Holbrook CC, Beilinson V, Nielsen NC, Stalker HT and Knapp SJ. 2010. Recombination is suppressed in an alien introgression in peanut harboring Rma, a dominant root-knot nematode resistance gene. Mol. Breeding., 26:357-370.

Naidu PH and Vasanthi RP. 1995. Influence of sowing dates on Tikka leaf spot in rabi and summer peanut (*Arachis hypogaea* L.). Legum Res., 25:275–281.

Narasimhulu R, Kenchanagoudar PV, Gowda MVC and Sekhar L. 2013. Genetic variability and correlation studies for selection of multiple disease resistance lines in two crosses of peanut. Bioinfolet. 10(1B):183-186.

Nautiyal PC, Bandyopadhyay A and Zala PV. 2001. In situ sprouting and regulation of fresh-seed dormancy in Spanish type groundnut (*Arachis hypogaea* L.). Field Crops Research. 70(3):233-241.

Nautiyal PC, Ravindra V, Rathnakumar AL, Ajay BC and Zala PV. 2012. Genetic variations in photosynthetic rate, pod yield and yield components in Spanish groundnut cultivars during three cropping seasons. Field Crops Res., 125:83-91.

Nawade B, Bosamia TC, Thankappan R, Rathnakumar AL, Kumar A, Dobaria JR, Kundu R, Mishra GP. 2016. Insights into the Indian peanut genotypes for ahFAD2 gene polymorphism regulating its oleic and linoleic acid fluxes. Frontiers in Plant Sci., 7:1271.

N'Doye O and Smith OD. 1992. Flowering pattern and fruiting characteristics of five short growth duration peanut lines. Oleagineux. 47:235-240

Nelson-Ehle H. 1909. Kreuzung, untersunchungen an Hafer and Weizenjunds. Univ. Asserter, N.F. Afala, 2:1-22.

Nevill DJ. 1982. Inheritance of resistance to *Cercosporidiumpersonatum* in groundnuts: a genetic model and its implications for selection. Oleagineux. 37:355-362.

Nigam SN, Dwivedi SL and Gibbons RW. 1991. Groundnut breeding: constraints, achievements and future possibilities. In Plant Breeding Abstracts. 61(10):1127-1136.

Nigam SN, Hildebrand GL, Bock KR, Ismael FM, Govinden N, Subrahmanyam, P and Reddy LJ. 1998. Registration of ICGV-SM 85048 Peanut Germplasm. Crop Sci., 38(2):572-573.

Nigam SN and Dwivedi SL. 2000. Enhanced resistance to leaf spot in cultivated groundnut on a partially-resistant peanut cultivar ICRISAT-Patancheru, Indian Soil and Crop Sci. Soc. Fla. Proc., 50:37-40.

Nigam SN. 2000. Some strategic issues in breeding for high and stable yield in groundnut in India. J. Oilseeds Res., 17:1-10.

Nigam SN, Prasada Rao RD, Mathur BP and Sharma KK. 2012. "Genetic management of virus diseases in peanut" in Plant Breeding Reviews, Vol. 36, ed. J. Janick (New York:John Wiley & Sons, Inc./Wiley-BlackwelL.). 293–356.

Norden AJ, Gorbet DW, Knauft DA and Young CT. 1987. Variability in oil quality among peanut genotypes in the Florida breeding program. Peanut Sci., 4, 7-11.

Ntare BR and Williams JH. 1998. Heritability and genotype × environment interaction for yield and components of a yield model in segregating populations of groundnut under semi-arid conditions. Afr. Crop Sci. J., 6(2):119-127.

Nunes da Luz L. Cavalcanti dos Santos R and Albuquerque Melo Filho P. 2011. Correlations and path analysis of peanut traits associated with the peg. Crop Breeding and Applied Biot., 11(1):88-93.

O'Keefe SF, Wiley VA, and Knauft DA. 1993. Comparison of oxidation stability of high and normal oleic peanutoils. J. American Oilseed Chem., 70:489-492.

Ohlrogge JB. 1994. Design of new plant products; Engineering of fatty acid metabolism. Pl. Physiol., 104:821-826.

Oliva ML, Shannon JG, Sleper DA, Ellersieck MR, Cardinal AJ, Paris RL, Lee JD. 2006. Stability of Fatty Acid Profile in Soybean Genotypes with Modified Seed Oil Composition. Crop Sci., 46:2069-2075.

Ory RL, Crippen KL and Lovegren NV. 1992. Off flavors in foods and beverages, Elsevier Science Publishers, New York.

Padmaja D, Brahmeswara Rao, Eswari KB and Reddy SM. 2013. Genetic variability, heritability for late leaf spot tolerance and productivity traits in a Recombinant Inbred Line population of groundnut (*Arachis hypogaea* L.). IOSR J Agric and Vet Sci. (IOSR-JAVS). 5(1):36-41.

Palmieri DA, Bechara RA, Curi MA, Gimenes and Lopes CR. 2005. Novel polymorphic microsatellite markers in section Caulorrhizae (*Arachis, Fabaceae*). Mol. Ecol. Notes., 5:77-79.

Pancholy SL, Despande AS and Krall S. 1978. Amino acids, oil and protein content of some selected peanut cultivars. American Peanut Research and Education Association. 10:30-37.

Pandey MK, Goutami B, Jayakumar T, Srishwathi M, Upadhyaya HD, Gowda MVC, Radhakrishnan T, Bertioli DJ, Knapp SJ, Cook DR and Varshney RK. 2012. Highly informative genic and genomic SSR markers to facilitate molecular breeding in cultivated groundnut (*Arachis hypogaea*). Plant Breed. 131:139-147.

Pandey MK, Upadhyaya HD, Rathore A, Vadez V, Sheshshayee MS, Sriswathi M, Mansee G, Kumar A, Gowda MVC, Sharma S, Hamidou F, Kumar VA, Khera P, Bhat RS, Khan AW, Singh S, Hongjie Li, Emmanuel M, Nadaf HL, Mukri G, Jackson SA, Baozhu G, Liang X and Varshney RK. 2014a. Genome-wide Association Studies for 50 Agronomic Traits in Peanut Using the 'Reference Set' Comprising 300 Genotypes from 48 Countries of the Semi-Arid Tropics of the World. PLoS ONE 9(8):e105228.

Pandey MK, Wang ML, Qiao L, Feng S, Khera P, Wang H, Tonnis B, Barkley NA, Wang J, Holbrook CC and Culbreath AK. 2014b. Identification of QTLs associated with oil content and mapping FAD2 genes and their relative contribution to oil quality in peanut (*Arachis hypogaea* L.). BMC genetics, 15(1), p.133.

Pandey MK, Wang H, Khera, P, Vishwakarma MK, Kale SM, Culbreath AK, Holbrook CC, Wang X, Varshney RK and Guo B. 2017. Genetic Dissection of Novel QTLs for Resistance to Leaf Spots and Tomato Spotted Wilt Virus in Peanut (*Arachis hypogaea* L.). Front. Plant Sci., 8:25.doi:10.3389/fpls.2017.00025.

Paramasivam JM, Jayasekhar M, Rajasekharan R and Veerabadhiran P. 1990. Inheritance of rust resistance in groundnut (*Arachis hypogaea* L.). Madras Agric. J., 77:50-52.

Parmar DH, Rathnakumar AH and Bharodia PS. 2000. Genotypic and interrelationship of oil and protein contents in crosses involving confectionery genotypes of groundnut. Internat. *Arachis* News Letter., 20:17-18.

Parmar DL, Ratna Kumar and Bharodia PS. 2002. Genetics and interrelationship of oil and protein content in crosses involving confectionary genotypes of groundnut (*Arachis hypogaea* L.). J. Oilseeds Res., 19:32-34.

Parameshwarappa KG and Kumar GB. 2007. Genetic analysis of pod yield and other confectionary traits in large seeded groundnut (*Arachis hypogaea* L.). J. Oilseeds Res., 24(3):237-240.

Parmeshwarappa KG, Malabasri. TA and Lingaraju BS. 2008. Analysis of correlation and path analysis among yield attributing traits in 2 crosses of large-seeded groundnut. J. Oilseed. Res., 25(1):4-7.

Pathirana R. 1993. Yield component analysis of bunch groundnut (*Arachis hypogaea* L. spp. *fastigata*) germplasm in Srilanka. Trop. Agric., 70(3):256-259.

Patil AS, Nandanwar HR, Punewar AA and Shah KP. 2014. Stability for yield and its component traits in groundnut (*Arachis hypogaea* L.). Int. J. of Bio-resource and Stress Management., 5(2):240-245.

Patra GJ and Mohanty JK. 1987. Stability of cross-derivatives of groundnut. Indian J. Agric. Sci., 57:51-56.

Patra GJ, Kar BB and Parhi G. 1995. Phenotypic stability for yield and quality factors in Spanish bunch groundnut (*Arachis hypogaea*subsp*fastigiata* var *vulgaris*). Indian J. Agric. Sci. 65(8):584-587.

Peakall R and Smouse PE 2006. GENALEX 6:genetic analysis in Excel. Population genetic software for teaching and research. Molecular Ecology. 6:288-295.

Pensuk V, Patanothai A, Jogloy S, Wongkaew S, Akkasaeng C and Vorasoot N. 2003. Reaction of peanut cultivars to late leaf spot and rust. Songklanakarin J. Sci. Technol., 25(3):289-295.

Perrier X and Jacquemoud-Collet JP. 2006. DARwin software.

Picket TA and Holley KT. 1951. Susceptibility of types of peanuts to rancidity development. J. Amer. Oil Chem. Soc., 28:478-479.

Powers L. 1942. The nature of the series of environmental variance and the estimation of genetic variances and geometric means of crosses involving species of Lycopersicum. Genetica. 27:561-575.

Prabhu R, Manivannan N, Mothilal A and Ibrahim SM. 2014. Magnitude and direction of association for yield and yield attributes in groundnut (*Arachis hypogaea* L.). Elect. J. Pl. Breed., 5(4):824-827.

Prabhu R, Manivannan N, Mothilal A and Ibrahim SM. 2015. Correlation coefficient analysis for yield and yield attributes in groundnut (*Arachis hypogaea* l.). Plant Archives. 15(2):685-689.

Pradhan K, Das PK and Patra RK. 2010. Genotype × environment interaction for pod yield and components of groundnut varieties in warm sub-humid climate and moderately acidic soil. Ind. J. Genet. 70(2):201-203.

Prakash BG, Khanare SK and Sajjanavar GM. 2000. Variability studies in spreading groundnut. Karnataka J. Agric. Sci., 13(4):988-990.

Prasad PVV, Craufurd PQ, Kakani VG, Wheeler TR and Boote KJ. 2001. Influence of high temperature during pre-and post-anthesis stages of floral development on fruit-set and pollen germination in peanut. Functional Plant Biology. 28(3):233-240.

Prathiba KM and Uma MR. 1994. Nutrient composition of groundnut cultures (*Arachis hypogaea* L.) in relation to their kernel size. Pl. Foods Human Nut., 45:365-369.

Pritchard JK, Stephens M, Rosenberg NA, and Donnelly P. 2000. Association mapping in structured populations. Am. J. Hum. Genet., 67:170-181.

Proite K, Leal-Bertioli SC, Bertioli DJ, Moretzsohn, MC, da Silva FR, Martins NF and Guimaraes PM. 2007. ESTs from a wild *Arachis* species for gene discovery and marker development. BMC Plant Biol., 7:7.

Punto NG and Lantinan RM. 1982. Genotype x Environment interaction for yield in field legumes:I Peanut, *Arachis hypogaea* L. Phillipp J. Crop Sci., 7(2):94-100.

Pushkaran K and Nair GV. 1993. Correlation studies in groundnut. J. Trop. Agric., 31:155-160.

Rabiei Z, Tahmasebi-Enferadi S, Giovanardi R and Vannozzi GP. 2007. Linolenic acid synthesis pathway: high and low oleic acid sunflower inbred lines after seeding. Current Advances in the Biochemistry and Cell Biology of Plant Lipids, pp199-202.

Raheja RK, Batta SK, Ahuja KL, Labana KS and Singh M. 1987. Comparison of oil content and fatty acid composition of peanut genotypes differing in growth habit. Pl. Foods Human Nutr., 37:103-108.

Rajgopal K, Chandran Misra, Bhalodia JB and Mathur RS. 2000. Evaluation of bold seeded groundnut association for confectionary attributes. Int. *Arachis* Newsletter,. 20:18-21.

Rasheed B, Rasheed H, Farid Abid UR and Khan A. 2015. Characters association and path analysis of peanut (*Arachis hypogaea* L.) for pod yield. J. Agric. Sci. and Res. , 2(1):79-84.

Ravi K, Vadez V, Isobe S, Mir RR, Guo Y, Nigam SN, Gowda MVC, Radhakrishnan T, Bertioli DJ, Knapp SJ, and Varshney RK. 2011. Identification of several small main-effect QTLs and a large number of epistatic QTLs for drought tolerance related traits in groundnut (*Arachis hypogaea* L.). Theor. Appl. Genet., 122:1119-1132.

Reddi MV, Reddy KR, Reddy KHP and Rao JA. 1991. Heritability, genetic advance and character association in groundnut over three environments. J. Maharashtra Agric. Univ., 16(3):383-385.

Reddy KHP. 1994. Variation in Spanish groundnut collection. J. Maharashtra Agric. Univ., 19 (3):423.

Reddy KR and Gupta RVS. 1992. Variability and inter-relationship of yield and its component characters in groundnut. J. Maharashtra Agric. Univ., 17(2):224-226.

Reddy LJ, Nigam SN, Dwivedi SL and Gibbons RW. 1987. Breeding groundnut cultivars resistant to rust (*Puccinia arachidis* Speg.). In:Groundnut Rust Disease; Proc. a Discussion Group Meeting, 24-28 September 1984, International Crops Research Institute for Semi-Arid Tropics, Patancheru, Andhra Pradesh, India. pp17-25.

Reddy LJ, Nigam SN and Reddy AGS. 1995. Stability of pod yield in foliar disease-resistant groundnut varieties. International *Arachis* Newsletter. (15):9-11.

Reddy PS. 1988. Groundnut, Indian council of Agricultural Research, pp 200-318

Reddy SBG.Moinuddin HH and Chenna Keshava BC. 2001. Variability studies in groundnut crosses across environment. In:National symposium on pulses and oilseeds for sustainable Agriculture. pp 59.

Ren X, Jiang H, Yan Z, Chen Y, Zhou X, Huang Li, Lei Y, Huang J, Yan L, Qi Y, Wei W and Liao B. 2014. Genetic Diversity and Population Structure of the Major Peanut (*Arachis hypogaea* L.) Cultivars Grown in China by SSR Markers. PLoS ONE.9 (2):e88091.

Reys GM and Romasata R. 1940. Varietal susceptibility of peanuts to black spot *Cercospora* perrorala. (Berk) Philippines J. Agric., 11:371-381.

Robinson HF, Comstoc RF and Harrey PH. 1949.Estimates of heritability and degree of dominance in corn. Agric. J., 41:353-359.

Roy D, Patel RK and Ojha OP. 2003. Study on podding index and other traits in groundnut (*Arachis hypogaea* L.). Legume Res., 26(4):310-312.

Sadeghi SM, Javid F and Niyaki SAN. 2011. Assessment of genetic diversity in peanut (*Arachis hypogaea* L.) genotypes using quantitative traits by cluster analysis method. Res. J. Biol. Sci., 6:293-297.

Sadhna K and Snehalatha R. 1998. Oil and protein quality of the selected groundnut varieties. J. Oilseeds Res., 15:339-342.

Salako EA and Adu JK. 1990. Effect of foliar fungicides on foliar diseases and pod, haulm and plant crude protein yields of groundnut. Tropical Pest Management. 36:4, 380-383.

Sanders TH. 1982. Peanut triacylglycerols: effect of season and production location. Journal of the American Oil Chemists' Society. 59(8):346-351.

Sarvamangala SC. 2009. Construction of genetic linkage map and QTLanalysis for foliar disease resistance, nutritional quality and productivity traitsin groundnut (*Arachis hypogaea* L.). Ph.D. Thesis, University of AgriculturalSciences, Dharwad.

Sarvamangala C, Gowda MVC and Nadaf HL. 2010. Genetic variation and association pattern among nutritional traits in recombinant inbred lines of groundnut (*Arachis hypogaea* L.). Indian J. Genet., 70(1):37-43.

Sarvamangala C, Gowda MVC and Varshney RK. 2011. Identification of quantitative trait loci for protein content, oil content and oil quality for groundnut (*Arachis hypogaea* L.). Field Crop Res., 122 (1):49-59.

SAS Institute Inc. 2013. SAS/STAT® 12.3 User's Guide. Cary, NC.

Savary S, Rao PV and Zadoks JC. 1989. A scale of reaction types of groundnut to *Puccinia arachidis* Speg. Journal of phytopathology, 124(3):259-266.

Savitzky A and Golay MJE. 1964. Smoothing and differentiation of data by simplified least squares procedures. Analytical Chemistry. 8:1627-1639.

Seijo JG, Lavia GI, Fernandez A, Krapovickas A, Ducasse D and Moscone EA. 2004. Physical mapping of the 5S and 18S-25S rRNA genes by fish as evidence that *Aduranensis* and *A ipaensis* are the wild diploid progenitors of A *hypogaea.* Am. J. Bot. 91:1294-1303.

Sekhon KS, Gupta SK, Ahuja KL and Jaswal SV. 1980. Variability in fatty acid composition in semi-spreading peanut types. Oleagineux. 35:409-411.

Selvaraj MG, Narayana M, Schubert AM, Ayers JL and Baring MR. 2009.Identification of QTLs for pod and kernel traits in cultivated peanut by bulked segregant analysis. Electronic J. Biotechnol., 12:DOI:10.2225/vol12.

Senapathi BK and Roy K. 1991. Stability analysis for pod yield and maturity of groundnut. Crop Res., 4(2):253-257.

Senapati BK and Roy K. 1998. Correlation coefficients among stability parameters of yield and yield contributing characters in groundnut (*Arachis hypogaea* L.). Legume Res., 21:37-40.

Senath PH and Sokal RR. 1973. Numerical taxonomy. The principles and practice of numerical classification. San Francisco: Freeman p573.

Serraj R, Bidinger FR, Chauhan YS, Seetharama N, Nigam SN and Saxena NP. 2003. Management of drought in ICRISAT cereal and legume mandate crops. Water Productivity in Agriculture: Limits and Opportunities for improvement. CABI Publishing, Wallingford, UK, pp127-144.

Sharma SB and McDonald D. 1990. Global status of nematode problems of groundnut, pigeonpea, chickpea, sorghum and pearl millet and suggestion for future work. Crop Prot., 9:453–458.

Sharma VK and Varshney SK. 1995. Analysis of harvest index in groundnut. J. Oilseeds Res., 12(2):171-175.

Shenk JS and Westerhaus MO. 1993. Analysis of agriculture and food products by near infrared reflectance Spectroscopy.Monograph.Infrasoft International (ISI), Port Matilda, PA, 26 pp 44-51.

Shenk JS and Westerhaus, MO. 1995. Routine operation, calibration, development and network system management manual. NIRSystems Inc., Silver Spring, MD, USA.

Shirasawa K, Koilkonda P, Aoki K, Hirakawa H, Tabata S and Watanabe M. 2012. In silico polymorphism analysis for the development of simple sequence repeat and transposon markers and construction of linkage map in cultivated peanut. BMC Plant Biol 12:80.

Shoba D, Manivannan N and Vindhiyavarman P. 2009. Studies on variability, heritability and genetic advance in groundnut (*Arachis hypogaea* L.). Electronic J. Plant Breed., 1:74-77.

Shoba D, Manivannan N. and Vindhiyavarman P. 2010. Genetic diversity analysis of groundnut genotypes using SSR markers., Electronic J. Plant Breed., 1(6):1420-1425.

Shoba D, Manivannan N and Vindhiyavarman P. 2012a. Correlation and path coefficient analysis in groundnut (*Arachis hypogaea* L.). Madras Agric. J., 99(1-3):18-20.

Shoba D, Manivannan N, Vindhiyavarman P and Nigam SN. 2012b. SSR markers associated for late leaf spot disease resistance by bulked segregant analysis in groundnut (*Arachis hypogaea* L.). Euphytica. 188:265-272.

Shridevi A, Jakkeral, Nadaf HL and Gowda MVC. 2014. Genotypic variability for yield, its component traits, and rust resistance in recombinants of groundnut (*Arachis hypogaea* L.). Karnataka J. Agric. Sci., 27(1):71-73.

Shukla GK. 1972. Some statistical aspects of partitioning genotype–environmental components of variability. Heredity 29:237–245.

Simpson CE, Baring MR, Schubert AM, Melouk HA, Black MC, Lopez, YKA and Keim A. 2003. Registration of 'Tamrun OL_{01}' peanut. Crop Sci., 43:2298.

Singh AK, Subrahmanyam P and Moss JP. 1984. The dominant nature of resistant to *Puccinia arachidis* in certain wild *Arachis* species. Oleagineux. 39:535-538.

Singh AK, Moss JP and Rao BG. 1987. Incorporation of rust resistance from wild *Arachis* species into cultivated groundnut. In: Groundnut Rust Disease: Proc Discuss Group Meet. 24-28 September, 1984, ICRI SAT, Patancheru, AP 502324, India. pp 41-48.

Singh AK and Simpson CE. 1994. Biosystematics and genetic resources In: Smartt J (ed) The Groundnut Crop: A Scientific Basis for Improvement Chapman and Hall, London, UK, pp 96-137.

Singh AK, Mehan VK and Nigam SN. 1997. Sources of resistance to groundnut fungal and bacterial diseases: an update and appraisal. Information Bulletin no. 50. International Crops Research Institute for the Semi-Arid Tropics, Hyderabad, p 48.

Singh JP and Sinha PK. 1993. Stability analysis for yield and quality characters in groundnut (*Arachis hypogaea* L.). Ind. J. Genet. & Pl. Breed., 53(1):97-98.

Singh RK and Chaudhary BD. 1977. Biometrical methods in quantitative genetic analysis. pp 318.

Singh SB and Singh JP. 2001. Genotype x environment interaction effects in groundnut (*Arachis hypogaea* L.) tested in mid-western plain zone of Uttar Pradesh. Indian J. Agril. Sci., 71 (2):126-127.

Singh SB and Chaubey AK. 2003. Variability and association amongst quantitative characters in peanut (*Arachis hypogaea* L.). New Agri., 14:97-101.

Slack CR and Browse JA. 1984. Synthesis of storage lipids in developing seeds, In D.R. Murray (ed.) Seed Physiology. Academic Press Inc., Orlando, FL. pp 209-244.

Smous TH. 1979. A review of soybean oil reversion flavor. J. American Oil Chem. Soc., 56:403-409.

Stalker HT and Simpson CE. 1995. Genetic resources in *Arachis* In: Pattee, H E and Stalker, H T (eds) Advances in Peanut Science, American Peanut Research Education Society, Stillwater, UK, pp 14-53.

Subrahmanyam P, McDonald D, Gibbons RW, Nigam SN and Nevill DJ. 1982. Resistance to rust and late leaf spot diseases in some genotypes of *Arachis hypogaea*. Peanut Sci., 9:6-10.

Subrahmanyam P, Moss JP and Rao VR.1983a. Resistance to peanut rust in wild *Arachis* species. Plant Dis 67:209-212.

Subrahamanyam P, McDonald D, Gibbons RW and Subbarao PV.1983b. Components of resistance to *Puccinia arachidis* in peanut. Phytopathology. 73:253-256.

Subrahmanyam P, Williams JH, McDonald D and Gibbons RW. 1984. The influence of foliar diseases and their control by selective fungicides on a range of groundnut genotypes. Ann. Appl. Biol., 104:467-476.

Subrahmanyam P, Ghanekhar AM, Nolt BL, Reddy DVR and McDonald D. 1985a. Resistance to groundnut diseases in wild *Arachis hypogaea*, In: Proc. of Intern, Workshop on Cytogenetics of *Arachis*, 31 Oct-Nov. 1983, ICRISAT, Patancheru, India. pp 55-59.

Subrahmanyam P, Reddy LJ, Gibbons RW and McDonald D. 1985b. Peanut rust: A major threat to peanut production in the semi-arid tropics. Plant Dis., 69:813-819.

Subrahmanyam P and McDonald, D. 1987. Groundnut Rust Disease: Epidemiology and Control In: Groundnut rust disease [*Pucciniaarachidis*]: proceedings of a Discussion Group Meeting, 24-28 Sep 1984, ICRISAT Patancheru, India.

Subrahmanyam P, Rao VR, McDonald D, Moss JP and Gibbons RW. 1989. Origins of resistance to rust and late leaf spot in peanut (*Arachis hypogaea* L.). Econ. Botany., 43:444-455.

Subrahmanyam P, McDonald D, Reddy LJ, Nigam SN and Smith DH. 1993. Origin and utilization of rust resistance in groundnut. In Durability of disease resistance. Springer Netherlands. pp 147-158.

Subrahmanyam P, McDonald D, Waliyar F, Reddy LJ, Nigam SN, Gibbons RW, Rao VR, Singh AK, Pande S, Reddy PM and Subbarao PV. 1995. Screening methods and sources of resistance to rust and late leaf spot of groundnut Information Bulletinno 47 ICRISAT, Patancheru, India: 24p

Subramanian V, Gurtu S, Nageswara Rao RC, Nigam SN. 2000. Identification of DNA polymorphism in cultivated groundnut using random amplified polymorphic DNA (RAPD) assay. Genome. 43:656-660.

Sudini H, Upadhyaya HD, Reddy SV, Mangala UN, Rathore A and Kumar KVK. 2015. Resistance to late leaf spot and rust diseases in ICRISAT's mini core collection of peanut (*Arachis hypogaea* L.)Australasian Plant Pathol. 44:557-566.

Sujay V, Kusuma VP, Yugandhar G, Sujatha B, Gowda MVC and Upadhyaya HD. 2008. Selection of accessions from mini-core to improve disease resistance in groundnut. In: 3rd International Conference for Peanut Genomics and Biotechnology on Advances in *Arachis* through Genomics and Biotechnology, 4-8 November 2008, ICRISAT Patancheru, Andhra Padesh, India.

Sujay V, Gowda MVC, Pandey MK, Bhat RS, Khedikar YP, Nadaf HL, Gautami B, Sarvamangala C, Lingaraju S, Radhakrishan T, Knapp SJ and Varshney RK. 2012. QTL analysis and construction of consensus genetic map for foliar disease resistance based on two RIL populations in cultivated groundnut (*Arachis hypogaea* L.). Mol. Breed., 30:773–788.

Sukruth M, Paratwagh SA, Sujay V, Kumari V, Gowda MVC, Nadaf HL, Motagi BN, Lingaraju S, Pandey MK, Varshney RK, and Bhat RS. 2015. Validation of markers linked to late leaf spot and rust resistance, and selection of superior genotypes among diverse recombinant inbred lines and backcross lines in peanut (*Arachis hypogaea* L.). Euphytica. 204:343-351.

Sumathi P and Muralidharan V. 2007. Character association and path coefficient analysis in confectionery type groundnut (*Arachis hypogaea* L.). Madras Agri. J., 94:105-109.

Sumathi P, Amalabalu P, Muralidharan V. 2009. Genetic variability for pod characters in large seeded genotypes of groundnut (*Arachis hypogaea* L.) Adv Plant Sci 22:281-283

Suneetha K. Dasaradha C, Reddy R and Ramana JV. 2004. Genetic variation and character association in groundnut (*Arachis hypogaea* L.). In: proceedings of National symposium on enhancing productivity for sustaining food and nutritional security, NRCG, Junagadh.

Suneetha N, Vasanthi RP, Sudhakar P and Raja Reddy K. 2013. Genetic diversity analysis among released and pre-release cultures in groundnut Legume Res., 36(3):208-213.

Suvarna SN, Kenchanagaudar PV and Talwar HS. 2004. Effect of imposed drought conditions on genetic variation and association of physiological and yield traits in groundnut. J. Oilseed Res., 21:234-239.

Swamy BM, Upadhyaya HD and Goudar PK. 2006. Characterization of Asian core-collection of groundnut for morphological traits. Indian Journal of Crop Science., 1(1-2):129-134.

Swamy BPM, Upadhyaya HD, Goudar PVK, Kullaiswamy BY and Singh S. 2003. Phenotypic variation for agronomic characteristics in a groundnut core collection for Asia. Field Crops Res., 84:359-371.

Swamy Rao T. 1979. Genetic variability in groundnut Crop Improv., 6:66-67.

Tai GCC. 1971. Genotypic stability analysis and its application to potato regional trials. Crop Sci., 11:184-190.

Tai TH and Tanksley SD. 1990. A rapid and inexpensive method for isolation of total DNA from dehydrated plant tissue. Plant Molecular Biology Reporter 8(4):297-303.

Taira H. 1985. Oil content and fatty acid composition of peanuts imported into Japan. J. Amer. Oilseed Chem. Soc., 62:699-702.

Takagi Y, Hossain ABM, Yanagita T, Mastueda T and Murayma A. 1990. Linolenic acid content in soybean improved by X-ray irradiation. Agric. Biol. Chem., 54:1735-1738.

Tang R, Gao G, He L, Han Z, Shan S, Zhong R, Zhou C, Jiang J, Li Y, and Zhuang W. 2007. Genetic diversity in cultivated groundnut based on SSR Markers. J. Genet. Genomics., 34:449-459.

Tekale GR, Dahiphale VV, Shelke VB, and Sondge VD. 1988. Correlation and regression studies in Groundnut. J. Maharastra Agric. Univ., 13:215.

Thaware BL. 2009. Stability analysis for dry pod yield in Spanish bunch groundnut. Agric. Sci. Digest. 29 (3):221-223.

Tiwari SP, Ghewande MP and Misra DP. 1984. Inheritance of resistance to rust and late leaf spot in groundnut (*Arachis hypogaea* L.). J. Cytology and Genetics., 19:97-101.

Uddin MJ, Chowdhary MAZ, Sultan MK and Mitra BN. 1995. Genetic variability, Correlation and path analysis in groundnut. Bangladesh J. Scient.Indust. Res., 30:235-241.

Upadhyaya HD. 2003. Phenotypic diversity in groundnut (*Arachis hypogaea* L.) core collection assessed by morphological and agronomical evaluations. Genet. Resour. Crop Evol., 50:539-550.

Upadhyaya HD, Ortiz R, Bramel PJ and Singh S. 2003. Development of a groundnut core collection using taxonomical, geographical and morphological descriptors. Genetic Resources and Crop Evolution. 50(2):139-148.

Upadhyaya HD, Mallikarjunaswamy BP, Kenchana Goudar PV, Kullaiswamy, BY and Singh S. 2005. Identification of diverse groundnut germplasm through multi-environment evaluation of a core collection for Asia. Field Crop Res., 93:293-299.

Upadhyaya, HD, Reddy LJ, Gowda CLL and Singh S. 2006. Identification of diverse groundnut germplasm: Sources of early maturity in a core collection. Field Crops Research. 97:261-271.

Upadhyaya HD, Dwivedi SL, Baum M, Varshney RK, Udupa SM, Gowda CL, Hoisington D and Singh S. 2008. Genetic structure, diversity, and allelic richness in composite collection and reference set in chickpea (Cicer arietinum L.). BMC Plant Biology. 8(1). p.106.

Upadhyaya HD, Reddy LJ, Dwivedi SL, Gowda CLL and Singh S. 2009. Phenotypic diversity in cold-tolerant peanut (*Arachis hypogaea* L.) germplasm. Euphytica. 165(2):279-291.

Upadhyaya HD, Sharma S and Dwivedi SL. 2011(a). *Arachis* In: Kole C (ed) Wild Crop Relatives: Genomic and Breeding Resources Vol: Legume Crops and Forages Springer Berlin, Heidelberg, Germany, pp 1-19.

Upadhyaya HD, Dwivedi SL, Ambrose M, Ellis N, Berger J, Smykal P, Duc G, Dumet D, Flavell A, Sharma SK, Mallikarjuna N and Gowda CLL. 2011b. Legume genetic resources: management, diversity assessment, and utilization in crop improvement. Euphytica. 180:27-47.

Upadhyaya HD, Ganapati Mukri, Nadaf HL, Singh S. 2012. Variability and stability analysis for nutritional traits in the mini core collection of peanut. Crop Sci., 52:168-178.

Upadhyaya HD, Dwivedi SL, Vadez V, Hamidou F, Singh S, Varshney RK and Liao B. 2014. Multiple resistant and nutritionally dense germplasm identified from mini core collection in peanut. Crop Sci., 54:679–693.

Vaddoria MA and Patel VJ. 1990. Genetic variability in Virginia runner groundnut (*Arachis hypogaea* L.). J. Oilseeds Res., 7:130-132.

Varma TSN, Dwivedi SL, Pande S and Gowda MVC. 2005. SSR markers associated with resistance to rust (*Puccinia arachidis* Speg.) in groundnut (*Arachis hypogaea* L.). SABRAO J. Breed Genet. 37:107–119.

Varman P, Ravendran TS and Ganapathy T. 1991. Genetic analysis of rust resistance in groundnut (*Arachis hypogaea* L.). J. Oilseed Res., 8:35-39.

Varman PV, Raveendran TS and Ganapathi T. 1993. Inheritance of rust resistance in groundnut. Madras Agric. J. 80:175-176.

Varshney RK and Tuberosa R. 2007. Genomic-assisted crop improvement An overview, In Genomics-Assisted Crop Improvement. Springer Verlag, Dordrecht, The Netherlands, pp1-12.

Varshney RK, Mahendar T, Aruna R, Nigam SN, Neelima K, Vadez, V and Hoisington, DA. 2009a. High level of natural variation in a groundnut (*Arachis hypogaea* L.) germplasm collection assayed by selected informative SSR markers. Plant Breed. 128(5):486-494.

Varshney RK, Bertioli DJ, Moretzsohn MC, Vadez V, Krishnamurthy L, Aruna R, Nigam SN, Moss BJ, Seetha K, Ravi K, He G, Knapp SJ and Hoisington DA. 2009b. The first SSR-based genetic linkage map for cultivated groundnut (*Arachis hypogaea* L.). Theor. Appl. Genet., 118:729-739.

Varshney RK, Mohan SM, Gaur PM, Gangarao NVPR, Pandey MK and Bohra A. 2013. Achievements and prospects of genomics-assisted breeding in three legume crops of the semi-arid tropics. Biotechnol. Adv.1-55.

Varshney RK, Pandey MK, Janila P, Nigam SN, Sudini H, Gowda MVC, Sriswathi M, Radhakrishnan T, Manohar SS and Nagesh P. 2014. Marker-assisted introgression of a QTL region to improve rust resistance in three elite and popular varieties of peanut (*Arachis hypogaea* L.). Theoretical and Applied Genetics. 127(8):1771-1781.

Vasanthi RP and Naidu PH. 1998. Evaluation of advanced groundnut lines for resistance to leaf spot. Int. *Arachis* Newsl. 18:14-16.

Vasanthi RP, Harinatha Naidu P and Sudhakar Rao A. 1998. Genetic variability and correlation of yield, component traits and foliar disease resistance in groundnut. J. Oilseed Res., 15(2):345-347.

Vasanthi RP, Suneetha N and Sudhakar P. 2015. Genetic variability and correlation studies for morphological, yield and yield attributes in groundnut (*Arachis hypogaea* L.). Legume Research. 38(1):9-15.

Vekariya HB, Khanpara MD, Vachhani JH, Jivani LL, Vagadiya KJ and Revar HJ. 2011. Correlation and path analysis in bunch groundnut (*Arachis hypogaea* L.). J. Plant Sci., (Muzaffarnagar) 6:11-15.

Venkataramana P, Janakiraman N and Madhuprasad. VL. 2001. Studies on genotype × environment interaction for oil content and its component characters in groundnut (*Arachis hypogaea* L.). Crop Res., 22(1):90-93.

Venkataravana P and Kumar S Injeti. 2008. Assessment of groundnut germplasm and advance breeding lines and isolation of foliar disease resistant genotypes for southern Karnataka. J. Soils and Crops. 18(2):282-286.

Venkataravana P, Sheriff RA, Shankaranarayana V, Reddy VSN, Reddy MNN and Prasad VLM. 2000. Stability analysis for pod yield and its components in groundnut (*Arachis hypogaea* L.). Mysore J. Agric Sci., 34(3):233-239.

Venkateswarlu O, Sudhakar BVG, Reddi M Sekhar and Sudhakar P. 2011. Genetic divergence in confectionary types of groundnut (*Arachis hypogaea* L.). Legume Res., 34(1):1-7.

Vindhiyavarman P, Raveendran TS and Ganapathi T. 1993.Inheritance of rust resistance in groundnut. Madras Agric J., 80:175–176.

Vishnuvardhan KM, Vasanthi RP, Hari Prasad Reddy K and Bhaskar Reddy BV. 2012. Genetic variability studies for yield attributes and resistance to foliar diseases in groundnut (*Arachis hypogaea* L.). Int. J. appl. Bio. and Pharma Tech., 3(1):390-394.

Viswanathan PL, Manivannan N, Murugan E and Mohansundaram K. 2001.Phenotypic stability analysis in groundnut (*Arachis* hypigeae L.). Agric. Sci. Digest., 21(3):164-166.

Vivekananda Y, Pramesh Khoyumthem and. Singh NB. 2015. Genetic Divergence Analysis in Groundnut (*Arachis hypogaea* L.). Electronic J. Plant Breed., 6(1):315-317.

Wambi W, Tukamuhabwa P, Puppala N, Okello DK, Nalugo RG and Kaaya NA. 2014. Narrow sense heritability and gene effects for late leaf spot resistance in *Valencia* groundnuts. African Crop Science Journal. 22(4):327–336.

Wang CT, Yang XD, Chen DX, Yu SL, Liu GZ, Tang YY and Xu JZ. 2007. Isolation of simple sequence repeats from groundnut. Electronic J. Biotech., 10(3):473-480.

Wang CB, Liu YF, Wu ZF, Zheng YP, Wan SB, Sun KX, Sun XW and Feng H. 2008. Diversity and stability of peanut kernel quality in different ecological regions of Shandong Province. Chinese Journal of Eco-Agriculture 16(5):1138-1142.

Wang ML, Chen CY, Davis J, Guo B, Stalker T and Pittman RN. 2009. Assessment of oil content and fatty acid composition variability in different peanut subspecies and botanical varieties. Plant Genet Resour., 8:71-73.

Wang ML, Barkley NL, Chinnan M, Stalker T and Pittman RN. 2010. Oil content and fatty acid composition variability in wild peanut species. Plant Genet. Resour., 8:232-234.

Wang ML, Sukumaran S, Barkley NA, Chen Z, Chen CY, et al. 2011. Population structure and marker-trait association analysis of the US peanut (*Arachis hypogaea* L.) mini-core collection. Theor. Appl. Genet., 123:1307-1317.

Wang H, Pandey MK, Qian L, Qin H, Culbreath AK, He G, Varshney RK, Scully BT, and Guo B. 2013. Genetic Mapping and Quantitative Trait Loci Analysis for Disease Resistance Using F2 and F5 Generation-based Genetic Maps Derived from ‘Tifrunner’ × ‘GT-C20’ in Peanut. The Plant Genome. 6:(3)1-10.

Ward JH.1963. Hierarchical grouping to optimize an objective function. J. Amer Statist. Assoc., 58:236-244.

Webber CR and Moorthy BR. 1952. Heritable and non-heritable relationship and variability of oil content and agronomic characteristics in the F2 generation of soybean crosses. J. Agron., 44:202-209.

Weber WE, Wricke G and Westermann T. 1996. Selection of genotypes and prediction of performance by analyzing GE interactions. In: Kang, M.S. and Gauch, H.G., Jr (eds) Genotype-by-Environment Interaction. CRC Press, Boca Raton, Florida, pp 353–371.

Wells MA, Grichar GS, Smith OD and Smith DH. 1994. Response of selected peanut germplasm lines to leaf spot and southern stem rot. Oleagineux. 49:21-26.

Wightman JA and Amin PW. 1988. Groundnut pests and their control in semiarid tropics. Trop. Pest Manag., 34:218–226.

Wilcox JR, Cavins JF and Nielsen NC. 1984. Genetic alteration of soybean oil composition by a chemical mutagen. J. Am. Oil Chem. Soc., 61:97-100.

Willet WC. 1994. Diet and health: Wheat should we eat? Sci., 264:532-537.

Wilson RF. 1991. Advances in the genetic alteration of soybean oil composition, pp 38-52.

Windham, WR, Mertens DR and Barton FE 1989. Protocol for NIRS calibration: sample selection and equation development and validation. In near infrared reflectance spectroscopy (NIRS): Analysis of forage quality, Marten G C(Ed) USDA Agriculture Handbook, Washington DC, USA 643.

Worthington RE and Hammons RO. 1971. Rancidity problems eyed by researchers. The Southeastern Peanut Farmer. 9:4.

Worthington RE, Hammons RO and Allison JR. 1972. Varietal differences and seasonal effects on fatty acid composition and stability of oil from 82 peanut genotypes. J. Agril. Food Chem., 20:727-730.

Wricke G. 1962. Uber eine Methode zur Erfassung der okologischen Streubreite in Feldversuchen.Zeitschrift für Pflanzenzucht 47, 92–96.

Wynne JC, Beute MK and Nigam SN. 1991. Breeding for disease resistance in peanut (*Arachis hypogaea* L.). Ann. Rev. Phytopathol., 29:279-303.

Xue HQ and Holbrook CG. 1998. Evaluation of peanut breeding lines for resistance to leaf spot. Biological and Cultural Tests and Control of Plant Diseases. 14:80.

Xue HQ and Holbrook CG. 1999. Evaluation of peanut breeding lines for resistance to leaf spot. Biological and Cultural Tests and Control of Plant Diseases. 15:84.

Yan W, Hunt LA, Sheng Q and Szlavnics Z. 2000. Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop Sci., 40:597-605.

Yan W. 2001. GGE biplot - a Windows application for graphical analysis of multi-environment trial data and other types of two-way data. Agronomy Journal. 93(5):1111-1118.

Yan W and Hunt LA. 2001. Genetic and environmental causes of genotype by environment interaction for winter wheat yield in Ontario. Crop Sci., 41:19–25.

Yan W and Hunt LA. 2002. Biplot analysis of diallel data. Crop Sci., 42:21-30.

Yan W and Rajcan I. 2002. Biplot analysis of test sites and trait relations of soybean in Ontario. Crop Sci., 42:11-20.

Yan W. 2002. Singular value partitioning in biplot analysis of multi-environment trial data. Agron. J., 94:990-996.

Yan W and Kang MS. 2003. GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists, and Agronomists. 1st Edn., CRC Press LLC., Boca Roton, Florida, pp 271

Yashoda MH. 2005. Evaluation of bold seeded groundnuts for confectionery characteristics M Sc (Agri) thesis submitted to Univ Agric Sci., Dharwad.

Yates F and Cochran WG. 1938. The analysis of groups of experiments. Journal of Agricultural Science. 28:556–580.

Yougandhar G. 2005. Evaluation of mini core set of germplasm in groundnut (*Arachis hypogaea* L.). M Sc (Agri) Thesis, University of Agricultural Sciences, Dharwad.

Young CT and Waller GR. 1972. Rapid oleic/linoleic microanalytical procedure for peanuts. J. Agri. Food Chem., 20:1116-1118.

Yu J, Pressoir G, Briggs WH, Bi IV, Yamasaki M, Doebley JF, McMullen MD, Gaut BS, Nielsen DM, Holland, JB and Kresovich S. 2006. A unified mixed-model method for association mapping that accounts for multiple levels of relatedness. Nature genetics. 38(2):203-208.

Yu S, Pan L, Yang Q, Min P, Ren Z and Zhang H. 2008. Comparison of the Δ 12 fatty acid desaturase gene between high-oleic and normal-oleic peanut genotypes. Journal of Genetics and Genomics.35(11):679-685.

Zaman MA, Tuhina-khatun M, Ullah MZ, Moniruzzam M and Alam KH. 2011. Genetic variability and path analysis of groundnut (*Arachis hypogaea* L.). The Agriculturists. 9:29-36.

Appendix I

List of genotypes of Genomic Selection Panel of groundnut with their botanical classification and origin used in present study

S. No.	Genotype	Sub-species	Botanical variety	Market type	Origin
1	ICGV 06423	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
2	ICGV 07246	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
3	ICGV 07247	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
4	ICGV 07268	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
5	ICGV 01005	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
6	ICGV 01060	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
7	ICGV 01124	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
8	ICGV 02206	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
9	ICGV 03397	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
10	ICGV 03398	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
11	ICGV 04044	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
12	ICGV 06347	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
13	ICGV 93280	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
14	ICGV 95469	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
15	ICGV 00387	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
16	ICGV 01393	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
17	ICGV 02242	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
18	ICGV 97058	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
19	ICGV 99083	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
20	ICGV 00343	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
21	ICGV 00349	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
22	ICGV 01263	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
23	ICGV 03056	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
24	ICGV 03064	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
25	ICGV 05161	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
26	ICGV 05163	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
27	ICGV 06422	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
28	ICGV 06431	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
29	ICGV 07220	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
30	ICGV 07223	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
31	ICGV 07227	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
32	ICGV 07235	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
33	ICGV 99233	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
34	ICGV 97165	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
35	ICGV 99029	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
36	ICGV 00191	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
37	ICGV 07120	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
38	ICGV 97092	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
39	ICGV 97120	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
40	ICGV 98163	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
41	ICGV 00005	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
42	ICGV 01273	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
43	ICGV 01274	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
44	ICGV 02321	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
45	ICGV 03043	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
46	ICGV 04124	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
47	ICGV 00290	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
48	ICGV 00321	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
49	ICGV 02125	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
50	ICGV 02144	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
51	ICGV 03184	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
52	ICGV 03207	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad

S. No.	Genotype	Sub-species	Botanical variety	Market type	Origin
53	ICGV 04018	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
54	ICGV 07210	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
55	ICGV 07217	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
56	ICGV 95290	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
57	ICGV 97261	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
58	ICGV 97262	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
59	ICGV 99181	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
60	ICGV 99195	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
61	ICGV 89104	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
62	ICGS 11	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
63	J 11	*fastigiata*	*vulgaris*	SB	DGR, Junagadh, India
64	ICGV 99085	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
65	TKG 19A	*fastigiata*	*vulgaris*	SB	BSKKV, Dapoli, India
66	TPG 41	*fastigiata*	*vulgaris*	SB	BARC, India
67	ICGV 00350	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
68	DH 86	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
69	ICGV 95058	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
70	ICGV 95070	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
71	GPBD 4	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
72	ICGV 91114	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
73	TMV 2	*fastigiata*	*vulgaris*	SB	TNAU, Tindivanam, India
74	Faizpur 1-5	*hypogaea*	*hypogaea*	VR	CSAUA &T Kanpur, India
75	Mutant 3	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
76	ICGV 03042	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
77	ICGV 05100	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
78	ICGV 06049	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
79	ICGV 06420	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
80	ICGV 06424	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
81	ICGV 07145	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
82	ICGV 07148	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
83	ICGV 07166	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
84	ICGV 06142	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
85	ICGV 91116	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
86	ICGV 97045	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
87	ICGV 94118	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
88	ICGV 05176	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
89	ICGV 04149	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
90	ICGV 00351	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
91	ICGV 92195	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
92	ICGV 87187	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
93	ICGV 86072	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
94	ICGV 86015	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
95	ICGV 93437	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
96	ICGV 86143	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
97	ICGV 90320	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
98	ICGV 07273	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
99	49 × 37-91	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
100	49 × 37-134	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
101	49 × 37-135	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
102	49 × 37-97-1	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
103	49 × 37- 99(b) tall	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
104	39 × 49 -8	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
105	39 × 49 -77	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
106	49 × 39-20-2	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
107	49 × 39-21-2	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
108	49 × 39-8	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
109	49 M-16	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India

S. No.	Genotype	Sub-species	Botanical variety	Market type	Origin
110	49 × 27-19	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
111	49 × 27-13 (ii)	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
112	27 × 49- 16	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
113	27 × 49- 12	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
114	27 × 49- 14	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
115	27 × 49- 27-1	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
116	26 M 156-2	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
117	26 M- 119-1	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
118	24 M-86	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
119	MN1-35	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
120	M 110-14	*fastigiata*	*fastigiata*	VL	UAS, Dharwad, India
121	M 28-2	*fastigiata*	*fastigiata*	VL	UAS, Dharwad, India
122	Somnath	*hypogaea*	*hypogaea*	VR	BARC, India
123	TG 41	*fastigiata*	*vulgaris*	SB	BARC, India
124	TG 42	*fastigiata*	*vulgaris*	SB	BARC, India
125	TG 49	*fastigiata*	*vulgaris*	SB	BARC, India
126	TG LPS 4	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
127	TG LPS 7	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
128	24 × 37-2275	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
129	24 × 39-31 MR	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
130	26 × M-95-1 RI	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
131	26 × 37-IV- 9IR	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
132	26 × 27-164	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
133	49 × 39-21-1	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
134	49 × 39-21-2(a)	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
135	49 × 39-74	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
136	39 × 49-81-1	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
137	49 × 27-37	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
138	TDG 10	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
139	TDG 13	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
140	TDG 14	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
141	DTG 3	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
142	DTG 15	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
143	M 28-2	*fastigiata*	*fastigiata*	VL	UAS, Dharwad, India
144	JL 24	*fastigiata*	*vulgaris*	SB	RORS, Jalgoan, India
145	TAG 24	*fastigiata*	*vulgaris*	SB	BARC, India
146	SPS 1	*hypogaea*	*hypogaea*	VB	UAS, Dharwad, India
147	SPS 9	*hypogaea*	*hypogaea*	VB	UAS, Dharwad, India
148	SPS 10	*hypogaea*	*hypogaea*	VB	UAS, Dharwad, India
149	SPS 13	*hypogaea*	*hypogaea*	VB	UAS, Dharwad, India
150	SPS 14	*hypogaea*	*hypogaea*	VB	UAS, Dharwad, India
151	SPS 17	*hypogaea*	*hypogaea*	VB	UAS, Dharwad, India
152	ICGV 02411	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
153	ICGV 05155	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
154	ICGV 06100	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
155	ICGV 07023	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
156	SunOleic 95R	*hypogaea*	*hypogaea*	VR	USA
157	ICG 434	*fastigiata*	*vulgaris*	SB	USA
158	ICG 2031	*fastigiata*	*vulgaris*	SB	India
159	ICG 3102	*fastigiata*	*vulgaris*	SB	India
160	ICG 3140	*fastigiata*	*vulgaris*	SB	UNK
161	ICG 3343	*fastigiata*	*vulgaris*	SB	India
162	ICG 3421	*fastigiata*	*vulgaris*	SB	India
163	ICG 4729	*fastigiata*	*vulgaris*	SB	China
164	ICG 6022	*fastigiata*	*fastigiata*	VL	Sudan
165	ICG 6646	*fastigiata*	*fastigiata*	VL	UNK
166	ICG 8517	*fastigiata*	*fastigiata*	VL	Bolivia

S. No.	Genotype	Sub-species	Botanical variety	Market type	Origin
167	ICG 8751	*fastigiata*	*Peruviana*	UNK	Peru
168	ICG 9315	*fastigiata*	*fastigiata*	VL	USA
169	ICG 10036	*fastigiata*	*Peruviana*	UNK	Peru
170	ICG 10053	*fastigiata*	*Peruviana*	UNK	Peru
171	ICG 10701	*fastigiata*	*vulgaris*	SB	China
172	ICG 11088	*fastigiata*	*Peruviana*	UNK	Peru
173	ICG 11651	*fastigiata*	*vulgaris*	SB	China
174	ICG 12625	*fastigiata*	*Aequatoriana*	UNK	Ecuador
175	ICG 12991	*fastigiata*	*vulgaris*	SB	India
176	ICG 14985	*fastigiata*	*vulgaris*	SB	China
177	ICG 15415	*hypogaea*	*UNK*	UNK	Indonesia
178	ICG 15419	*hypogaea*	*hirsuta*	UNK	Ecuador
179	ICGV 01232	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
180	ICGV 01276	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
181	ICGV 01328	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
182	ICGV 02022	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
183	ICGV 02038	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
184	ICGV 02189	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
185	ICGV 02194	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
186	ICGV 02266	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
187	ICGV 02271	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
188	ICGV 02286	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
189	ICGV 86011	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
190	ICGV 86590	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
191	ICGV 87160	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
192	ICGV 87354	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
193	ICGV 87378	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
194	ICGV 87921	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
195	ICGV 88145	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
196	ICGV 92267	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
197	ICGV 93470	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
198	ICGV 94169	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
199	ICGV 94361	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
200	ICGV 95377	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
201	ICGV 96466	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
202	ICGV 96468	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
203	ICGV 97182	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
204	ICGV 97183	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
205	ICGV 98294	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
206	Gangapuri	*fastigiata*	*fastigiata*	VL	JNKVV, Jabalpur, India
207	ICGS 44	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
208	ICG 3312	*fastigiata*	*vulgaris*	SB	Argentina
209	ICG 14705	*hypogaea*	*hypogaea*	VB	Cameroon
210	ICG 3746	*fastigiata*	*vulgaris*	SB	Argentina
211	ICG 4955	*fastigiata*	*vulgaris*	SB	India
212	ICG 12879	*fastigiata*	*vulgaris*	SB	Myanmar
213	ICG 5221	*fastigiata*	*fastigiata*	VL	Argentina
214	ICG 4543	*fastigiata*	*vulgaris*	SB	UNK
215	ICG 1834	*fastigiata*	*vulgaris*	SB	Tanzania
216	ICG 2106	*fastigiata*	*vulgaris*	SB	India
217	ICG 9507	*fastigiata*	*vulgaris*	SB	Philippines
218	ICG 1973	*fastigiata*	*vulgaris*	SB	India
219	ICG 3673	*fastigiata*	*fastigiata*	VL	Korea
220	ICG 3584	*fastigiata*	*vulgaris*	SB	India
221	ICG 442	*fastigiata*	*vulgaris*	SB	USA
222	ICGV 01464	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
223	ICGV 01478	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad

S. No.	Genotype	Sub-species	Botanical variety	Market type	Origin
224	ICGV 02251	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
225	ICGV 03136	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
226	ICGV 05198	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
227	ICGV 06234	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
228	ICGV 00346	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
229	ICGV 00362	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
230	ICGV 00371	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
231	ICGV 02287	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
232	ICGV 02298	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
233	ICGV 02317	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
234	ICGV 97232	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
235	ICGV 99051	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
236	ICGV 99052	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
237	ICGV 00246	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
238	ICGV 00248	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
239	ICGV 01361	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
240	ICGV 02434	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
241	ICGV 04087	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
242	ICGV 06175	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
243	ICGV 97116	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
244	ICGV 97128	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
245	ICGV 98184	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
246	ICGV 00068	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
247	ICGV 01495	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
248	ICGV 05057	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
249	ICGV 07168	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
250	ICGV 01265	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
251	ICGV 98105	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
252	ICGV 99160	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
253	ICGV 02323	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
254	ICGV 04115	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
255	ICGV 05036	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
256	ICGV 06042	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
257	ICGV 86564	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
258	ICGV 98432	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
259	BAU 13	*hypogaea*	*hypogaea*	VB	BAU, Ranchi, India
260	ICGV 87846	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
261	ICR 48	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
262	ICGV 86699	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
263	ICGV 98373	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
264	ICGV 97115	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
265	ICGV 06040	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
266	ICGV 06099	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
267	CS 39	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
268	ICGV 05032	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
269	ICGV 05141	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
270	ICGV 07359	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
271	ICGV 07368	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
272	ICGV 06110	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
273	ICGV 06188	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
274	ICGV 00440	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
275	ICGV 86352	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
276	ICGV 09112	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
277	ICGV 93920	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
278	ICGV 93216	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
279	ICGV 88438	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
280	ICG 11337	*fastigiata*	*vulgaris*	SB	India

S. No.	Genotype	Sub-species	Botanical variety	Market type	Origin
281	49 × 37-90	*hypogaea*	*hypogaea*	VB	UAS, Dharwad, India
282	49 M-2-2	*hypogaea*	*hypogaea*	VB	UAS, Dharwad, India
283	49 M- 1-1	*hypogaea*	*hypogaea*	VB	UAS, Dharwad, India
284	TG 19	*fastigiata*	*vulgaris*	SB	BARC, India
285	TG 39	*hypogaea*	*hypogaea*	VB	BARC, India
286	TG LPS 3	*hypogaea*	*hypogaea*	VB	UAS, Dharwad, India
287	26 × M-223-1	*fastigiata*	*vulgaris*	SB	UAS, Dharwad, India
288	SPS 2	*hypogaea*	*hypogaea*	VB	UAS, Dharwad, India
289	SPS 3	*hypogaea*	*hypogaea*	VB	UAS, Dharwad, India
290	SPS 6	*hypogaea*	*hypogaea*	VB	UAS, Dharwad, India
291	SPS 7	*hypogaea*	*hypogaea*	VB	UAS, Dharwad, India
292	SPS 8	*hypogaea*	*hypogaea*	VB	UAS, Dharwad, India
293	SPS 11	*hypogaea*	*hypogaea*	VB	UAS, Dharwad, India
294	SPS 15	*hypogaea*	*hypogaea*	VB	UAS, Dharwad, India
295	SPS 20	*hypogaea*	*hypogaea*	VB	UAS, Dharwad, India
296	SPS 21	*hypogaea*	*hypogaea*	VB	UAS, Dharwad, India
297	ICGV 03128	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
298	TMV 2 NLM	*hypogaea*	*hypogaea*	VB	TNAU, Tindivanam, India
299	ICG 1668	*hypogaea*	*hypogaea*	VB	USA
300	ICG 8285	*hypogaea*	*hypogaea*	VB	USA
301	ICG 11426	*hypogaea*	*hypogaea*	VB	India
302	ICGV 02290	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
303	ICGV 02446	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
304	ICG 156 (M 13)	*hypogaea*	*hypogaea*	VR	PAU, Ludhiana, India
305	ICGS 76	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
306	ICG 5891	*hypogaea*	*hypogaea*	VB	India
307	CSMG 84-1	*hypogaea*	*hypogaea*	VR	CSAUA&T Kanpur, India
308	ICG 111	*hypogaea*	*hypogaea*	VB	UNK
309	ICG 14834	*hypogaea*	*hypogaea*	VB	Pakistan
310	ICG 11322	*hypogaea*	*hypogaea*	VB	India
311	ICG 532	*hypogaea*	*hypogaea*	VB	UNK
312	ICG 12509	*hypogaea*	*hypogaea*	VB	Bolivia
313	ICG 12672	*hypogaea*	*hypogaea*	VB	Bolivia
314	ICG 10185	*hypogaea*	*hypogaea*	VB	USA
315	ICG 2773	*hypogaea*	*hypogaea*	VR	Tanzania
316	ICG 3027	*hypogaea*	*hypogaea*	VB	India
317	ICG 5745	*hypogaea*	*hypogaea*	VB	Puerto Rico
318	ICG 14482	*hypogaea*	*hypogaea*	VB	Nigeria
319	ICG 4527	*hypogaea*	*hypogaea*	VB	Uganda
320	ICG 4343	*hypogaea*	*hypogaea*	VR	India
321	ICG 13895	*hypogaea*	*hypogaea*	VB	India
322	ICG 5663	*hypogaea*	*hypogaea*	VB	China
323	ICG 721	*hypogaea*	*hypogaea*	VB	USA
324	ICG 12276	*hypogaea*	*hypogaea*	VB	Bolivia
325	ICG 875	*hypogaea*	*hypogaea*	VR	India
326	ICG 14475	*hypogaea*	*hypogaea*	VB	Nigeria
327	ICG 15190	*hypogaea*	*hypogaea*	VB	Costa Rica
328	ICG 12370	*hypogaea*	*hypogaea*	VR	India
329	ICGV 86325	*hypogaea*	*hypogaea*	VB	ICRISAT, Hyderabad
330	ICG 5662	*hypogaea*	*hypogaea*	VB	China
331	ICG 9961	*hypogaea*	*hypogaea*	VB	UNK
332	ICG 14466	*hypogaea*	*hypogaea*	VB	Nigeria
333	ICG 3053	*hypogaea*	*hypogaea*	VB	India
334	ICG 6766	*hypogaea*	*hypogaea*	VB	USA
335	ICG 2381	*hypogaea*	*hypogaea*	VR	Brazil
336	ICG 2857	*hypogaea*	*hypogaea*	VR	Argentina
337	ICGV 13238	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad

S. No.	Genotype	Sub-species	Botanical variety	Market type	Origin
338	ICGV 13241	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
339	ICGV 13242	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad
340	ICGV 13245	*fastigiata*	*vulgaris*	SB	ICRISAT, Hyderabad

Where *SB= Spanish Bunch; VB= Virginia Bunch; VR= Virginia Runner; VL= Valencia and UNK= Unknown;*

Appendix II

Best linear unbiased prediction of mean for different yield and its contributing traits of genomic selection panel evaluated at Aliyarnagar during rainy 2015

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
1	ICGV 06423	32	2.0	4.0	7.0	1.0	3.0	5.0	6.0	38.6	18.0	10.6	6.2	59.3	26.7	118.1	337.6	2250.7
2	ICGV 07246	35	1.0	5.0	8.0	1.0	4.0	8.0	5.0	30.4	21.0	16.8	11.2	62.4	35.8	106.1	467.6	3117.2
3	ICGV 07247	33	1.0	6.0	8.0	1.0	4.0	7.0	7.0	32.9	20.0	13.7	8.6	63.0	34.0	106.0	393.8	2625.4
4	ICGV 07268	30	2.0	5.0	8.0	2.0	6.0	8.0	6.0	31.2	20.0	18.3	13.0	69.3	40.8	106.0	188.9	1259.3
5	ICGV 01005	29	2.0	5.0	8.0	4.0	7.0	7.0	4.0	54.9	7.0	6.3	3.9	63.6	33.0	106.6	97.4	649.6
6	ICGV 01060	30	2.0	4.0	6.0	1.0	4.0	5.0	4.0	40.5	14.0	9.8	6.7	67.9	29.9	107.0	223.3	1488.4
7	ICGV 01124	30	3.0	5.0	7.0	2.0	4.0	7.0	5.0	33.3	16.0	10.0	6.2	61.9	32.1	107.9	155.6	1037.5
8	ICGV 02206	29	2.0	5.0	7.0	1.0	4.0	7.0	5.0	40.9	10.0	7.5	4.8	65.0	34.8	108.1	94.7	631.5
9	ICGV 03397	34	2.0	5.0	8.0	1.0	4.0	8.0	5.0	34.2	11.0	7.5	4.8	64.6	27.0	106.0	170.2	1134.5
10	ICGV 03398	32	3.0	6.0	7.0	1.0	5.0	8.0	7.0	35.2	18.0	13.0	7.7	60.1	27.6	105.2	259.5	1729.7
11	ICGV 04044	30	1.0	5.0	6.0	1.0	4.0	6.0	5.0	34.9	22.0	14.5	8.2	56.6	35.2	105.9	313.9	2092.9
12	ICGV 06347	32	2.0	5.0	7.0	2.0	7.0	8.0	4.0	29.0	12.0	8.2	5.5	65.8	28.8	105.0	339.1	2260.8
13	ICGV 93280	30	2.0	4.0	8.0	1.0	3.0	7.0	5.0	28.8	20.0	10.4	6.1	59.8	27.1	107.0	211.4	1409.2
14	ICGV 95469	29	3.0	6.0	8.0	3.0	5.0	6.0	5.0	33.8	20.0	14.5	10.2	70.6	33.8	101.5	177.9	1186.2
15	ICGV 00387	30	2.0	5.0	6.0	2.0	5.0	8.0	5.0	42.6	11.0	9.5	5.4	57.2	31.1	106.0	312.6	2084.1
16	ICGV 01393	28	3.0	6.0	7.0	3.0	5.0	7.0	5.0	42.8	7.0	7.6	4.7	60.9	57.7	110.0	196.9	1312.4
17	ICGV 02242	28	2.0	4.0	7.0	1.0	3.0	8.0	5.0	41.3	12.0	13.7	7.5	54.3	40.3	107.0	376.5	2510.3
18	ICGV 97058	31	2.0	5.0	6.0	1.0	6.0	7.0	5.0	37.4	13.0	13.8	8.2	59.7	40.1	111.1	318.1	2120.5
19	ICGV 99083	28	2.0	6.0	8.0	3.0	6.0	8.0	5.0	37.4	9.0	7.8	4.3	53.7	50.3	106.4	136.3	908.6
20	ICGV 00343	31	2.0	5.0	8.0	3.0	7.0	8.0	4.0	42.7	12.0	11.1	6.6	60.0	32.4	107.2	96.4	642.5
21	ICGV 00349	30	2.0	6.0	8.0	3.0	6.0	7.0	4.0	30.0	12.0	10.1	5.6	57.2	25.5	106.1	106.1	707.3
22	ICGV 01263	29	2.0	5.0	7.0	3.0	6.0	8.0	4.0	43.5	22.0	21.5	12.2	62.4	42.7	105.9	293.9	1959.1
23	ICGV 03056	31	2.0	5.0	8.0	2.0	4.0	7.0	6.0	40.4	10.0	9.4	6.3	65.5	26.4	104.0	278.3	1855.1
24	ICGV 03064	30	2.0	4.0	8.0	1.0	2.0	6.0	7.0	38.6	9.0	9.3	5.4	57.8	35.6	108.6	391.0	2606.8
25	ICGV 05161	29	2.0	4.0	8.0	1.0	3.0	8.0	6.0	40.0	11.0	9.8	6.8	68.7	34.6	111.0	384.7	2564.4
26	ICGV 05163	31	1.0	2.0	8.0	1.0	3.0	7.0	5.0	33.7	23.0	18.6	11.4	60.6	36.7	108.0	534.1	3560.6
27	ICGV 06422	31	1.0	3.0	4.0	1.0	2.0	3.0	7.0	43.0	25.0	10.8	6.8	60.6	28.3	120.6	309.1	2060.4
28	ICGV 06431	26	3.0	6.0	8.0	3.0	7.0	8.0	4.0	37.9	23.0	17.1	10.1	60.8	32.4	108.1	315.0	2099.9
29	ICGV 07220	33	1.0	4.0	8.0	1.0	4.0	7.0	6.0	36.4	21.0	12.3	6.7	55.4	25.6	116.5	187.8	1251.8
30	ICGV 07223	30	1.0	4.0	7.0	1.0	2.0	6.0	6.0	27.9	16.0	12.6	8.6	68.0	37.1	106.6	352.7	2351.2

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
31	ICGV 07227	32	2.0	5.0	7.0	1.0	3.0	6.0	7.0	34.0	19.0	11.6	7.0	60.8	29.3	102.5	334.3	2228.8
32	ICGV 07235	33	1.0	2.0	8.0	1.0	2.0	6.0	6.0	30.9	22.0	16.4	10.4	63.4	30.5	111.0	400.3	2668.6
33	ICGV 99233	28	1.0	5.0	7.0	1.0	3.0	6.0	4.0	34.7	18.0	14.0	7.6	55.1	27.8	104.4	141.3	941.9
34	ICGV 97165	32	1.0	3.0	6.0	2.0	4.0	6.0	5.0	39.7	10.0	8.8	4.5	51.6	23.8	105.1	215.4	1436.2
35	ICGV 99029	29	1.0	3.0	4.0	1.0	4.0	5.0	5.0	34.6	23.0	14.7	8.4	56.3	29.2	118.9	299.8	1998.9
36	ICGV 00191	28	1.0	3.0	5.0	1.0	2.0	3.0	5.0	37.1	18.0	12.9	8.0	61.7	29.9	118.1	264.1	1760.6
37	ICGV 07120	30	1.0	2.0	4.0	1.0	3.0	5.0	6.0	37.1	25.0	16.1	10.3	64.0	31.2	119.4	410.5	2736.7
38	ICGV 97092	29	2.0	5.0	8.0	1.0	4.0	7.0	5.0	33.7	17.0	12.0	8.3	69.6	27.2	105.0	343.3	2288.7
39	ICGV 97120	31	2.0	4.0	7.0	1.0	2.0	4.0	4.0	42.3	11.0	9.2	5.9	65.3	35.5	105.9	324.3	2162.3
40	ICGV 98163	32	2.0	4.0	8.0	2.0	4.0	7.0	6.0	41.7	22.0	13.6	8.0	58.7	28.6	104.1	305.2	2034.8
41	ICGV 00005	31	1.0	3.0	6.0	1.0	2.0	5.0	5.0	35.6	20.0	13.5	7.6	58.9	26.4	104.0	184.5	1230.3
42	ICGV 01273	28	1.0	3.0	7.0	1.0	3.0	5.0	5.0	29.3	23.0	15.8	10.3	67.0	34.9	104.0	316.9	2112.5
43	ICGV 01274	32	1.0	2.0	5.0	1.0	2.0	6.0	5.0	29.2	20.0	14.2	8.8	61.4	32.0	104.6	386.6	2577.1
44	ICGV 02321	32	2.0	4.0	7.0	1.0	2.0	6.0	5.0	32.3	20.0	10.5	7.3	63.0	28.7	106.0	332.1	2214.2
45	ICGV 03043	30	1.0	2.0	4.0	1.0	2.0	3.0	6.0	33.3	17.0	12.8	7.8	61.4	38.9	117.5	442.1	2947.2
46	ICGV 04124	30	3.0	6.0	8.0	3.0	6.0	8.0	4.0	32.3	14.0	7.6	4.6	59.1	25.4	106.1	93.5	623.1
47	ICGV 00290	31	2.0	4.0	6.0	2.0	4.0	5.0	5.0	33.3	16.0	13.2	8.0	58.2	36.8	103.6	425.8	2838.9
48	ICGV 00321	29	2.0	6.0	8.0	3.0	6.0	8.0	5.0	38.5	12.0	10.0	6.8	65.5	36.2	106.1	466.3	3108.6
49	ICGV 02125	29	2.0	6.0	7.0	3.0	6.0	8.0	4.0	33.8	10.0	6.0	3.6	61.1	22.8	102.4	327.8	2185.1
50	ICGV 02144	29	2.0	5.0	6.0	3.0	7.0	8.0	5.0	40.4	10.0	6.9	4.3	62.2	26.2	105.5	237.9	1585.9
51	ICGV 03184	28	3.0	6.0	8.0	4.0	7.0	9.0	4.0	50.0	7.0	5.6	3.8	69.5	27.9	104.0	151.3	1008.4
52	ICGV 03207	28	3.0	6.0	7.0	2.0	4.0	7.0	5.0	44.1	28.0	21.3	13.9	65.4	26.9	110.0	222.6	1483.7
53	ICGV 04018	28	3.0	7.0	8.0	4.0	7.0	8.0	4.0	44.0	12.0	8.7	5.8	66.5	30.4	102.4	78.6	523.7
54	ICGV 07210	27	3.0	6.0	7.0	2.0	4.0	6.0	4.0	36.4	16.0	8.2	5.3	63.4	25.7	102.8	221.7	1478.1
55	ICGV 07217	29	2.0	7.0	8.0	4.0	8.0	7.0	4.0	31.4	10.0	5.1	3.4	68.2	21.4	101.9	100.2	667.9
56	ICGV 95290	28	2.0	5.0	8.0	3.0	7.0	8.0	4.0	35.5	17.0	13.2	8.9	66.5	33.8	106.1	115.0	766.7
57	ICGV 97261	29	2.0	5.0	7.0	3.0	6.0	7.0	4.0	35.9	15.0	8.5	5.8	65.9	27.1	105.6	164.8	1098.8
58	ICGV 97262	29	3.0	7.0	8.0	4.0	7.0	8.0	5.0	37.5	24.0	17.8	11.8	66.1	29.6	103.6	135.2	901.1
59	ICGV 99181	27	3.0	6.0	8.0	3.0	6.0	7.0	4.0	34.0	12.0	10.7	6.5	60.7	29.2	102.9	228.6	1524.2
60	ICGV 99195	29	4.0	6.0	8.0	2.0	5.0	8.0	5.0	30.8	14.0	9.5	6.3	66.5	39.0	106.1	107.3	715.4
61	ICGV 89104	30	2.0	6.0	7.0	3.0	7.0	8.0	4.0	37.7	13.0	7.2	4.5	61.6	22.6	106.1	90.3	602.0
62	ICGS 11	29	2.0	6.0	8.0	3.0	6.0	8.0	5.0	37.9	13.0	8.3	5.5	66.1	25.4	106.1	201.1	1340.4
63	J 11	29	3.0	6.0	7.0	4.0	7.0	8.0	4.0	37.7	14.0	8.5	5.4	63.1	23.5	105.5	113.0	753.5
64	ICGV 99085	29	1.0	3.0	8.0	1.0	2.0	7.0	4.0	37.3	15.0	9.0	5.3	64.0	29.3	115.4	201.7	1344.5
65	TKG 19A	30	2.0	5.0	8.0	3.0	6.0	7.0	5.0	43.8	12.0	8.9	5.0	56.9	28.5	105.9	192.9	1285.7

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
66	TPG 41	30	2.0	5.0	8.0	3.0	7.0	8.0	4.0	45.7	15.0	12.6	7.5	57.0	56.8	109.1	209.3	1395.3
67	ICGV 00350	32	1.0	3.0	7.0	2.0	5.0	8.0	4.0	36.6	14.0	8.1	5.3	69.2	24.9	105.9	224.7	1498.0
68	DH 86	31	2.0	6.0	7.0	2.0	5.0	6.0	7.0	36.8	15.0	11.7	8.3	70.4	36.4	106.6	459.6	3063.7
69	ICGV 95058	30	2.0	4.0	8.0	3.0	6.0	8.0	5.0	33.8	17.0	11.4	7.5	65.1	30.2	105.9	235.7	1571.5
70	ICGV 95070	30	3.0	6.0	8.0	4.0	7.0	8.0	4.0	31.5	12.0	6.6	3.9	59.1	26.1	106.0	108.3	722.1
71	GPBD 4	29	1.0	2.0	3.0	1.0	2.0	3.0	5.0	34.8	17.0	10.5	6.4	59.8	25.6	118.6	259.7	1731.3
72	ICGV 91114	29	2.0	6.0	8.0	3.0	6.0	7.0	4.0	35.9	9.0	5.1	3.6	67.8	28.0	105.9	98.2	654.9
73	TMV 2	29	2.0	8.0	9.0	4.0	7.0	9.0	5.0	33.2	7.0	5.8	2.8	48.9	29.3	106.0	158.7	1057.8
74	Faizpur 1-5	28	3.0	6.0	8.0	4.0	7.0	8.0	4.0	34.5	11.0	7.7	4.8	64.3	27.2	106.0	99.4	662.4
75	Mutant 3	27	3.0	6.0	8.0	4.0	7.0	9.0	4.0	47.1	15.0	10.7	6.9	63.8	29.6	106.4	193.0	1286.7
76	ICGV 03042	31	1.0	3.0	8.0	1.0	2.0	7.0	5.0	29.6	18.0	13.1	8.1	62.3	32.0	108.4	301.5	2009.7
77	ICGV 05100	31	1.0	2.0	6.0	1.0	2.0	6.0	5.0	33.4	17.0	10.8	6.2	58.1	29.3	118.0	317.7	2117.9
78	ICGV 06049	27	2.0	5.0	7.0	4.0	6.0	7.0	4.0	35.8	11.0	8.9	6.3	60.3	31.6	110.0	101.5	676.7
79	ICGV 06420	31	2.0	5.0	8.0	2.0	3.0	5.0	4.0	35.3	22.0	13.6	7.6	57.0	28.0	114.9	283.3	1888.4
80	ICGV 06424	33	1.0	4.0	7.0	1.0	2.0	5.0	5.0	29.6	17.0	9.7	5.7	58.6	24.2	101.5	291.8	1945.2
81	ICGV 07145	31	1.0	4.0	6.0	1.0	2.0	7.0	5.0	34.5	14.0	11.4	5.7	50.2	26.8	115.5	227.4	1516.1
82	ICGV 07148	30	1.0	4.0	3.0	1.0	2.0	4.0	5.0	34.5	18.0	12.4	6.5	52.3	31.3	103.5	235.7	1571.6
83	ICGV 07166	29	1.0	4.0	7.0	1.0	4.0	8.0	5.0	37.3	27.0	18.6	11.0	59.5	33.5	106.0	394.1	2627.5
84	ICGV 06142	32	1.0	2.0	4.0	1.0	2.0	5.0	5.0	39.7	27.0	17.3	10.7	64.3	28.2	120.4	492.5	3283.4
85	ICGV 91116	28	4.0	8.0	8.0	5.0	7.0	8.0	4.0	46.9	18.0	13.9	8.4	66.0	26.4	107.5	120.9	806.2
86	ICGV 97045	28	2.0	5.0	7.0	3.0	6.0	7.0	4.0	40.9	11.0	11.1	5.8	52.7	53.7	118.4	301.7	2011.4
87	ICGV 94118	29	2.0	4.0	7.0	1.0	3.0	4.0	6.0	35.7	10.0	8.4	5.4	66.0	31.6	106.1	82.0	546.9
88	ICGV 05176	30	2.0	5.0	7.0	3.0	6.0	8.0	5.0	46.2	11.0	15.1	9.5	62.5	52.6	110.5	248.2	1654.5
89	ICGV 04149	26	2.0	5.0	7.0	3.0	7.0	8.0	4.0	31.4	10.0	6.3	3.6	56.8	24.6	110.1	93.8	625.3
90	ICGV 00351	30	2.0	5.0	8.0	2.0	4.0	7.0	5.0	38.1	16.0	10.9	6.9	64.4	27.9	105.0	240.9	1606.2
91	ICGV 92195	29	2.0	5.0	8.0	4.0	7.0	9.0	4.0	40.5	13.0	6.9	4.2	59.7	23.1	101.5	124.6	830.6
92	ICGV 87187	32	2.0	5.0	7.0	3.0	6.0	8.0	6.0	39.5	17.0	10.9	6.8	63.3	29.6	106.0	132.0	879.9
93	ICGV 86072	29	2.0	6.0	8.0	3.0	6.0	8.0	6.0	34.4	13.0	11.3	7.1	62.4	33.8	108.5	171.6	1144.0
94	ICGV 86015	30	2.0	5.0	8.0	3.0	6.0	8.0	5.0	28.3	12.0	7.4	4.5	60.9	28.0	106.2	104.5	696.9
95	ICGV 93437	27	2.0	6.0	8.0	3.0	6.0	7.0	4.0	41.1	12.0	9.9	6.4	69.5	28.6	106.0	192.5	1283.5
96	ICGV 86143	31	3.0	7.0	8.0	4.0	6.0	8.0	5.0	35.2	17.0	13.0	8.6	67.3	31.9	105.9	157.5	1049.9
97	ICGV 90320	28	2.0	4.0	8.0	2.0	5.0	7.0	5.0	33.4	17.0	13.4	8.0	59.7	33.2	106.0	261.2	1741.2
98	ICGV 07273	31	2.0	6.0	8.0	3.0	6.0	8.0	5.0	34.5	14.0	8.8	5.9	67.4	27.5	105.9	140.6	937.0
99	49 × 37-91	27	2.0	6.0	8.0	4.0	8.0	9.0	4.0	32.3	18.0	9.0	4.6	56.2	33.3	111.4	138.4	922.6
100	49 × 37-134	30	2.0	4.0	7.0	2.0	4.0	7.0	4.0	43.4	19.0	13.5	7.2	52.9	35.6	106.0	112.0	746.9

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
101	49 × 37-135	28	2.0	6.0	7.0	4.0	7.0	8.0	4.0	37.3	13.0	7.5	4.8	66.7	23.0	107.1	124.3	828.9
102	49 × 37-97-1	32	2.0	6.0	8.0	5.0	7.0	9.0	5.0	35.6	8.0	10.2	6.1	58.1	61.1	110.5	111.0	739.8
103	49 × 37- 99(b) tall	32	2.0	5.0	8.0	4.0	7.0	8.0	5.0	31.7	10.0	12.3	6.7	59.0	57.1	110.9	113.2	754.6
104	39 × 49 -8	28	1.0	4.0	5.0	1.0	3.0	4.0	5.0	32.5	17.0	11.9	6.8	57.7	43.1	108.0	258.0	1719.9
105	39 × 49 -77	27	1.0	3.0	6.0	1.0	4.0	7.0	4.0	29.8	8.0	6.6	3.6	53.3	45.1	105.7	216.5	1443.3
106	49 × 39-20-2	27	2.0	6.0	8.0	3.0	7.0	9.0	4.0	26.1	16.0	12.3	6.6	52.9	34.0	105.9	189.4	1262.7
107	49 × 39-21-2	29	2.0	5.0	7.0	2.0	4.0	5.0	5.0	41.3	15.0	9.5	5.8	53.7	31.5	119.6	169.5	1129.9
108	49 × 39-8	28	1.0	2.0	6.0	1.0	4.0	7.0	4.0	27.2	11.0	8.2	4.7	57.7	30.3	103.5	206.1	1373.8
109	49 M-16	33	1.0	2.0	8.0	1.0	3.0	5.0	6.0	39.2	21.0	12.5	7.7	59.4	31.0	118.0	243.5	1623.1
110	49 × 27-19	31	2.0	6.0	8.0	3.0	6.0	7.0	4.0	34.9	19.0	13.1	6.9	53.9	41.0	107.5	135.0	900.3
111	49 × 27-13 (ii)	30	2.0	6.0	8.0	3.0	5.0	8.0	4.0	38.6	9.0	8.3	4.3	52.1	42.8	113.4	157.7	1051.2
112	27 × 49- 16	31	1.0	4.0	8.0	2.0	5.0	7.0	6.0	41.8	7.0	4.9	2.6	53.1	41.6	108.0	144.1	960.5
113	27 × 49- 12	29	1.0	4.0	6.0	1.0	5.0	7.0	4.0	27.0	13.0	10.9	6.2	57.9	32.8	107.5	153.2	1021.3
114	27 × 49- 14	29	2.0	4.0	8.0	2.0	6.0	8.0	4.0	36.3	9.0	8.2	4.3	52.9	44.7	106.5	151.4	1009.4
115	27 × 49- 27-1	29	2.0	5.0	8.0	3.0	6.0	7.0	4.0	25.9	17.0	9.9	5.5	55.9	44.1	105.9	113.6	757.5
116	26 M 156-2	29	1.0	4.0	8.0	2.0	6.0	8.0	4.0	26.0	8.0	6.7	2.6	52.1	31.3	105.0	261.2	1741.2
117	26 M- 119-1	28	2.0	6.0	8.0	3.0	7.0	8.0	4.0	35.8	17.0	12.9	8.0	67.6	30.9	104.9	136.2	907.7
118	24 M-86	28	1.0	3.0	4.0	2.0	4.0	6.0	6.0	36.1	14.0	9.4	4.6	46.8	31.5	117.9	83.7	557.7
119	MN1-35	28	2.0	4.0	6.0	1.0	4.0	6.0	4.0	33.8	12.0	7.4	3.1	39.0	24.9	105.9	325.0	2166.9
120	M 110-14	29	1.0	5.0	8.0	1.0	4.0	7.0	5.0	30.9	16.0	13.2	8.1	57.7	40.6	105.1	141.8	945.3
121	M 28-2	30	2.0	4.0	8.0	2.0	4.0	8.0	4.0	28.1	18.0	13.6	6.5	47.1	33.9	101.4	167.2	1114.6
122	Somnath	29	2.0	5.0	8.0	3.0	6.0	7.0	5.0	49.8	15.0	10.5	6.3	60.6	29.8	102.5	115.8	772.0
123	TG 41	28	2.0	6.0	8.0	3.0	7.0	9.0	4.0	35.0	9.0	9.3	5.2	55.5	57.4	106.0	198.2	1321.2
124	TG 42	29	2.0	5.0	7.0	3.0	6.0	7.0	4.0	32.1	9.0	9.9	6.0	59.8	56.3	106.0	192.7	1284.9
125	TG 49	27	2.0	6.0	8.0	3.0	7.0	8.0	4.0	25.7	9.0	7.5	4.1	55.2	34.9	104.0	140.8	938.9
126	TG LPS 4	26	2.0	6.0	8.0	3.0	6.0	8.0	5.0	33.4	16.0	14.3	9.5	68.8	50.0	104.1	128.6	857.1
127	TG LPS 7	28	2.0	6.0	8.0	3.0	6.0	7.0	5.0	32.2	8.0	6.3	4.0	63.0	42.6	106.0	81.9	546.1
128	24 × 37-2275	29	2.0	5.0	7.0	1.0	5.0	8.0	4.0	30.6	19.0	14.9	8.9	61.5	33.6	107.5	288.0	1920.1
129	24 × 39-31 MR	28	2.0	4.0	7.0	1.0	3.0	5.0	5.0	34.2	11.0	6.0	2.4	40.0	25.1	115.5	218.6	1457.5
130	26 × M-95-1 RI	27	2.0	4.0	7.0	2.0	4.0	6.0	5.0	26.1	17.0	10.4	5.1	49.7	28.6	103.4	248.6	1657.3
131	26 × 37-IV- 9IR	30	1.0	4.0	7.0	2.0	5.0	6.0	4.0	35.6	20.0	12.7	7.9	62.9	27.3	106.0	156.4	1042.6
132	26 × 27-164	30	2.0	6.0	8.0	3.0	7.0	8.0	5.0	37.6	14.0	10.5	6.9	65.4	29.7	101.5	132.1	880.7
133	49 × 39-21-1	29	2.0	4.0	6.0	1.0	3.0	7.0	4.0	30.4	13.0	8.6	5.3	61.2	27.9	104.3	152.3	1015.6
134	49 × 39-21-2(a)	28	2.0	4.0	8.0	1.0	4.0	8.0	5.0	28.6	34.0	22.1	13.1	63.6	28.3	102.5	144.3	962.0
135	49 × 39-74	29	1.0	3.0	5.0	1.0	3.0	6.0	4.0	29.3	20.0	9.1	5.8	64.3	24.7	103.4	179.0	1193.1

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
136	39 × 49-81-1	30	1.0	2.0	6.0	1.0	3.0	6.0	4.0	29.4	18.0	10.7	6.4	59.1	29.2	104.7	178.2	1187.7
137	49 × 27-37	31	1.0	4.0	8.0	1.0	3.0	6.0	5.0	28.4	16.0	7.9	4.2	54.0	30.8	102.1	127.9	852.4
138	TDG 10	29	2.0	4.0	7.0	2.0	6.0	8.0	4.0	33.3	17.0	10.5	5.9	53.7	27.4	105.9	233.9	1559.0
139	TDG 13	29	2.0	5.0	8.0	3.0	6.0	8.0	5.0	35.5	16.0	10.6	6.4	60.8	29.3	105.9	276.5	1843.2
140	TDG 14	27	2.0	5.0	8.0	3.0	6.0	7.0	4.0	29.6	14.0	9.0	5.5	61.6	36.6	106.4	179.6	1197.3
141	DTG 3	28	2.0	5.0	8.0	3.0	7.0	7.0	5.0	31.5	16.0	10.6	6.8	64.4	27.8	109.1	239.4	1596.0
142	DTG 15	27	2.0	6.0	8.0	4.0	7.0	8.0	4.0	36.3	12.0	8.1	5.0	64.0	26.4	108.6	162.2	1081.2
143	M 28-2	32	1.0	2.0	7.0	3.0	5.0	7.0	4.0	28.7	13.0	9.8	5.1	51.9	31.2	106.1	88.3	588.4
144	JL 24	29	3.0	6.0	8.0	4.0	7.0	9.0	4.0	45.6	11.0	7.1	4.7	65.3	26.0	106.0	82.4	549.5
145	TAG 24	27	2.0	6.0	8.0	4.0	5.0	7.0	4.0	39.2	12.0	8.4	5.5	67.9	25.4	107.6	127.5	849.7
146	SPS 1	30	1.0	4.0	6.0	1.0	4.0	8.0	4.0	39.3	11.0	6.9	4.0	59.2	19.6	108.0	174.1	1160.5
147	SPS 9	30	1.0	3.0	6.0	2.0	4.0	6.0	4.0	41.0	17.0	11.1	5.7	51.7	23.7	103.0	254.4	1696.1
148	SPS 10	27	3.0	6.0	8.0	5.0	7.0	8.0	4.0	36.8	10.0	7.0	3.8	54.8	24.5	104.1	418.3	2788.9
149	SPS 13	29	2.0	4.0	6.0	4.0	6.0	8.0	4.0	25.5	11.0	11.3	6.4	56.2	51.6	105.9	159.4	1062.7
150	SPS 14	29	2.0	4.0	8.0	2.0	4.0	7.0	4.0	28.4	12.0	6.6	3.9	61.4	22.8	114.9	126.3	842.3
151	SPS 17	28	3.0	6.0	8.0	2.0	4.0	7.0	4.0	36.3	8.0	6.2	3.1	51.9	43.0	105.9	146.4	976.2
152	ICGV 02411	30	1.0	2.0	3.0	1.0	2.0	5.0	5.0	40.8	19.0	13.9	7.4	52.9	32.4	116.5	346.1	2307.5
153	ICGV 05155	30	1.0	2.0	6.0	1.0	2.0	3.0	5.0	35.0	22.0	15.7	9.1	58.1	31.9	101.0	429.4	2862.7
154	ICGV 06100	30	2.0	4.0	8.0	1.0	3.0	7.0	6.0	36.7	23.0	20.3	12.8	63.0	42.3	108.0	490.4	3269.2
155	ICGV 07023	27	2.0	5.0	8.0	3.0	7.0	8.0	6.0	43.0	8.0	5.7	4.1	69.5	31.0	106.0	129.4	862.6
156	SunOleic 95R	29	2.0	6.0	8.0	3.0	5.0	7.0	5.0	29.0	10.0	7.1	4.1	56.8	28.6	104.6	134.6	897.2
157	ICG 434	28	3.0	6.0	7.0	4.0	7.0	8.0	4.0	42.1	7.0	4.6	2.9	64.4	28.5	107.4	103.9	692.4
158	ICG 2031	27	2.0	6.0	8.0	3.0	7.0	9.0	4.0	40.9	10.0	5.4	3.7	69.7	21.2	105.0	80.5	536.8
159	ICG 3102	27	2.0	5.0	8.0	4.0	7.0	7.0	4.0	44.0	11.0	8.6	5.7	67.0	30.7	107.0	186.4	1242.4
160	ICG 3140	28	3.0	5.0	8.0	5.0	7.0	8.0	4.0	42.3	10.0	6.1	3.6	59.0	26.5	106.9	88.5	590.3
161	ICG 3343	28	2.0	6.0	7.0	3.0	7.0	8.0	4.0	43.7	15.0	11.6	7.3	58.4	27.9	106.1	75.7	504.9
162	ICG 3421	28	2.0	6.0	8.0	4.0	7.0	8.0	4.0	39.5	15.0	9.3	5.9	65.0	23.6	102.1	107.4	716.3
163	ICG 4729	28	3.0	7.0	8.0	5.0	8.0	9.0	4.0	45.8	14.0	9.4	6.1	67.1	23.7	105.0	96.9	646.3
164	ICG 6022	28	1.0	2.0	7.0	2.0	4.0	7.0	4.0	59.0	11.0	15.2	8.1	52.7	38.2	106.0	168.3	1121.7
165	ICG 6646	29	1.0	3.0	6.0	3.0	5.0	7.0	4.0	53.0	5.0	8.4	4.4	54.4	29.9	105.5	129.3	862.0
166	ICG 8517	28	2.0	5.0	8.0	2.0	6.0	8.0	4.0	47.7	8.0	6.2	3.8	62.4	24.5	105.6	104.3	695.5
167	ICG 8751	29	2.0	5.0	8.0	2.0	3.0	7.0	4.0	53.5	10.0	11.1	6.7	59.2	29.5	106.0	255.4	1703.0
168	ICG 9315	28	2.0	6.0	8.0	4.0	7.0	7.0	4.0	42.1	15.0	8.7	4.5	55.4	24.4	108.0	111.7	744.5
169	ICG 10036	29	2.0	5.0	6.0	1.0	4.0	7.0	4.0	43.6	13.0	13.2	7.3	54.7	25.2	103.4	207.2	1381.5
170	ICG 10053	30	2.0	3.0	5.0	2.0	4.0	6.0	4.0	39.9	13.0	11.1	7.3	59.6	35.9	104.6	147.3	982.1

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
171	ICG 10701	26	2.0	6.0	9.0	4.0	7.0	8.0	4.0	27.2	9.0	5.4	3.5	58.9	26.8	110.0	102.8	685.2
172	ICG 11088	28	2.0	5.0	8.0	2.0	4.0	6.0	3.0	43.1	14.0	12.0	6.9	56.3	26.8	104.5	234.2	1561.3
173	ICG 11651	29	2.0	5.0	7.0	3.0	6.0	6.0	4.0	36.8	18.0	15.6	8.1	52.0	32.9	103.6	227.0	1513.5
174	ICG 12625	30	1.0	3.0	7.0	2.0	5.0	6.0	4.0	41.3	10.0	6.4	3.4	53.1	29.9	120.5	99.3	661.8
175	ICG 12991	27	3.0	7.0	8.0	5.0	7.0	8.0	4.0	45.0	16.0	8.7	5.6	63.9	21.3	105.1	65.5	436.9
176	ICG 14985	26	3.0	6.0	8.0	4.0	7.0	8.0	5.0	33.6	13.0	10.6	6.4	59.9	35.0	107.5	154.6	1030.5
177	ICG 15415	27	2.0	4.0	8.0	1.0	4.0	8.0	4.0	40.7	14.0	11.0	6.5	59.3	23.6	104.4	153.9	1025.9
178	ICG 15419	28	2.0	4.0	7.0	2.0	4.0	6.0	4.0	67.3	3.0	4.8	2.6	53.4	36.7	107.0	188.7	1257.8
179	ICGV 01232	28	3.0	6.0	8.0	4.0	7.0	8.0	4.0	44.0	10.0	11.3	6.4	56.3	44.3	104.9	250.6	1670.4
180	ICGV 01276	30	1.0	2.0	5.0	1.0	3.0	6.0	6.0	31.5	28.0	20.2	13.6	65.6	32.0	120.5	341.1	2273.8
181	ICGV 01328	28	1.0	2.0	5.0	2.0	5.0	7.0	5.0	34.3	20.0	15.0	8.7	62.5	29.1	112.5	448.6	2990.5
182	ICGV 02022	27	2.0	5.0	8.0	4.0	6.0	7.0	5.0	38.9	13.0	8.6	5.6	66.1	25.1	108.2	187.1	1247.3
183	ICGV 02038	27	3.0	7.0	8.0	5.0	7.0	9.0	4.0	44.0	15.0	5.2	3.5	67.2	28.9	105.5	87.6	583.7
184	ICGV 02189	28	3.0	5.0	8.0	4.0	7.0	9.0	4.0	36.6	11.0	10.1	6.4	66.2	29.9	105.9	179.5	1196.5
185	ICGV 02194	29	3.0	6.0	8.0	2.0	5.0	8.0	4.0	44.1	16.0	8.7	5.4	60.6	23.5	106.1	278.5	1856.9
186	ICGV 02266	30	1.0	5.0	6.0	1.0	3.0	5.0	6.0	41.3	20.0	16.0	10.0	62.0	37.8	102.9	347.3	2315.6
187	ICGV 02271	30	2.0	6.0	8.0	3.0	6.0	7.0	5.0	34.5	16.0	12.8	8.7	67.3	30.9	105.5	168.3	1121.8
188	ICGV 02286	29	1.0	4.0	7.0	2.0	4.0	6.0	5.0	46.0	18.0	10.8	6.7	62.0	27.0	103.4	234.5	1563.3
189	ICGV 86011	29	2.0	6.0	7.0	3.0	7.0	9.0	5.0	45.7	21.0	14.2	8.5	60.6	28.9	103.9	177.8	1185.2
190	ICGV 86590	28	2.0	4.0	6.0	1.0	3.0	4.0	5.0	41.3	15.0	13.3	7.6	56.7	30.0	105.9	335.8	2238.4
191	ICGV 87160	27	2.0	5.0	8.0	3.0	6.0	8.0	4.0	32.5	17.0	9.3	5.6	60.0	28.0	104.4	103.5	690.0
192	ICGV 87354	31	3.0	6.0	7.0	4.0	6.0	8.0	4.0	36.7	6.0	5.2	2.7	53.6	21.9	103.9	98.7	657.7
193	ICGV 87378	26	3.0	6.0	6.0	4.0	6.0	7.0	4.0	43.7	12.0	10.0	6.5	64.6	28.8	108.0	169.3	1129.0
194	ICGV 87921	29	3.0	6.0	8.0	2.0	4.0	7.0	4.0	39.1	14.0	10.5	5.7	54.9	36.9	103.0	333.7	2224.6
195	ICGV 88145	28	2.0	5.0	8.0	3.0	6.0	7.0	4.0	54.1	14.0	10.6	6.7	63.6	32.5	110.4	234.3	1561.8
196	ICGV 92267	29	2.0	5.0	7.0	3.0	6.0	8.0	5.0	47.5	12.0	10.6	5.4	61.7	33.7	102.6	195.1	1300.5
197	ICGV 93470	28	3.0	6.0	8.0	5.0	7.0	9.0	4.0	37.0	16.0	12.5	7.5	60.0	28.0	104.5	339.7	2264.6
198	ICGV 94169	29	2.0	5.0	7.0	3.0	6.0	9.0	5.0	39.3	8.0	10.6	6.3	61.9	42.3	107.0	188.1	1254.3
199	ICGV 94361	29	2.0	6.0	8.0	3.0	7.0	8.0	5.0	35.8	14.0	9.1	6.5	69.1	28.8	102.9	111.8	745.0
200	ICGV 95377	30	2.0	6.0	7.0	3.0	7.0	8.0	4.0	40.1	9.0	8.1	5.7	67.8	37.5	102.5	159.2	1061.2
201	ICGV 96466	29	2.0	7.0	8.0	4.0	6.0	8.0	4.0	32.6	11.0	6.3	4.3	65.9	32.4	103.0	187.1	1247.6
202	ICGV 96468	28	3.0	6.0	8.0	4.0	7.0	8.0	4.0	41.5	8.0	6.1	3.4	55.1	40.2	104.0	199.9	1332.8
203	ICGV 97182	29	2.0	5.0	6.0	1.0	3.0	7.0	5.0	34.3	10.0	6.5	3.6	56.7	26.2	104.9	113.4	756.0
204	ICGV 97183	29	2.0	5.0	8.0	5.0	7.0	8.0	4.0	38.4	12.0	9.8	6.3	64.5	40.3	103.5	204.4	1362.5
205	ICGV 98294	33	3.0	5.0	7.0	3.0	6.0	8.0	5.0	35.0	12.0	10.4	6.4	62.3	36.6	103.4	283.5	1890.0

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
206	Gangapuri	27	2.0	4.0	8.0	4.0	6.0	8.0	4.0	38.2	8.0	6.7	4.1	59.0	27.1	105.9	129.5	863.0
207	ICGS 44	30	2.0	6.0	8.0	2.0	6.0	7.0	5.0	29.6	20.0	15.9	9.7	63.6	32.2	106.0	144.6	964.1
208	ICG 3312	30	2.0	7.0	8.0	4.0	6.0	8.0	4.0	35.3	14.0	7.8	5.7	70.6	23.9	108.0	112.7	751.6
209	ICG 14705	28	2.0	4.0	6.0	3.0	6.0	7.0	5.0	32.9	11.0	7.2	4.8	69.2	33.1	109.9	136.7	911.3
210	ICG 3746	28	3.0	6.0	8.0	5.0	7.0	8.0	4.0	44.2	14.0	8.3	5.9	70.5	21.7	114.0	84.0	559.9
211	ICG 4955	28	3.0	7.0	7.0	4.0	7.0	8.0	4.0	49.2	13.0	8.6	5.5	65.4	28.4	104.6	187.0	1246.7
212	ICG 12879	29	2.0	6.0	7.0	3.0	7.0	8.0	4.0	36.7	7.0	3.8	2.3	59.7	25.3	107.5	65.1	434.2
213	ICG 5221	28	3.0	6.0	8.0	3.0	7.0	8.0	4.0	48.6	9.0	8.6	5.0	58.9	30.3	104.9	141.0	939.7
214	ICG 4543	26	3.0	7.0	8.0	4.0	7.0	8.0	4.0	38.6	16.0	7.4	4.8	66.3	22.1	105.6	103.2	687.9
215	ICG 1834	30	2.0	6.0	8.0	4.0	7.0	8.0	4.0	40.9	17.0	11.1	7.4	65.4	27.1	106.6	153.6	1024.1
216	ICG 2106	29	3.0	5.0	8.0	5.0	7.0	8.0	4.0	41.2	22.0	12.5	8.6	69.6	27.2	105.4	69.0	460.3
217	ICG 9507	29	2.0	7.0	6.0	3.0	6.0	7.0	4.0	38.6	10.0	6.4	4.3	68.4	28.1	108.2	94.8	632.2
218	ICG 1973	29	2.0	6.0	8.0	4.0	7.0	9.0	4.0	41.7	19.0	10.2	6.9	69.2	24.7	107.0	57.9	386.3
219	ICG 3673	29	2.0	6.0	8.0	4.0	7.0	8.0	4.0	41.0	5.0	4.3	2.6	59.0	26.2	116.6	213.2	1421.1
220	ICG 3584	28	3.0	7.0	8.0	5.0	7.0	9.0	4.0	44.2	10.0	8.5	3.7	43.7	24.9	107.5	149.0	993.4
221	ICG 442	27	3.0	7.0	8.0	5.0	7.0	8.0	4.0	42.2	12.0	8.0	5.3	66.2	27.1	113.0	143.3	955.6
222	ICGV 01464	32	2.0	5.0	7.0	1.0	3.0	4.0	6.0	39.3	10.0	11.0	5.6	50.0	42.7	121.4	266.5	1776.7
223	ICGV 01478	34	2.0	6.0	8.0	3.0	5.0	7.0	6.0	36.8	19.0	23.8	14.6	64.0	53.2	113.1	454.9	3033.0
224	ICGV 02251	28	2.0	6.0	8.0	3.0	6.0	8.0	4.0	36.1	14.0	10.1	6.8	67.7	28.2	117.0	192.6	1284.2
225	ICGV 03136	33	2.0	5.0	8.0	3.0	5.0	7.0	5.0	31.5	9.0	10.5	6.4	60.3	44.2	107.0	67.9	452.9
226	ICGV 05198	29	4.0	7.0	7.0	3.0	5.0	6.0	4.0	43.3	20.0	29.0	17.2	60.2	61.2	110.1	454.9	3032.4
227	ICGV 06234	32	3.0	6.0	8.0	2.0	5.0	7.0	5.0	33.6	11.0	9.5	5.8	63.5	39.2	112.7	154.1	1027.1
228	ICGV 00346	31	1.0	3.0	6.0	1.0	2.0	4.0	7.0	39.9	10.0	9.6	5.3	56.8	37.2	109.2	260.6	1737.5
229	ICGV 00362	33	1.0	2.0	6.0	1.0	2.0	3.0	4.0	36.7	23.0	15.4	9.6	65.7	31.1	108.6	251.0	1673.0
230	ICGV 00371	33	2.0	4.0	8.0	3.0	6.0	8.0	5.0	36.2	14.0	8.0	4.1	51.5	24.8	108.0	137.3	915.0
231	ICGV 02287	33	2.0	5.0	7.0	1.0	3.0	6.0	6.0	33.7	22.0	16.7	11.1	66.4	41.7	106.1	167.3	1115.1
232	ICGV 02298	33	2.0	6.0	8.0	4.0	6.0	7.0	6.0	31.1	15.0	13.6	8.9	66.2	34.8	108.0	189.4	1262.5
233	ICGV 02317	32	1.0	3.0	5.0	1.0	3.0	5.0	6.0	33.0	13.0	9.0	5.6	62.4	35.7	106.9	187.7	1251.3
234	ICGV 97232	28	2.0	6.0	8.0	3.0	7.0	8.0	4.0	35.7	11.0	7.5	4.9	64.7	29.4	110.9	274.7	1831.1
235	ICGV 99051	33	1.0	2.0	4.0	1.0	2.0	5.0	6.0	40.2	35.0	25.9	14.6	59.0	34.4	118.0	330.1	2201.0
236	ICGV 99052	32	1.0	2.0	3.0	1.0	2.0	4.0	6.0	41.9	18.0	12.9	7.0	55.2	30.2	117.9	345.1	2300.6
237	ICGV 00246	33	1.0	2.0	4.0	1.0	2.0	3.0	6.0	42.4	12.0	8.6	5.3	60.9	31.6	119.5	240.7	1604.8
238	ICGV 00248	32	1.0	2.0	5.0	1.0	2.0	4.0	6.0	39.4	12.0	9.0	5.3	58.6	28.2	119.1	366.0	2439.8
239	ICGV 01361	32	1.0	2.0	3.0	1.0	2.0	3.0	6.0	37.1	12.0	12.1	7.1	59.1	27.7	117.9	379.5	2530.1
240	ICGV 02434	32	2.0	4.0	5.0	2.0	4.0	6.0	6.0	33.0	17.0	9.6	5.4	56.0	30.9	104.6	245.4	1636.1

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
241	ICGV 04087	34	1.0	2.0	6.0	1.0	2.0	4.0	5.0	35.7	29.0	19.6	10.9	60.1	28.0	117.5	243.9	1625.9
242	ICGV 06175	33	2.0	5.0	6.0	1.0	3.0	5.0	5.0	36.2	21.0	14.6	8.3	57.2	31.2	114.9	206.7	1378.0
243	ICGV 97116	32	1.0	4.0	7.0	3.0	5.0	8.0	6.0	33.7	17.0	12.2	8.0	63.5	32.7	106.9	212.5	1416.8
244	ICGV 97128	31	1.0	5.0	8.0	1.0	3.0	6.0	6.0	38.0	16.0	10.8	6.0	55.9	29.5	117.0	362.7	2418.3
245	ICGV 98184	29	2.0	4.0	7.0	1.0	3.0	6.0	5.0	39.4	19.0	11.6	6.5	55.0	31.1	120.9	269.7	1797.7
246	ICGV 00068	33	1.0	2.0	5.0	1.0	3.0	5.0	5.0	32.4	19.0	14.6	7.9	55.2	28.1	117.1	200.5	1336.7
247	ICGV 01495	31	1.0	2.0	4.0	1.0	4.0	8.0	7.0	36.4	19.0	18.1	11.4	62.1	47.3	112.0	396.1	2640.9
248	ICGV 05057	32	1.0	4.0	8.0	1.0	3.0	6.0	6.0	35.3	17.0	13.1	7.7	58.1	33.5	115.4	422.0	2813.2
249	ICGV 07168	32	2.0	5.0	6.0	2.0	5.0	7.0	6.0	38.6	13.0	10.9	6.7	62.4	35.0	106.9	242.3	1615.3
250	ICGV 01265	34	2.0	4.0	6.0	1.0	3.0	8.0	6.0	35.8	24.0	11.7	6.0	46.1	32.1	110.4	326.5	2176.9
251	ICGV 98105	30	1.0	4.0	6.0	1.0	2.0	7.0	6.0	32.0	22.0	16.1	10.3	63.7	41.4	118.9	409.0	2726.9
252	ICGV 99160	33	1.0	2.0	7.0	2.0	2.0	7.0	6.0	36.7	16.0	13.6	7.8	58.1	34.7	117.5	334.1	2227.4
253	ICGV 02323	32	1.0	2.0	5.0	1.0	2.0	7.0	5.0	34.9	30.0	20.5	14.6	70.4	33.3	121.4	335.2	2234.7
254	ICGV 04115	33	2.0	4.0	6.0	2.0	3.0	5.0	5.0	33.1	15.0	11.4	6.6	58.5	30.2	102.5	160.9	1072.7
255	ICGV 05036	30	1.0	2.0	7.0	1.0	2.0	5.0	5.0	35.6	16.0	13.0	7.6	58.6	34.2	115.4	338.1	2254.1
256	ICGV 06042	30	1.0	2.0	5.0	1.0	2.0	6.0	5.0	36.3	19.0	13.0	8.2	62.9	30.4	106.0	355.2	2368.2
257	ICGV 86564	33	2.0	5.0	7.0	3.0	5.0	8.0	6.0	41.0	14.0	17.0	9.8	57.3	50.3	121.4	161.5	1076.8
258	ICGV 98432	33	2.0	4.0	8.0	2.0	4.0	7.0	7.0	40.9	20.0	20.6	12.1	57.7	44.1	118.5	181.4	1209.5
259	BAU 13	33	2.0	5.0	7.0	2.0	6.0	8.0	6.0	42.1	11.0	13.9	9.7	70.8	53.8	119.6	211.7	1411.6
260	ICGV 87846	32	1.0	3.0	4.0	1.0	2.0	3.0	6.0	37.1	21.0	14.3	8.4	57.8	32.5	120.0	306.4	2042.7
261	ICR 48	33	2.0	4.0	9.0	3.0	5.0	8.0	5.0	29.7	13.0	8.4	5.2	63.3	27.7	107.6	169.0	1126.7
262	ICGV 86699	32	1.0	2.0	4.0	1.0	2.0	5.0	6.0	39.5	27.0	15.5	8.5	53.7	26.6	103.1	183.7	1224.8
263	ICGV 98373	33	2.0	5.0	7.0	1.0	2.0	3.0	5.0	31.3	21.0	16.4	9.8	56.5	42.2	113.5	318.1	2121.0
264	ICGV 97115	33	2.0	4.0	6.0	2.0	4.0	6.0	6.0	37.6	18.0	12.9	7.6	60.1	30.8	106.0	219.4	1462.4
265	ICGV 06040	30	2.0	3.0	6.0	1.0	3.0	5.0	5.0	36.6	18.0	13.9	8.5	61.0	39.4	107.1	350.8	2338.6
266	ICGV 06099	31	1.0	4.0	6.0	1.0	2.0	6.0	6.0	33.9	23.0	21.4	13.2	62.0	43.5	109.0	427.0	2846.5
267	CS 39	32	2.0	4.0	8.0	1.0	3.0	8.0	6.0	35.6	11.0	6.9	3.7	50.9	36.2	110.9	175.1	1167.6
268	ICGV 05032	30	1.0	3.0	6.0	1.0	1.0	2.0	6.0	32.8	12.0	9.5	5.4	50.7	33.9	116.5	336.7	2244.4
269	ICGV 05141	31	1.0	2.0	6.0	1.0	2.0	4.0	5.0	34.7	10.0	7.7	4.7	61.1	31.6	114.0	223.7	1491.0
270	ICGV 07359	32	2.0	6.0	8.0	3.0	7.0	8.0	6.0	43.2	8.0	8.9	5.5	63.2	51.2	114.1	236.5	1576.7
271	ICGV 07368	33	2.0	5.0	8.0	3.0	6.0	7.0	5.0	42.0	9.0	9.6	6.1	63.2	48.5	114.5	224.5	1497.0
272	ICGV 06110	30	2.0	4.0	8.0	3.0	6.0	7.0	6.0	35.9	10.0	9.7	5.0	50.5	41.4	113.1	137.5	916.7
273	ICGV 06188	27	2.0	5.0	8.0	2.0	4.0	7.0	5.0	39.3	12.0	14.3	9.4	65.0	48.4	111.5	374.0	2493.2
274	ICGV 00440	32	2.0	5.0	8.0	2.0	4.0	8.0	6.0	37.4	9.0	12.4	7.9	62.8	66.2	107.5	353.3	2355.2
275	ICGV 86352	28	2.0	5.0	8.0	3.0	6.0	8.0	4.0	34.0	11.0	8.2	4.9	60.5	24.7	106.0	173.5	1156.4

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
276	ICGV 09112	31	2.0	6.0	8.0	3.0	6.0	8.0	8.0	42.0	16.0	9.6	5.6	58.8	26.8	106.0	123.3	822.0
277	ICGV 93920	30	2.0	4.0	7.0	2.0	4.0	7.0	5.0	38.6	22.0	13.7	8.4	60.3	29.4	105.1	370.3	2468.8
278	ICGV 93216	29	1.0	5.0	8.0	2.0	4.0	7.0	5.0	34.7	21.0	13.9	9.2	66.2	29.6	105.0	301.1	2007.3
279	ICGV 88438	34	1.0	5.0	7.0	1.0	5.0	6.0	5.0	27.6	10.0	6.4	3.8	58.2	26.3	111.5	213.9	1426.2
280	ICG 11337	32	1.0	2.0	5.0	1.0	2.0	7.0	5.0	33.6	16.0	11.4	5.7	49.5	32.8	116.4	113.5	756.7
281	49 × 37-90	31	2.0	4.0	7.0	3.0	5.0	8.0	5.0	32.1	15.0	11.5	7.0	60.4	28.8	102.5	246.1	1640.6
282	49 M-2-2	31	1.0	4.0	7.0	2.0	5.0	7.0	6.0	30.6	18.0	19.2	9.3	62.0	36.8	116.5	303.9	2026.0
283	49 M- 1-1	31	1.0	2.0	7.0	1.0	2.0	6.0	4.0	25.6	14.0	13.6	8.1	59.4	39.1	114.6	130.3	868.5
284	TG 19	28	3.0	6.0	8.0	4.0	7.0	7.0	4.0	31.3	18.0	13.8	9.0	65.1	27.8	103.5	109.0	726.4
285	TG 39	29	2.0	5.0	8.0	3.0	6.0	8.0	5.0	25.2	8.0	7.7	4.6	60.2	48.4	107.6	245.6	1637.3
286	TG LPS 3	31	2.0	5.0	8.0	3.0	6.0	8.0	5.0	28.1	11.0	15.5	8.7	58.1	49.3	107.4	190.5	1269.8
287	26 × M-223-1	29	2.0	4.0	7.0	2.0	6.0	8.0	5.0	28.9	11.0	7.4	4.5	58.4	30.6	105.9	167.7	1118.3
288	SPS 2	33	1.0	2.0	5.0	1.0	2.0	6.0	6.0	36.5	13.0	8.4	4.7	55.3	26.6	104.4	252.4	1682.9
289	SPS 3	27	2.0	5.0	8.0	4.0	7.0	8.0	4.0	37.1	15.0	11.8	7.6	64.0	32.1	103.4	164.7	1098.1
290	SPS 6	26	2.0	6.0	8.0	3.0	7.0	7.0	4.0	38.9	14.0	10.9	7.5	68.8	29.4	104.9	98.3	655.0
291	SPS 7	34	1.0	2.0	3.0	1.0	2.0	6.0	7.0	33.8	24.0	16.1	10.6	62.5	32.9	103.6	365.0	2433.4
292	SPS 8	32	1.0	2.0	4.0	1.0	3.0	6.0	7.0	36.2	14.0	9.4	5.6	61.1	26.0	106.0	312.0	2079.7
293	SPS 11	33	1.0	2.0	6.0	1.0	2.0	5.0	6.0	34.7	30.0	21.8	13.4	61.0	33.5	118.6	571.4	3809.3
294	SPS 15	34	1.0	3.0	4.0	1.0	4.0	6.0	6.0	34.8	11.0	8.1	4.7	57.9	39.1	118.0	272.0	1813.3
295	SPS 20	33	1.0	2.0	5.0	1.0	2.0	4.0	5.0	29.9	17.0	10.4	6.0	57.7	26.4	119.0	112.2	747.7
296	SPS 21	32	1.0	2.0	4.0	1.0	2.0	6.0	5.0	34.6	22.0	14.5	8.8	62.0	27.7	117.0	139.4	929.2
297	ICGV 03128	31	1.0	4.0	6.0	1.0	4.0	7.0	6.0	28.2	30.0	22.9	13.5	64.6	34.9	110.1	260.5	1736.9
298	TMV 2 NLM	28	3.0	6.0	8.0	4.0	7.0	7.0	4.0	38.2	15.0	10.2	6.9	66.6	27.2	106.4	160.0	1066.3
299	ICG 1668	28	3.0	6.0	8.0	4.0	7.0	7.0	4.0	37.5	11.0	6.8	4.6	66.8	25.0	108.0	130.8	872.3
300	ICG 8285	33	2.0	4.0	8.0	3.0	6.0	7.0	6.0	32.9	16.0	13.1	8.0	59.5	36.4	109.0	114.9	766.3
301	ICG 11426	33	1.0	3.0	5.0	1.0	2.0	6.0	5.0	34.8	17.0	12.1	7.7	60.8	32.9	107.5	149.3	995.2
302	ICGV 02290	31	2.0	4.0	8.0	3.0	6.0	7.0	6.0	35.4	13.0	11.2	7.8	70.2	35.6	106.2	223.2	1487.8
303	ICGV 02446	34	1.0	2.0	4.0	1.0	2.0	6.0	5.0	33.7	12.0	10.2	5.2	51.9	27.8	116.6	149.2	994.8
304	ICG 156	31	1.0	4.0	8.0	2.0	6.0	7.0	6.0	32.6	18.0	4.7	3.6	71.3	38.6	109.5	164.2	1094.5
305	ICGS 76	34	1.0	6.0	8.0	1.0	5.0	8.0	6.0	32.3	19.0	14.5	7.7	53.5	32.9	104.0	170.9	1139.4
306	ICG 5891	35	2.0	5.0	8.0	3.0	6.0	8.0	6.0	32.7	14.0	8.7	5.4	62.1	29.1	107.9	112.2	748.0
307	CSMG 84-1	27	2.0	5.0	7.0	2.0	6.0	6.0	5.0	33.9	15.0	9.6	4.7	59.4	28.3	103.5	164.2	1094.8
308	ICG 111	32	2.0	6.0	8.0	3.0	6.0	8.0	6.0	32.0	14.0	10.4	6.3	61.4	27.5	108.0	87.2	581.5
309	ICG 14834	31	2.0	4.0	8.0	2.0	4.0	7.0	6.0	32.0	5.0	3.9	2.2	54.1	31.7	104.4	94.8	631.7
310	ICG 11322	32	2.0	5.0	8.0	3.0	6.0	7.0	5.0	32.3	11.0	6.4	3.9	60.1	23.4	105.0	146.6	977.2

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
311	ICG 532	34	2.0	5.0	8.0	2.0	4.0	7.0	6.0	31.8	16.0	9.2	5.6	60.9	29.9	102.0	75.4	502.9
312	ICG 12509	32	2.0	5.0	8.0	2.0	6.0	8.0	6.0	40.1	9.0	6.1	4.1	69.6	28.4	108.6	194.1	1294.3
313	ICG 12672	28	2.0	4.0	6.0	3.0	6.0	8.0	4.0	51.9	18.0	9.7	5.8	59.9	22.5	106.0	122.1	814.2
314	ICG 10185	32	2.0	5.0	7.0	2.0	5.0	7.0	6.0	39.8	12.0	8.9	5.2	59.1	38.3	107.1	75.7	505.0
315	ICG 2773	33	2.0	5.0	8.0	2.0	4.0	7.0	7.0	30.0	11.0	8.3	5.5	66.6	29.9	107.6	63.5	423.5
316	ICG 3027	33	2.0	6.0	8.0	3.0	6.0	8.0	6.0	38.4	11.0	7.8	4.8	61.6	34.0	105.9	126.3	842.3
317	ICG 5745	33	2.0	5.0	8.0	3.0	6.0	8.0	5.0	33.6	8.0	7.7	4.9	63.8	41.0	109.5	157.3	1048.5
318	ICG 14482	35	1.0	5.0	6.0	2.0	6.0	8.0	5.0	34.7	10.0	8.6	5.2	63.6	36.3	108.1	164.8	1098.7
319	ICG 4527	33	2.0	4.0	8.0	3.0	5.0	7.0	6.0	38.8	17.0	13.6	8.3	60.7	34.4	104.5	163.4	1089.3
320	ICG 4343	33	3.0	5.0	7.0	3.0	5.0	7.0	6.0	30.1	9.0	7.4	4.8	62.4	29.6	105.4	112.0	746.5
321	ICG 13895	34	2.0	3.0	6.0	2.0	4.0	6.0	6.0	31.9	5.0	3.6	2.2	60.5	33.5	105.0	106.6	710.5
322	ICG 5663	33	2.0	5.0	7.0	2.0	6.0	8.0	5.0	38.7	8.0	7.2	5.0	68.2	35.4	109.9	78.2	521.6
323	ICG 721	34	2.0	5.0	8.0	3.0	6.0	7.0	6.0	37.9	23.0	20.2	12.9	64.7	41.0	108.5	133.1	887.5
324	ICG 12276	31	1.0	4.0	8.0	1.0	5.0	7.0	5.0	39.3	10.0	7.1	3.9	54.9	28.3	116.0	94.5	629.9
325	ICG 875	34	3.0	6.0	7.0	3.0	6.0	8.0	7.0	33.8	13.0	10.1	6.2	62.7	35.3	105.1	58.1	387.4
326	ICG 14475	33	1.0	4.0	7.0	3.0	6.0	8.0	6.0	39.3	10.0	8.3	5.1	61.9	32.6	106.0	109.9	732.7
327	ICG 15190	34	3.0	6.0	7.0	2.0	5.0	6.0	6.0	35.7	9.0	6.4	4.5	69.0	35.8	103.5	83.3	555.6
328	ICG 12370	32	1.0	3.0	8.0	2.0	4.0	5.0	6.0	35.3	16.0	10.3	5.9	57.3	33.8	106.0	98.7	657.7
329	ICGV 86325	31	1.0	4.0	6.0	3.0	6.0	8.0	6.0	35.6	9.0	5.8	3.8	64.1	30.2	104.5	150.1	1000.4
330	ICG 5662	34	2.0	4.0	8.0	2.0	5.0	7.0	6.0	35.0	11.0	13.6	4.9	40.9	32.5	105.0	330.8	2205.2
331	ICG 9961	32	2.0	5.0	8.0	3.0	7.0	7.0	7.0	40.5	14.0	8.5	5.5	64.3	27.5	110.5	132.7	884.5
332	ICG 14466	32	1.0	4.0	5.0	2.0	4.0	7.0	5.0	33.4	17.0	10.7	7.1	63.2	30.7	108.1	413.5	2756.8
333	ICG 3053	33	2.0	5.0	8.0	2.0	5.0	7.0	6.0	34.5	15.0	11.7	7.1	61.2	34.2	119.4	113.2	754.7
334	ICG 6766	33	2.0	4.0	5.0	2.0	3.0	6.0	6.0	40.3	8.0	7.6	4.5	59.4	44.3	104.0	70.8	472.0
335	ICG 2381	35	1.0	3.0	7.0	1.0	3.0	5.0	6.0	34.0	13.0	11.1	6.0	55.2	29.2	105.1	457.5	3049.9
336	ICG 2857	33	2.0	4.0	8.0	2.0	4.0	6.0	5.0	30.4	13.0	10.1	6.2	62.5	33.1	110.0	99.8	665.6
337	ICGV 13238	27	2.0	6.0	8.0	3.0	7.0	8.0	4.0	31.4	13.0	9.1	6.2	66.3	29.2	106.0	150.0	999.7
338	ICGV 13241	28	2.0	6.0	8.0	3.0	6.0	8.0	4.0	33.3	9.0	5.9	3.8	65.8	26.4	108.2	103.7	691.5
339	ICGV 13242	26	3.0	6.0	8.0	3.0	7.0	8.0	5.0	36.2	16.0	11.6	6.9	59.5	28.6	101.5	146.7	977.8
340	ICGV 13245	29	2.0	6.0	8.0	3.0	7.0	8.0	4.0	38.9	11.0	7.5	5.0	64.9	26.1	102.9	152.1	1013.8
Mean		**30**	**1.9**	**4.6**	**7.1**	**2.4**	**4.9**	**6.9**	**5.0**	**36.7**	**15**	**15.0**	**6.6**	**60.7**	**32.6**	**108.2**	**209.5**	**1396.8**
CV		**3.4**	**16.4**	**6.6**	**7.2**	**15.5**	**8.0**	**6.8**	**10.6**	**5.5**	**18.2**	**19.3**	**20.2**	**4.4**	**6.2**	**1.6**	**23.3**	**23.3**
LSD at 5 % level		**1.7**	**0.1**	**0.1**	**0.1**	**0.1**	**0.1**	**0.1**	**0.9**	**3.3**	**4.4**	**3.5**	**2.2**	**4.4**	**3.3**	**2.9**	**80.4**	**536.0**

X1= Days to 50% flowering; **X2, X3, X4=** Disease score of late leaf spot at 75, 90 and 105 days after sowing, respectively; **X5, X6, X7=** Disease score of rust at 75, 90 and 105 days after sowing, respectively; **X8=** Number of primary branches per plant; **X9=** Plant height (cm); **X10=** Number of pods per plant; **X11=** Pod yield per plant (g); **X12=**Seed yield per plant (g); **X13=** Shelling percent; **X14=** Hundred seed weight (g); **X15=** Days to maturity; **X16=**Yield per plot (g); **X17=** Yield per hectare (Kg)

Appendix III

Best linear unbiased prediction of mean for nutritional quality traits of Genomic Selection Panel of groundnut evaluated at Aliyarnagar during rainy 2015

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
1	ICGV 06423	56.0	19.9	35.0	45.9	12.4	1.9	0.8
2	ICGV 07246	54.5	21.2	38.6	42.2	12.3	2.7	0.9
3	ICGV 07247	54.3	22.4	34.9	45.2	12.8	2.3	0.8
4	ICGV 07268	50.2	21.5	38.8	41.6	11.4	2.4	0.9
5	ICGV 01005	54.8	18.2	48.4	35.7	10.4	1.8	1.4
6	ICGV 01060	58.0	20.8	36.3	45.2	11.9	3.2	0.8
7	ICGV 01124	55.9	18.8	43.7	39.2	11.4	2.6	1.2
8	ICGV 02206	57.2	19.6	38.8	43.8	12.3	2.6	0.9
9	ICGV 03397	51.7	23.3	33.1	46.2	13.5	2.2	0.7
10	ICGV 03398	49.5	23.5	36.2	43.1	13.3	2.3	0.8
11	ICGV 04044	54.5	19.2	34.7	47.4	13.0	2.3	0.7
12	ICGV 06347	50.6	21.4	33.7	46.0	12.9	1.6	0.8
13	ICGV 93280	54.5	20.1	34.2	45.6	13.1	2.3	0.7
14	ICGV 95469	51.9	20.2	30.7	48.1	13.4	2.2	0.6
15	ICGV 00387	51.6	19.9	32.8	47.2	13.4	2.1	0.7
16	ICGV 01393	52.2	19.3	48.1	35.7	9.9	2.1	1.4
17	ICGV 02242	51.4	21.5	43.8	38.9	11.0	2.6	1.1
18	ICGV 97058	53.7	17.1	49.4	34.2	10.3	2.5	1.4
19	ICGV 99083	51.9	20.9	46.3	36.2	10.7	2.6	1.3
20	ICGV 00343	52.1	21.1	40.3	41.4	11.5	2.8	1.0
21	ICGV 00349	55.9	21.5	34.4	45.7	12.9	2.8	0.7
22	ICGV 01263	53.7	22.7	45.6	36.6	10.8	2.6	1.3
23	ICGV 03056	55.7	17.9	39.2	42.1	12.4	2.1	0.9
24	ICGV 03064	52.6	20.6	42.9	39.9	11.1	2.4	1.1
25	ICGV 05161	55.2	19.0	40.7	41.6	11.8	2.5	1.0
26	ICGV 05163	58.5	16.0	35.2	46.4	12.5	2.4	0.8
27	ICGV 06422	56.8	18.5	35.4	45.8	12.4	2.1	0.8
28	ICGV 06431	57.5	17.0	38.0	44.1	11.8	2.6	0.9
29	ICGV 07220	58.0	19.4	49.2	35.1	12.6	1.5	1.4
30	ICGV 07223	59.4	18.3	35.6	45.6	12.4	2.6	0.8
31	ICGV 07227	55.5	20.6	37.1	42.0	13.4	2.5	0.9
32	ICGV 07235	53.0	20.4	39.6	41.2	11.8	2.4	1.0
33	ICGV 99233	54.7	22.0	39.5	42.0	11.5	2.8	0.9
34	ICGV 97165	55.3	17.0	37.7	42.3	12.8	2.6	0.9
35	ICGV 99029	52.5	21.7	40.1	38.5	13.0	3.1	1.1
36	ICGV 00191	54.0	21.8	38.6	40.9	12.9	2.8	1.0
37	ICGV 07120	51.4	18.9	39.5	40.8	12.2	2.1	1.0
38	ICGV 97092	50.8	20.0	34.1	44.9	13.3	2.0	0.8
39	ICGV 97120	53.9	21.3	53.8	30.9	12.5	1.3	1.7
40	ICGV 98163	53.7	22.3	37.2	42.4	12.7	2.3	0.9
41	ICGV 00005	55.2	22.2	37.3	41.1	12.6	2.6	0.9
42	ICGV 01273	56.1	21.2	35.2	44.3	13.0	2.8	0.8
43	ICGV 01274	52.6	22.5	37.5	43.0	12.5	1.7	0.9
44	ICGV 02321	53.7	22.3	37.0	42.0	12.9	2.2	0.9
45	ICGV 03043	57.5	18.7	31.8	48.6	13.1	2.3	0.7
46	ICGV 04124	54.0	16.4	42.9	40.3	10.5	2.1	1.1
47	ICGV 00290	54.3	20.3	37.7	43.5	11.8	2.3	0.9
48	ICGV 00321	50.1	23.3	39.0	41.5	11.8	2.2	1.0
49	ICGV 02125	53.6	20.2	42.9	39.1	11.4	2.1	1.1
50	ICGV 02144	53.5	18.4	49.4	33.9	10.5	2.0	1.5
51	ICGV 03184	49.1	24.0	41.8	37.8	11.5	2.4	1.1
52	ICGV 03207	55.6	20.5	42.6	39.3	11.6	2.3	1.1

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
53	ICGV 04018	49.2	25.3	43.3	36.4	11.5	2.9	1.3
54	ICGV 07210	56.1	21.1	44.3	37.8	11.3	2.6	1.2
55	ICGV 07217	57.5	16.2	40.9	42.4	11.6	2.4	1.0
56	ICGV 95290	54.0	21.0	37.0	43.3	12.6	2.4	0.9
57	ICGV 97261	55.6	18.8	39.3	42.5	12.0	2.0	0.9
58	ICGV 97262	56.9	21.6	40.9	39.4	12.3	3.3	1.0
59	ICGV 99181	60.0	16.5	38.0	43.4	12.3	3.1	0.9
60	ICGV 99195	53.9	23.6	31.7	48.4	13.3	2.4	0.7
61	ICGV 89104	56.4	17.7	44.6	37.8	10.9	2.4	1.2
62	ICGS 11	48.3	21.5	37.5	43.0	12.1	1.6	0.9
63	J 11	55.2	19.9	39.3	42.0	12.0	2.2	0.9
64	ICGV 99085	62.7	16.7	52.9	31.4	9.5	3.3	1.7
65	TKG 19A	54.3	19.6	34.5	46.3	12.2	2.5	0.7
66	TPG 41	51.8	22.6	42.1	40.1	11.2	2.8	1.1
67	ICGV 00350	53.5	19.3	36.0	44.8	12.6	2.1	0.8
68	DH 86	52.4	21.2	38.5	42.0	11.7	2.2	0.9
69	ICGV 95058	51.7	19.7	45.7	35.3	11.5	2.0	1.3
70	ICGV 95070	52.6	17.0	38.3	42.8	11.9	1.7	0.9
71	GPBD 4	59.5	18.3	50.7	33.1	10.0	2.9	1.5
72	ICGV 91114	56.1	16.5	51.2	32.9	10.1	2.2	1.6
73	TMV 2	45.9	24.1	46.8	31.6	10.6	2.6	1.5
74	Faizpur 1-5	50.1	26.7	34.4	45.8	12.9	2.6	0.7
75	Mutant 3	55.7	17.1	40.9	41.2	11.6	2.1	1.0
76	ICGV 03042	56.5	18.3	29.4	51.2	13.6	1.8	0.6
77	ICGV 05100	56.3	18.9	35.6	45.2	13.0	1.9	0.8
78	ICGV 06049	54.6	19.8	38.1	44.1	11.8	2.1	0.9
79	ICGV 06420	55.6	21.1	38.5	43.3	11.9	2.1	0.9
80	ICGV 06424	55.3	19.4	40.0	41.8	11.6	2.2	1.0
81	ICGV 07145	51.7	20.2	37.3	44.9	12.0	2.3	0.8
82	ICGV 07148	55.2	17.5	38.1	43.5	12.4	2.6	0.9
83	ICGV 07166	54.1	19.3	42.9	39.2	11.5	2.4	1.1
84	ICGV 06142	59.2	19.7	38.0	43.3	12.1	3.1	0.9
85	ICGV 91116	50.9	21.3	41.3	38.1	12.1	2.1	1.1
86	ICGV 97045	52.5	19.4	43.7	38.6	12.1	2.5	1.1
87	ICGV 94118	52.4	21.8	35.9	43.4	13.0	2.3	0.8
88	ICGV 05176	52.0	22.6	48.7	33.2	10.7	3.0	1.5
89	ICGV 04149	54.3	18.0	43.8	39.0	11.3	2.2	1.1
90	ICGV 00351	50.7	20.5	44.5	37.0	10.9	2.1	1.2
91	ICGV 92195	51.9	17.8	46.3	36.2	11.3	1.8	1.3
92	ICGV 87187	49.0	21.6	45.2	36.5	11.3	1.8	1.2
93	ICGV 86072	50.8	18.6	48.8	33.5	11.1	1.7	1.5
94	ICGV 86015	49.5	22.3	35.3	43.9	12.7	1.9	0.8
95	ICGV 93437	50.7	21.9	39.8	41.4	12.1	1.8	1.0
96	ICGV 86143	48.3	22.4	42.6	38.0	11.2	2.1	1.1
97	ICGV 90320	53.1	17.1	43.0	39.1	11.0	2.2	1.1
98	ICGV 07273	59.0	16.2	43.8	38.5	11.7	2.4	1.2
99	49 × 37-91	47.7	20.1	47.9	34.6	10.6	1.7	1.4
100	49 × 37-134	53.5	19.5	50.1	33.6	10.1	2.2	1.5
101	49 × 37-135	53.9	17.6	45.3	37.2	10.9	2.2	1.2
102	49 × 37-97-1	48.0	21.9	48.6	33.5	10.7	1.6	1.5
103	49 × 37- 99(b) tall	49.5	21.8	48.8	33.8	10.4	1.7	1.4
104	39 × 49 -8	52.9	20.0	45.4	36.7	10.8	1.9	1.3
105	39 × 49 -77	57.9	19.6	43.1	41.3	10.9	2.7	1.0
106	49 × 39-20-2	48.8	20.3	45.4	36.5	10.8	1.7	1.3
107	49 × 39-21-2	51.7	19.9	50.9	32.7	9.9	2.3	1.6
108	49 × 39-8	52.4	18.2	52.7	31.5	9.9	1.8	1.7

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
109	49 M-16	56.5	22.8	33.3	47.9	12.5	2.7	0.7
110	49 × 27-19	50.6	21.7	41.2	39.9	11.3	1.9	1.0
111	49 × 27-13 (ii)	46.9	23.9	50.1	30.8	11.1	2.2	1.7
112	27 × 49- 16	49.0	24.5	44.8	35.9	11.1	2.4	1.3
113	27 × 49- 12	56.5	18.1	39.0	42.7	12.1	2.0	1.0
114	27 × 49- 14	53.6	17.3	45.4	37.0	11.6	1.5	1.2
115	27 × 49- 27-1	48.3	23.1	45.7	38.0	10.5	1.6	1.2
116	26 M 156-2	54.8	20.1	44.7	38.2	10.8	2.7	1.2
117	26 M- 119-1	54.2	19.0	44.3	38.6	11.4	2.3	1.1
118	24 M-86	51.4	21.5	38.8	41.7	12.3	2.7	0.9
119	MN1-35	60.8	18.7	42.0	41.3	13.5	1.7	1.0
120	M 110-14	52.0	21.7	37.1	43.0	12.0	2.7	0.9
121	M 28-2	52.6	21.7	38.7	42.2	12.3	2.5	0.9
122	Somnath	56.8	18.5	35.1	46.9	11.9	2.8	0.8
123	TG 41	50.2	21.0	45.6	36.3	11.7	1.4	1.2
124	TG 42	52.7	18.2	40.4	41.5	12.0	1.6	1.0
125	TG 49	48.2	22.7	44.1	37.2	11.3	1.8	1.2
126	TG LPS 4	51.3	20.9	41.5	38.8	11.9	1.9	1.1
127	TG LPS 7	54.0	18.2	41.4	39.8	11.8	1.9	1.0
128	24 × 37-2275	51.0	18.6	53.2	30.6	9.6	1.9	1.7
129	24 × 39-31 MR	54.3	21.9	38.2	42.4	11.8	2.6	0.9
130	26 × M-95-1 RI	57.3	19.0	51.9	32.3	9.5	2.8	1.6
131	26 × 37-IV- 9IR	51.3	16.4	45.4	38.0	11.0	1.5	1.2
132	26 × 27-164	50.0	16.8	33.7	46.4	13.1	1.5	0.7
133	49 × 39-21-1	54.6	18.5	44.1	38.4	11.5	2.1	1.2
134	49 × 39-21-2(a)	59.1	17.6	45.9	36.8	10.9	3.4	1.2
135	49 × 39-74	54.9	16.4	45.1	38.4	10.6	1.9	1.2
136	39 × 49-81-1	53.8	18.4	44.0	38.8	10.9	2.4	1.2
137	49 × 27-37	53.7	19.7	33.4	47.1	12.4	2.3	0.7
138	TDG 10	50.8	20.1	40.4	42.4	11.1	2.3	1.0
139	TDG 13	55.7	18.5	41.7	40.9	11.2	2.5	1.0
140	TDG 14	50.9	23.2	41.5	39.8	11.7	2.2	1.1
141	DTG 3	47.6	16.4	49.0	33.9	10.6	1.1	1.5
142	DTG 15	52.0	19.7	42.6	39.7	11.4	1.6	1.1
143	M 28-2	55.0	19.5	40.0	41.7	11.9	2.9	1.0
144	JL 24	53.4	16.9	48.5	35.3	10.2	1.5	1.4
145	TAG 24	53.9	19.2	39.8	41.5	11.7	1.8	1.0
146	SPS 1	58.0	22.7	36.5	43.6	14.9	2.0	0.8
147	SPS 9	57.9	21.9	40.8	41.0	14.1	1.9	1.0
148	SPS 10	50.2	21.7	44.3	38.3	11.2	1.5	1.2
149	SPS 13	54.1	19.6	46.1	36.8	12.0	1.6	1.3
150	SPS 14	58.8	18.2	44.2	38.3	12.4	2.2	1.2
151	SPS 17	49.5	20.8	44.3	37.4	11.2	1.6	1.2
152	ICGV 02411	57.4	20.6	35.1	45.9	12.4	2.8	0.8
153	ICGV 05155	59.8	16.5	40.0	43.1	11.7	2.1	0.9
154	ICGV 06100	59.0	22.3	30.8	49.2	13.7	2.7	0.6
155	ICGV 07023	51.4	20.2	43.3	39.4	11.2	1.6	1.1
156	SunOleic 95R	52.2	21.5	74.4	5.3	8.5	2.1	14.0
157	ICG 434	55.9	22.4	37.6	43.2	12.5	2.9	0.9
158	ICG 2031	55.6	16.0	40.5	41.4	11.6	1.8	1.0
159	ICG 3102	53.3	21.3	42.9	38.6	11.9	2.1	1.1
160	ICG 3140	49.0	21.5	43.8	36.8	11.4	1.7	1.2
161	ICG 3343	49.1	20.4	41.2	39.7	11.7	1.5	1.0
162	ICG 3421	53.9	17.4	47.5	34.9	10.7	2.1	1.4
163	ICG 4729	55.4	17.9	40.5	41.3	11.5	2.0	1.0
164	ICG 6022	62.6	16.6	49.6	40.9	8.1	3.2	1.2

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
165	ICG 6646	54.2	16.2	48.5	37.5	9.0	2.6	1.3
166	ICG 8517	52.4	22.0	42.2	39.6	14.0	1.4	1.1
167	ICG 8751	53.2	16.7	37.1	43.1	12.3	2.1	0.9
168	ICG 9315	53.2	21.4	41.9	40.1	11.7	1.9	1.1
169	ICG 10036	48.9	18.7	36.7	44.2	11.6	2.4	0.8
170	ICG 10053	52.8	23.7	45.7	36.9	10.7	2.4	1.2
171	ICG 10701	48.8	22.1	40.4	40.9	12.2	1.6	1.0
172	ICG 11088	57.8	16.2	45.4	39.6	10.9	2.3	1.2
173	ICG 11651	51.6	21.5	35.7	45.6	11.9	1.8	0.8
174	ICG 12625	63.5	17.5	46.0	44.7	8.2	2.9	1.0
175	ICG 12991	53.4	16.4	48.2	35.3	10.5	1.6	1.4
176	ICG 14985	47.9	23.1	40.5	39.2	12.7	1.6	1.0
177	ICG 15415	51.1	18.6	36.6	44.8	11.9	2.7	0.8
178	ICG 15419	62.1	19.0	48.5	42.2	7.5	3.5	1.2
179	ICGV 01232	52.1	19.2	35.5	46.5	11.9	2.3	0.8
180	ICGV 01276	50.5	25.5	30.4	48.2	13.2	2.1	0.6
181	ICGV 01328	58.5	19.0	43.5	38.6	14.3	1.3	1.1
182	ICGV 02022	53.0	20.0	40.2	42.2	11.6	2.0	1.0
183	ICGV 02038	49.5	28.4	36.5	42.6	12.5	2.4	0.9
184	ICGV 02189	50.4	21.0	43.7	38.2	11.3	1.6	1.1
185	ICGV 02194	55.8	19.6	35.4	45.0	12.6	2.7	0.8
186	ICGV 02266	52.2	21.0	45.1	36.2	11.7	2.4	1.3
187	ICGV 02271	55.7	20.4	31.9	47.9	13.1	2.7	0.7
188	ICGV 02286	54.4	18.2	35.1	45.7	12.5	2.2	0.8
189	ICGV 86011	50.9	19.0	46.3	36.0	10.5	1.9	1.3
190	ICGV 86590	51.3	19.5	33.4	47.2	12.0	2.4	0.7
191	ICGV 87160	54.0	20.0	45.9	36.2	11.0	2.6	1.3
192	ICGV 87354	55.1	20.1	47.0	35.7	10.9	2.5	1.3
193	ICGV 87378	53.6	21.4	37.3	43.8	12.2	2.4	0.8
194	ICGV 87921	57.4	16.7	43.0	40.3	11.3	2.5	1.1
195	ICGV 88145	51.5	21.4	45.2	36.7	11.0	1.8	1.3
196	ICGV 92267	56.0	21.1	41.3	41.6	11.3	2.8	1.0
197	ICGV 93470	51.6	20.4	40.0	40.8	12.3	1.6	1.0
198	ICGV 94169	50.9	20.1	45.7	37.0	11.1	1.9	1.2
199	ICGV 94361	54.6	20.8	37.9	43.8	12.2	2.5	0.9
200	ICGV 95377	52.0	23.6	38.1	42.0	12.3	2.6	0.9
201	ICGV 96466	55.5	21.2	40.1	41.1	11.6	2.9	1.0
202	ICGV 96468	51.7	22.6	33.4	47.0	12.5	2.4	0.7
203	ICGV 97182	49.9	24.6	38.3	41.6	12.1	2.0	0.9
204	ICGV 97183	51.7	20.8	43.8	38.2	11.2	2.0	1.2
205	ICGV 98294	55.6	24.3	38.2	43.3	11.8	3.4	0.9
206	Gangapuri	49.5	22.1	41.4	39.7	14.1	1.3	1.1
207	ICGS 44	50.1	22.6	36.3	44.6	12.2	2.0	0.8
208	ICG 3312	58.3	16.5	48.3	35.1	10.7	2.7	1.4
209	ICG 14705	53.1	21.5	41.6	39.6	11.5	2.7	1.0
210	ICG 3746	55.9	17.8	45.5	37.2	10.9	2.1	1.2
211	ICG 4955	54.1	17.8	50.5	31.9	12.6	0.7	1.6
212	ICG 12879	54.9	18.2	48.2	34.1	10.6	2.0	1.4
213	ICG 5221	60.3	21.7	45.6	43.2	7.7	2.9	1.1
214	ICG 4543	56.7	16.5	48.9	34.6	10.9	2.2	1.4
215	ICG 1834	54.2	19.3	40.8	40.8	11.6	2.7	1.0
216	ICG 2106	55.1	17.9	46.1	36.7	11.0	2.2	1.3
217	ICG 9507	49.9	22.0	38.5	40.9	12.1	1.9	0.9
218	ICG 1973	54.9	18.4	49.9	32.6	10.5	2.4	1.5
219	ICG 3673	58.0	16.0	42.9	40.2	13.4	1.1	1.1
220	ICG 3584	55.5	16.8	44.2	38.6	11.0	2.0	1.1

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
221	ICG 442	56.0	19.9	35.0	45.9	12.4	1.9	0.8
222	ICGV 01464	50.2	24.1	41.8	38.0	11.5	1.9	1.1
223	ICGV 01478	49.8	23.2	42.5	39.2	11.0	2.7	1.1
224	ICGV 02251	53.6	18.1	45.2	37.6	10.9	2.1	1.2
225	ICGV 03136	56.0	19.9	35.0	45.9	12.4	1.9	0.8
226	ICGV 05198	50.3	21.3	51.1	31.7	10.2	2.1	1.6
227	ICGV 06234	52.4	23.7	52.5	30.8	9.6	2.6	1.7
228	ICGV 00346	53.5	19.4	37.9	42.6	12.1	2.4	0.9
229	ICGV 00362	55.3	21.9	45.5	36.2	10.6	2.9	1.3
230	ICGV 00371	51.8	20.3	32.7	47.6	12.5	2.3	0.7
231	ICGV 02287	53.8	22.0	46.4	36.1	11.5	2.0	1.3
232	ICGV 02298	47.6	22.0	47.9	34.0	10.0	1.7	1.4
233	ICGV 02317	55.0	17.9	38.4	42.2	11.8	2.3	0.9
234	ICGV 97232	50.5	24.2	40.9	40.2	11.5	2.2	1.0
235	ICGV 99051	53.8	21.8	35.4	44.6	12.6	2.4	0.8
236	ICGV 99052	54.7	22.9	34.4	45.0	12.8	2.3	0.8
237	ICGV 00246	55.9	21.0	33.6	46.6	12.7	2.5	0.7
238	ICGV 00248	58.8	18.2	33.3	47.1	13.1	2.7	0.7
239	ICGV 01361	51.8	18.9	37.2	42.7	12.3	1.6	0.9
240	ICGV 02434	52.7	20.6	35.0	44.1	12.4	2.4	0.8
241	ICGV 04087	55.7	20.5	33.2	45.4	13.0	2.5	0.7
242	ICGV 06175	51.0	21.6	41.3	39.0	11.7	2.1	1.1
243	ICGV 97116	53.6	19.9	43.2	38.4	11.0	2.4	1.2
244	ICGV 97128	60.9	16.2	34.6	46.3	12.9	2.7	0.8
245	ICGV 98184	54.3	18.4	37.4	45.0	12.3	2.2	0.8
246	ICGV 00068	53.9	19.8	42.3	39.8	10.8	2.4	1.1
247	ICGV 01495	56.1	18.7	40.0	41.6	11.8	2.7	1.0
248	ICGV 05057	54.4	19.1	32.8	47.7	13.2	2.1	0.7
249	ICGV 07168	52.9	21.5	38.5	41.5	12.2	2.2	0.9
250	ICGV 01265	51.6	21.3	38.1	41.4	12.8	2.4	0.9
251	ICGV 98105	59.7	16.1	34.1	48.2	12.7	2.2	0.7
252	ICGV 99160	55.1	21.1	31.1	49.8	13.0	2.0	0.6
253	ICGV 02323	51.3	22.3	35.9	44.3	12.5	1.7	0.8
254	ICGV 04115	50.5	22.8	40.9	40.1	12.0	2.1	1.0
255	ICGV 05036	52.4	22.4	35.0	45.3	12.6	1.9	0.8
256	ICGV 06042	53.1	22.5	37.6	40.9	13.1	2.0	0.9
257	ICGV 86564	51.2	21.2	45.1	36.0	10.5	3.2	1.3
258	ICGV 98432	50.1	20.8	47.3	35.5	10.0	2.3	1.3
259	BAU 13	49.1	21.7	42.9	37.8	11.2	2.0	1.1
260	ICGV 87846	51.7	21.0	35.2	44.5	12.7	2.2	0.8
261	ICR 48	46.1	24.7	51.1	29.8	10.2	1.8	1.7
262	ICGV 86699	54.5	23.5	49.8	34.2	12.3	1.2	1.5
263	ICGV 98373	51.1	23.6	37.6	41.6	12.3	1.8	0.9
264	ICGV 97115	51.9	18.9	41.6	37.9	12.4	2.2	1.1
265	ICGV 06040	59.1	20.5	35.1	45.6	13.0	2.8	0.8
266	ICGV 06099	58.5	19.2	39.4	42.2	12.4	3.0	0.9
267	CS 39	52.2	21.7	42.4	38.9	11.3	2.3	1.1
268	ICGV 05032	52.5	18.4	40.3	40.4	12.2	2.0	1.0
269	ICGV 05141	58.2	17.9	44.9	37.5	11.5	2.4	1.2
270	ICGV 07359	49.6	22.4	38.5	40.2	12.7	2.5	1.0
271	ICGV 07368	46.4	23.4	43.5	35.4	12.0	2.1	1.2
272	ICGV 06110	45.0	24.3	46.4	32.4	12.1	2.2	1.4
273	ICGV 06188	49.6	23.1	50.2	32.5	9.9	1.8	1.5
274	ICGV 00440	49.8	22.7	45.9	35.0	10.8	2.8	1.3
275	ICGV 86352	52.9	18.7	48.3	35.4	10.7	2.0	1.4
276	ICGV 09112	48.0	18.5	48.6	33.9	10.6	1.2	1.4

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
277	ICGV 93920	47.9	20.0	40.5	39.1	11.6	1.9	1.0
278	ICGV 93216	48.8	20.1	46.5	35.7	10.6	1.6	1.3
279	ICGV 88438	54.6	19.3	47.3	37.5	11.1	1.7	1.3
280	ICG 11337	57.0	18.8	51.0	35.0	12.5	1.4	1.5
281	49 × 37-90	58.8	16.9	43.6	40.4	11.5	2.9	1.1
282	49 M-2-2	52.5	20.2	46.8	36.2	10.7	2.0	1.3
283	49 M- 1-1	51.9	21.0	37.2	43.5	12.8	2.1	0.8
284	TG 19	55.1	20.1	40.4	41.1	11.5	2.5	1.0
285	TG 39	49.0	18.9	47.0	35.7	11.0	1.5	1.3
286	TG LPS 3	47.9	27.2	42.4	38.4	11.7	1.6	1.1
287	26 × M-223-1	55.2	22.2	40.9	41.2	12.0	2.8	1.0
288	SPS 2	54.9	22.3	52.2	32.5	11.8	1.3	1.6
289	SPS 3	54.4	18.5	43.8	39.2	11.2	2.3	1.1
290	SPS 6	53.6	18.9	42.7	40.0	11.2	1.8	1.1
291	SPS 7	57.6	21.9	49.7	35.4	12.2	1.4	1.4
292	SPS 8	56.3	21.2	50.9	35.0	11.6	1.4	1.5
293	SPS 11	57.7	22.4	35.7	44.2	12.4	3.0	0.8
294	SPS 15	56.2	18.2	47.2	38.5	10.9	2.0	1.2
295	SPS 20	57.6	21.4	52.6	33.5	11.4	1.6	1.6
296	SPS 21	60.5	16.6	49.8	35.8	12.2	1.8	1.4
297	ICGV 03128	56.2	22.0	39.2	40.6	12.7	2.5	1.0
298	TMV 2 NLM	51.8	22.7	40.2	40.4	11.9	2.0	1.0
299	ICG 1668	56.6	18.2	41.2	41.2	11.1	2.2	1.0
300	ICG 8285	51.0	22.8	44.2	36.1	11.7	2.3	1.2
301	ICG 11426	56.9	21.7	52.7	31.6	12.2	1.6	1.7
302	ICGV 02290	50.3	20.6	47.8	33.0	10.7	2.1	1.5
303	ICGV 02446	52.7	22.3	38.7	39.4	13.0	2.7	1.0
304	ICG 156	48.6	20.2	48.9	33.5	9.8	1.9	1.5
305	ICGS 76	53.8	22.3	39.5	42.1	12.0	2.4	0.9
306	ICG 5891	53.9	19.9	47.8	33.9	10.9	2.4	1.4
307	CSMG 84-1	49.2	19.5	46.5	34.4	11.3	1.7	1.4
308	ICG 111	51.8	18.9	43.9	37.2	11.4	2.0	1.2
309	ICG 14834	50.3	21.3	47.5	33.5	10.9	1.6	1.4
310	ICG 11322	48.5	21.4	39.5	41.5	11.8	1.4	1.0
311	ICG 532	53.1	18.5	44.5	37.2	11.2	1.9	1.2
312	ICG 12509	60.6	22.5	58.6	28.6	9.7	2.3	2.1
313	ICG 12672	54.7	20.5	44.2	39.4	13.3	1.1	1.1
314	ICG 10185	51.3	21.0	43.6	37.4	11.3	2.1	1.2
315	ICG 2773	49.4	20.4	42.5	38.7	11.3	1.8	1.1
316	ICG 3027	53.0	20.7	34.5	45.0	13.3	2.0	0.8
317	ICG 5745	48.6	18.3	49.4	32.5	10.3	1.7	1.5
318	ICG 14482	64.2	20.9	57.5	30.2	10.0	2.8	1.9
319	ICG 4527	51.8	20.5	38.6	43.2	10.9	2.4	0.9
320	ICG 4343	49.5	21.1	42.8	36.4	12.0	1.6	1.2
321	ICG 13895	51.0	23.7	38.9	41.2	12.1	1.8	1.0
322	ICG 5663	52.1	19.5	42.9	39.3	11.0	1.9	1.1
323	ICG 721	52.8	19.4	42.4	38.6	11.1	2.3	1.1
324	ICG 12276	54.5	20.0	60.3	24.1	10.0	2.3	2.5
325	ICG 875	48.0	23.4	40.6	39.7	11.9	1.9	1.0
326	ICG 14475	61.5	19.0	50.0	37.4	10.8	2.3	1.4
327	ICG 15190	52.5	19.8	40.2	40.7	12.0	2.1	1.0
328	ICG 12370	52.3	19.5	41.9	38.7	11.4	1.9	1.1
329	ICGV 86325	53.0	19.2	44.8	36.5	11.3	2.2	1.2
330	ICG 5662	55.6	17.8	37.0	44.8	12.0	2.2	0.8
331	ICG 9961	52.4	19.2	49.7	33.0	10.6	1.8	1.5
332	ICG 14466	52.0	21.2	40.6	39.8	11.8	1.9	1.0

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
333	ICG 3053	52.0	19.4	44.0	35.7	11.8	1.9	1.2
334	ICG 6766	50.5	20.1	43.6	37.8	11.3	1.9	1.2
335	ICG 2381	54.8	22.3	35.5	45.9	9.3	3.6	0.8
336	ICG 2857	51.8	20.8	46.5	35.8	10.8	2.2	1.3
337	ICGV 13238	55.2	16.1	44.5	38.4	11.4	1.8	1.2
338	ICGV 13241	52.7	19.8	45.1	37.3	11.4	2.0	1.2
339	ICGV 13242	54.1	19.2	40.6	40.6	11.7	2.0	1.0
340	ICGV 13245	53.5	17.4	42.7	39.6	11.6	2.1	1.1
Mean		**53.5**	**20.2**	**42.0**	**39.7**	**11.7**	**2.2**	**1.1**
CV		**4.5**	**10.1**	**8.4**	**7.7**	**5.4**	**14.9**	**16.5**
LSD at 5 % level		**4.0**	**3.3**	**5.8**	**5.0**	**1.0**	**0.5**	**0.3**

Appendix IV

Best linear unbiased prediction (BLUPs) of mean for different traits of Genomic Selection Panel of groundnut evaluated at Jalgaon during rainy 2015

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
1	ICGV 06423	35.0	1.0	2.0	3.0	1.0	2.0	2.0	7.0	43.1	25.0	18.2	10.4	56.3	33.5	136.0	501.8	3345.4
2	ICGV 07246	32.0	1.0	2.0	2.0	1.0	2.0	2.0	9.0	41.9	19.0	11.1	6.6	61.0	35.1	121.1	362.4	2415.7
3	ICGV 07247	29.0	1.0	3.0	4.0	1.0	2.0	3.0	9.0	38.9	35.0	21.0	13.2	63.0	32.2	120.9	532.2	3547.9
4	ICGV 07268	29.0	1.0	5.0	7.0	1.0	3.0	5.0	7.0	39.7	21.0	16.8	11.6	69.1	40.6	123.0	471.9	3146.3
5	ICGV 01005	33.0	3.0	4.0	6.0	1.0	5.0	7.0	5.0	49.5	15.0	11.1	7.3	66.2	34.4	123.0	258.3	1722.3
6	ICGV 01060	28.0	1.0	2.0	4.0	1.0	3.0	5.0	6.0	48.6	14.0	7.5	4.3	61.4	28.5	126.1	110.6	737.5
7	ICGV 01124	31.0	1.0	3.0	5.0	1.0	2.0	3.0	8.0	44.6	15.0	8.0	4.8	59.2	33.1	118.0	211.2	1407.7
8	ICGV 02206	33.0	1.0	4.0	6.0	1.0	2.0	4.0	7.0	50.2	25.0	17.2	11.1	66.0	40.8	128.0	388.7	2591.5
9	ICGV 03397	37.0	1.0	3.0	4.0	1.0	2.0	3.0	7.0	27.2	21.0	9.5	5.7	61.6	25.0	114.0	155.6	1037.5
10	ICGV 03398	34.0	1.0	5.0	8.0	1.0	3.0	5.0	8.0	39.3	27.0	17.1	11.5	63.8	28.0	118.0	294.6	1964.2
11	ICGV 04044	31.0	1.0	3.0	5.0	1.0	2.0	4.0	6.0	44.6	16.0	9.8	4.8	48.4	31.9	122.9	252.3	1682.0
12	ICGV 06347	33.0	2.0	3.0	4.0	2.0	4.0	6.0	6.0	42.8	23.0	15.6	10.1	64.3	37.5	121.0	355.1	2367.1
13	ICGV 93280	33.0	1.0	4.0	6.0	1.0	3.0	5.0	6.0	49.1	22.0	15.0	9.4	61.7	31.9	120.9	274.4	1829.1
14	ICGV 95469	26.0	1.0	3.0	4.0	1.0	3.0	4.0	6.0	48.1	27.0	14.6	9.4	67.6	32.7	114.0	366.1	2440.9
15	ICGV 00387	29.0	1.0	4.0	6.0	1.0	3.0	4.0	7.0	48.4	17.0	12.7	5.8	46.5	30.0	123.1	385.5	2569.8
16	ICGV 01393	29.0	1.0	3.0	4.0	1.0	3.0	4.0	5.0	44.7	13.0	9.0	4.7	51.6	40.9	135.0	213.2	1421.5
17	ICGV 02242	27.0	1.0	3.0	5.0	1.0	3.0	6.0	5.0	45.1	15.0	13.5	7.3	54.7	41.8	127.0	323.1	2154.1
18	ICGV 97058	33.0	1.0	2.0	4.0	1.0	2.0	4.0	5.0	51.9	12.0	8.7	4.3	54.0	38.4	130.0	330.8	2205.3
19	ICGV 99083	26.0	1.0	4.0	6.0	1.0	2.0	4.0	7.0	53.0	15.0	11.4	4.9	42.0	35.3	126.0	300.0	1999.8
20	ICGV 00343	33.0	1.0	5.0	7.0	1.0	3.0	4.0	5.0	43.3	12.0	10.5	5.5	54.6	37.7	121.5	381.3	2541.9
21	ICGV 00349	30.0	2.0	5.0	8.0	1.0	4.0	6.0	6.0	34.9	19.0	11.2	6.7	59.4	30.0	122.0	287.1	1914.0
22	ICGV 01263	29.0	2.0	4.0	5.0	1.0	2.0	2.0	4.0	55.4	16.0	15.3	9.2	59.9	42.2	119.0	273.3	1821.7
23	ICGV 03056	26.0	1.0	4.0	5.0	1.0	3.0	3.0	6.0	45.3	21.0	16.4	10.3	63.1	32.0	116.0	729.7	4864.5
24	ICGV 03064	30.0	1.0	2.0	3.0	1.0	3.0	3.0	6.0	43.4	27.0	23.8	12.9	53.9	40.5	123.0	682.3	4549.0
25	ICGV 05161	32.0	1.0	3.0	4.0	1.0	3.0	3.0	6.0	46.0	20.0	16.6	8.2	51.8	35.4	130.0	425.7	2838.1
26	ICGV 05163	29.0	1.0	2.0	4.0	1.0	3.0	3.0	7.0	46.7	32.0	24.0	13.9	57.5	36.9	120.0	520.2	3468.2
27	ICGV 06422	31.0	1.0	3.0	5.0	1.0	2.0	2.0	8.0	48.4	25.0	17.6	10.5	60.3	34.7	138.0	490.6	3270.5
28	ICGV 06431	26.0	1.0	4.0	6.0	1.0	4.0	6.0	5.0	45.5	12.0	7.7	4.1	54.5	34.7	114.5	175.4	1169.1
29	ICGV 07220	31.0	1.0	2.0	3.0	1.0	2.0	3.0	8.0	38.3	18.0	9.0	4.7	54.0	28.9	138.0	161.8	1078.9
30	ICGV 07223	32.0	1.0	3.0	4.0	1.0	2.0	2.0	8.0	42.9	30.0	20.5	13.0	63.4	32.0	121.0	508.1	3387.3

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
31	ICGV 07227	30.0	1.0	3.0	5.0	1.0	2.0	3.0	8.0	43.1	11.0	5.7	3.3	60.9	31.2	120.0	167.9	1119.0
32	ICGV 07235	33.0	1.0	2.0	3.0	1.0	2.0	3.0	8.0	39.1	26.0	15.6	9.5	61.8	33.5	130.0	494.4	3296.0
33	ICGV 99233	27.0	1.0	4.0	5.0	1.0	2.0	3.0	6.0	48.6	17.0	7.3	3.9	55.8	30.1	119.0	199.4	1329.6
34	ICGV 97165	30.0	1.0	3.0	5.0	1.0	2.0	3.0	5.0	58.2	6.0	6.1	3.2	47.1	28.2	116.1	182.7	1217.8
35	ICGV 99029	26.0	1.0	3.0	5.0	1.0	2.0	2.0	5.0	52.1	14.0	8.6	4.7	57.4	36.3	138.0	310.6	2070.4
36	ICGV 00191	28.0	1.0	3.0	5.0	1.0	3.0	4.0	6.0	50.1	23.0	13.2	7.7	60.6	30.9	138.0	416.0	2773.4
37	ICGV 07120	36.0	1.0	3.0	3.0	1.0	2.0	2.0	7.0	45.4	22.0	15.1	9.6	64.8	36.8	138.0	429.8	2865.2
38	ICGV 97092	31.0	1.0	3.0	6.0	1.0	3.0	4.0	8.0	47.1	19.0	12.1	5.8	48.5	31.2	116.0	371.3	2475.1
39	ICGV 97120	31.0	1.0	3.0	6.0	1.0	4.0	6.0	6.0	43.0	13.0	10.0	5.9	58.5	37.3	121.0	261.1	1740.9
40	ICGV 98163	32.0	1.0	3.0	4.0	1.0	2.0	3.0	7.0	49.0	23.0	13.9	8.6	61.1	31.8	116.1	340.8	2272.0
41	ICGV 00005	28.0	1.0	3.0	4.0	1.0	3.0	3.0	8.0	42.3	29.0	17.7	11.2	62.2	28.3	116.0	531.9	3546.3
42	ICGV 01273	32.0	1.0	3.0	4.0	1.0	2.0	3.0	8.0	43.0	26.0	15.6	9.5	61.2	32.0	112.0	442.5	2950.1
43	ICGV 01274	35.0	1.0	2.0	3.0	1.0	3.0	3.0	7.0	45.3	27.0	20.2	12.5	60.5	31.7	116.0	597.3	3982.1
44	ICGV 02321	32.0	1.0	3.0	4.0	1.0	2.0	4.0	7.0	43.0	21.0	12.6	7.7	61.1	29.5	116.0	283.5	1890.0
45	ICGV 03043	32.0	1.0	2.0	3.0	1.0	3.0	2.0	7.0	43.7	27.0	19.4	11.1	57.0	37.0	136.5	371.5	2476.8
46	ICGV 04124	29.0	1.0	4.0	4.0	1.0	2.0	3.0	5.0	39.8	17.0	12.1	7.1	62.9	33.5	116.1	288.2	1921.1
47	ICGV 00290	35.0	1.0	2.0	4.0	1.0	2.0	3.0	8.0	37.9	24.0	15.0	8.7	57.8	36.0	115.0	333.0	2220.0
48	ICGV 00321	26.0	2.0	5.0	7.0	1.0	4.0	6.0	5.0	37.2	15.0	11.8	7.6	62.7	36.6	122.0	188.7	1258.0
49	ICGV 02125	29.0	1.0	4.0	6.0	1.0	3.0	4.0	5.0	42.8	16.0	8.7	5.5	64.6	29.1	114.4	291.4	1942.8
50	ICGV 02144	29.0	1.0	5.0	7.0	1.0	4.0	6.0	6.0	40.6	18.0	13.4	7.6	59.7	34.1	116.5	247.4	1649.1
51	ICGV 03184	27.0	1.0	3.0	5.0	1.0	3.0	3.0	5.0	71.6	15.0	10.4	6.3	63.3	36.2	121.9	217.3	1448.8
52	ICGV 03207	33.0	1.0	3.0	4.0	1.0	4.0	5.0	5.0	38.0	17.0	9.9	6.4	64.7	25.0	125.4	214.7	1431.5
53	ICGV 04018	26.0	1.0	2.0	4.0	1.0	3.0	4.0	5.0	61.0	15.0	14.2	9.6	68.8	47.8	116.6	254.0	1693.5
54	ICGV 07210	29.0	1.0	3.0	5.0	1.0	3.0	5.0	5.0	40.3	19.0	9.6	6.2	64.0	29.1	115.5	179.4	1196.1
55	ICGV 07217	33.0	1.0	4.0	6.0	1.0	3.0	4.0	4.0	42.9	18.0	8.4	5.4	60.8	26.6	112.0	168.1	1120.8
56	ICGV 95290	27.0	2.0	4.0	6.0	1.0	3.0	4.0	5.0	39.1	16.0	8.3	5.6	67.3	35.4	119.5	191.3	1275.2
57	ICGV 97261	27.0	1.0	5.0	7.0	1.0	4.0	6.0	5.0	39.6	15.0	9.3	5.2	61.6	32.5	115.5	249.9	1666.0
58	ICGV 97262	29.0	1.0	4.0	6.0	1.0	3.0	4.0	5.0	43.7	21.0	11.8	7.4	62.6	31.1	115.9	307.0	2046.7
59	ICGV 99181	27.0	1.0	5.0	7.0	1.0	6.0	8.0	3.0	39.2	20.0	12.0	7.6	64.1	29.6	116.4	307.4	2049.0
60	ICGV 99195	26.0	1.0	4.0	6.0	1.0	4.0	6.0	6.0	44.9	16.0	10.6	6.6	62.6	29.9	113.0	260.4	1736.3
61	ICGV 89104	30.0	1.0	4.0	6.0	1.0	3.0	5.0	6.0	38.0	12.0	6.6	3.6	50.5	26.5	120.9	127.6	850.7
62	ICGS 11	28.0	1.0	3.0	4.0	1.0	4.0	6.0	6.0	38.0	17.0	10.5	6.2	58.0	33.3	122.0	231.6	1544.3
63	J 11	31.0	1.0	5.0	6.0	1.0	5.0	6.0	5.0	42.2	21.0	13.0	8.1	63.0	27.2	114.0	245.8	1638.9
64	ICGV 99085	31.0	1.0	3.0	3.0	1.0	3.0	4.0	6.0	47.2	16.0	6.5	3.8	61.3	27.8	136.4	184.0	1226.3
65	TKG 19A	26.0	1.0	3.0	5.0	1.0	3.0	4.0	5.0	52.4	15.0	8.3	5.0	59.4	32.1	114.5	219.0	1460.0

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
66	TPG 41	31.0	1.0	2.0	4.0	1.0	4.0	6.0	4.0	59.2	11.0	10.2	4.8	47.9	42.8	128.0	248.8	1658.6
67	ICGV 00350	33.0	1.0	2.0	5.0	1.0	3.0	5.0	5.0	39.3	29.0	18.2	10.7	59.9	32.2	120.0	366.3	2442.2
68	DH 86	31.0	2.0	3.0	4.0	1.0	2.0	4.0	8.0	37.7	22.0	17.3	13.2	67.1	36.5	114.5	341.7	2278.3
69	ICGV 95058	32.0	1.0	3.0	4.0	1.0	3.0	5.0	5.0	37.4	15.0	9.3	6.1	66.3	29.9	118.9	167.3	1115.0
70	ICGV 95070	29.0	1.0	4.0	7.0	1.0	4.0	6.0	7.0	37.6	31.0	18.0	11.8	67.2	31.5	122.0	407.4	2716.1
71	GPBD 4	27.0	1.0	2.0	3.0	1.0	2.0	3.0	5.0	51.9	17.0	6.2	3.7	60.1	28.9	136.5	164.7	1098.2
72	ICGV 91114	26.0	1.0	3.0	5.0	1.0	5.0	6.0	6.0	43.7	11.0	7.5	4.6	60.9	29.1	116.5	340.6	2270.9
73	TMV 2	29.0	1.0	5.0	7.0	3.0	5.0	7.0	5.0	43.0	8.0	7.0	4.2	56.4	30.1	107.5	251.2	1674.9
74	Faizpur 1-5	26.0	1.0	3.0	4.0	1.0	6.0	8.0	5.0	49.7	18.0	11.2	7.0	62.0	31.4	114.5	371.1	2474.2
75	Mutant 3	31.0	1.0	4.0	6.0	1.0	5.0	6.0	5.0	44.8	9.0	6.0	3.6	58.9	33.3	122.0	171.4	1142.8
76	ICGV 03042	34.0	1.0	2.0	3.0	1.0	2.0	3.0	5.0	43.5	26.0	18.3	11.2	61.5	38.4	119.0	699.0	4660.2
77	ICGV 05100	34.0	1.0	2.0	2.0	1.0	2.0	2.0	8.0	37.0	26.0	15.5	8.4	55.2	33.9	135.6	223.9	1492.9
78	ICGV 06049	25.0	1.0	3.0	4.0	1.0	3.0	5.0	6.0	40.5	15.0	9.9	6.4	63.6	33.6	123.5	203.7	1357.9
79	ICGV 06420	27.0	1.0	3.0	4.0	1.0	3.0	4.0	8.0	46.4	28.0	18.5	11.3	61.1	32.2	136.0	604.8	4032.1
80	ICGV 06424	31.0	1.0	2.0	3.0	1.0	2.0	3.0	7.0	39.9	26.0	16.7	10.4	58.9	30.0	110.5	293.6	1957.4
81	ICGV 07145	30.0	2.0	3.0	5.0	1.0	2.0	3.0	8.0	43.4	25.0	16.3	8.6	54.3	35.6	135.5	190.6	1270.4
82	ICGV 07148	32.0	1.0	2.0	3.0	1.0	2.0	3.0	6.0	45.4	8.0	5.4	2.6	48.4	30.1	114.4	269.2	1795.0
83	ICGV 07166	31.0	1.0	3.0	3.0	1.0	3.0	4.0	7.0	35.2	15.0	7.4	3.6	53.0	35.0	119.6	182.0	1213.3
84	ICGV 06142	32.0	1.0	3.0	6.0	1.0	2.0	4.0	8.0	49.6	28.0	17.7	10.5	59.2	27.6	138.5	427.7	2851.4
85	ICGV 91116	26.0	1.0	4.0	7.0	1.0	4.0	5.0	5.0	57.9	19.0	13.4	8.9	67.9	34.3	116.5	302.6	2017.2
86	ICGV 97045	27.0	1.0	3.0	5.0	1.0	3.0	5.0	5.0	48.0	8.0	7.7	4.3	54.0	39.3	138.5	126.8	845.2
87	ICGV 94118	28.0	1.0	3.0	4.0	1.0	3.0	3.0	5.0	52.2	12.0	7.5	4.5	62.1	40.7	120.0	241.5	1609.8
88	ICGV 05176	31.0	1.0	4.0	6.0	1.0	2.0	4.0	7.0	44.1	7.0	7.6	4.3	57.7	48.6	130.5	163.9	1092.9
89	ICGV 04149	25.0	1.0	5.0	7.0	2.0	6.0	8.0	4.0	38.1	27.0	17.4	9.4	65.6	34.8	126.0	357.0	2379.7
90	ICGV 00351	32.0	1.0	2.0	3.0	1.0	3.0	3.0	4.0	40.5	19.0	10.7	6.6	59.9	32.0	116.5	421.6	2810.6
91	ICGV 92195	29.0	1.0	5.0	7.0	1.0	4.0	6.0	6.0	49.1	14.0	5.3	2.8	55.7	22.9	110.1	128.5	856.8
92	ICGV 87187	29.0	1.0	3.0	4.0	1.0	2.0	3.0	6.0	45.0	16.0	8.6	5.2	58.8	39.5	122.1	128.2	854.8
93	ICGV 86072	32.0	1.0	4.0	6.0	1.0	4.0	6.0	5.0	51.2	20.0	14.4	8.5	58.5	36.5	121.0	298.5	1990.1
94	ICGV 86015	28.0	1.0	4.0	6.0	1.0	4.0	5.0	6.0	37.8	13.0	9.6	6.0	65.3	30.1	117.6	275.5	1837.0
95	ICGV 93437	31.0	1.0	2.0	5.0	1.0	5.0	6.0	5.0	48.5	10.0	7.0	4.2	61.4	26.8	121.0	139.6	930.9
96	ICGV 86143	32.0	1.0	2.0	3.0	1.0	2.0	3.0	7.0	50.6	8.0	5.9	3.5	66.1	29.6	114.5	175.4	1169.4
97	ICGV 90320	29.0	1.0	3.0	5.0	1.0	3.0	4.0	5.0	36.5	19.0	13.9	7.5	54.8	33.8	116.5	367.2	2448.3
98	ICGV 07273	34.0	2.0	5.0	7.0	1.0	4.0	5.0	5.0	44.9	12.0	7.0	4.5	63.5	31.2	122.0	181.3	1208.5
99	49 × 37-91	30.0	2.0	6.0	8.0	1.0	5.0	7.0	6.0	32.9	16.0	13.4	8.6	63.2	47.2	130.5	457.6	3050.6
100	49 × 37-134	32.0	1.0	2.0	4.0	1.0	3.0	4.0	5.0	49.2	14.0	7.4	3.8	55.5	40.6	118.5	149.8	998.4

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
101	49 × 37-135	32.0	1.0	5.0	7.0	1.0	5.0	7.0	6.0	45.2	11.0	9.7	5.2	55.5	24.5	121.0	125.3	835.3
102	49 × 37-97-1	32.0	1.0	3.0	4.0	1.0	4.0	6.0	5.0	36.5	15.0	12.4	5.7	49.5	43.3	129.5	273.0	1820.3
103	49 × 37- 99(b) tall	28.0	1.0	4.0	6.0	1.0	5.0	7.0	6.0	38.9	13.0	13.6	8.5	62.0	54.1	130.5	253.4	1689.5
104	39 × 49 -8	34.0	1.0	4.0	6.0	1.0	3.0	5.0	6.0	38.9	21.0	13.7	7.5	53.6	44.2	116.5	260.9	1739.5
105	39 × 49 -77	29.0	1.0	4.0	6.0	1.0	2.0	4.0	6.0	34.5	22.0	16.8	8.3	48.1	38.5	119.0	254.5	1696.5
106	49 × 39-20-2	30.0	1.0	5.0	7.0	1.0	4.0	6.0	4.0	31.6	10.0	9.7	5.8	59.6	43.9	127.5	303.5	2023.6
107	49 × 39-21-2	25.0	1.0	3.0	4.0	1.0	3.0	4.0	6.0	43.1	13.0	7.7	3.1	42.2	28.3	136.0	138.8	925.0
108	49 × 39-8	28.0	1.0	3.0	5.0	1.0	2.0	4.0	6.0	37.2	16.0	10.7	6.3	59.5	34.1	116.4	219.5	1463.1
109	49 M-16	35.0	1.0	3.0	3.0	1.0	2.0	4.0	8.0	44.3	22.0	11.0	6.2	57.2	28.2	136.5	289.8	1931.8
110	49 × 27-19	30.0	1.0	3.0	4.0	1.0	3.0	5.0	4.0	40.9	11.0	8.6	4.5	53.2	41.2	123.0	201.4	1342.5
111	49 × 27-13 (ii)	31.0	1.0	5.0	7.0	1.0	5.0	7.0	5.0	41.7	14.0	15.0	8.1	56.0	47.5	130.5	264.9	1765.8
112	27 × 49- 16	31.0	1.0	3.0	4.0	1.0	4.0	4.0	5.0	66.6	12.0	10.3	6.4	62.6	45.3	123.0	223.4	1489.5
113	27 × 49- 12	27.0	1.0	2.0	5.0	1.0	2.0	4.0	4.0	41.8	14.0	7.5	4.2	55.9	31.1	123.5	147.6	984.0
114	27 × 49- 14	29.0	1.0	3.0	5.0	1.0	3.0	4.0	5.0	49.1	15.0	10.9	6.5	57.6	44.8	123.0	192.0	1280.0
115	27 × 49- 27-1	28.0	1.0	4.0	7.0	1.0	4.0	6.0	5.0	33.2	18.0	14.6	7.3	51.0	45.9	127.5	314.0	2093.3
116	26 M 156-2	34.0	1.0	3.0	5.0	1.0	4.0	6.0	5.0	47.4	26.0	14.7	7.4	48.5	36.2	114.5	215.0	1433.5
117	26 M- 119-1	31.0	1.0	4.0	7.0	1.0	4.0	6.0	6.0	37.2	12.0	8.2	5.2	64.5	33.7	115.5	153.6	1024.2
118	24 M-86	30.0	1.0	3.0	3.0	1.0	3.0	3.0	7.0	42.5	10.0	6.7	3.2	51.2	33.5	136.5	159.1	1060.8
119	MN1-35	31.0	1.0	4.0	6.0	1.0	2.0	4.0	6.0	35.3	4.0	2.7	1.4	47.5	13.6	114.5	174.6	1164.2
120	M 110-14	30.0	1.0	2.0	3.0	1.0	3.0	4.0	7.0	32.3	14.0	9.1	5.3	59.3	37.3	135.1	145.2	968.3
121	M 28-2	32.0	1.0	2.0	3.0	1.0	3.0	5.0	6.0	28.7	17.0	14.8	9.1	60.6	34.4	115.0	305.4	2036.0
122	Somnath	31.0	1.0	3.0	4.0	1.0	3.0	4.0	5.0	53.7	16.0	9.1	5.4	59.0	29.6	121.0	167.0	1113.1
123	TG 41	33.0	1.0	3.0	5.0	1.0	4.0	6.0	5.0	43.0	22.0	13.7	8.4	60.1	51.3	123.9	251.2	1674.4
124	TG 42	31.0	1.0	4.0	6.0	1.0	3.0	5.0	6.0	32.0	16.0	11.0	6.2	56.2	51.9	119.9	280.7	1871.6
125	TG 49	26.0	1.0	4.0	7.0	1.0	3.0	6.0	6.0	31.1	24.0	17.2	10.5	61.3	43.9	114.9	340.0	2266.6
126	TG LPS 4	32.0	1.0	3.0	4.0	1.0	2.0	5.0	4.0	43.9	16.0	12.8	7.1	53.0	43.3	117.0	292.4	1949.2
127	TG LPS 7	28.0	1.0	3.0	4.0	1.0	5.0	7.0	4.0	36.6	10.0	7.9	4.3	56.1	41.0	120.0	238.7	1591.6
128	24 × 37-2275	27.0	1.0	4.0	5.0	1.0	3.0	4.0	5.0	40.2	14.0	9.5	4.9	53.6	28.7	124.0	114.8	765.2
129	24 × 39-31 MR	26.0	1.0	3.0	5.0	1.0	3.0	5.0	6.0	44.5	15.0	7.4	3.9	51.8	29.1	135.1	181.9	1212.8
130	26 × M-95-1 RI	28.0	2.0	3.0	6.0	1.0	3.0	4.0	6.0	41.2	18.0	8.7	5.6	63.4	30.3	108.0	153.8	1025.5
131	26 × 37-IV- 9IR	32.0	1.0	3.0	4.0	1.0	4.0	6.0	5.0	49.6	24.0	16.4	10.6	66.1	34.2	120.0	456.5	3043.6
132	26 × 27-164	32.0	1.0	3.0	5.0	1.0	3.0	5.0	6.0	58.0	15.0	11.5	7.6	63.4	36.5	113.0	435.5	2903.6
133	49 × 39-21-1	30.0	1.0	3.0	5.0	1.0	3.0	5.0	5.0	47.9	15.0	8.6	5.0	57.7	30.2	120.0	199.8	1332.0
134	49 × 39-21-2(a)	33.0	1.0	4.0	6.0	1.0	4.0	6.0	5.0	40.1	23.0	13.8	8.2	58.6	29.2	113.0	286.0	1906.8
135	49 × 39-74	31.0	1.0	3.0	5.0	1.0	3.0	4.0	6.0	44.6	32.0	15.0	9.6	63.0	28.9	115.0	257.9	1719.4

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
136	39× 49-81-1	28.0	1.0	3.0	4.0	1.0	3.0	4.0	5.0	43.3	21.0	14.7	8.1	54.7	31.8	107.0	311.9	2079.4
137	49 × 27-37	29.0	1.0	2.0	3.0	1.0	4.0	6.0	5.0	33.0	12.0	6.1	2.9	49.4	28.2	113.0	133.3	888.4
138	TDG 10	29.0	1.0	4.0	6.0	1.0	5.0	7.0	5.0	36.4	17.0	10.9	6.6	60.3	31.6	120.0	166.8	1111.9
139	TDG 13	29.0	1.0	4.0	4.0	1.0	2.0	3.0	5.0	30.2	12.0	7.9	4.9	63.0	34.7	120.0	169.3	1128.5
140	TDG 14	26.0	1.0	3.0	3.0	1.0	3.0	3.0	6.0	37.8	23.0	16.5	9.8	57.4	38.4	120.0	253.4	1689.2
141	DTG 3	35.0	1.0	3.0	3.0	1.0	3.0	3.0	6.0	39.8	21.0	12.0	7.4	61.8	34.2	121.0	324.2	2161.4
142	DTG 15	28.0	1.0	5.0	7.0	1.0	4.0	6.0	6.0	37.3	21.0	13.5	8.8	64.5	29.2	118.0	189.3	1262.3
143	M 28-2	31.0	1.0	3.0	4.0	1.0	3.0	4.0	5.0	33.3	14.0	10.3	5.8	55.0	37.1	115.4	230.2	1534.6
144	JL 24	26.0	1.0	4.0	6.0	1.0	4.0	6.0	5.0	47.8	15.0	10.4	6.5	62.4	28.9	114.5	201.9	1345.9
145	TAG 24	26.0	2.0	5.0	8.0	1.0	4.0	6.0	5.0	45.2	13.0	7.2	4.0	58.1	31.0	114.5	144.3	961.7
146	SPS 1	27.0	1.0	2.0	3.0	1.0	2.0	2.0	5.0	41.4	16.0	10.3	6.4	61.6	31.2	114.4	265.0	1766.8
147	SPS 9	25.0	1.0	2.0	3.0	1.0	2.0	3.0	6.0	36.7	8.0	5.6	3.2	50.6	20.7	114.5	89.0	593.1
148	SPS 10	28.0	1.0	2.0	4.0	1.0	5.0	7.0	6.0	40.3	13.0	7.8	5.2	65.7	30.5	112.4	173.2	1154.6
149	SPS 13	32.0	1.0	4.0	6.0	1.0	3.0	5.0	4.0	34.1	21.0	18.2	9.6	54.9	47.7	115.5	253.6	1690.4
150	SPS 14	31.0	1.0	2.0	3.0	1.0	2.0	3.0	4.0	26.1	4.0	2.3	1.5	63.5	16.9	136.5	63.2	421.2
151	SPS 17	30.0	1.0	3.0	5.0	1.0	3.0	5.0	6.0	47.4	10.0	10.3	5.9	57.9	41.6	121.0	326.7	2177.8
152	ICGV 02411	27.0	1.0	3.0	5.0	1.0	2.0	3.0	6.0	51.2	21.0	15.3	8.5	55.4	34.4	135.9	413.1	2753.8
153	ICGV 05155	33.0	1.0	3.0	3.0	1.0	2.0	3.0	5.0	44.9	22.0	16.1	10.0	62.8	37.7	112.9	541.6	3610.4
154	ICGV 06100	30.0	2.0	4.0	6.0	1.0	2.0	4.0	7.0	47.5	24.0	20.8	12.2	62.4	41.9	128.0	473.1	3154.2
155	ICGV 07023	27.0	1.0	5.0	7.0	1.0	4.0	6.0	5.0	44.8	10.0	6.0	3.6	56.8	29.7	121.1	169.6	1130.6
156	SunOleic 95R	28.0	1.0	3.0	5.0	1.0	3.0	4.0	5.0	37.4	16.0	10.6	6.7	63.1	32.9	114.0	212.3	1415.3
157	ICG 434	26.0	1.0	4.0	6.0	1.0	5.0	7.0	5.0	42.9	18.0	9.6	5.9	61.7	29.8	125.1	169.5	1130.1
158	ICG 2031	31.0	2.0	5.0	6.0	1.0	3.0	5.0	5.0	41.1	17.0	6.9	4.5	64.8	25.6	114.0	182.1	1214.0
159	ICG 3102	26.0	2.0	5.0	7.0	1.0	4.0	6.0	5.0	41.4	15.0	10.4	6.2	62.4	32.8	125.0	193.5	1289.8
160	ICG 3140	29.0	1.0	3.0	3.0	1.0	3.0	4.0	6.0	42.1	11.0	8.5	5.1	58.4	34.6	122.0	166.1	1107.1
161	ICG 3343	30.0	1.0	5.0	7.0	1.0	3.0	5.0	5.0	47.6	17.0	12.3	7.2	58.3	29.1	121.1	232.9	1552.5
162	ICG 3421	30.0	1.0	4.0	6.0	1.0	4.0	7.0	5.0	47.7	14.0	7.3	4.7	65.0	28.7	112.0	223.7	1491.3
163	ICG 4729	26.0	1.0	5.0	7.0	1.0	5.0	7.0	5.0	48.1	20.0	11.7	7.2	64.0	28.6	121.0	197.0	1313.0
164	ICG 6022	27.0	1.0	2.0	4.0	1.0	3.0	5.0	3.0	69.8	8.0	8.8	3.9	47.0	31.1	114.0	139.3	928.6
165	ICG 6646	31.0	1.0	4.0	6.0	1.0	4.0	6.0	4.0	51.1	5.0	6.9	3.0	43.9	26.6	119.5	93.5	623.1
166	ICG 8517	36.0	1.0	4.0	6.0	1.0	4.0	6.0	4.0	42.8	8.0	7.3	3.9	56.6	29.5	117.5	162.6	1084.2
167	ICG 8751	33.0	1.0	3.0	4.0	1.0	3.0	4.0	3.0	48.7	5.0	3.9	1.9	52.4	26.9	115.5	160.0	1066.4
168	ICG 9315	34.0	1.0	5.0	7.0	1.0	5.0	7.0	5.0	41.7	15.0	9.4	5.6	60.9	29.4	122.0	229.3	1528.8
169	ICG 10036	30.0	1.0	3.0	4.0	1.0	2.0	3.0	4.0	54.2	12.0	7.8	3.4	44.1	21.3	120.5	143.1	954.2
170	ICG 10053	29.0	2.0	3.0	4.0	1.0	3.0	4.0	6.0	52.1	14.0	14.7	8.9	57.0	43.8	114.6	255.1	1700.7

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
171	ICG 10701	31.0	1.0	4.0	6.0	1.0	4.0	6.0	7.0	38.5	17.0	13.4	8.6	64.3	37.8	122.0	260.6	1737.2
172	ICG 11088	34.0	1.0	5.0	7.0	1.0	6.0	8.0	5.0	52.3	10.0	5.8	3.6	59.4	26.8	117.5	113.2	754.4
173	ICG 11651	30.0	1.0	3.0	4.0	1.0	3.0	5.0	5.0	31.0	5.0	3.7	1.8	51.3	33.1	116.1	266.7	1778.0
174	ICG 12625	32.0	1.0	3.0	3.0	1.0	3.0	4.0	4.0	41.7	9.0	6.3	3.2	53.5	26.5	140.0	176.3	1175.7
175	ICG 12991	27.0	1.0	4.0	5.0	1.0	3.0	6.0	7.0	38.5	24.0	14.8	10.3	68.6	29.2	118.0	198.9	1325.7
176	ICG 14985	28.0	1.0	4.0	6.0	1.0	6.0	8.0	6.0	40.2	16.0	11.7	7.2	60.9	40.4	118.5	366.3	2441.7
177	ICG 15415	26.0	1.0	4.0	6.0	1.0	3.0	4.0	5.0	45.7	16.0	10.3	5.8	56.3	25.1	115.6	174.2	1161.2
178	ICG 15419	28.0	1.0	3.0	3.0	1.0	3.0	3.0	4.0	64.4	8.0	10.5	5.2	47.7	35.4	120.9	206.6	1377.4
179	ICGV 01232	33.0	1.0	5.0	7.0	1.0	3.0	4.0	5.0	49.4	14.0	12.6	6.4	51.5	35.9	118.0	212.3	1415.6
180	ICGV 01276	29.0	1.0	4.0	5.0	1.0	2.0	3.0	7.0	47.5	23.0	15.4	9.2	60.2	36.1	136.5	422.1	2813.9
181	ICGV 01328	30.0	1.0	2.0	4.0	1.0	2.0	3.0	5.0	23.8	6.0	3.0	1.5	55.4	20.9	136.5	88.2	587.7
182	ICGV 02022	27.0	1.0	3.0	5.0	1.0	3.0	3.0	6.0	43.8	20.0	12.1	7.2	61.4	30.7	122.0	223.9	1492.5
183	ICGV 02038	29.0	1.0	5.0	7.0	1.0	4.0	5.0	5.0	44.0	18.0	14.0	9.2	70.2	38.4	115.5	224.6	1497.1
184	ICGV 02189	26.0	2.0	3.0	6.0	1.0	3.0	4.0	5.0	37.5	16.0	8.6	5.3	62.6	29.4	116.0	145.4	969.0
185	ICGV 02194	35.0	1.0	5.0	6.0	1.0	3.0	5.0	5.0	46.5	12.0	7.3	4.4	60.1	25.2	114.5	148.2	988.3
186	ICGV 02266	30.0	1.0	4.0	6.0	1.0	3.0	5.0	6.0	35.4	8.0	5.0	2.8	58.3	38.6	114.0	123.2	821.2
187	ICGV 02271	27.0	1.0	3.0	6.0	1.0	3.0	6.0	5.0	46.4	16.0	9.1	5.0	55.9	34.7	114.5	340.5	2270.3
188	ICGV 02286	32.0	1.0	3.0	5.0	1.0	4.0	5.0	4.0	57.3	17.0	11.1	7.4	67.7	32.0	114.5	261.6	1743.9
189	ICGV 86011	26.0	1.0	4.0	6.0	1.0	4.0	6.0	6.0	48.2	20.0	12.4	7.2	59.2	27.1	113.5	227.2	1514.6
190	ICGV 86590	33.0	1.0	3.0	4.0	1.0	2.0	4.0	4.0	48.8	16.0	10.6	5.7	54.2	41.1	121.5	204.7	1364.9
191	ICGV 87160	32.0	1.0	3.0	5.0	1.0	3.0	4.0	5.0	39.7	11.0	6.6	3.3	53.2	26.3	113.5	86.7	577.9
192	ICGV 87354	36.0	1.0	3.0	5.0	1.0	3.0	5.0	5.0	33.9	13.0	8.0	2.8	51.1	19.4	110.4	93.5	623.4
193	ICGV 87378	26.0	1.0	4.0	6.0	1.0	4.0	6.0	5.0	49.2	19.0	15.5	9.3	61.0	30.7	124.5	225.2	1501.2
194	ICGV 87921	32.0	1.0	3.0	5.0	1.0	2.0	4.0	6.0	45.8	23.0	18.7	10.9	56.9	38.3	113.5	468.6	3124.3
195	ICGV 88145	27.0	2.0	5.0	7.0	1.0	4.0	6.0	6.0	58.0	17.0	11.9	7.0	57.7	33.7	124.4	181.9	1212.5
196	ICGV 92267	35.0	2.0	5.0	7.0	1.0	4.0	6.0	6.0	47.6	18.0	12.3	7.6	61.1	33.9	113.6	195.8	1305.4
197	ICGV 93470	28.0	1.0	6.0	8.0	1.0	4.0	6.0	5.0	43.9	17.0	8.8	5.5	62.7	33.8	113.5	162.5	1083.6
198	ICGV 94169	30.0	1.0	4.0	5.0	1.0	4.0	5.0	6.0	45.3	23.0	19.6	12.6	62.5	44.3	124.5	429.7	2864.6
199	ICGV 94361	27.0	1.0	4.0	6.0	1.0	2.0	3.0	5.0	40.5	14.0	9.2	5.4	59.5	36.4	113.5	282.0	1880.0
200	ICGV 95377	26.0	1.0	3.0	5.0	1.0	3.0	6.0	6.0	54.3	12.0	10.3	5.8	57.6	45.7	113.5	198.2	1321.3
201	ICGV 96466	35.0	1.0	5.0	6.0	1.0	2.0	4.0	6.0	34.2	16.0	10.9	6.5	59.4	35.3	112.5	172.0	1146.9
202	ICGV 96468	28.0	1.0	4.0	6.0	1.0	5.0	6.0	6.0	59.7	16.0	15.9	9.4	58.7	44.8	114.5	448.2	2987.8
203	ICGV 97182	34.0	1.0	2.0	3.0	1.0	2.0	3.0	6.0	48.3	28.0	18.4	10.2	56.5	30.4	122.5	314.3	2095.4
204	ICGV 97183	31.0	1.0	4.0	6.0	1.0	3.0	5.0	5.0	32.5	11.0	8.2	4.7	55.2	35.0	113.6	231.4	1542.9
205	ICGV 98294	32.0	1.0	5.0	7.0	1.0	3.0	4.0	5.0	39.0	19.0	14.1	8.0	56.3	35.1	115.5	375.6	2504.0

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
206	Gangapuri	28.0	1.0	4.0	6.0	1.0	3.0	5.0	6.0	48.8	9.0	6.1	3.5	57.5	30.2	113.5	155.9	1039.6
207	ICGS 44	33.0	1.0	4.0	7.0	1.0	4.0	6.0	7.0	38.8	11.0	9.1	5.2	59.5	29.9	120.5	170.3	1135.5
208	ICG 3312	31.0	2.0	5.0	7.0	1.0	3.0	4.0	4.0	37.2	12.0	5.2	3.1	61.4	27.3	113.6	111.7	744.4
209	ICG 14705	31.0	1.0	4.0	5.0	1.0	3.0	4.0	5.0	35.2	15.0	10.8	6.5	62.6	39.1	113.5	270.7	1804.9
210	ICG 3746	30.0	1.0	4.0	6.0	1.0	4.0	6.0	6.0	59.2	23.0	9.8	6.3	65.9	24.7	125.1	168.7	1124.6
211	ICG 4955	28.0	1.0	3.0	4.0	1.0	3.0	4.0	6.0	42.7	22.0	12.8	8.2	64.9	29.9	114.0	146.5	976.7
212	ICG 12879	27.0	1.0	5.0	7.0	1.0	3.0	5.0	5.0	40.0	23.0	13.6	9.2	66.7	27.4	121.0	257.5	1716.9
213	ICG 5221	26.0	1.0	2.0	4.0	1.0	3.0	4.0	5.0	47.5	12.0	11.2	6.5	55.7	37.5	117.1	160.0	1066.6
214	ICG 4543	26.0	2.0	4.0	6.0	1.0	4.0	5.0	5.0	51.0	19.0	9.6	6.1	64.2	28.4	113.1	184.5	1230.3
215	ICG 1834	33.0	1.0	3.0	5.0	1.0	5.0	6.0	5.0	26.5	12.0	8.7	5.6	60.7	26.4	114.5	148.7	991.5
216	ICG 2106	27.0	1.0	3.0	5.0	1.0	2.0	4.0	6.0	42.0	17.0	10.5	6.8	64.6	29.4	114.5	121.5	809.9
217	ICG 9507	29.0	1.0	6.0	8.0	1.0	4.0	6.0	5.0	38.5	11.0	9.4	5.7	62.0	33.8	121.0	286.2	1907.9
218	ICG 1973	26.0	1.0	5.0	7.0	1.0	5.0	7.0	5.0	46.7	18.0	10.1	6.8	66.4	28.0	121.0	239.7	1597.7
219	ICG 3673	29.0	1.0	5.0	6.0	1.0	4.0	7.0	5.0	49.3	9.0	5.8	4.3	60.4	34.5	128.5	138.8	925.2
220	ICG 3584	26.0	1.0	6.0	8.0	1.0	4.0	6.0	6.0	45.4	25.0	15.2	9.1	58.9	34.2	120.0	352.0	2346.6
221	ICG 442	27.0	1.0	4.0	6.0	1.0	5.0	7.0	5.0	49.7	10.0	5.9	3.9	62.6	27.0	118.5	93.6	624.1
222	ICGV 01464	33.0	1.0	3.0	4.0	1.0	2.0	3.0	6.0	45.1	8.0	5.8	2.6	47.9	37.1	136.5	124.3	828.6
223	ICGV 01478	37.0	1.0	5.0	7.0	1.0	2.0	4.0	6.0	33.0	12.0	10.3	5.1	51.2	38.2	126.9	138.9	926.0
224	ICGV 02251	28.0	1.0	4.0	6.0	1.0	4.0	5.0	5.0	40.4	9.0	5.0	3.0	62.4	34.7	125.0	114.0	759.7
225	ICGV 03136	32.0	1.0	4.0	6.0	1.0	2.0	3.0	8.0	36.6	9.0	9.0	5.0	57.3	38.6	118.5	169.9	1132.4
226	ICGV 05198	32.0	1.0	4.0	5.0	1.0	3.0	4.0	5.0	43.3	8.0	9.9	4.7	46.2	39.5	123.0	163.0	1086.9
227	ICGV 06234	31.0	1.0	3.0	5.0	1.0	4.0	6.0	6.0	42.7	8.0	7.7	4.6	57.8	55.2	128.5	163.6	1090.8
228	ICGV 00346	32.0	1.0	3.0	4.0	1.0	2.0	2.0	6.0	44.7	13.0	7.1	4.1	63.3	37.5	114.1	214.5	1429.7
229	ICGV 00362	31.0	1.0	3.0	3.0	1.0	2.0	3.0	7.0	46.5	11.0	5.6	2.8	52.2	23.3	118.5	166.1	1107.2
230	ICGV 00371	33.0	1.0	3.0	4.0	1.0	4.0	5.0	6.0	40.0	19.0	9.1	5.1	54.2	26.8	117.5	197.5	1316.6
231	ICGV 02287	31.0	1.0	2.0	3.0	1.0	3.0	4.0	7.0	44.0	15.0	9.2	5.8	61.4	36.4	114.5	263.4	1755.8
232	ICGV 02298	32.0	1.0	3.0	4.0	1.0	3.0	4.0	8.0	43.5	21.0	15.1	9.3	62.2	39.0	121.0	166.1	1107.4
233	ICGV 02317	34.0	1.0	4.0	5.0	1.0	3.0	4.0	6.0	40.9	16.0	9.2	5.4	59.8	33.2	120.4	367.6	2450.4
234	ICGV 97232	31.0	1.0	4.0	5.0	1.0	3.0	5.0	5.0	35.4	17.0	10.6	6.9	63.9	27.4	125.0	190.0	1266.9
235	ICGV 99051	34.0	1.0	2.0	4.0	1.0	3.0	3.0	8.0	49.7	16.0	8.9	4.5	51.4	29.5	136.4	196.8	1311.8
236	ICGV 99052	31.0	1.0	3.0	4.0	1.0	2.0	3.0	9.0	49.0	28.0	16.4	8.2	53.1	33.5	136.5	204.1	1360.5
237	ICGV 00246	33.0	1.0	3.0	4.0	1.0	2.0	3.0	7.0	46.3	9.0	5.9	3.0	50.8	29.5	136.5	97.4	649.3
238	ICGV 00248	27.0	1.0	2.0	3.0	1.0	2.0	3.0	7.0	43.1	19.0	11.1	6.4	57.3	28.3	135.5	248.5	1656.8
239	ICGV 01361	35.0	1.0	3.0	4.0	1.0	2.0	4.0	9.0	40.1	18.0	12.4	7.9	65.3	30.0	136.5	256.8	1712.0
240	ICGV 02434	28.0	1.0	3.0	4.0	1.0	2.0	3.0	6.0	35.1	7.0	3.0	1.5	51.0	35.5	114.5	55.1	367.3

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
241	ICGV 04087	28.0	1.0	2.0	3.0	1.0	2.0	2.0	9.0	54.9	21.0	14.7	7.5	52.2	27.2	136.5	290.6	1937.6
242	ICGV 06175	30.0	1.0	2.0	3.0	1.0	2.0	3.0	6.0	36.9	14.0	8.1	4.4	55.4	31.6	121.6	157.5	1049.9
243	ICGV 97116	32.0	1.0	2.0	3.0	1.0	2.0	3.0	7.0	39.6	9.0	4.9	2.9	61.0	31.6	122.0	153.3	1021.7
244	ICGV 97128	34.0	1.0	2.0	4.0	1.0	2.0	2.0	9.0	39.5	22.0	11.9	6.7	56.1	29.1	136.5	217.5	1449.9
245	ICGV 98184	35.0	1.0	4.0	4.0	1.0	3.0	3.0	5.0	34.5	12.0	6.5	3.1	48.6	31.7	135.5	225.3	1502.0
246	ICGV 00068	30.0	1.0	3.0	3.0	1.0	2.0	3.0	8.0	42.5	15.0	9.5	4.7	55.1	26.4	136.5	324.0	2159.9
247	ICGV 01495	30.0	1.0	4.0	6.0	1.0	2.0	4.0	6.0	41.5	20.0	18.8	11.3	57.1	42.1	123.0	342.2	2281.6
248	ICGV 05057	28.0	1.0	2.0	3.0	1.0	1.0	2.0	7.0	33.0	13.0	8.8	5.3	59.9	35.8	136.5	183.3	1222.3
249	ICGV 07168	32.0	1.0	3.0	3.0	1.0	2.0	2.0	6.0	34.6	14.0	7.4	4.6	63.5	34.9	121.1	203.7	1358.2
250	ICGV 01265	29.0	1.0	2.0	2.0	1.0	2.0	2.0	9.0	37.8	18.0	11.2	6.3	56.6	37.1	119.0	217.0	1446.6
251	ICGV 98105	34.0	1.0	3.0	3.0	1.0	3.0	4.0	6.0	38.7	20.0	11.6	6.6	55.9	32.8	135.5	314.9	2099.5
252	ICGV 99160	28.0	1.0	2.0	2.0	1.0	2.0	2.0	5.0	48.9	20.0	16.1	9.5	57.8	39.3	136.4	394.4	2629.3
253	ICGV 02323	31.0	1.0	2.0	3.0	1.0	2.0	2.0	9.0	39.5	29.0	21.2	11.9	57.0	35.5	136.5	473.6	3157.5
254	ICGV 04115	33.0	1.0	3.0	3.0	1.0	3.0	3.0	8.0	31.3	10.0	5.6	4.0	60.4	34.1	117.0	104.5	696.5
255	ICGV 05036	30.0	1.0	2.0	3.0	1.0	3.0	3.0	7.0	45.2	27.0	19.9	11.0	55.9	40.2	136.4	388.6	2590.9
256	ICGV 06042	30.0	1.0	3.0	5.0	1.0	3.0	4.0	8.0	48.2	27.0	15.1	9.3	62.8	31.3	114.6	364.2	2427.7
257	ICGV 86564	33.0	1.0	4.0	6.0	1.0	3.0	4.0	7.0	36.4	6.0	4.8	2.5	53.1	43.9	129.4	212.6	1417.0
258	ICGV 98432	30.0	1.0	2.0	3.0	1.0	2.0	3.0	7.0	41.1	10.0	6.7	3.9	59.8	44.6	128.5	170.1	1133.8
259	BAU 13	30.0	1.0	2.0	3.0	1.0	2.0	2.0	8.0	46.5	10.0	10.1	5.1	54.9	48.6	136.5	183.9	1226.0
260	ICGV 87846	35.0	1.0	3.0	4.0	1.0	2.0	3.0	8.0	40.6	13.0	10.2	5.8	56.2	38.6	135.5	358.7	2391.4
261	ICR 48	32.0	1.0	3.0	5.0	1.0	4.0	5.0	8.0	42.3	21.0	16.4	10.5	64.8	35.7	122.0	267.0	1780.3
262	ICGV 86699	31.0	1.0	2.0	3.0	1.0	3.0	3.0	8.0	43.3	12.0	7.3	4.7	58.7	28.2	108.5	142.4	949.6
263	ICGV 98373	31.0	1.0	3.0	5.0	1.0	3.0	5.0	5.0	47.0	9.0	5.3	2.2	43.1	33.5	130.5	178.9	1192.9
264	ICGV 97115	32.0	1.0	3.0	4.0	1.0	3.0	4.0	6.0	36.0	12.0	7.2	3.9	50.2	29.5	116.6	122.7	817.8
265	ICGV 06040	32.0	1.0	3.0	4.0	1.0	3.0	3.0	8.0	39.5	18.0	14.3	8.9	63.8	40.4	123.0	498.3	3321.8
266	ICGV 06099	35.0	1.0	4.0	6.0	1.0	3.0	4.0	7.0	47.2	26.0	20.8	14.0	66.5	42.7	127.5	518.6	3457.5
267	CS 39	33.0	1.0	3.0	5.0	1.0	2.0	3.0	7.0	31.5	12.0	8.1	4.5	55.4	31.8	126.4	141.4	942.9
268	ICGV 05032	28.0	1.0	2.0	3.0	1.0	2.0	3.0	8.0	43.1	20.0	12.8	6.5	52.5	37.1	136.5	330.7	2204.4
269	ICGV 05141	34.0	1.0	2.0	3.0	1.0	3.0	3.0	10.0	45.8	22.0	15.3	9.0	58.7	35.5	136.5	387.2	2581.1
270	ICGV 07359	33.0	1.0	3.0	4.0	1.0	2.0	3.0	7.0	48.1	11.0	9.8	4.6	50.2	42.4	128.0	164.3	1095.3
271	ICGV 07368	33.0	1.0	2.0	3.0	1.0	3.0	4.0	6.0	46.6	9.0	9.3	4.8	53.2	42.1	136.6	246.8	1645.0
272	ICGV 06110	32.0	1.0	3.0	5.0	1.0	5.0	7.0	8.0	35.7	11.0	14.3	7.9	53.9	51.8	134.0	293.1	1954.2
273	ICGV 06188	33.0	1.0	2.0	3.0	1.0	3.0	3.0	7.0	35.8	12.0	10.9	6.3	57.2	50.0	124.5	231.9	1545.8
274	ICGV 00440	33.0	1.0	4.0	6.0	1.0	4.0	5.0	9.0	42.7	11.0	11.6	6.3	52.9	46.9	123.5	210.8	1405.2
275	ICGV 86352	32.0	1.0	3.0	5.0	1.0	4.0	5.0	5.0	49.8	12.0	8.4	4.5	56.8	40.2	114.5	158.4	1055.7

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
276	ICGV 09112	31.0	1.0	4.0	7.0	1.0	3.0	4.0	7.0	38.0	10.0	5.3	3.2	62.2	31.5	124.5	131.6	877.1
277	ICGV 93920	31.0	1.0	2.0	3.0	1.0	2.0	3.0	7.0	30.0	18.0	8.5	4.6	57.5	30.9	115.5	141.0	940.2
278	ICGV 93216	32.0	1.0	4.0	5.0	1.0	3.0	4.0	6.0	42.4	13.0	7.0	4.2	57.7	25.7	124.5	109.1	727.6
279	ICGV 88438	34.0	1.0	3.0	4.0	1.0	2.0	2.0	8.0	34.4	9.0	7.5	4.2	54.4	39.5	129.5	138.4	922.8
280	ICG 11337	29.0	1.0	2.0	3.0	1.0	3.0	3.0	7.0	50.3	9.0	6.7	4.5	56.1	31.0	137.5	109.4	729.1
281	49 × 37-90	33.0	1.0	3.0	4.0	1.0	2.0	4.0	7.0	31.6	14.0	10.1	6.2	60.4	31.1	115.5	268.7	1791.6
282	49 M-2-2	28.0	1.0	3.0	5.0	1.0	2.0	3.0	8.0	50.9	13.0	8.7	5.1	59.0	39.7	137.5	140.7	938.1
283	49 M- 1-1	29.0	1.0	2.0	4.0	1.0	3.0	5.0	5.0	26.5	20.0	15.6	9.7	67.4	54.3	137.5	187.9	1252.5
284	TG 19	31.0	1.0	4.0	6.0	1.0	6.0	8.0	4.0	35.0	17.0	10.4	6.7	62.7	31.8	115.4	232.7	1551.3
285	TG 39	34.0	1.0	5.0	7.0	1.0	5.0	7.0	7.0	30.4	16.0	10.7	5.6	51.7	43.5	122.5	237.1	1580.4
286	TG LPS 3	31.0	1.0	4.0	6.0	1.0	4.0	6.0	6.0	34.1	17.0	13.7	8.7	61.1	51.6	119.5	326.2	2174.6
287	26 × M-223-1	30.0	1.0	4.0	6.0	1.0	3.0	4.0	7.0	41.6	21.0	9.0	4.4	51.8	26.4	108.5	199.5	1329.9
288	SPS 2	35.0	1.0	2.0	3.0	1.0	2.0	3.0	8.0	35.0	14.0	7.6	4.3	55.0	36.0	122.5	127.7	851.3
289	SPS 3	26.0	1.0	5.0	7.0	1.0	2.0	4.0	6.0	64.2	9.0	6.7	4.2	62.7	36.5	114.5	203.5	1356.5
290	SPS 6	27.0	1.0	4.0	6.0	1.0	3.0	5.0	5.0	41.6	16.0	11.6	7.5	66.4	28.1	115.5	256.3	1708.7
291	SPS 7	32.0	1.0	3.0	4.0	1.0	2.0	2.0	8.0	38.3	15.0	7.8	5.4	68.9	40.4	115.5	110.3	735.3
292	SPS 8	30.0	1.0	2.0	3.0	1.0	2.0	2.0	8.0	40.3	21.0	10.0	4.0	54.5	24.6	119.6	160.8	1072.2
293	SPS 11	31.0	1.0	3.0	5.0	1.0	2.0	3.0	9.0	52.0	22.0	16.1	9.4	58.5	27.7	137.5	529.3	3528.5
294	SPS 15	30.0	1.0	2.0	3.0	1.0	2.0	2.0	7.0	47.1	8.0	4.4	2.3	55.7	27.6	137.5	159.2	1061.4
295	SPS 20	33.0	1.0	2.0	5.0	1.0	2.0	3.0	7.0	36.8	17.0	9.4	6.1	66.1	26.9	137.5	136.6	910.8
296	SPS 21	32.0	1.0	4.0	3.0	1.0	2.0	2.0	8.0	44.0	7.0	3.5	1.9	53.0	21.3	137.5	96.5	643.5
297	ICGV 03128	33.0	1.0	3.0	5.0	1.0	3.0	5.0	6.0	39.7	21.0	13.4	8.8	67.2	34.4	122.0	557.8	3718.8
298	TMV 2 NLM	26.0	1.0	4.0	6.0	1.0	3.0	5.0	6.0	41.7	16.0	9.3	5.7	61.8	30.4	121.9	136.1	907.4
299	ICG 1668	26.0	1.0	2.0	5.0	1.0	2.0	5.0	5.0	36.9	14.0	9.1	6.1	65.8	33.0	124.0	235.2	1568.0
300	ICG 8285	34.0	1.0	2.0	3.0	1.0	2.0	3.0	9.0	40.1	10.0	6.0	2.9	50.6	31.3	122.0	99.5	663.1
301	ICG 11426	30.0	1.0	2.0	6.0	1.0	2.0	3.0	5.0	35.1	5.0	2.1	0.9	54.1	24.1	122.0	102.7	684.8
302	ICGV 02290	31.0	1.0	4.0	5.0	1.0	3.0	3.0	7.0	37.0	11.0	6.1	3.6	60.2	33.4	129.0	99.2	661.6
303	ICGV 02446	32.0	1.0	2.0	3.0	1.0	2.0	2.0	7.0	43.4	18.0	10.3	5.9	54.1	32.2	136.9	187.6	1250.4
304	ICG 156	32.0	1.0	2.0	3.0	1.0	3.0	4.0	6.0	30.3	10.0	6.7	4.0	61.8	43.3	122.0	151.7	1011.3
305	ICGS 76	31.0	1.0	2.0	2.0	1.0	2.0	3.0	5.0	36.3	13.0	9.5	5.4	55.5	33.3	115.0	186.4	1242.8
306	ICG 5891	36.0	1.0	3.0	4.0	1.0	3.0	3.0	6.0	32.3	18.0	11.8	7.0	58.8	31.3	121.9	144.8	965.1
307	CSMG 84-1	28.0	1.0	1.0	2.0	1.0	2.0	3.0	7.0	43.1	21.0	13.1	8.2	65.9	29.5	111.0	277.9	1852.6
308	ICG 111	33.0	1.0	3.0	4.0	1.0	3.0	3.0	7.0	36.5	20.0	16.1	8.8	56.8	32.8	126.0	133.5	890.1
309	ICG 14834	33.0	1.0	2.0	3.0	1.0	3.0	3.0	7.0	39.3	18.0	10.5	6.3	56.2	26.2	120.0	245.4	1636.0
310	ICG 11322	34.0	1.0	2.0	5.0	1.0	4.0	5.0	6.0	36.2	15.0	8.2	5.1	61.9	31.2	124.0	187.9	1252.6

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
311	ICG 532	35.0	1.0	3.0	4.0	1.0	3.0	3.0	6.0	30.0	10.0	5.3	3.0	52.4	30.3	118.0	99.7	665.0
312	ICG 12509	29.0	1.0	3.0	5.0	1.0	3.0	4.0	5.0	40.4	8.0	5.2	2.9	48.4	40.3	124.0	99.6	664.2
313	ICG 12672	33.0	1.0	5.0	7.0	1.0	3.0	5.0	4.0	46.0	15.0	8.9	4.9	57.1	24.0	115.0	121.0	806.6
314	ICG 10185	31.0	1.0	3.0	5.0	1.0	4.0	5.0	7.0	54.0	10.0	6.5	3.6	53.7	38.7	123.1	120.9	806.2
315	ICG 2773	29.0	1.0	2.0	4.0	1.0	2.0	3.0	7.0	32.8	5.0	2.5	1.8	49.4	17.6	126.0	74.3	495.6
316	ICG 3027	31.0	1.0	3.0	5.0	1.0	2.0	3.0	8.0	46.2	9.0	6.0	3.2	54.0	33.9	122.1	132.1	880.8
317	ICG 5745	32.0	1.0	3.0	5.0	1.0	2.0	3.0	7.0	31.1	11.0	6.4	3.8	62.1	39.9	126.0	112.4	749.1
318	ICG 14482	36.0	1.0	2.0	3.0	1.0	2.0	4.0	8.0	44.9	7.0	6.2	3.3	50.7	29.3	125.0	131.8	878.6
319	ICG 4527	33.0	1.0	2.0	3.0	1.0	3.0	3.0	7.0	43.3	9.0	5.3	2.8	52.4	36.8	114.9	68.5	456.5
320	ICG 4343	32.0	1.0	2.0	3.0	1.0	2.0	3.0	5.0	36.7	9.0	5.5	2.9	55.8	30.6	119.0	102.3	681.9
321	ICG 13895	31.0	1.0	2.0	4.0	1.0	3.0	5.0	7.0	43.7	11.0	7.4	3.6	49.1	34.1	119.0	120.3	801.9
322	ICG 5663	27.0	1.0	4.0	7.0	1.0	3.0	5.0	6.0	49.3	6.0	3.5	1.7	55.9	37.8	126.0	81.5	543.4
323	ICG 721	34.0	1.0	3.0	4.0	1.0	4.0	5.0	7.0	46.4	13.0	7.3	3.4	49.6	28.1	124.0	110.4	735.9
324	ICG 12276	32.0	1.0	3.0	3.0	1.0	2.0	3.0	5.0	44.6	5.0	2.0	0.8	46.3	22.4	137.0	77.3	515.3
325	ICG 875	29.0	1.0	2.0	3.0	1.0	3.0	5.0	6.0	39.6	13.0	7.0	3.8	52.7	35.2	122.0	116.7	778.2
326	ICG 14475	35.0	1.0	2.0	3.0	1.0	2.0	3.0	5.0	40.7	17.0	8.4	3.9	45.6	27.0	123.0	439.2	2927.7
327	ICG 15190	30.0	1.0	3.0	3.0	1.0	2.0	3.0	8.0	42.4	8.0	4.2	2.0	50.5	30.5	137.0	99.7	664.8
328	ICG 12370	33.0	1.0	3.0	5.0	1.0	2.0	3.0	7.0	46.3	6.0	2.3	1.2	49.4	19.0	119.0	72.4	482.4
329	ICGV 86325	31.0	1.0	3.0	4.0	1.0	2.0	4.0	7.0	39.7	22.0	11.6	7.5	63.9	34.8	120.0	258.6	1723.9
330	ICG 5662	30.0	1.0	2.0	3.0	1.0	2.0	3.0	6.0	41.0	6.0	4.0	1.8	43.7	41.0	122.0	55.8	371.7
331	ICG 9961	32.0	1.0	3.0	4.0	1.0	3.0	4.0	5.0	38.2	13.0	6.4	3.6	58.1	29.9	126.1	149.4	996.1
332	ICG 14466	32.0	1.0	3.0	3.0	1.0	3.0	3.0	6.0	46.1	8.0	3.2	1.7	52.4	24.5	124.0	111.2	741.6
333	ICG 3053	29.0	1.0	4.0	5.0	1.0	3.0	3.0	5.0	36.7	7.0	3.9	2.4	62.6	36.5	137.1	94.4	629.2
334	ICG 6766	32.0	1.0	2.0	3.0	1.0	2.0	3.0	5.0	41.6	4.0	4.3	2.3	54.7	31.8	119.0	87.4	582.6
335	ICG 2381	30.0	1.0	2.0	4.0	1.0	2.0	5.0	7.0	46.3	4.0	2.3	1.3	48.9	28.9	118.0	171.1	1140.9
336	ICG 2857	33.0	1.0	2.0	3.0	1.0	2.0	3.0	7.0	45.0	10.0	7.6	4.1	52.2	25.6	124.0	102.5	683.3
337	ICGV 13238	26.0	1.0	3.0	5.0	1.0	4.0	6.0	5.0	42.3	11.0	7.9	4.9	62.3	29.5	115.0	229.3	1528.5
338	ICGV 13241	30.0	1.0	4.0	6.0	1.0	2.0	4.0	6.0	33.1	10.0	7.1	4.3	59.4	29.7	122.0	116.2	774.5
339	ICGV 13242	31.0	3.0	4.0	6.0	1.0	3.0	5.0	5.0	38.3	12.0	8.7	5.1	55.7	29.4	111.0	196.6	1310.8
340	ICGV 13245	28.0	1.0	4.0	6.0	1.0	3.0	5.0	5.0	39.2	14.0	9.7	6.3	63.0	32.0	112.0	188.6	1257.5
Mean		**30.0**	**1.1**	**3.3**	**4.8**	**1.0**	**3.0**	**4.3**	**6.0**	**42.8**	**16.0**	**10.5**	**6.1**	**58.1**	**33.7**	**122.2**	**238.9**	**1592.3**
CV (%)		**6.09**	**10.54**	**11.80**	**9.52**	**3.54**	**14.62**	**19.96**	**8.01**	**7.52**	**17.91**	**20.12**	**21.93**	**3.91**	**7.29**	**1.10**	**21.58**	**21.58**
LSD at 5 % level		**3.05**	**0.05**	**0.11**	**0.11**	**0.02**	**0.13**	**0.18**	**0.78**	**5.30**	**4.64**	**3.48**	**2.22**	**3.74**	**4.04**	**2.22**	**84.91**	**566.09**

X1= Days to 50% flowering; **X2, X3, X4=** Disease score of late leaf spot at 75, 90 and 105 days after sowing, respectively; **X5, X6, X7=** Disease score of rust at 75, 90 and 105 days after sowing, respectively; **X8=** Number of primary branches per plant; **X9=** Plant height (cm); **X10=** Number of pods per plant; **X11=** Pod yield per plant (g); **X12=**Seed yield per plant (g); **X13=** Shelling percent; **X14=** Hundred seed weight (g); **X15=** Days to maturity; **X16=**Yield per plot (g); **X17=** Yield per hectare (Kg)

Appendix V

Best linear unbiased prediction of mean for nutritional quality traits of Genomic Selection Panel of groundnut evaluated at Jalgaon during rainy 2015

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
1	ICGV 06423	56.4	18.2	32.0	48.5	13.0	2.0	0.7
2	ICGV 07246	54.3	19.9	33.5	46.7	12.6	2.1	0.7
3	ICGV 07247	55.4	20.4	32.6	47.6	12.9	2.2	0.7
4	ICGV 07268	51.9	18.7	39.5	41.2	11.1	2.3	1.0
5	ICGV 01005	52.1	20.0	42.1	39.3	11.0	2.0	1.1
6	ICGV 01060	56.4	19.6	34.8	46.0	11.8	2.9	0.8
7	ICGV 01124	53.2	19.7	38.6	40.3	13.6	1.4	1.0
8	ICGV 02206	56.2	20.5	34.1	46.9	12.6	2.6	0.7
9	ICGV 03397	55.1	20.4	29.3	50.1	13.5	2.4	0.6
10	ICGV 03398	48.9	23.9	29.9	49.0	13.6	2.2	0.6
11	ICGV 04044	53.9	18.1	33.4	47.9	12.6	2.6	0.7
12	ICGV 06347	54.8	19.7	27.1	52.1	13.8	2.3	0.5
13	ICGV 93280	56.6	18.3	33.1	45.9	13.2	2.6	0.7
14	ICGV 95469	55.6	18.0	28.7	49.8	14.0	2.3	0.6
15	ICGV 00387	51.3	18.2	31.3	47.4	13.4	1.9	0.7
16	ICGV 01393	49.4	19.1	40.5	41.3	11.4	1.4	1.0
17	ICGV 02242	49.6	21.0	40.4	39.9	11.9	2.6	1.0
18	ICGV 97058	53.1	19.0	42.9	38.7	11.6	2.2	1.1
19	ICGV 99083	54.3	21.2	37.7	44.2	12.3	2.0	0.8
20	ICGV 00343	51.6	22.2	34.3	46.2	12.6	2.4	0.7
21	ICGV 00349	56.1	18.9	40.3	41.1	11.7	2.3	1.0
22	ICGV 01263	51.6	22.3	43.0	39.0	11.1	2.2	1.1
23	ICGV 03056	56.6	18.8	36.1	45.0	12.8	2.2	0.8
24	ICGV 03064	57.7	18.0	35.4	46.4	12.1	2.6	0.8
25	ICGV 05161	57.0	17.8	33.0	49.0	12.6	2.3	0.7
26	ICGV 05163	58.8	17.0	35.6	47.1	12.1	2.0	0.8
27	ICGV 06422	55.5	18.3	32.7	49.0	12.3	2.3	0.7
28	ICGV 06431	55.0	17.7	42.7	40.5	10.7	2.3	1.1
29	ICGV 07220	57.3	19.0	47.7	36.5	12.7	1.0	1.3
30	ICGV 07223	54.1	20.7	32.7	48.4	12.7	1.9	0.7
31	ICGV 07227	57.8	19.8	27.4	51.3	14.2	2.3	0.5
32	ICGV 07235	55.7	22.0	28.0	51.8	13.3	2.1	0.5
33	ICGV 99233	57.2	18.4	35.7	46.0	12.2	2.3	0.8
34	ICGV 97165	50.6	20.7	33.5	44.9	13.3	2.1	0.8
35	ICGV 99029	53.3	21.3	34.3	45.0	13.0	2.8	0.8
36	ICGV 00191	56.1	17.6	31.3	47.7	13.5	2.8	0.7
37	ICGV 07120	56.1	17.2	30.5	48.2	13.7	2.3	0.6
38	ICGV 97092	50.6	19.0	31.0	48.4	13.1	1.6	0.6
39	ICGV 97120	55.7	19.3	53.7	32.3	12.1	1.5	1.7
40	ICGV 98163	58.7	20.5	28.9	49.0	14.2	2.5	0.6
41	ICGV 00005	58.2	21.0	29.9	48.5	13.8	2.8	0.6
42	ICGV 01273	56.5	19.3	30.6	48.7	13.3	2.2	0.6
43	ICGV 01274	52.5	19.0	38.7	41.7	11.9	1.6	1.0
44	ICGV 02321	58.0	20.8	31.0	47.0	13.6	2.7	0.7
45	ICGV 03043	56.6	17.8	32.4	48.5	13.0	1.9	0.7
46	ICGV 04124	52.1	19.8	34.7	47.0	11.9	1.8	0.7
47	ICGV 00290	53.7	19.8	35.4	45.3	12.1	2.1	0.8
48	ICGV 00321	50.6	25.1	41.6	38.4	11.1	2.4	1.1
49	ICGV 02125	55.3	20.1	37.2	44.5	11.9	1.8	0.8
50	ICGV 02144	48.1	24.6	41.6	38.8	10.9	1.6	1.1
51	ICGV 03184	50.1	23.3	38.8	40.5	11.6	2.3	1.0

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
52	ICGV 03207	56.5	17.6	40.1	42.2	11.7	2.0	1.0
53	ICGV 04018	55.3	22.2	36.4	43.3	12.0	2.9	0.8
54	ICGV 07210	58.2	18.5	40.2	42.2	11.4	2.8	0.9
55	ICGV 07217	54.9	19.2	32.1	48.8	12.4	2.1	0.7
56	ICGV 95290	51.7	23.0	35.5	44.2	12.1	2.4	0.8
57	ICGV 97261	56.6	20.2	40.2	41.6	11.6	2.4	1.0
58	ICGV 97262	53.3	19.5	38.7	41.8	11.9	2.4	0.9
59	ICGV 99181	53.8	20.4	38.0	44.0	11.5	2.4	0.9
60	ICGV 99195	54.2	20.2	28.5	52.1	13.2	2.3	0.6
61	ICGV 89104	54.6	19.9	41.1	40.4	11.8	1.9	1.0
62	ICGS 11	52.9	20.1	35.6	45.6	11.8	2.2	0.8
63	J 11	55.7	19.0	34.0	47.5	12.4	2.1	0.7
64	ICGV 99085	62.5	18.5	45.3	37.0	10.5	3.6	1.2
65	TKG 19A	56.7	17.3	38.5	43.4	11.3	3.0	0.9
66	TPG 41	53.1	18.8	43.6	38.1	10.4	2.7	1.2
67	ICGV 00350	57.1	17.3	31.2	49.3	12.7	2.2	0.6
68	DH 86	53.4	21.9	32.3	47.3	12.6	2.4	0.7
69	ICGV 95058	53.2	18.8	44.6	36.1	11.4	2.2	1.2
70	ICGV 95070	57.6	16.4	36.6	45.1	12.1	2.4	0.8
71	GPBD 4	62.0	17.4	48.2	35.4	10.0	3.3	1.4
72	ICGV 91114	53.0	19.0	45.9	37.4	10.5	2.0	1.2
73	TMV 2	46.1	27.8	45.4	33.0	10.9	2.3	1.4
74	Faizpur 1-5	52.0	22.7	33.9	46.7	12.5	2.3	0.7
75	Mutant 3	54.3	18.0	37.5	43.2	12.2	1.8	0.9
76	ICGV 03042	60.3	16.4	31.5	50.1	13.1	2.0	0.6
77	ICGV 05100	58.7	16.5	32.6	48.8	12.9	1.9	0.7
78	ICGV 06049	52.7	21.4	39.8	42.0	11.8	1.8	0.9
79	ICGV 06420	64.9	16.2	24.8	55.3	14.2	2.6	0.5
80	ICGV 06424	59.8	16.8	32.0	48.6	13.1	2.2	0.7
81	ICGV 07145	54.7	18.8	34.3	46.4	12.5	2.6	0.7
82	ICGV 07148	54.3	17.4	34.0	46.4	13.0	1.9	0.7
83	ICGV 07166	53.1	18.8	35.3	45.8	12.2	2.4	0.8
84	ICGV 06142	58.6	20.6	35.4	46.2	12.1	2.8	0.8
85	ICGV 91116	52.6	23.6	33.7	45.5	12.8	2.0	0.7
86	ICGV 97045	52.9	18.7	37.5	43.0	12.4	2.6	0.9
87	ICGV 94118	53.4	20.2	37.8	40.9	12.8	2.9	0.9
88	ICGV 05176	49.8	24.4	39.2	40.4	11.6	2.5	1.0
89	ICGV 04149	57.0	19.7	39.4	42.5	11.9	2.4	0.9
90	ICGV 00351	58.6	18.5	21.3	57.2	14.1	2.8	0.4
91	ICGV 92195	51.8	18.7	41.1	39.3	11.3	1.6	1.0
92	ICGV 87187	51.9	20.0	43.8	38.3	10.9	1.9	1.2
93	ICGV 86072	51.8	16.5	40.2	41.0	11.7	1.6	1.0
94	ICGV 86015	51.0	20.5	36.1	43.4	12.7	1.9	0.8
95	ICGV 93437	51.1	22.6	34.5	45.9	12.1	2.0	0.8
96	ICGV 86143	55.1	19.1	50.2	32.7	11.5	1.9	1.5
97	ICGV 90320	53.4	16.4	36.3	45.2	11.7	2.3	0.8
98	ICGV 07273	48.3	22.5	41.8	39.8	11.0	1.3	1.1
99	49 × 37-91	52.1	18.6	45.5	36.8	10.6	1.8	1.2
100	49 × 37-134	54.7	19.8	40.6	41.8	11.1	1.7	1.0
101	49 × 37-135	51.6	17.5	43.2	38.4	10.9	1.5	1.1
102	49 × 37-97-1	47.8	21.6	42.1	38.5	11.5	1.5	1.1
103	49 × 37- 99(b) tall	51.7	20.4	44.9	36.8	11.3	1.9	1.2
104	39 × 49 -8	49.6	23.6	40.1	41.3	10.8	1.9	1.0
105	39 × 49 -77	54.5	19.9	36.5	45.1	11.7	2.5	0.8
106	49 × 39-20-2	50.6	19.2	44.8	37.5	10.4	1.8	1.2
107	49 × 39-21-2	51.8	20.6	40.8	39.6	11.5	2.6	1.0

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
108	49 × 39-8	54.0	17.1	47.9	35.4	10.5	1.8	1.4
109	49 M-16	60.8	18.5	36.3	45.4	12.2	2.8	0.8
110	49 × 27-19	49.3	21.0	44.6	36.6	10.3	1.8	1.2
111	49 × 27-13 (ii)	46.2	20.9	43.5	38.4	11.2	1.4	1.2
112	27 × 49- 16	50.9	22.0	41.2	39.4	11.0	2.6	1.1
113	27 × 49- 12	52.8	17.9	44.0	39.1	10.8	1.7	1.1
114	27 × 49- 14	54.3	20.3	41.5	39.5	11.6	2.0	1.0
115	27 × 49- 27-1	50.0	19.0	42.0	40.1	11.1	1.5	1.0
116	26 M 156-2	55.0	18.6	39.8	41.4	12.0	2.3	1.0
117	26 M- 119-1	50.2	23.5	36.9	43.9	11.5	1.8	0.8
118	24 M-86	50.5	23.7	35.2	44.8	12.7	1.9	0.8
119	MN1-35	51.5	20.9	46.7	35.4	11.9	1.2	1.3
120	M 110-14	56.3	19.3	35.4	44.7	12.7	2.8	0.8
121	M 28-2	56.5	19.7	35.6	44.4	12.7	3.0	0.8
122	Somnath	55.1	19.5	33.3	47.4	12.2	2.6	0.7
123	TG 41	50.3	21.2	39.1	42.0	12.1	1.6	0.9
124	TG 42	48.8	20.2	37.0	43.3	12.3	1.6	0.9
125	TG 49	50.0	19.9	45.3	36.5	10.8	1.9	1.2
126	TG LPS 4	48.6	22.1	40.5	40.1	11.6	1.5	1.0
127	TG LPS 7	49.7	19.7	36.4	44.2	11.8	1.6	0.8
128	24 × 37-2275	54.3	20.1	49.2	33.7	9.8	2.5	1.5
129	24 × 39-31 MR	54.7	20.6	39.5	41.9	11.5	2.6	0.9
130	26 × M-95-1 RI	54.4	21.2	36.9	44.1	11.6	2.2	0.9
131	26 × 37-IV- 9IR	50.3	16.7	42.4	39.3	11.3	1.3	1.1
132	26 × 27-164	46.7	20.7	32.2	47.4	12.9	1.4	0.7
133	49 × 39-21-1	52.4	18.2	37.0	45.0	11.9	1.7	0.8
134	49 × 39-21-2(a)	54.9	20.4	41.5	40.1	10.9	2.8	1.0
135	49 × 39-74	57.5	16.5	49.4	34.7	10.0	2.2	1.4
136	39× 49-81-1	55.6	16.7	42.2	40.2	10.9	2.1	1.1
137	49 × 27-37	53.9	19.0	36.6	43.3	12.3	2.4	0.8
138	TDG 10	53.1	21.1	39.8	43.3	11.2	2.5	0.9
139	TDG 13	53.9	20.3	38.9	42.2	11.7	2.0	0.9
140	TDG 14	52.7	21.8	37.1	42.8	11.9	2.1	0.9
141	DTG 3	50.7	19.5	38.1	42.9	11.5	1.5	0.9
142	DTG 15	54.6	17.9	43.8	38.6	11.2	2.0	1.1
143	M 28-2	55.5	21.0	38.6	41.4	12.3	3.3	0.9
144	JL 24	51.5	18.2	42.6	39.3	10.6	1.6	1.1
145	TAG 24	49.8	22.5	43.6	37.8	11.3	1.8	1.2
146	SPS 1	54.2	21.4	40.3	40.7	13.0	1.9	1.0
147	SPS 9	55.8	18.6	39.3	40.5	14.4	1.6	1.0
148	SPS 10	54.4	18.3	40.9	40.2	11.3	2.1	1.0
149	SPS 13	52.5	20.6	39.0	42.1	12.1	1.5	0.9
150	SPS 14	56.3	18.7	43.3	38.9	14.1	1.3	1.1
151	SPS 17	47.5	22.9	44.0	37.3	10.9	2.1	1.2
152	ICGV 02411	58.0	17.8	34.4	46.2	12.7	2.7	0.7
153	ICGV 05155	62.0	16.5	37.4	45.1	11.6	2.6	0.8
154	ICGV 06100	59.3	20.0	32.6	47.0	13.6	2.7	0.7
155	ICGV 07023	54.1	20.6	40.2	40.7	11.3	2.3	1.0
156	SunOleic 95R	54.2	19.0	80.5	5.1	7.0	1.9	15.7
157	ICG 434	52.6	22.3	31.4	48.3	12.9	2.0	0.7
158	ICG 2031	51.6	18.5	45.8	36.5	10.5	1.6	1.3
159	ICG 3102	55.0	19.0	39.3	42.0	11.9	1.8	0.9
160	ICG 3140	51.9	20.1	41.5	39.4	11.4	1.9	1.1
161	ICG 3343	51.9	21.1	38.1	42.7	11.8	1.6	0.9
162	ICG 3421	53.9	18.2	43.0	39.3	10.8	1.8	1.1
163	ICG 4729	53.8	16.6	43.5	37.9	10.7	1.9	1.2

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
164	ICG 6022	58.9	18.0	45.2	43.7	8.8	3.0	1.0
165	ICG 6646	55.1	17.1	43.7	41.6	9.3	3.0	1.1
166	ICG 8517	52.7	21.7	43.2	38.9	13.9	1.1	1.1
167	ICG 8751	48.1	18.3	36.8	43.5	11.6	1.7	0.9
168	ICG 9315	54.6	19.2	42.8	40.4	11.2	2.1	1.1
169	ICG 10036	48.1	18.4	39.2	41.8	11.2	2.1	0.9
170	ICG 10053	51.8	19.8	46.7	35.8	10.5	2.4	1.3
171	ICG 10701	52.9	21.5	35.8	45.4	12.1	2.3	0.8
172	ICG 11088	54.5	18.6	47.0	37.8	9.7	2.1	1.3
173	ICG 11651	50.2	22.6	36.5	43.3	11.9	1.9	0.8
174	ICG 12625	58.9	17.9	49.1	42.7	7.0	2.6	1.2
175	ICG 12991	52.3	18.9	43.7	37.3	11.2	1.7	1.2
176	ICG 14985	50.0	19.0	39.6	41.5	11.4	1.8	1.0
177	ICG 15415	50.7	20.2	37.1	44.9	11.6	2.7	0.8
178	ICG 15419	59.4	21.5	46.4	44.0	6.5	3.9	1.1
179	ICGV 01232	53.4	19.8	33.9	46.4	12.5	2.0	0.7
180	ICGV 01276	53.6	22.8	31.4	48.7	13.0	2.0	0.7
181	ICGV 01328	55.5	20.0	44.6	36.2	14.5	1.0	1.3
182	ICGV 02022	50.8	23.8	34.7	45.7	12.1	2.1	0.8
183	ICGV 02038	49.2	25.1	32.8	45.6	12.7	2.4	0.7
184	ICGV 02189	51.3	21.9	41.0	40.4	11.5	1.8	1.0
185	ICGV 02194	55.5	19.0	37.7	43.3	12.0	2.7	0.9
186	ICGV 02266	53.4	20.3	40.7	39.4	11.8	2.3	1.0
187	ICGV 02271	54.9	24.8	29.3	50.4	13.0	3.1	0.6
188	ICGV 02286	52.9	21.7	32.1	47.5	12.8	2.1	0.7
189	ICGV 86011	52.6	18.3	46.6	35.9	10.4	1.8	1.3
190	ICGV 86590	51.8	20.8	34.5	46.4	12.0	2.3	0.7
191	ICGV 87160	47.1	23.4	44.9	36.3	10.6	1.6	1.3
192	ICGV 87354	50.6	21.1	43.3	36.3	11.7	1.4	1.2
193	ICGV 87378	53.3	18.5	39.4	42.7	11.1	2.2	0.9
194	ICGV 87921	54.3	18.8	32.4	49.3	12.3	2.5	0.7
195	ICGV 88145	53.3	20.4	42.7	40.0	11.0	1.8	1.1
196	ICGV 92267	54.0	19.1	41.6	40.7	11.1	2.4	1.0
197	ICGV 93470	53.2	22.5	38.1	42.4	11.9	2.1	0.9
198	ICGV 94169	55.5	17.2	45.5	36.3	11.2	2.0	1.2
199	ICGV 94361	54.7	21.5	29.7	49.8	13.0	2.3	0.6
200	ICGV 95377	55.5	20.3	40.7	42.6	11.1	2.9	1.0
201	ICGV 96466	51.9	21.6	37.0	42.6	12.4	2.1	0.9
202	ICGV 96468	57.6	18.3	33.8	47.3	12.9	2.8	0.7
203	ICGV 97182	56.5	17.4	32.2	48.4	13.2	2.7	0.7
204	ICGV 97183	53.7	19.7	39.1	41.5	11.6	2.1	1.0
205	ICGV 98294	54.6	22.3	37.0	43.3	11.9	3.4	0.9
206	Gangapuri	50.0	19.1	42.0	38.3	13.7	1.1	1.1
207	ICGS 44	51.6	18.7	33.7	46.5	12.4	1.9	0.7
208	ICG 3312	52.6	18.1	42.2	39.8	11.0	1.8	1.1
209	ICG 14705	54.3	21.5	35.4	44.5	12.5	2.4	0.8
210	ICG 3746	51.4	19.1	43.5	37.6	10.7	1.5	1.2
211	ICG 4955	53.6	19.1	49.7	33.4	12.8	0.3	1.5
212	ICG 12879	52.8	18.8	42.8	39.5	10.9	1.8	1.1
213	ICG 5221	61.0	18.6	44.1	44.0	8.6	2.9	1.0
214	ICG 4543	54.2	17.3	40.6	41.3	11.6	1.9	1.0
215	ICG 1834	52.3	22.9	47.6	31.9	10.7	1.8	1.6
216	ICG 2106	50.8	17.3	44.9	36.6	10.5	1.2	1.3
217	ICG 9507	51.9	24.7	33.6	46.7	12.3	2.3	0.7
218	ICG 1973	52.8	16.6	44.6	38.0	10.5	1.7	1.2
219	ICG 3673	52.2	20.8	41.0	40.6	12.9	1.6	1.1

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
220	ICG 3584	54.9	17.1	46.5	35.6	10.6	2.1	1.3
221	ICG 442	57.1	16.4	43.2	38.2	13.8	0.8	1.1
222	ICGV 01464	49.2	19.3	40.9	37.6	12.7	1.7	1.1
223	ICGV 01478	48.8	20.9	42.3	38.3	11.2	2.5	1.1
224	ICGV 02251	54.1	22.8	36.4	45.0	11.9	2.4	0.8
225	ICGV 03136	48.8	22.2	38.5	40.6	12.0	2.2	1.0
226	ICGV 05198	47.6	25.4	47.4	34.4	10.6	1.7	1.4
227	ICGV 06234	55.4	19.1	47.1	34.6	10.9	2.3	1.4
228	ICGV 00346	55.3	17.9	30.1	50.1	13.4	2.0	0.6
229	ICGV 00362	53.6	22.4	42.4	38.4	11.0	2.9	1.1
230	ICGV 00371	54.8	16.3	29.4	51.2	12.8	2.3	0.6
231	ICGV 02287	53.2	21.1	38.9	41.7	11.9	2.2	0.9
232	ICGV 02298	52.5	17.9	45.4	37.0	10.6	2.3	1.2
233	ICGV 02317	57.9	18.8	30.8	48.2	13.6	2.3	0.6
234	ICGV 97232	52.3	21.6	39.9	42.5	11.2	1.7	1.0
235	ICGV 99051	59.6	16.5	28.5	51.8	13.2	2.5	0.6
236	ICGV 99052	58.6	17.7	32.1	47.0	13.3	2.7	0.7
237	ICGV 00246	60.5	17.0	28.6	51.3	13.5	2.5	0.6
238	ICGV 00248	61.5	16.5	32.4	49.5	12.5	2.9	0.7
239	ICGV 01361	54.2	18.7	36.5	43.0	12.6	1.9	0.9
240	ICGV 02434	51.8	20.6	37.9	41.6	11.9	2.0	0.9
241	ICGV 04087	56.4	19.8	26.7	51.3	13.7	2.5	0.5
242	ICGV 06175	52.4	18.9	32.7	45.2	13.4	2.0	0.7
243	ICGV 97116	50.5	20.0	43.8	37.0	10.6	2.1	1.2
244	ICGV 97128	59.2	17.5	27.8	52.3	13.3	2.6	0.5
245	ICGV 98184	54.2	18.2	34.1	46.6	12.9	2.1	0.7
246	ICGV 00068	52.2	22.4	35.7	45.8	11.9	1.9	0.8
247	ICGV 01495	54.8	19.0	39.4	41.1	12.0	2.3	1.0
248	ICGV 05057	54.6	18.7	33.8	45.3	13.0	2.2	0.7
249	ICGV 07168	51.5	19.3	44.6	36.6	10.5	2.4	1.2
250	ICGV 01265	54.7	17.6	40.8	38.3	12.9	2.3	1.1
251	ICGV 98105	56.7	16.5	27.4	52.4	13.8	1.6	0.5
252	ICGV 99160	54.9	19.8	33.8	47.4	12.8	1.9	0.7
253	ICGV 02323	52.2	20.8	33.7	46.7	12.9	1.6	0.7
254	ICGV 04115	56.4	17.6	34.3	46.5	12.2	1.9	0.7
255	ICGV 05036	56.2	19.9	33.8	47.7	12.8	1.9	0.7
256	ICGV 06042	55.8	21.4	34.5	44.1	12.8	2.5	0.8
257	ICGV 86564	50.3	21.4	46.0	35.2	10.6	3.0	1.3
258	ICGV 98432	52.1	19.0	42.6	40.9	10.8	1.9	1.0
259	BAU 13	49.6	21.4	43.7	36.0	11.1	2.7	1.2
260	ICGV 87846	55.4	20.1	31.7	47.9	13.3	2.3	0.7
261	ICR 48	53.1	19.2	40.4	40.0	11.1	2.6	1.1
262	ICGV 86699	58.5	17.7	45.7	38.1	13.3	1.1	1.2
263	ICGV 98373	49.9	18.6	34.3	45.6	12.0	1.9	0.7
264	ICGV 97115	53.1	17.9	36.7	42.9	12.6	2.1	0.9
265	ICGV 06040	58.4	22.6	28.6	50.7	13.9	3.0	0.6
266	ICGV 06099	60.3	19.1	29.8	50.5	14.0	2.8	0.6
267	CS 39	52.0	22.1	36.8	41.9	12.4	2.3	0.9
268	ICGV 05032	59.1	17.7	31.3	49.7	13.5	2.3	0.6
269	ICGV 05141	56.4	17.7	42.5	39.0	11.9	2.2	1.1
270	ICGV 07359	48.7	23.0	40.1	38.4	12.3	2.4	1.0
271	ICGV 07368	46.0	23.0	39.3	39.8	12.3	2.0	1.0
272	ICGV 06110	46.2	23.0	38.2	40.7	12.6	1.5	0.9
273	ICGV 06188	51.3	21.4	43.4	38.2	10.9	1.8	1.1
274	ICGV 00440	48.9	20.3	39.1	40.3	11.9	2.7	1.0
275	ICGV 86352	51.9	23.6	37.8	42.3	11.9	2.4	0.9

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
276	ICGV 09112	51.1	19.6	44.5	37.5	11.6	1.9	1.2
277	ICGV 93920	52.9	21.0	38.7	42.6	11.9	2.2	0.9
278	ICGV 93216	49.4	17.9	39.6	40.8	11.1	2.3	1.0
279	ICGV 88438	50.3	18.8	42.6	38.2	11.0	2.2	1.1
280	ICG 11337	59.6	17.1	47.1	37.0	12.8	1.5	1.3
281	49 × 37-90	57.1	16.4	36.8	45.4	12.3	2.6	0.8
282	49 M-2-2	50.1	20.6	39.5	41.2	11.4	1.7	1.0
283	49 M- 1-1	52.3	20.9	34.8	44.5	12.8	2.2	0.8
284	TG 19	59.8	18.7	39.6	42.4	11.5	2.9	0.9
285	TG 39	51.2	22.2	44.6	38.1	10.8	1.7	1.2
286	TG LPS 3	51.8	19.6	45.2	37.9	10.7	1.6	1.2
287	26 × M-223-1	50.8	24.6	32.1	46.8	12.8	2.3	0.7
288	SPS 2	57.2	18.4	45.3	39.1	12.9	1.0	1.2
289	SPS 3	53.8	19.7	43.7	38.9	10.9	2.0	1.1
290	SPS 6	49.0	21.9	43.0	38.3	11.0	1.6	1.1
291	SPS 7	54.4	19.1	42.6	40.2	12.2	1.7	1.1
292	SPS 8	55.7	17.9	46.1	38.0	13.0	1.1	1.2
293	SPS 11	59.0	18.9	36.6	44.5	12.3	2.8	0.8
294	SPS 15	56.5	17.0	47.7	36.4	12.9	1.2	1.3
295	SPS 20	54.2	21.0	48.6	34.5	13.1	0.9	1.5
296	SPS 21	56.0	19.1	46.7	37.1	13.1	0.9	1.3
297	ICGV 03128	56.7	20.9	31.3	47.1	13.6	2.7	0.7
298	TMV 2 NLM	52.7	20.2	37.0	44.7	11.7	2.0	0.8
299	ICG 1668	54.9	18.4	41.8	39.4	11.7	2.6	1.1
300	ICG 8285	52.3	17.4	40.0	39.0	12.0	2.0	1.0
301	ICG 11426	57.3	18.4	52.0	32.1	11.7	1.6	1.6
302	ICGV 02290	54.8	20.2	32.4	47.3	13.4	2.2	0.7
303	ICGV 02446	59.0	18.2	38.5	44.0	9.6	2.9	0.9
304	ICG 156	49.1	20.7	45.3	36.2	10.4	1.8	1.3
305	ICGS 76	52.8	16.9	40.3	40.6	11.5	1.7	1.1
306	ICG 5891	55.3	16.2	40.0	41.7	11.6	2.2	1.0
307	CSMG 84-1	49.7	19.1	43.2	37.6	11.2	1.5	1.2
308	ICG 111	52.2	21.3	37.8	42.6	12.1	2.5	0.9
309	ICG 14834	52.0	19.9	39.1	41.2	12.0	1.8	0.9
310	ICG 11322	52.3	16.6	32.9	48.1	12.3	1.8	0.7
311	ICG 532	52.0	18.1	41.0	40.3	11.4	1.5	1.0
312	ICG 12509	52.9	18.6	38.4	42.1	12.2	1.8	0.9
313	ICG 12672	57.7	18.1	44.5	39.4	12.7	1.2	1.2
314	ICG 10185	52.6	18.7	43.1	37.8	11.4	1.9	1.1
315	ICG 2773	50.2	17.7	41.6	39.7	11.6	1.1	1.1
316	ICG 3027	51.9	18.5	34.1	45.1	12.8	1.6	0.8
317	ICG 5745	49.4	19.1	44.2	36.6	10.6	2.2	1.3
318	ICG 14482	59.3	18.2	56.9	30.7	11.2	1.4	2.0
319	ICG 4527	51.9	20.0	34.1	45.9	12.3	2.0	0.7
320	ICG 4343	51.7	19.4	41.4	39.5	11.3	1.8	1.1
321	ICG 13895	52.1	20.1	34.5	44.2	13.2	2.2	0.8
322	ICG 5663	53.1	20.6	36.1	42.9	12.6	2.3	0.8
323	ICG 721	50.3	18.0	41.1	39.9	11.6	1.6	1.0
324	ICG 12276	51.3	19.3	55.8	26.7	10.6	1.6	2.1
325	ICG 875	52.3	18.8	38.6	40.5	12.6	2.3	0.9
326	ICG 14475	54.2	19.3	53.1	34.1	10.8	1.8	1.5
327	ICG 15190	51.0	19.2	39.8	39.2	12.3	1.9	1.0
328	ICG 12370	48.9	22.3	36.6	41.8	12.2	1.6	0.9
329	ICGV 86325	53.5	16.5	41.8	39.8	11.6	2.0	1.1
330	ICG 5662	53.2	16.7	40.1	41.7	10.9	2.1	1.0
331	ICG 9961	51.6	18.9	43.7	36.7	11.6	1.6	1.2

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
332	ICG 14466	49.6	19.6	41.9	37.3	12.2	1.6	1.1
333	ICG 3053	54.2	18.6	36.7	43.9	12.1	1.8	0.9
334	ICG 6766	51.1	21.2	40.2	39.5	12.0	2.0	1.0
335	ICG 2381	61.3	16.6	42.2	43.9	7.3	3.6	1.0
336	ICG 2857	49.4	21.0	40.8	39.3	11.8	1.5	1.0
337	ICGV 13238	53.8	18.1	40.4	41.1	11.5	2.0	1.0
338	ICGV 13241	52.1	19.5	40.0	40.7	11.8	1.9	1.0
339	ICGV 13242	51.7	22.3	43.0	39.4	11.8	1.4	1.1
340	ICGV 13245	51.7	20.0	42.3	39.7	11.4	1.6	1.1
Mean		**53.7**	**19.6**	**38.9**	**42.2**	**11.9**	**2.1**	**1.0**
CV (%)		**3.9**	**10.5**	**9.0**	**7.3**	**5.4**	**16.8**	**18.2**
LSD at 5 % level		**3.5**	**3.4**	**5.8**	**5.1**	**1.1**	**0.6**	**0.3**

Appendix VI

Best linear unbiased prediction of mean for different traits of Genomic Selection Panel of groundnut evaluated at ICRISAT during rainy 2015

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17	X18
1	ICGV 06423	32.0	2.0	5.0	8.0	2.0	3.0	6.0	6.0	39.2	23.0	16.9	10.5	62.0	27.5	121.8	435.3	2901.7	20.0
2	ICGV 07246	31.0	2.0	5.0	8.0	1.0	4.0	6.0	7.0	32.0	23.0	16.4	9.9	59.8	37.6	106.9	450.5	3003.6	18.3
3	ICGV 07247	32.0	2.0	5.0	8.0	1.0	3.0	6.0	9.0	29.4	22.0	17.3	11.0	63.8	38.2	107.1	433.0	2886.5	18.6
4	ICGV 07268	28.0	5.0	7.0	9.0	5.0	7.0	9.0	6.0	33.8	7.0	6.0	3.9	66.0	39.4	109.1	227.8	1518.6	13.6
5	ICGV 01005	27.0	4.0	7.0	9.0	4.0	7.0	9.0	4.0	47.4	11.0	7.1	3.7	52.3	30.9	108.6	202.2	1348.2	17.1
6	ICGV 01060	29.0	2.0	6.0	9.0	2.0	5.0	7.0	6.0	35.8	21.0	15.7	10.1	63.8	32.7	112.0	357.8	2385.4	14.2
7	ICGV 01124	28.0	4.0	7.0	9.0	2.0	6.0	8.0	7.0	40.0	16.0	10.0	5.6	55.7	25.1	104.1	246.1	1640.8	18.8
8	ICGV 02206	29.0	5.0	7.0	9.0	5.0	7.0	8.0	5.0	35.4	12.0	7.9	5.7	60.6	31.3	114.1	260.9	1739.1	12.4
9	ICGV 03397	32.0	3.0	7.0	8.0	3.0	5.0	7.0	8.0	34.6	15.0	6.5	4.0	60.1	25.0	100.0	255.4	1702.6	14.6
10	ICGV 03398	32.0	4.0	7.0	9.0	2.0	6.0	7.0	7.0	37.7	18.0	11.2	6.5	58.7	29.5	104.0	216.6	1443.8	14.1
11	ICGV 04044	29.0	3.0	7.0	8.0	3.0	6.0	8.0	6.0	30.4	18.0	12.8	6.3	48.9	34.7	108.7	336.5	2243.5	18.3
12	ICGV 06347	29.0	3.0	8.0	9.0	2.0	7.0	8.0	6.0	33.0	15.0	10.7	6.5	60.3	32.7	107.4	261.5	1743.1	11.2
13	ICGV 93280	29.0	3.0	7.0	9.0	2.0	5.0	7.0	6.0	31.0	22.0	12.0	7.2	59.9	26.7	107.0	350.3	2335.6	12.6
14	ICGV 95469	29.0	3.0	7.0	8.0	2.0	6.0	8.0	4.0	32.7	15.0	10.1	7.0	68.7	28.8	99.8	290.0	1933.1	14.4
15	ICGV 00387	32.0	3.0	8.0	9.0	3.0	7.0	8.0	5.0	39.6	13.0	7.7	3.8	51.0	25.3	109.3	234.5	1563.2	13.4
16	ICGV 01393	29.0	3.0	6.0	9.0	3.0	5.0	8.0	5.0	38.9	9.0	9.8	5.0	51.6	48.4	121.1	248.0	1653.1	16.9
17	ICGV 02242	28.0	5.0	7.0	9.0	4.0	4.0	8.0	4.0	38.9	14.0	14.5	7.9	54.2	39.2	113.2	344.4	2295.7	12.4
18	ICGV 97058	29.0	4.0	8.0	9.0	3.0	6.0	8.0	4.0	34.1	10.0	7.8	4.9	63.7	37.2	116.1	222.3	1481.9	12.3
19	ICGV 99083	25.0	5.0	8.0	9.0	4.0	7.0	9.0	6.0	35.5	7.0	5.0	2.2	45.1	28.2	111.6	137.1	914.1	12.5
20	ICGV 00343	29.0	4.0	7.0	9.0	4.0	7.0	9.0	5.0	34.2	8.0	6.6	4.1	59.5	38.7	108.7	194.6	1297.2	18.0
21	ICGV 00349	32.0	5.0	9.0	9.0	5.0	8.0	9.0	5.0	30.2	13.0	7.2	4.6	64.6	25.0	108.0	157.0	1046.5	9.8
22	ICGV 01263	27.0	4.0	7.0	9.0	3.0	7.0	8.0	5.0	40.3	16.0	14.3	8.4	58.4	36.1	104.6	259.8	1732.0	16.5
23	ICGV 03056	30.0	2.0	6.0	8.0	1.0	5.0	8.0	7.0	36.1	24.0	14.6	4.6	48.3	30.3	102.1	347.5	2316.5	16.9
24	ICGV 03064	31.0	2.0	6.0	9.0	2.0	4.0	7.0	6.0	40.9	23.0	19.8	11.1	55.9	37.8	110.0	522.6	3484.0	18.0
25	ICGV 05161	31.0	2.0	7.0	9.0	2.0	5.0	7.0	6.0	38.7	21.0	18.8	10.8	57.3	36.5	115.9	472.5	3149.8	13.1
26	ICGV 05163	29.0	2.0	5.0	7.0	2.0	3.0	6.0	6.0	40.0	20.0	18.3	10.0	54.2	39.7	106.6	471.3	3142.3	21.1
27	ICGV 06422	30.0	2.0	5.0	8.0	2.0	3.0	6.0	6.0	33.1	22.0	17.4	10.8	61.8	35.9	123.6	421.9	2812.9	16.3
28	ICGV 06431	26.0	5.0	8.0	9.0	5.0	8.0	9.0	5.0	38.4	17.0	10.0	5.7	58.9	25.0	101.7	165.9	1105.9	18.6
29	ICGV 07220	30.0	1.0	4.0	5.0	1.0	3.0	4.0	7.0	37.1	20.0	14.5	7.8	53.9	31.1	123.8	262.9	1752.4	24.7
30	ICGV 07223	33.0	2.0	5.0	8.0	2.0	3.0	7.0	6.0	27.2	13.0	8.8	4.7	51.9	36.5	108.8	416.9	2779.1	12.7
31	ICGV 07227	29.0	3.0	7.0	9.0	2.0	4.0	7.0	8.0	31.8	23.0	14.1	8.4	59.3	31.5	106.3	418.3	2788.5	15.0

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17	X18
32	ICGV 07235	32.0	2.0	5.0	7.0	2.0	3.0	6.0	9.0	27.7	19.0	14.7	8.8	59.5	37.3	115.7	421.7	2811.4	15.0
33	ICGV 99233	27.0	4.0	7.0	9.0	3.0	7.0	8.0	5.0	38.5	19.0	15.2	8.7	56.8	35.1	104.8	290.8	1938.6	13.0
34	ICGV 97165	29.0	2.0	7.0	8.0	2.0	4.0	6.0	6.0	39.2	9.0	8.7	4.7	54.5	22.8	102.0	130.8	871.8	15.3
35	ICGV 99029	27.0	2.0	5.0	6.0	1.0	3.0	5.0	6.0	38.2	21.0	14.7	8.7	59.5	34.2	124.5	361.1	2407.3	27.8
36	ICGV 00191	28.0	2.0	5.0	5.0	1.0	4.0	5.0	5.0	40.7	20.0	15.4	9.4	61.1	37.0	124.5	335.8	2238.5	16.9
37	ICGV 07120	31.0	2.0	5.0	6.0	1.0	3.0	5.0	6.0	33.1	17.0	13.6	8.5	62.3	40.9	124.2	369.5	2463.2	25.2
38	ICGV 97092	28.0	4.0	7.0	8.0	2.0	6.0	8.0	5.0	38.7	17.0	10.9	5.8	53.9	30.4	102.5	280.7	1871.4	16.1
39	ICGV 97120	28.0	3.0	7.0	9.0	3.0	4.0	8.0	5.0	37.6	13.0	12.0	5.8	47.3	37.5	107.0	343.0	2286.6	14.7
40	ICGV 98163	28.0	3.0	7.0	9.0	2.0	7.0	8.0	7.0	37.3	19.0	11.7	7.3	62.0	29.7	101.9	328.6	2191.0	14.6
41	ICGV 00005	33.0	3.0	6.0	9.0	2.0	4.0	7.0	7.0	35.3	15.0	10.0	6.5	53.8	30.2	101.7	174.5	1163.1	12.1
42	ICGV 01273	31.0	2.0	4.0	8.0	1.0	3.0	7.0	7.0	29.9	20.0	12.6	8.0	63.6	31.3	97.8	436.2	2908.3	13.4
43	ICGV 01274	30.0	2.0	5.0	7.0	2.0	3.0	6.0	7.0	27.7	16.0	14.5	9.3	63.6	37.1	103.2	403.2	2688.0	13.0
44	ICGV 02321	32.0	2.0	7.0	9.0	2.0	6.0	7.0	8.0	33.6	22.0	16.2	9.9	61.1	34.2	102.1	458.9	3059.3	14.2
45	ICGV 03043	29.0	3.0	5.0	6.0	4.0	3.0	4.0	6.0	32.1	23.0	19.2	11.5	60.3	37.1	124.2	433.2	2887.8	14.8
46	ICGV 04124	29.0	5.0	6.0	9.0	5.0	5.0	8.0	6.0	32.9	14.0	10.9	6.4	59.3	39.0	101.8	225.2	1501.6	13.9
47	ICGV 00290	29.0	4.0	7.0	9.0	4.0	4.0	6.0	4.0	36.0	16.0	13.5	9.2	60.8	34.6	100.5	228.3	1522.1	22.6
48	ICGV 00321	28.0	4.0	8.0	9.0	4.0	8.0	9.0	5.0	36.8	13.0	11.1	6.7	60.4	30.5	108.7	271.7	1811.2	14.2
49	ICGV 02125	26.0	4.0	8.0	9.0	4.0	7.0	9.0	5.0	30.2	9.0	6.0	4.4	66.5	21.6	102.8	108.8	725.2	14.7
50	ICGV 02144	27.0	5.0	7.0	9.0	5.0	7.0	9.0	6.0	37.9	17.0	11.4	6.5	56.4	28.2	102.4	255.6	1703.8	12.2
51	ICGV 03184	27.0	4.0	7.0	9.0	3.0	7.0	8.0	5.0	45.2	22.0	15.2	9.5	62.4	34.6	109.8	339.5	2263.4	16.6
52	ICGV 03207	27.0	4.0	8.0	9.0	3.0	7.0	9.0	5.0	32.7	18.0	8.0	4.5	57.5	24.3	111.4	180.1	1200.4	10.4
53	ICGV 04018	25.0	3.0	8.0	9.0	4.0	7.0	9.0	5.0	44.6	11.0	6.9	4.3	62.3	36.0	102.5	189.1	1260.8	19.6
54	ICGV 07210	27.0	4.0	7.0	9.0	2.0	6.0	9.0	4.0	30.6	22.0	10.4	8.6	68.9	25.3	102.5	279.5	1863.1	10.7
55	ICGV 07217	27.0	3.0	8.0	9.0	3.0	7.0	9.0	4.0	28.9	19.0	10.3	6.5	67.4	25.3	100.0	150.6	1004.1	8.8
56	ICGV 95290	26.0	3.0	8.0	9.0	4.0	7.0	9.0	5.0	33.0	20.0	12.8	8.7	67.7	36.0	105.0	253.3	1689.0	12.0
57	ICGV 97261	27.0	5.0	8.0	9.0	5.0	7.0	9.0	4.0	36.5	21.0	10.5	6.7	67.6	24.9	101.8	177.9	1185.7	14.5
58	ICGV 97262	28.0	4.0	8.0	9.0	4.0	7.0	9.0	5.0	32.4	11.0	6.6	4.7	71.2	24.1	103.2	175.5	1170.2	11.1
59	ICGV 99181	24.0	4.0	8.0	9.0	4.0	8.0	9.0	4.0	33.6	12.0	8.0	5.3	65.8	31.3	102.8	158.9	1059.4	14.6
60	ICGV 99195	28.0	4.0	8.0	9.0	3.0	6.0	8.0	5.0	36.9	10.0	8.9	5.4	60.3	33.1	101.3	213.0	1419.9	10.6
61	ICGV 89104	29.0	5.0	8.0	9.0	5.0	8.0	9.0	4.0	37.9	7.0	3.7	1.9	53.8	16.1	109.4	84.6	564.0	10.9
62	ICGS 11	26.0	5.0	9.0	9.0	5.0	8.0	9.0	6.0	29.1	12.0	6.5	3.9	60.3	28.9	109.2	160.6	1070.4	11.7
63	J 11	25.0	5.0	8.0	9.0	5.0	7.0	9.0	4.0	39.2	19.0	9.6	5.5	58.5	21.7	102.4	176.4	1176.3	15.7
64	ICGV 99085	27.0	2.0	5.0	6.0	2.0	4.0	5.0	6.0	40.4	25.0	14.5	7.9	55.3	31.6	124.5	272.6	1817.4	18.2
65	TKG 19A	28.0	2.0	7.0	8.0	3.0	7.0	9.0	6.0	39.0	14.0	8.3	4.8	57.6	24.9	102.7	228.9	1526.3	15.1
66	TPG 41	27.0	3.0	8.0	8.0	3.0	7.0	9.0	4.0	35.4	7.0	7.5	3.6	46.9	50.8	115.9	200.3	1335.3	18.2

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17	X18
67	ICGV 00350	28.0	3.0	7.0	9.0	3.0	6.0	9.0	5.0	35.8	13.0	10.9	6.4	58.9	29.6	107.6	377.6	2517.2	17.3
68	DH 86	30.0	3.0	6.0	9.0	2.0	6.0	8.0	6.0	31.6	17.0	11.4	6.3	56.5	34.3	102.5	257.6	1717.2	12.8
69	ICGV 95058	30.0	3.0	7.0	8.0	3.0	7.0	9.0	6.0	35.9	10.0	8.4	5.4	63.6	29.0	106.6	274.9	1832.7	14.1
70	ICGV 95070	31.0	4.0	8.0	9.0	3.0	8.0	9.0	5.0	31.4	21.0	10.5	5.1	51.9	28.0	109.6	196.4	1309.2	13.8
71	GPBD 4	27.0	2.0	3.0	4.0	2.0	3.0	3.0	5.0	40.0	21.0	13.3	8.9	66.5	29.9	124.6	291.1	1940.4	20.9
72	ICGV 91114	26.0	5.0	9.0	9.0	5.0	8.0	9.0	4.0	38.2	13.0	9.7	6.1	62.6	30.1	104.7	208.3	1388.6	17.8
73	TMV 2	34.0	3.0	8.0	9.0	4.0	8.0	9.0	5.0	36.5	7.0	10.1	4.4	49.6	30.7	105.9	128.8	858.6	10.7
74	Faizpur 1-5	28.0	4.0	8.0	9.0	4.0	7.0	9.0	5.0	36.6	13.0	8.9	5.7	62.7	33.1	102.4	215.4	1436.2	9.6
75	Mutant 3	28.0	4.0	8.0	9.0	4.0	7.0	9.0	5.0	35.3	13.0	5.7	3.0	57.7	24.5	109.4	124.7	831.5	15.8
76	ICGV 03042	27.0	2.0	5.0	7.0	1.0	4.0	5.0	7.0	31.3	20.0	19.1	10.9	57.2	36.9	107.7	372.5	2483.1	17.5
77	ICGV 05100	31.0	2.0	5.0	7.0	2.0	3.0	4.0	6.0	31.2	20.0	15.5	6.2	59.9	34.2	124.1	358.0	2386.9	21.4
78	ICGV 06049	26.0	5.0	9.0	9.0	5.0	8.0	9.0	5.0	37.4	16.0	8.2	4.4	53.1	26.9	110.2	170.8	1139.0	14.7
79	ICGV 06420	33.0	2.0	5.0	7.0	1.0	4.0	6.0	7.0	33.2	16.0	11.9	7.4	61.5	32.0	124.6	355.1	2367.4	19.2
80	ICGV 06424	29.0	3.0	6.0	7.0	3.0	4.0	5.0	6.0	29.2	23.0	13.9	8.3	59.6	27.4	98.4	361.8	2411.9	24.8
81	ICGV 07145	28.0	2.0	5.0	8.0	1.0	4.0	6.0	6.0	34.7	18.0	11.3	5.8	50.4	32.3	124.5	357.0	2380.2	14.5
82	ICGV 07148	26.0	3.0	8.0	9.0	4.0	8.0	9.0	4.0	38.0	19.0	10.7	6.4	60.6	27.3	101.9	171.7	1144.7	12.0
83	ICGV 07166	28.0	2.0	5.0	8.0	1.0	4.0	7.0	7.0	32.3	21.0	14.3	8.1	56.9	34.5	105.6	382.0	2546.3	16.5
84	ICGV 06142	30.0	2.0	3.0	4.0	1.0	3.0	4.0	7.0	33.0	21.0	21.1	11.8	57.6	35.9	124.5	521.7	3477.8	23.0
85	ICGV 91116	24.0	4.0	8.0	9.0	4.0	7.0	9.0	4.0	40.3	15.0	8.5	5.1	59.4	23.4	102.4	151.3	1009.0	16.4
86	ICGV 97045	31.0	2.0	7.0	8.0	2.0	6.0	8.0	5.0	34.6	10.0	11.0	6.3	56.3	41.1	124.3	252.5	1683.4	21.3
87	ICGV 94118	29.0	2.0	6.0	8.0	1.0	4.0	8.0	5.0	43.0	15.0	11.9	6.6	55.7	39.1	108.2	344.6	2297.3	17.3
88	ICGV 05176	31.0	3.0	7.0	9.0	3.0	6.0	9.0	6.0	42.0	11.0	13.1	8.3	63.8	47.2	116.9	278.3	1855.6	20.2
89	ICGV 04149	26.0	5.0	8.0	9.0	5.0	7.0	9.0	4.0	31.6	17.0	11.7	6.9	61.1	28.5	113.8	243.7	1624.4	11.8
90	ICGV 00351	26.0	2.0	7.0	9.0	2.0	5.0	8.0	4.0	36.7	18.0	13.5	9.4	58.6	32.9	102.5	429.4	2862.3	11.4
91	ICGV 92195	28.0	3.0	7.0	9.0	4.0	7.0	9.0	5.0	38.8	19.0	8.7	5.0	56.7	21.1	97.4	138.4	922.7	20.3
92	ICGV 87187	28.0	3.0	7.0	8.0	2.0	7.0	8.0	8.0	37.0	17.0	9.2	6.4	69.4	33.7	110.3	293.2	1954.7	19.0
93	ICGV 86072	29.0	5.0	8.0	9.0	5.0	8.0	9.0	6.0	32.2	15.0	10.8	5.6	52.7	32.1	109.5	249.4	1662.8	15.4
94	ICGV 86015	26.0	3.0	7.0	9.0	3.0	7.0	9.0	6.0	28.2	15.0	9.6	5.9	61.8	28.9	103.3	248.7	1657.8	18.4
95	ICGV 93437	26.0	4.0	8.0	9.0	4.0	7.0	9.0	4.0	38.2	23.0	10.2	6.5	62.9	23.0	109.6	203.8	1358.8	16.0
96	ICGV 86143	30.0	4.0	8.0	9.0	3.0	8.0	8.0	7.0	31.3	11.0	8.7	5.7	65.7	30.1	102.0	205.9	1372.9	13.2
97	ICGV 90320	27.0	3.0	6.0	9.0	3.0	6.0	8.0	4.0	32.3	13.0	11.0	6.2	56.6	32.5	102.7	369.0	2459.7	12.5
98	ICGV 07273	26.0	4.0	8.0	9.0	3.0	7.0	9.0	5.0	32.5	21.0	11.7	7.5	63.9	22.9	109.6	175.5	1169.7	15.3
99	49 x 37-91	26.0	4.0	8.0	9.0	4.0	8.0	9.0	5.0	25.6	11.0	8.2	4.5	55.3	37.0	116.5	184.9	1232.5	7.9
100	49 x 37-134	26.0	3.0	5.0	8.0	2.0	3.0	8.0	4.0	32.7	13.0	7.2	3.7	52.2	45.1	106.4	218.1	1454.3	15.0
101	49 x 37-135	27.0	4.0	7.0	9.0	4.0	7.0	9.0	5.0	31.6	18.0	7.8	4.7	61.6	20.4	109.1	88.0	586.4	12.9

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17	X18
102	49 x 37-97-1	34.0	4.0	8.0	9.0	4.0	7.0	9.0	4.0	22.6	6.0	6.4	3.4	52.8	43.6	116.7	147.7	984.4	11.2
103	49 x 37- 99(b) tall	34.0	4.0	8.0	9.0	4.0	7.0	9.0	6.0	24.4	10.0	9.2	4.0	42.2	41.8	116.2	155.2	1034.7	13.2
104	39 x 49 -8	27.0	2.0	5.0	8.0	2.0	4.0	8.0	5.0	26.0	9.0	9.2	4.9	53.6	49.9	104.6	283.6	1890.7	10.7
105	39 x 49 -77	25.0	3.0	5.0	7.0	2.0	6.0	7.0	5.0	28.2	19.0	10.4	4.0	39.3	37.5	107.8	297.6	1984.3	11.8
106	49 x 39-20-2	26.0	4.0	8.0	9.0	4.0	7.0	8.0	5.0	26.8	12.0	8.9	4.0	45.1	36.9	114.1	218.3	1455.4	11.3
107	49 x 39-21-2	31.0	4.0	6.0	8.0	4.0	6.0	8.0	5.0	29.5	18.0	7.0	2.7	41.8	33.4	125.0	108.6	723.7	13.1
108	49 x 39-8	32.0	2.0	6.0	8.0	2.0	6.0	8.0	6.0	25.5	12.0	8.7	4.7	53.6	32.6	102.3	227.6	1517.3	11.4
109	49 M-16	29.0	1.0	4.0	4.0	1.0	2.0	3.0	7.0	36.5	29.0	20.3	12.9	64.5	31.7	124.0	564.7	3764.5	18.2
110	49 x 27-19	27.0	4.0	8.0	8.0	3.0	7.0	9.0	5.0	33.4	11.0	6.8	3.0	46.6	30.0	111.5	181.3	1208.4	15.9
111	49 x 27-13 (ii)	25.0	5.0	8.0	8.0	5.0	7.0	9.0	4.0	36.1	9.0	9.0	4.1	46.5	43.6	116.5	267.3	1782.2	16.6
112	27 x 49- 16	29.0	3.0	7.0	9.0	3.0	7.0	9.0	5.0	40.3	10.0	7.6	4.3	56.9	36.6	111.5	175.1	1167.4	15.4
113	27 x 49- 12	28.0	3.0	6.0	8.0	3.0	5.0	8.0	5.0	35.2	28.0	15.9	9.5	64.7	33.9	109.5	167.2	1114.5	12.5
114	27 x 49- 14	28.0	3.0	6.0	9.0	3.0	6.0	9.0	5.0	31.8	10.0	7.4	3.4	50.1	37.0	111.4	143.5	956.9	14.1
115	27 x 49- 27-1	26.0	3.0	8.0	9.0	3.0	8.0	9.0	4.0	20.6	8.0	6.7	3.8	56.1	55.6	113.3	148.5	989.8	8.9
116	26 M 156-2	31.0	3.0	6.0	8.0	3.0	6.0	9.0	5.0	39.6	10.0	5.4	2.9	53.0	29.7	102.4	192.2	1281.3	17.4
117	26 M- 119-1	27.0	6.0	8.0	9.0	6.0	7.0	9.0	4.0	36.6	15.0	8.6	5.8	69.3	24.3	102.6	171.3	1142.0	14.6
118	24 M-86	28.0	2.0	4.0	7.0	2.0	4.0	8.0	7.0	26.1	9.0	8.0	5.0	66.0	33.5	124.7	137.0	913.3	13.3
119	MN1-35	27.0	3.0	7.0	8.0	2.0	6.0	7.0	5.0	37.2	7.0	5.3	2.5	48.7	15.3	102.4	215.3	1435.4	17.9
120	M 110-14	29.0	2.0	5.0	8.0	2.0	5.0	7.0	6.0	30.4	9.0	9.4	5.2	52.1	37.0	121.5	180.0	1199.8	17.8
121	M 28-2	30.0	2.0	4.0	7.0	2.0	5.0	6.0	5.0	27.0	13.0	10.7	6.6	56.5	36.3	100.7	333.7	2224.6	11.3
122	Somnath	27.0	4.0	7.0	9.0	5.0	7.0	9.0	5.0	40.2	19.0	11.1	6.5	59.5	25.4	106.8	241.4	1609.6	16.0
123	TG 41	26.0	3.0	8.0	9.0	3.0	8.0	9.0	4.0	31.9	12.0	9.9	4.9	49.3	50.0	109.8	249.5	1663.1	11.0
124	TG 42	27.0	3.0	7.0	9.0	3.0	6.0	9.0	6.0	31.9	8.0	7.3	4.6	63.4	54.0	106.5	236.3	1575.3	11.4
125	TG 49	25.0	4.0	8.0	9.0	4.0	8.0	9.0	5.0	28.0	10.0	9.2	5.0	56.0	37.3	100.7	188.1	1254.1	8.4
126	TG LPS 4	26.0	4.0	8.0	9.0	3.0	7.0	9.0	5.0	34.4	10.0	7.6	4.2	55.0	34.0	102.8	210.1	1400.9	13.1
127	TG LPS 7	26.0	4.0	8.0	9.0	4.0	8.0	9.0	4.0	35.5	14.0	7.1	3.9	56.7	35.1	106.2	184.2	1228.2	10.0
128	24 x 37-2275	30.0	3.0	7.0	8.0	3.0	6.0	9.0	5.0	31.3	13.0	9.3	5.2	54.5	31.3	110.1	252.7	1684.5	11.5
129	24 x 39-31 MR	28.0	2.0	4.0	6.0	2.0	4.0	5.0	5.0	34.9	13.0	8.7	4.3	50.1	27.1	121.0	272.7	1817.8	19.1
130	26 x M-95-1 RI	25.0	2.0	5.0	7.0	2.0	5.0	5.0	5.0	21.0	19.0	10.3	6.0	57.9	31.9	97.3	417.9	2785.9	16.0
131	26 x 37-IV- 9IR	29.0	3.0	7.0	9.0	3.0	7.0	9.0	5.0	34.0	12.0	7.1	4.2	59.3	28.2	106.4	199.9	1332.5	19.6
132	26 x 27-164	33.0	4.0	7.0	9.0	4.0	7.0	9.0	6.0	34.2	11.0	7.9	5.3	66.4	36.3	99.4	214.8	1431.8	13.1
133	49 x 39-21-1	30.0	3.0	7.0	8.0	3.0	5.0	8.0	4.0	35.9	13.0	8.4	5.3	63.5	29.9	106.0	200.6	1337.6	12.8
134	49 x 39-21-2(a)	27.0	3.0	7.0	9.0	2.0	6.0	9.0	5.0	26.7	16.0	8.9	4.9	55.8	35.4	99.3	204.5	1363.3	7.2
135	49 x 39-74	29.0	2.0	5.0	8.0	2.0	3.0	9.0	5.0	29.9	22.0	10.7	5.7	56.1	25.6	100.9	259.0	1726.6	9.9
136	39 x 49-81-1	28.0	1.0	5.0	6.0	2.0	3.0	8.0	5.0	28.8	26.0	16.8	9.7	57.8	33.6	97.1	358.1	2387.4	12.4

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17	X18
137	49 x 27-37	27.0	3.0	7.0	9.0	3.0	7.0	9.0	5.0	35.8	24.0	18.4	9.8	53.4	30.5	99.1	245.6	1637.4	15.4
138	TDG 10	27.0	4.0	8.0	9.0	4.0	8.0	9.0	5.0	37.7	11.0	7.6	4.7	61.9	29.2	105.9	219.4	1462.9	9.7
139	TDG 13	27.0	2.0	6.0	8.0	2.0	6.0	7.0	5.0	34.3	17.0	10.0	5.7	57.3	30.8	106.2	224.6	1497.3	12.3
140	TDG 14	26.0	3.0	6.0	8.0	2.0	5.0	7.0	5.0	30.5	11.0	8.4	5.1	60.2	39.4	106.1	222.2	1481.2	13.0
141	DTG 3	26.0	4.0	8.0	9.0	4.0	8.0	9.0	6.0	30.1	12.0	6.0	3.6	59.3	24.5	109.2	175.0	1166.9	9.2
142	DTG 15	27.0	4.0	8.0	9.0	3.0	7.0	9.0	5.0	32.8	17.0	10.4	6.5	62.6	28.8	109.8	192.4	1282.7	16.9
143	M 28-2	31.0	2.0	4.0	8.0	2.0	4.0	7.0	5.0	29.3	20.0	5.7	3.5	62.1	37.1	102.6	101.1	674.1	10.6
144	JL 24	30.0	5.0	8.0	9.0	4.0	7.0	9.0	5.0	43.7	23.0	10.0	6.2	62.0	24.3	102.1	192.4	1282.8	15.7
145	TAG 24	28.0	5.0	8.0	9.0	5.0	8.0	9.0	5.0	36.9	11.0	5.4	2.8	58.6	23.2	102.2	110.0	733.4	13.5
146	SPS 1	27.0	2.0	5.0	6.0	3.0	5.0	7.0	5.0	39.1	21.0	13.7	8.8	63.9	29.4	102.4	261.6	1744.3	29.3
147	SPS 9	31.0	3.0	5.0	6.0	3.0	5.0	6.0	6.0	38.0	13.0	8.1	3.9	47.9	23.2	102.3	175.3	1169.0	19.5
148	SPS 10	27.0	6.0	8.0	9.0	6.0	7.0	9.0	5.0	39.4	12.0	6.6	2.6	51.4	21.8	100.8	148.3	988.7	20.1
149	SPS 13	26.0	3.0	8.0	9.0	3.0	7.0	9.0	5.0	20.9	11.0	10.1	4.7	44.9	41.5	102.1	232.3	1548.9	8.7
150	SPS 14	27.0	2.0	4.0	4.0	2.0	4.0	5.0	7.0	25.5	12.0	7.7	5.0	57.6	24.9	124.3	108.7	724.8	12.1
151	SPS 17	27.0	5.0	7.0	9.0	5.0	7.0	9.0	5.0	34.6	10.0	9.3	4.5	48.3	40.2	110.0	210.8	1405.1	17.6
152	ICGV 02411	29.0	2.0	3.0	5.0	1.0	3.0	4.0	7.0	40.3	23.0	21.0	13.3	63.4	38.4	122.4	458.8	3058.4	26.7
153	ICGV 05155	27.0	2.0	6.0	8.0	2.0	3.0	8.0	7.0	35.9	22.0	15.6	10.0	64.4	37.9	98.7	488.6	3257.3	16.6
154	ICGV 06100	29.0	3.0	7.0	9.0	2.0	6.0	7.0	7.0	39.3	18.0	15.4	7.2	51.8	35.1	114.0	504.1	3360.5	16.3
155	ICGV 07023	26.0	6.0	8.0	9.0	6.0	7.0	9.0	4.0	40.9	16.0	10.2	5.1	53.4	31.0	107.3	184.9	1232.7	16.7
156	SunOleic 95R	27.0	4.0	8.0	9.0	4.0	8.0	9.0	5.0	28.2	12.0	7.1	4.4	62.2	25.7	100.3	146.7	977.8	15.4
157	ICG 434	27.0	5.0	8.0	9.0	5.0	8.0	9.0	4.0	36.5	10.0	6.2	3.1	54.6	25.0	111.2	147.2	981.0	11.4
158	ICG 2031	27.0	4.0	8.0	9.0	4.0	7.0	9.0	6.0	42.2	18.0	8.9	4.1	49.1	25.4	100.0	230.1	1534.2	11.3
159	ICG 3102	25.0	4.0	8.0	9.0	4.0	7.0	9.0	5.0	44.4	14.0	7.5	3.6	46.8	29.2	111.4	164.5	1096.7	14.7
160	ICG 3140	27.0	4.0	8.0	9.0	4.0	8.0	9.0	5.0	43.0	12.0	5.2	2.6	51.7	24.8	108.0	141.5	943.3	11.5
161	ICG 3343	26.0	5.0	8.0	9.0	5.0	7.0	9.0	5.0	35.8	17.0	9.0	4.7	51.6	22.5	106.5	168.2	1121.2	15.2
162	ICG 3421	27.0	5.0	8.0	9.0	5.0	8.0	9.0	5.0	35.2	10.0	4.6	2.6	55.6	19.2	97.5	102.6	683.7	11.1
163	ICG 4729	28.0	4.0	9.0	9.0	5.0	8.0	9.0	4.0	45.2	16.0	7.7	5.0	65.4	20.3	106.6	109.8	732.3	13.3
164	ICG 6022	26.0	2.0	5.0	6.0	2.0	4.0	5.0	4.0	57.0	6.0	8.4	4.8	57.7	33.3	101.6	149.3	995.6	22.6
165	ICG 6646	26.0	3.0	6.0	8.0	3.0	4.0	7.0	4.0	58.2	6.0	5.2	2.8	55.2	28.4	108.0	117.2	781.4	24.2
166	ICG 8517	26.0	5.0	8.0	9.0	5.0	8.0	9.0	5.0	45.7	9.0	8.5	4.7	55.7	28.4	105.9	165.7	1104.5	13.3
167	ICG 8751	27.0	3.0	6.0	8.0	2.0	3.0	7.0	4.0	57.0	15.0	15.7	8.2	52.8	34.0	104.1	312.5	2083.4	23.9
168	ICG 9315	32.0	3.0	8.0	9.0	3.0	8.0	9.0	5.0	38.4	15.0	7.5	4.3	58.8	25.3	111.0	198.6	1324.1	16.8
169	ICG 10036	29.0	3.0	6.0	8.0	2.0	5.0	7.0	4.0	42.1	10.0	10.5	5.8	56.0	25.5	103.8	161.6	1077.3	12.7
170	ICG 10053	27.0	3.0	7.0	9.0	3.0	7.0	9.0	5.0	32.5	13.0	12.2	6.4	52.6	37.2	103.8	207.3	1382.1	15.1
171	ICG 10701	25.0	5.0	8.0	9.0	5.0	8.0	9.0	4.0	25.2	18.0	10.0	5.7	56.5	34.9	111.3	202.5	1350.2	7.1

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17	X18
172	ICG 11088	29.0	4.0	6.0	8.0	3.0	4.0	7.0	4.0	38.0	7.0	7.6	4.9	63.4	27.8	106.2	220.8	1471.8	14.8
173	ICG 11651	28.0	5.0	8.0	9.0	5.0	7.0	9.0	5.0	34.4	12.0	8.6	5.1	59.0	30.3	104.0	240.6	1604.3	11.8
174	ICG 12625	28.0	2.0	5.0	6.0	2.0	3.0	5.0	4.0	46.3	9.0	7.3	3.8	53.9	34.3	126.1	183.4	1222.4	17.0
175	ICG 12991	26.0	5.0	8.0	9.0	5.0	8.0	9.0	5.0	42.2	16.0	6.8	4.3	62.6	22.2	106.0	127.2	847.9	12.2
176	ICG 14985	24.0	4.0	8.0	9.0	4.0	7.0	9.0	6.0	33.8	9.0	6.5	2.9	51.1	22.9	108.2	170.6	1137.1	15.2
177	ICG 15415	25.0	3.0	7.0	8.0	2.0	5.0	7.0	5.0	40.0	14.0	10.6	6.2	59.0	27.0	103.8	299.1	1994.3	13.2
178	ICG 15419	26.0	3.0	6.0	8.0	3.0	5.0	8.0	4.0	59.7	7.0	8.5	4.7	54.2	35.6	109.3	190.2	1268.0	20.3
179	ICGV 01232	26.0	5.0	8.0	9.0	4.0	8.0	9.0	7.0	45.1	17.0	16.8	8.9	52.8	39.1	106.0	342.1	2280.9	19.4
180	ICGV 01276	30.0	4.0	5.0	8.0	4.0	3.0	7.0	6.0	31.9	26.0	19.7	12.1	61.6	37.3	126.0	430.2	2868.3	17.7
181	ICGV 01328	27.0	2.0	4.0	5.0	2.0	5.0	6.0	6.0	33.2	15.0	9.2	6.1	65.7	30.5	126.0	202.6	1350.4	20.3
182	ICGV 02022	27.0	3.0	8.0	9.0	3.0	8.0	9.0	5.0	42.0	13.0	6.9	4.1	58.4	25.6	111.3	176.1	1174.2	11.4
183	ICGV 02038	26.0	5.0	8.0	9.0	5.0	7.0	9.0	4.0	45.0	5.0	3.1	1.9	62.9	25.3	104.1	53.5	356.8	15.0
184	ICGV 02189	25.0	5.0	7.0	9.0	5.0	7.0	9.0	5.0	39.2	20.0	14.2	8.6	60.2	30.6	103.8	231.0	1539.7	17.5
185	ICGV 02194	28.0	4.0	8.0	9.0	3.0	7.0	9.0	4.0	39.1	18.0	8.4	5.0	58.0	26.4	104.0	212.1	1413.8	18.4
186	ICGV 02266	27.0	4.0	8.0	9.0	4.0	8.0	8.0	5.0	45.6	19.0	9.7	5.6	59.3	30.3	104.0	312.8	2085.4	19.8
187	ICGV 02271	26.0	3.0	8.0	8.0	3.0	7.0	9.0	5.0	31.6	16.0	11.4	7.0	61.1	32.5	104.7	286.4	1909.1	12.7
188	ICGV 02286	30.0	2.0	6.0	9.0	3.0	6.0	8.0	5.0	35.3	27.0	19.9	13.5	61.8	33.2	100.3	350.5	2336.6	17.8
189	ICGV 86011	26.0	4.0	8.0	9.0	4.0	7.0	9.0	5.0	39.2	20.0	10.5	6.1	57.6	29.1	99.7	210.6	1403.9	16.2
190	ICGV 86590	29.0	3.0	4.0	6.0	2.0	4.0	5.0	4.0	40.3	15.0	12.4	7.0	56.3	34.6	107.8	265.8	1771.9	14.9
191	ICGV 87160	27.0	3.0	7.0	9.0	4.0	7.0	9.0	5.0	31.6	9.0	4.1	2.5	60.2	21.0	99.2	104.4	696.1	10.1
192	ICGV 87354	28.0	4.0	8.0	9.0	4.0	7.0	9.0	6.0	38.7	10.0	4.8	2.2	46.0	19.1	96.0	105.1	700.5	12.3
193	ICGV 87378	23.0	5.0	8.0	9.0	5.0	7.0	9.0	4.0	40.9	15.0	10.7	6.5	61.6	23.9	110.6	190.5	1270.0	16.2
194	ICGV 87921	27.0	3.0	7.0	9.0	2.0	4.0	7.0	5.0	43.2	19.0	11.8	5.8	49.2	32.7	99.2	237.9	1585.9	16.7
195	ICGV 88145	25.0	5.0	8.0	9.0	5.0	7.0	9.0	5.0	41.2	16.0	12.0	6.4	52.5	26.1	110.2	183.3	1222.2	22.0
196	ICGV 92267	27.0	5.0	8.0	9.0	5.0	7.0	9.0	5.0	39.6	16.0	11.7	6.4	58.7	33.0	99.7	376.9	2512.7	14.7
197	ICGV 93470	25.0	4.0	9.0	9.0	4.0	8.0	9.0	5.0	33.8	16.0	9.5	5.8	59.9	27.8	100.0	201.0	1339.9	16.9
198	ICGV 94169	28.0	3.0	7.0	9.0	3.0	7.0	9.0	6.0	33.1	17.0	12.0	6.7	55.5	36.3	110.0	271.3	1808.4	18.4
199	ICGV 94361	29.0	5.0	8.0	9.0	5.0	8.0	9.0	5.0	36.3	11.0	6.9	4.0	58.1	30.3	99.6	188.7	1257.8	11.1
200	ICGV 95377	31.0	3.0	7.0	8.0	3.0	7.0	8.0	5.0	41.9	14.0	9.6	5.8	62.1	39.9	99.3	259.4	1729.2	15.0
201	ICGV 96466	27.0	4.0	8.0	9.0	3.0	7.0	9.0	4.0	35.3	13.0	8.4	5.3	64.2	33.8	98.6	165.0	1099.7	16.3
202	ICGV 96468	25.0	5.0	8.0	9.0	5.0	8.0	9.0	5.0	37.4	12.0	9.2	5.3	57.5	31.5	100.5	255.4	1702.5	15.7
203	ICGV 97182	27.0	3.0	8.0	9.0	3.0	7.0	7.0	6.0	38.2	17.0	11.1	6.8	60.8	30.6	108.6	286.0	1906.8	17.1
204	ICGV 97183	32.0	4.0	7.0	9.0	4.0	7.0	9.0	5.0	36.2	11.0	8.7	5.0	56.7	30.8	99.7	182.7	1218.0	12.4
205	ICGV 98294	30.0	3.0	8.0	9.0	2.0	6.0	8.0	6.0	43.7	14.0	13.7	8.0	58.6	40.0	101.2	361.6	2410.9	12.6
206	Gangapuri	25.0	3.0	7.0	8.0	3.0	7.0	8.0	5.0	36.9	9.0	8.3	5.2	63.4	27.6	100.1	137.0	913.6	19.6

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17	X18
207	ICGS 44	32.0	4.0	8.0	9.0	4.0	7.0	9.0	6.0	28.8	12.0	7.1	4.3	62.6	25.9	107.0	164.5	1096.5	11.2
208	ICG 3312	27.0	4.0	8.0	9.0	4.0	7.0	9.0	5.0	35.8	21.0	10.0	5.6	55.2	27.8	99.9	197.1	1313.8	12.0
209	ICG 14705	27.0	4.0	7.0	9.0	4.0	7.0	9.0	5.0	30.6	9.0	6.8	4.2	60.0	31.7	99.7	182.9	1219.6	10.1
210	ICG 3746	27.0	5.0	7.0	9.0	5.0	7.0	9.0	4.0	42.4	13.0	6.4	3.7	57.4	17.9	114.4	130.3	868.3	13.4
211	ICG 4955	26.0	4.0	8.0	9.0	4.0	7.0	9.0	5.0	43.0	14.0	7.3	4.7	67.0	29.3	103.9	154.5	1029.9	16.7
212	ICG 12879	26.0	4.0	8.0	9.0	4.0	8.0	9.0	5.0	34.7	21.0	9.4	5.3	55.4	22.7	110.3	174.5	1163.2	13.4
213	ICG 5221	28.0	5.0	7.0	8.0	5.0	6.0	9.0	4.0	50.9	10.0	7.3	4.0	53.6	26.6	106.3	98.5	656.6	19.2
214	ICG 4543	27.0	6.0	8.0	9.0	5.0	7.0	9.0	5.0	41.8	13.0	6.1	3.0	47.8	22.1	102.2	109.4	729.4	13.2
215	ICG 1834	31.0	4.0	7.0	9.0	4.0	7.0	9.0	5.0	36.1	12.0	7.9	5.0	64.4	22.2	104.3	122.8	818.7	13.8
216	ICG 2106	27.0	6.0	9.0	9.0	5.0	8.0	9.0	4.0	36.7	18.0	8.3	5.1	63.5	22.8	103.6	147.0	979.9	12.1
217	ICG 9507	31.0	5.0	8.0	9.0	6.0	7.0	9.0	5.0	37.0	10.0	5.3	2.8	54.2	25.9	110.6	162.8	1085.1	14.6
218	ICG 1973	25.0	5.0	8.0	9.0	5.0	7.0	9.0	4.0	41.9	14.0	6.4	3.3	52.8	20.9	110.6	129.6	864.2	16.1
219	ICG 3673	28.0	4.0	8.0	9.0	4.0	7.0	9.0	4.0	38.9	14.0	6.2	3.8	59.2	22.6	117.9	110.4	735.7	18.3
220	ICG 3584	27.0	5.0	8.0	9.0	5.0	8.0	9.0	5.0	38.7	14.0	6.4	4.1	61.5	24.4	109.9	118.9	792.6	12.6
221	ICG 442	26.0	4.0	8.0	9.0	4.0	7.0	9.0	5.0	42.6	14.0	5.9	3.5	60.0	19.8	107.7	95.6	637.5	14.9
222	ICGV 01464	30.0	3.0	6.0	9.0	2.0	3.0	7.0	6.0	38.9	10.0	11.3	4.7	40.6	44.3	125.4	262.2	1747.7	27.7
223	ICGV 01478	30.0	2.0	7.0	8.0	2.0	7.0	8.0	8.0	33.0	10.0	11.9	5.5	50.3	42.4	116.5	254.2	1694.5	20.4
224	ICGV 02251	28.0	4.0	8.0	9.0	4.0	7.0	9.0	5.0	33.6	17.0	9.3	4.9	63.2	29.4	114.8	136.1	907.5	14.1
225	ICGV 03136	35.0	3.0	6.0	8.0	3.0	5.0	8.0	8.0	36.2	9.0	11.9	5.3	44.8	50.1	107.5	309.1	2060.7	17.8
226	ICGV 05198	29.0	4.0	7.0	9.0	3.0	6.0	8.0	5.0	36.7	7.0	8.7	4.8	57.6	59.0	112.1	295.6	1971.0	15.0
227	ICGV 06234	30.0	4.0	8.0	9.0	3.0	7.0	8.0	5.0	34.6	11.0	9.3	5.0	53.5	42.0	117.8	238.2	1587.8	16.9
228	ICGV 00346	31.0	2.0	6.0	8.0	2.0	4.0	7.0	6.0	35.9	14.0	13.6	6.6	57.7	40.9	103.7	318.0	2120.2	21.2
229	ICGV 00362	34.0	2.0	4.0	6.0	2.0	3.0	4.0	6.0	34.3	19.0	13.5	7.0	50.4	29.5	107.3	336.1	2240.5	24.4
230	ICGV 00371	33.0	3.0	7.0	9.0	3.0	7.0	9.0	5.0	36.9	13.0	8.4	4.3	52.0	28.7	105.3	182.5	1216.7	17.1
231	ICGV 02287	30.0	3.0	7.0	8.0	3.0	5.0	7.0	7.0	37.6	15.0	14.3	6.7	55.6	30.3	102.8	300.2	2001.5	19.3
232	ICGV 02298	34.0	5.0	8.0	9.0	4.0	8.0	9.0	6.0	29.7	9.0	6.8	3.4	52.7	30.0	110.4	157.3	1048.4	12.6
233	ICGV 02317	28.0	2.0	5.0	7.0	2.0	3.0	6.0	7.0	37.3	23.0	17.3	6.1	36.5	32.4	108.5	373.9	2492.4	21.7
234	ICGV 97232	27.0	5.0	8.0	9.0	5.0	8.0	9.0	4.0	34.8	15.0	6.9	4.1	59.1	23.8	113.9	148.9	992.4	15.0
235	ICGV 99051	32.0	2.0	4.0	6.0	1.0	2.0	4.0	5.0	44.0	18.0	16.8	10.2	60.7	43.1	124.7	334.5	2230.0	21.4
236	ICGV 99052	32.0	2.0	4.0	4.0	1.0	2.0	4.0	6.0	48.7	16.0	17.2	10.7	62.2	38.6	124.7	436.4	2909.6	26.2
237	ICGV 00246	32.0	1.0	3.0	4.0	1.0	3.0	4.0	6.0	50.1	14.0	15.4	9.5	61.8	43.0	124.7	324.4	2162.9	27.7
238	ICGV 00248	33.0	2.0	3.0	4.0	2.0	3.0	4.0	5.0	44.9	14.0	12.4	6.6	58.6	37.4	124.9	299.0	1993.4	21.5
239	ICGV 01361	30.0	2.0	5.0	7.0	2.0	3.0	5.0	7.0	32.6	15.0	12.5	7.8	62.5	37.3	124.5	396.6	2644.2	15.9
240	ICGV 02434	30.0	2.0	6.0	8.0	2.0	4.0	7.0	6.0	32.9	23.0	15.3	8.6	55.7	29.9	102.9	353.3	2355.6	15.6
241	ICGV 04087	33.0	2.0	5.0	6.0	2.0	4.0	4.0	7.0	40.7	16.0	13.4	7.5	55.9	35.6	125.3	376.2	2508.2	23.3

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17	X18
242	ICGV 06175	33.0	3.0	5.0	8.0	2.0	4.0	6.0	6.0	33.6	18.0	12.9	7.4	57.2	30.3	109.3	295.8	1971.9	19.2
243	ICGV 97116	35.0	3.0	7.0	9.0	3.0	7.0	9.0	6.0	34.0	7.0	5.2	3.2	61.8	33.1	109.7	128.3	855.6	14.3
244	ICGV 97128	30.0	1.0	5.0	6.0	1.0	3.0	5.0	6.0	39.0	21.0	18.2	11.4	62.0	38.4	125.2	413.1	2754.2	18.6
245	ICGV 98184	30.0	2.0	6.0	8.0	2.0	5.0	6.0	5.0	34.6	22.0	14.9	7.6	51.1	38.7	125.1	279.9	1866.2	16.3
246	ICGV 00068	32.0	2.0	3.0	4.0	1.0	3.0	4.0	6.0	30.8	20.0	17.6	9.5	54.2	32.8	124.8	332.9	2219.5	14.8
247	ICGV 01495	34.0	4.0	6.0	9.0	4.0	6.0	8.0	7.0	38.8	13.0	13.9	8.4	60.2	44.2	111.9	407.8	2718.8	13.9
248	ICGV 05057	30.0	2.0	6.0	6.0	2.0	4.0	5.0	8.0	28.8	19.0	19.6	11.7	59.3	38.9	125.1	278.5	1856.6	16.0
249	ICGV 07168	33.0	3.0	7.0	8.0	3.0	7.0	9.0	6.0	28.2	15.0	10.0	5.7	63.6	34.1	109.2	156.6	1043.9	19.2
250	ICGV 01265	32.0	2.0	6.0	7.0	2.0	3.0	6.0	6.0	31.9	15.0	12.7	7.8	61.5	41.7	107.2	236.3	1575.4	24.8
251	ICGV 98105	30.0	2.0	4.0	7.0	4.0	4.0	6.0	6.0	33.5	17.0	14.2	7.8	55.9	35.8	125.2	345.3	2302.3	24.2
252	ICGV 99160	29.0	2.0	5.0	6.0	2.0	3.0	5.0	6.0	37.9	19.0	17.2	10.5	60.9	39.1	124.9	380.4	2536.2	21.0
253	ICGV 02323	30.0	2.0	5.0	7.0	2.0	3.0	5.0	7.0	30.4	18.0	14.7	9.5	65.1	39.4	125.0	420.6	2803.7	17.1
254	ICGV 04115	30.0	2.0	6.0	9.0	2.0	5.0	7.0	7.0	31.3	23.0	18.6	10.4	56.1	35.3	102.9	275.8	1838.5	21.3
255	ICGV 05036	29.0	2.0	4.0	6.0	1.0	3.0	4.0	7.0	36.2	16.0	15.1	8.4	54.6	37.5	125.5	436.4	2909.1	19.5
256	ICGV 06042	33.0	3.0	7.0	8.0	2.0	6.0	7.0	7.0	34.4	15.0	11.4	7.1	62.0	31.1	103.3	384.5	2563.4	11.7
257	ICGV 86564	36.0	3.0	7.0	9.0	2.0	4.0	8.0	7.0	36.0	7.0	5.9	4.2	54.8	40.3	117.7	150.8	1005.4	16.9
258	ICGV 98432	30.0	3.0	7.0	9.0	3.0	6.0	7.0	6.0	34.0	8.0	8.0	4.6	61.4	29.0	117.9	127.8	852.0	16.5
259	BAU 13	35.0	3.0	6.0	8.0	2.0	5.0	6.0	7.0	47.2	12.0	13.0	7.4	57.7	43.9	124.9	255.3	1702.2	17.1
260	ICGV 87846	31.0	2.0	5.0	6.0	2.0	3.0	4.0	5.0	38.1	12.0	11.6	5.6	55.6	43.1	125.1	324.7	2164.3	23.6
261	ICR 48	32.0	3.0	7.0	9.0	3.0	7.0	9.0	8.0	29.6	15.0	11.2	7.2	64.0	35.5	110.3	254.5	1696.9	14.2
262	ICGV 86699	33.0	1.0	2.0	4.0	1.0	2.0	4.0	6.0	34.7	12.0	9.0	5.2	58.4	33.0	96.8	176.0	1173.1	19.4
263	ICGV 98373	32.0	2.0	6.0	8.0	2.0	4.0	7.0	6.0	33.2	17.0	10.4	5.7	55.4	38.7	118.7	182.6	1217.4	19.3
264	ICGV 97115	32.0	3.0	6.0	9.0	2.0	4.0	7.0	6.0	33.9	22.0	15.1	8.5	55.9	31.0	104.8	265.9	1772.9	15.7
265	ICGV 06040	31.0	3.0	7.0	8.0	2.0	6.0	7.0	7.0	38.3	20.0	13.4	5.9	44.6	41.6	112.3	371.6	2477.1	19.8
266	ICGV 06099	30.0	3.0	7.0	9.0	2.0	6.0	8.0	7.0	38.2	15.0	11.4	6.6	57.4	35.7	117.0	271.0	1806.6	16.4
267	CS 39	33.0	2.0	5.0	8.0	2.0	4.0	8.0	6.0	31.7	16.0	12.0	7.0	59.2	37.8	114.8	329.8	2198.8	22.1
268	ICGV 05032	31.0	2.0	5.0	7.0	2.0	4.0	5.0	7.0	34.8	16.0	13.8	6.7	48.6	36.9	124.8	354.1	2360.6	15.9
269	ICGV 05141	30.0	2.0	4.0	4.0	1.0	3.0	4.0	6.0	32.1	22.0	19.9	12.7	63.9	40.9	124.4	443.9	2959.2	20.1
270	ICGV 07359	32.0	4.0	7.0	9.0	4.0	7.0	8.0	8.0	42.3	17.0	11.6	5.8	50.7	40.0	117.2	247.3	1648.5	21.8
271	ICGV 07368	34.0	4.0	7.0	9.0	3.0	6.0	9.0	6.0	37.0	9.0	8.7	5.7	65.9	51.8	125.0	176.6	1177.6	21.0
272	ICGV 06110	31.0	4.0	8.0	8.0	4.0	8.0	9.0	7.0	30.0	11.0	12.8	6.8	52.6	45.9	122.5	307.3	2048.8	14.6
273	ICGV 06188	30.0	4.0	6.0	8.0	2.0	5.0	8.0	5.0	35.7	11.0	12.7	7.6	56.1	52.0	110.7	235.0	1566.4	13.1
274	ICGV 00440	35.0	4.0	7.0	8.0	4.0	6.0	8.0	7.0	37.7	10.0	10.2	4.5	48.6	49.4	109.8	250.3	1668.4	15.6
275	ICGV 86352	30.0	5.0	8.0	9.0	4.0	7.0	9.0	4.0	37.4	18.0	10.6	6.5	61.7	26.4	100.8	212.3	1415.7	19.0
276	ICGV 09112	32.0	4.0	7.0	9.0	4.0	7.0	9.0	8.0	36.7	18.0	9.8	5.9	60.8	31.4	110.9	260.0	1733.2	15.8

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17	X18
277	ICGV 93920	31.0	2.0	7.0	9.0	2.0	4.0	8.0	7.0	36.3	17.0	10.2	6.1	60.2	27.6	101.8	350.3	2335.1	12.8
278	ICGV 93216	26.0	2.0	6.0	8.0	2.0	6.0	8.0	6.0	31.0	22.0	12.6	7.1	55.8	29.1	110.2	337.7	2251.1	10.4
279	ICGV 88438	32.0	3.0	8.0	9.0	3.0	8.0	9.0	8.0	28.1	11.0	9.1	4.3	48.6	38.5	115.8	127.8	851.7	15.9
280	ICG 11337	32.0	2.0	4.0	6.0	1.0	3.0	4.0	6.0	38.3	9.0	7.5	4.0	54.8	36.7	123.7	179.8	1198.9	23.7
281	49 x 37-90	28.0	4.0	5.0	9.0	3.0	5.0	8.0	6.0	34.7	11.0	7.7	4.6	60.6	34.3	101.9	200.8	1338.4	17.8
282	49 M-2-2	30.0	2.0	6.0	7.0	3.0	5.0	7.0	10.0	33.1	10.0	6.7	3.8	56.7	35.9	123.1	131.3	875.6	21.9
283	49 M- 1-1	33.0	2.0	5.0	6.0	2.0	3.0	4.0	5.0	27.1	13.0	10.6	6.4	59.7	43.3	123.3	223.9	1492.6	16.1
284	TG 19	30.0	4.0	8.0	9.0	4.0	8.0	9.0	5.0	29.7	12.0	7.7	4.9	63.7	23.1	101.0	214.2	1428.2	10.0
285	TG 39	29.0	4.0	8.0	9.0	4.0	7.0	9.0	5.0	21.4	13.0	8.2	3.9	48.0	44.2	108.5	189.9	1266.3	10.6
286	TG LPS 3	32.0	3.0	8.0	9.0	4.0	7.0	9.0	6.0	24.3	10.0	8.3	4.8	56.7	44.6	104.9	205.8	1372.1	20.0
287	26 X M-223-1	25.0	2.0	6.0	8.0	3.0	5.0	8.0	6.0	26.3	19.0	10.9	4.4	49.6	32.6	94.2	266.9	1779.2	10.6
288	SPS 2	32.0	2.0	4.0	5.0	2.0	3.0	4.0	7.0	37.4	15.0	12.3	7.2	58.0	37.4	108.5	321.9	2146.0	23.8
289	SPS 3	26.0	5.0	8.0	9.0	5.0	8.0	9.0	5.0	38.3	15.0	8.7	5.9	60.9	25.1	99.9	140.2	934.9	16.3
290	SPS 6	28.0	5.0	8.0	9.0	5.0	7.0	9.0	4.0	36.2	17.0	10.0	6.1	60.6	25.5	101.5	157.2	1048.0	13.0
291	SPS 7	31.0	1.0	5.0	6.0	1.0	3.0	4.0	8.0	35.4	14.0	13.1	7.8	59.5	34.6	101.8	301.5	2009.7	23.1
292	SPS 8	33.0	1.0	4.0	5.0	1.0	3.0	4.0	6.0	37.4	10.0	9.4	5.4	58.6	37.4	105.5	196.2	1308.2	24.7
293	SPS 11	31.0	2.0	3.0	4.0	1.0	3.0	4.0	8.0	39.6	28.0	20.3	12.7	62.7	30.9	123.9	512.7	3418.1	17.2
294	SPS 15	33.0	3.0	5.0	7.0	1.0	6.0	9.0	6.0	40.5	18.0	13.2	7.6	58.0	33.4	123.4	198.0	1320.1	15.3
295	SPS 20	32.0	1.0	3.0	4.0	1.0	2.0	3.0	6.0	35.8	16.0	12.5	7.4	58.7	36.2	123.4	228.3	1522.1	21.0
296	SPS 21	32.0	2.0	5.0	5.0	1.0	3.0	4.0	7.0	32.6	12.0	10.9	6.3	61.3	29.2	123.5	189.5	1263.3	28.2
297	ICGV 03128	33.0	2.0	6.0	9.0	2.0	4.0	6.0	7.0	32.2	13.0	9.2	6.4	69.4	29.1	108.3	306.8	2045.4	11.1
298	TMV 2 NLM	26.0	5.0	8.0	9.0	5.0	7.0	9.0	5.0	37.3	19.0	10.1	6.2	61.3	29.6	107.8	187.9	1252.4	18.9
299	ICG 1668	26.0	5.0	8.0	9.0	5.0	8.0	9.0	6.0	34.7	13.0	8.0	4.7	58.2	26.6	109.6	196.6	1310.4	18.9
300	ICG 8285	34.0	3.0	7.0	8.0	3.0	6.0	8.0	7.0	32.3	13.0	5.7	3.6	63.1	27.9	107.6	86.7	578.1	16.1
301	ICG 11426	32.0	2.0	6.0	7.0	2.0	4.0	5.0	5.0	27.7	13.0	9.6	5.4	56.0	35.3	108.1	179.8	1198.4	16.2
302	ICGV 02290	33.0	3.0	7.0	9.0	3.0	6.0	9.0	7.0	35.2	11.0	8.4	5.0	59.9	33.2	114.9	201.2	1341.2	16.3
303	ICGV 02446	33.0	2.0	5.0	6.0	1.0	3.0	4.0	7.0	30.8	11.0	10.6	6.4	60.2	36.6	123.0	226.5	1510.3	16.0
304	ICG 156	33.0	3.0	7.0	9.0	3.0	7.0	8.0	6.0	29.9	11.0	8.9	5.4	61.3	35.9	107.7	219.7	1464.8	13.5
305	ICGS 76	32.0	2.0	5.0	8.0	2.0	3.0	7.0	6.0	34.3	13.0	11.7	6.6	56.3	37.8	101.0	289.6	1930.8	20.1
306	ICG 5891	31.0	4.0	7.0	9.0	4.0	7.0	8.0	8.0	31.4	10.0	6.6	3.1	56.8	24.4	108.4	100.8	671.7	12.8
307	CSMG 84-1	27.0	3.0	7.0	8.0	3.0	6.0	8.0	6.0	32.5	14.0	10.3	5.2	50.3	30.6	97.0	222.8	1485.6	15.9
308	ICG 111	36.0	3.0	7.0	8.0	3.0	6.0	8.0	7.0	29.0	6.0	4.0	1.9	51.5	26.0	111.9	71.8	478.8	17.2
309	ICG 14834	34.0	3.0	7.0	9.0	3.0	6.0	8.0	6.0	32.3	9.0	7.4	4.4	61.8	37.5	106.1	127.1	847.5	15.6
310	ICG 11322	30.0	3.0	7.0	9.0	3.0	7.0	9.0	7.0	23.5	13.0	8.3	4.7	63.9	30.2	110.0	142.2	947.7	13.0
311	ICG 532	34.0	3.0	6.0	9.0	3.0	6.0	8.0	9.0	29.9	8.0	7.1	4.3	60.3	43.2	104.2	170.2	1134.8	14.7

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17	X18
312	ICG 12509	33.0	3.0	6.0	8.0	2.0	6.0	8.0	7.0	40.4	9.0	6.4	3.6	56.0	33.2	109.9	98.9	659.1	18.8
313	ICG 12672	26.0	4.0	7.0	9.0	4.0	7.0	9.0	5.0	41.6	16.0	8.9	5.0	55.0	24.9	101.0	150.6	1003.7	16.9
314	ICG 10185	32.0	4.0	7.0	9.0	4.0	7.0	8.0	6.0	34.1	7.0	4.2	2.6	60.8	29.0	109.2	99.1	660.7	19.4
315	ICG 2773	34.0	3.0	8.0	9.0	3.0	7.0	8.0	6.0	25.9	5.0	3.2	1.5	55.5	21.5	111.7	79.1	527.3	14.5
316	ICG 3027	35.0	3.0	7.0	8.0	2.0	6.0	7.0	7.0	32.7	9.0	5.1	2.8	56.0	29.2	108.2	96.0	639.9	20.1
317	ICG 5745	33.0	4.0	7.0	9.0	4.0	7.0	9.0	6.0	29.9	10.0	9.5	5.5	65.9	40.9	112.3	227.1	1513.9	13.4
318	ICG 14482	33.0	3.0	6.0	8.0	3.0	6.0	7.0	8.0	32.2	10.0	8.7	5.1	59.0	36.5	110.9	164.9	1099.5	28.4
319	ICG 4527	31.0	3.0	7.0	8.0	2.0	7.0	8.0	7.0	31.8	9.0	6.0	4.0	67.2	29.7	101.2	135.1	901.0	22.9
320	ICG 4343	35.0	3.0	7.0	9.0	3.0	7.0	9.0	5.0	28.6	5.0	3.4	2.1	65.2	25.2	104.9	90.8	605.0	15.2
321	ICG 13895	36.0	4.0	8.0	9.0	4.0	7.0	9.0	7.0	24.6	4.0	2.7	1.6	59.8	18.3	104.7	69.9	465.8	10.4
322	ICG 5663	32.0	3.0	7.0	9.0	3.0	8.0	8.0	7.0	39.3	9.0	7.6	4.1	54.6	32.3	112.3	120.0	800.0	16.0
323	ICG 721	36.0	4.0	6.0	8.0	4.0	6.0	8.0	6.0	36.8	8.0	4.7	2.7	58.9	28.9	110.7	93.5	623.2	18.4
324	ICG 12276	33.0	3.0	6.0	7.0	2.0	5.0	6.0	5.0	46.4	6.0	5.2	2.7	52.9	26.0	123.4	81.2	541.6	22.2
325	ICG 875	35.0	3.0	7.0	9.0	3.0	6.0	9.0	7.0	28.2	5.0	2.5	1.6	54.0	20.6	108.3	59.2	394.9	19.1
326	ICG 14475	32.0	2.0	6.0	9.0	3.0	6.0	7.0	7.0	34.9	9.0	5.7	3.1	54.7	32.1	108.7	86.4	575.8	23.2
327	ICG 15190	36.0	3.0	7.0	7.0	2.0	5.0	6.0	7.0	36.4	11.0	4.6	2.5	56.7	31.4	123.2	85.9	572.5	17.2
328	ICG 12370	33.0	2.0	5.0	7.0	2.0	4.0	6.0	6.0	30.7	7.0	4.1	2.0	50.6	24.8	105.0	64.7	431.0	17.5
329	ICGV 86325	31.0	2.0	6.0	9.0	2.0	5.0	9.0	7.0	37.1	22.0	12.9	7.7	60.1	34.4	105.9	259.4	1729.6	18.0
330	ICG 5662	35.0	3.0	6.0	8.0	4.0	6.0	8.0	8.0	30.9	5.0	6.2	2.8	45.8	43.1	107.9	142.3	948.8	18.4
331	ICG 9961	37.0	3.0	7.0	9.0	2.0	6.0	8.0	8.0	31.3	17.0	9.0	5.3	61.8	28.5	111.9	164.8	1098.7	12.9
332	ICG 14466	33.0	4.0	8.0	8.0	4.0	7.0	8.0	7.0	33.0	5.0	2.9	1.8	60.0	28.6	110.3	92.7	617.8	24.9
333	ICG 3053	36.0	3.0	7.0	7.0	2.0	6.0	6.0	7.0	34.0	5.0	5.0	2.5	48.7	30.6	122.8	69.8	465.3	16.3
334	ICG 6766	34.0	2.0	6.0	8.0	2.0	6.0	8.0	6.0	34.4	4.0	4.2	2.6	60.6	36.3	105.2	70.7	471.5	18.9
335	ICG 2381	32.0	3.0	7.0	8.0	4.0	5.0	8.0	8.0	40.2	11.0	6.2	3.3	53.1	36.3	103.8	150.6	1004.1	17.4
336	ICG 2857	33.0	3.0	6.0	8.0	3.0	5.0	7.0	7.0	29.1	9.0	5.0	2.2	43.8	24.6	109.8	100.8	672.1	13.6
337	ICGV 13238	27.0	4.0	8.0	9.0	4.0	7.0	9.0	4.0	34.0	17.0	8.9	5.1	58.1	21.0	101.0	158.0	1053.3	14.0
338	ICGV 13241	25.0	6.0	8.0	9.0	6.0	7.0	9.0	4.0	39.5	17.0	11.0	5.3	48.5	30.2	108.2	189.4	1262.8	17.4
339	ICGV 13242	26.0	5.0	9.0	9.0	5.0	8.0	9.0	5.0	36.6	16.0	11.1	7.1	62.8	27.3	97.0	228.5	1523.0	15.2
340	ICGV 13245	26.0	6.0	8.0	9.0	5.0	7.0	9.0	5.0	39.6	13.0	8.3	4.9	58.7	26.4	97.8	167.5	1116.4	19.9
Mean		**29.0**	**3.3**	**6.7**	**8.2**	**3.1**	**5.8**	**7.7**	**6.0**	**35.4**	**14.0**	**10.2**	**5.9**	**57.5**	**32.4**	**109.3**	**235.3**	**1569.0**	**16.1**
CV (%)		**5.4**	**11.7**	**4.9**	**3.7**	**13.2**	**6.6**	**4.7**	**6.9**	**6.6**	**23.4**	**22.7**	**27.2**	**8.4**	**10.8**	**1.9**	**18.1**	**18.1**	**18.7**
LSD at 5 % level		**4.2**	**0.2**	**0.1**	**0.1**	**0.2**	**0.2**	**0.2**	**0.1**	**8.7**	**5.6**	**3.8**	**2.6**	**8.0**	**5.7**	**3.4**	**70.2**	**467.9**	**0.4**

X1= Days to 50% flowering; **X2, X3, X4=** Disease score of late leaf spot at 75, 90 and 105 days after sowing, respectively; **X5, X6, X7=** Disease score of rust at 75, 90 and 105 days after sowing, respectively; **X8=** Number of primary branches per plant; **X9=** Plant height (cm); **X10=** Number of pods per plant; **X11=** Pod yield per plant (g); **X12=**Seed yield per plant (g); **X13=** Shelling percent; **X14=** Hundred seed weight (g**); X15=** Days to maturity; **X16=**Yield per plot (g); **X17=** Yield per hectare (Kg); **X18=** Haulm yield per plant (g)

Appendix VII

Best linear unbiased prediction of mean for nutritional quality traits of Genomic Selection Panel of groundnut evaluated at ICRISAT during rainy 2015

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
1	ICGV 06423	52.2	21.9	35.1	43.4	12.5	1.8	0.8
2	ICGV 07246	49.8	26.8	39.6	39.2	12.0	1.8	1.0
3	ICGV 07247	49.3	26.7	38.5	39.9	12.3	1.9	1.0
4	ICGV 07268	50.1	19.2	41.9	38.2	11.0	2.1	1.1
5	ICGV 01005	49.3	24.6	47.4	34.0	10.5	1.5	1.4
6	ICGV 01060	51.4	24.4	37.0	41.8	11.8	2.4	0.9
7	ICGV 01124	46.4	26.6	51.7	28.2	10.4	1.7	1.7
8	ICGV 02206	50.8	21.7	37.2	41.6	12.2	2.2	0.9
9	ICGV 03397	48.4	25.3	37.2	41.2	12.5	2.3	0.9
10	ICGV 03398	46.4	27.9	40.2	37.9	12.4	2.1	1.1
11	ICGV 04044	48.8	24.8	35.2	43.0	12.6	2.2	0.8
12	ICGV 06347	45.6	24.2	34.1	43.8	12.6	1.3	0.8
13	ICGV 93280	48.6	23.2	39.8	38.8	12.2	1.8	1.1
14	ICGV 95469	47.2	24.7	33.2	44.9	12.7	1.6	0.7
15	ICGV 00387	46.7	22.3	36.6	40.9	12.5	1.7	0.9
16	ICGV 01393	46.8	24.5	48.7	33.1	10.0	1.5	1.5
17	ICGV 02242	46.5	24.6	47.6	31.8	10.8	2.2	1.5
18	ICGV 97058	46.7	23.1	47.6	31.6	11.1	2.0	1.5
19	ICGV 99083	44.8	25.2	41.3	37.4	11.9	1.5	1.1
20	ICGV 00343	46.7	26.3	39.9	38.5	11.7	2.1	1.0
21	ICGV 00349	47.2	25.6	38.2	40.3	12.0	1.5	1.0
22	ICGV 01263	48.1	25.5	50.2	29.7	10.8	1.9	1.7
23	ICGV 03056	52.6	21.5	38.7	40.1	12.0	2.0	1.0
24	ICGV 03064	52.0	24.4	41.0	38.3	11.7	2.3	1.1
25	ICGV 05161	51.6	24.1	40.1	39.2	11.8	2.5	1.0
26	ICGV 05163	54.1	22.6	31.4	46.7	12.8	2.1	0.7
27	ICGV 06422	53.3	22.8	35.4	42.7	12.3	2.1	0.8
28	ICGV 06431	49.0	21.6	48.4	32.3	10.6	0.9	1.5
29	ICGV 07220	51.3	22.7	50.3	30.0	13.0	1.1	1.7
30	ICGV 07223	49.7	25.3	39.7	39.4	11.6	1.7	1.0
31	ICGV 07227	49.8	26.8	37.7	38.5	13.1	2.2	1.0
32	ICGV 07235	50.7	26.3	36.8	42.0	12.2	1.9	0.9
33	ICGV 99233	53.8	22.6	38.6	42.2	11.8	2.5	0.9
34	ICGV 97165	44.1	26.2	36.0	39.4	13.1	1.7	0.9
35	ICGV 99029	49.9	25.4	37.4	38.2	13.4	2.6	1.0
36	ICGV 00191	50.8	24.9	37.9	37.9	13.6	2.9	1.0
37	ICGV 07120	49.9	24.3	35.3	40.9	13.2	2.1	0.9
38	ICGV 97092	46.3	24.8	36.4	40.3	12.6	1.9	0.9
39	ICGV 97120	50.6	24.6	52.3	28.6	13.3	1.4	1.8
40	ICGV 98163	50.8	25.5	34.5	41.8	13.0	2.2	0.8
41	ICGV 00005	51.3	26.7	33.7	42.1	13.3	2.2	0.8
42	ICGV 01273	49.8	25.6	33.4	42.9	12.9	2.1	0.8
43	ICGV 01274	50.3	25.7	35.4	42.9	12.4	1.8	0.8
44	ICGV 02321	50.1	26.0	35.2	41.0	13.1	2.1	0.9
45	ICGV 03043	53.1	22.7	37.5	40.0	13.4	1.8	0.9
46	ICGV 04124	49.6	24.7	35.4	42.6	12.1	1.6	0.8
47	ICGV 00290	50.2	25.4	34.5	43.6	12.2	1.7	0.8
48	ICGV 00321	47.3	27.4	43.9	34.9	11.2	1.5	1.3
49	ICGV 02125	49.0	23.8	41.9	37.7	11.5	1.1	1.1
50	ICGV 02144	51.6	24.5	47.7	33.4	10.7	1.7	1.4
51	ICGV 03184	47.1	27.3	41.5	36.3	11.7	1.7	1.2

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
52	ICGV 03207	49.3	24.1	47.6	33.6	10.4	1.7	1.4
53	ICGV 04018	50.4	25.1	41.6	37.9	11.7	2.1	1.1
54	ICGV 07210	50.9	22.8	44.8	35.8	11.2	1.8	1.3
55	ICGV 07217	51.0	21.8	41.4	39.7	11.7	1.5	1.1
56	ICGV 95290	49.2	25.6	40.6	38.6	11.5	1.9	1.0
57	ICGV 97261	48.8	25.0	44.8	35.4	11.1	1.3	1.3
58	ICGV 97262	48.2	25.2	43.1	36.1	11.2	1.7	1.2
59	ICGV 99181	52.4	22.7	43.7	37.6	11.2	1.9	1.2
60	ICGV 99195	49.5	26.5	33.2	44.7	13.0	2.1	0.7
61	ICGV 89104	45.5	23.3	43.9	34.9	11.0	0.6	1.3
62	ICGS 11	45.5	25.5	34.6	43.6	12.3	1.3	0.8
63	J 11	50.5	24.7	41.0	38.3	11.7	1.3	1.1
64	ICGV 99085	57.9	23.2	52.1	29.4	10.1	3.1	1.8
65	TKG 19A	48.2	23.5	38.0	41.2	11.3	1.8	0.9
66	TPG 41	44.7	24.9	44.5	34.1	10.9	1.9	1.3
67	ICGV 00350	50.9	20.6	35.5	42.6	12.4	1.7	0.8
68	DH 86	46.6	27.4	40.7	37.9	11.4	1.9	1.1
69	ICGV 95058	45.7	23.2	47.2	31.7	11.3	1.4	1.5
70	ICGV 95070	49.2	20.4	38.9	39.9	11.6	1.7	1.0
71	GPBD 4	57.1	22.5	51.4	30.5	10.0	2.6	1.7
72	ICGV 91114	48.8	22.5	47.8	33.1	10.4	1.2	1.4
73	TMV 2	45.0	25.1	50.0	29.6	10.7	1.4	1.7
74	Faizpur 1-5	47.3	26.5	39.6	38.2	12.4	2.3	1.0
75	Mutant 3	49.1	23.9	43.2	36.1	11.4	1.2	1.2
76	ICGV 03042	53.7	24.2	32.1	46.9	12.9	1.9	0.7
77	ICGV 05100	51.9	24.3	36.8	41.7	13.0	1.5	0.9
78	ICGV 06049	49.2	20.9	47.7	33.3	10.7	1.2	1.4
79	ICGV 06420	55.6	21.9	33.8	44.9	12.9	1.8	0.8
80	ICGV 06424	52.5	22.3	42.7	36.7	11.6	2.2	1.2
81	ICGV 07145	48.6	26.1	36.3	41.9	12.6	2.0	0.9
82	ICGV 07148	47.3	24.3	44.9	35.0	11.1	0.8	1.3
83	ICGV 07166	50.8	24.7	36.3	42.9	12.5	2.2	0.9
84	ICGV 06142	54.8	28.0	38.3	39.5	12.5	2.9	1.0
85	ICGV 91116	47.2	24.1	42.2	36.0	11.7	1.5	1.2
86	ICGV 97045	45.9	24.5	45.8	31.9	12.1	2.0	1.5
87	ICGV 94118	52.5	23.9	43.0	35.8	12.9	2.5	1.2
88	ICGV 05176	46.2	28.0	40.5	36.1	11.8	2.3	1.1
89	ICGV 04149	54.8	20.1	46.6	34.3	11.2	1.7	1.4
90	ICGV 00351	53.3	23.1	31.4	46.5	13.1	2.4	0.7
91	ICGV 92195	45.4	25.5	46.2	33.2	10.8	0.9	1.4
92	ICGV 87187	46.3	23.6	46.3	33.4	11.4	1.3	1.4
93	ICGV 86072	45.3	21.6	47.4	30.7	11.6	1.4	1.5
94	ICGV 86015	45.7	25.7	37.0	39.9	12.9	1.5	0.9
95	ICGV 93437	51.0	20.3	36.4	42.4	12.6	1.0	0.9
96	ICGV 86143	44.4	26.7	44.6	34.4	10.8	1.7	1.3
97	ICGV 90320	47.7	21.6	42.0	37.0	11.5	1.9	1.1
98	ICGV 07273	44.9	26.0	46.1	33.5	11.0	0.8	1.4
99	49 x 37-91	51.0	23.5	47.3	30.4	11.6	1.6	1.7
100	49 x 37-134	47.9	22.3	46.0	34.1	10.5	1.5	1.4
101	49 x 37-135	46.3	23.0	46.2	33.6	10.7	0.9	1.4
102	49 x 37-97-1	42.3	26.0	50.2	28.1	10.7	1.0	1.8
103	49 x 37- 99(b) tall	43.5	22.9	48.5	29.6	10.9	1.0	1.6
104	39 x 49 -8	49.3	24.4	43.8	36.4	10.8	1.9	1.2
105	39 x 49 -77	52.1	25.6	40.3	40.1	11.2	2.2	1.0
106	49 x 39-20-2	47.7	25.3	39.4	38.9	11.7	1.7	1.0
107	49 x 39-21-2	44.6	25.3	46.4	32.4	11.0	1.7	1.4

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
108	49 x 39-8	49.9	21.7	50.6	30.5	10.3	1.4	1.7
109	49 M-16	53.7	27.4	39.7	39.0	12.1	2.4	1.0
110	49 x 27-19	42.3	26.0	46.2	31.6	10.9	0.9	1.5
111	49 x 27-13 (ii)	41.6	26.7	45.6	33.0	11.3	1.1	1.4
112	27 x 49- 16	45.2	27.0	45.2	32.8	11.1	1.8	1.4
113	27 x 49- 12	53.3	21.8	47.7	34.4	10.7	2.0	1.4
114	27 x 49- 14	46.2	25.5	45.6	32.7	11.9	1.2	1.4
115	27 x 49- 27-1	46.5	22.7	42.0	38.2	11.4	1.1	1.1
116	26 M 156-2	47.5	24.3	40.2	39.2	11.4	1.5	1.0
117	26 M- 119-1	47.3	23.0	44.4	35.3	10.8	1.0	1.2
118	24 M-86	50.6	26.9	38.4	38.7	13.0	2.3	1.0
119	MN1-35	51.0	24.1	51.5	29.4	12.7	0.9	1.8
120	M 110-14	51.7	23.3	39.7	37.3	12.9	2.5	1.1
121	M 28-2	54.0	22.1	40.0	38.8	12.9	2.6	1.0
122	Somnath	48.1	24.8	36.6	42.6	11.7	1.6	0.9
123	TG 41	46.5	25.3	43.8	34.1	12.0	1.4	1.3
124	TG 42	45.3	24.7	40.0	37.1	12.4	1.0	1.1
125	TG 49	43.0	24.9	45.3	34.0	11.1	1.1	1.4
126	TG LPS 4	44.8	25.0	44.1	33.1	12.1	1.3	1.3
127	TG LPS 7	44.3	24.7	43.5	35.0	11.6	1.0	1.2
128	24 x 37-2275	44.9	25.4	50.4	29.1	10.3	1.4	1.7
129	24 x 39-31 MR	52.8	24.3	42.7	37.3	11.3	2.6	1.1
130	26 X M-95-1 RI	51.9	24.5	49.3	32.4	9.9	2.5	1.5
131	26 X 37-IV- 9IR	43.9	21.0	44.1	35.5	11.1	0.8	1.3
132	26X 27-164	43.0	23.5	37.5	40.2	12.4	0.6	0.9
133	49 X 39-21-1	50.1	23.1	46.8	35.0	10.9	1.5	1.3
134	49 X 39-21-2(a)	50.8	23.7	44.4	36.1	11.0	2.4	1.2
135	49 x 39-74	51.8	22.3	47.0	33.4	10.7	1.9	1.4
136	39x 49-81-1	50.7	22.8	47.0	33.0	10.5	2.0	1.4
137	49 x 27-37	46.0	24.8	39.7	40.1	11.2	1.3	1.0
138	TDG 10	47.8	22.7	39.3	40.2	11.6	1.5	1.0
139	TDG 13	51.8	23.1	39.6	39.4	12.0	1.9	1.0
140	TDG 14	47.2	26.4	44.9	35.8	10.9	1.9	1.3
141	DTG 3	42.4	20.3	45.0	33.4	11.5	0.5	1.3
142	DTG 15	48.6	23.0	44.7	35.7	10.7	1.2	1.3
143	M 28-2	51.1	25.1	40.2	38.0	12.4	2.4	1.1
144	JL 24	48.4	22.5	47.4	32.8	10.6	0.9	1.4
145	TAG 24	45.4	23.9	46.1	33.8	10.7	0.5	1.4
146	SPS 1	54.0	23.2	45.0	34.1	14.4	1.9	1.3
147	SPS 9	55.3	20.3	42.1	36.9	14.7	1.4	1.1
148	SPS 10	48.2	23.3	43.6	36.0	11.2	0.9	1.2
149	SPS 13	44.9	23.2	49.2	31.6	10.9	0.6	1.6
150	SPS 14	52.4	24.1	42.5	36.2	13.5	2.0	1.2
151	SPS 17	42.0	26.3	48.4	30.7	11.1	0.9	1.6
152	ICGV 02411	53.1	26.5	36.3	41.3	13.1	2.5	0.9
153	ICGV 05155	53.9	23.7	36.3	43.1	12.4	1.9	0.9
154	ICGV 06100	49.3	24.2	34.9	41.9	12.9	2.0	0.8
155	ICGV 07023	47.2	25.5	49.2	31.1	10.4	1.3	1.6
156	SunOleic 95R	46.1	25.4	76.0	6.1	7.9	1.4	12.8
157	ICG 434	49.7	25.5	39.6	39.2	12.0	1.7	1.0
158	ICG 2031	50.4	23.0	45.8	34.0	11.0	1.8	1.4
159	ICG 3102	50.3	22.6	40.2	38.8	11.9	1.1	1.0
160	ICG 3140	44.8	22.8	46.9	32.6	10.8	0.8	1.4
161	ICG 3343	46.7	23.8	44.8	33.7	11.5	0.8	1.3
162	ICG 3421	50.0	21.2	45.0	35.0	10.8	1.2	1.3
163	ICG 4729	45.4	22.8	47.3	32.3	10.6	0.7	1.5

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
164	ICG 6022	57.6	21.5	53.3	34.5	7.9	3.4	1.6
165	ICG 6646	48.6	22.6	46.0	36.0	10.4	1.9	1.3
166	ICG 8517	50.1	22.6	45.6	33.6	14.1	1.0	1.4
167	ICG 8751	46.7	21.9	35.5	42.1	12.6	1.9	0.9
168	ICG 9315	50.5	21.4	39.7	40.7	11.7	1.3	1.0
169	ICG 10036	43.6	25.0	41.1	38.3	11.0	2.2	1.1
170	ICG 10053	47.4	26.8	46.8	32.1	11.3	1.9	1.5
171	ICG 10701	46.8	22.4	44.0	35.6	11.4	1.6	1.2
172	ICG 11088	51.7	22.5	53.2	31.6	10.0	2.0	1.7
173	ICG 11651	45.9	24.5	38.5	40.0	11.5	1.3	1.0
174	ICG 12625	55.6	21.7	57.3	30.8	8.9	2.4	1.9
175	ICG 12991	47.5	21.8	43.8	36.0	10.9	0.7	1.2
176	ICG 14985	38.2	29.8	47.9	27.7	11.6	1.1	1.7
177	ICG 15415	47.9	22.1	40.4	39.3	11.5	2.7	1.0
178	ICG 15419	59.9	21.2	51.6	36.6	8.1	3.1	1.4
179	ICGV 01232	49.9	24.6	36.6	42.1	12.1	1.8	0.9
180	ICGV 01276	51.6	25.1	35.3	41.9	13.1	2.1	0.8
181	ICGV 01328	51.0	23.2	52.2	27.8	13.6	1.1	1.9
182	ICGV 02022	48.1	22.9	43.6	36.8	11.1	1.3	1.2
183	ICGV 02038	47.5	24.4	40.7	38.0	11.5	1.5	1.1
184	ICGV 02189	49.9	23.0	43.7	37.4	11.3	0.9	1.2
185	ICGV 02194	50.3	23.8	42.8	36.7	11.7	1.4	1.2
186	ICGV 02266	46.1	26.9	39.6	37.4	12.3	1.3	1.1
187	ICGV 02271	50.2	26.8	32.8	46.0	12.6	2.5	0.7
188	ICGV 02286	53.0	19.8	34.6	44.3	12.4	2.4	0.8
189	ICGV 86011	51.6	22.0	49.4	31.9	10.6	1.7	1.6
190	ICGV 86590	46.8	25.1	37.1	42.1	11.9	2.4	0.9
191	ICGV 87160	49.8	23.0	44.4	35.8	11.4	1.7	1.2
192	ICGV 87354	45.4	23.9	41.9	36.8	11.1	1.0	1.2
193	ICGV 87378	47.9	24.4	45.9	34.3	11.0	1.8	1.3
194	ICGV 87921	49.9	23.4	38.0	41.4	11.7	1.6	0.9
195	ICGV 88145	51.3	21.4	45.8	35.7	10.5	1.8	1.3
196	ICGV 92267	50.4	25.1	40.9	38.2	11.7	1.8	1.1
197	ICGV 93470	48.0	22.7	46.1	34.7	10.7	1.0	1.3
198	ICGV 94169	47.3	22.3	47.0	32.0	11.1	2.0	1.5
199	ICGV 94361	50.7	22.3	37.0	42.6	12.4	1.4	0.9
200	ICGV 95377	48.1	25.3	43.7	36.8	10.8	2.3	1.2
201	ICGV 96466	50.3	24.3	43.9	36.5	11.0	1.7	1.2
202	ICGV 96468	45.7	23.0	38.9	39.1	12.0	1.4	1.0
203	ICGV 97182	51.5	22.1	34.5	43.4	12.8	2.5	0.8
204	ICGV 97183	46.2	26.6	47.3	32.9	10.9	1.4	1.4
205	ICGV 98294	48.2	27.7	38.9	39.9	11.9	2.8	1.0
206	Gangapuri	50.9	20.3	44.9	34.1	14.2	1.1	1.3
207	ICGS 44	44.4	24.0	35.9	42.2	12.2	1.3	0.9
208	ICG 3312	51.9	19.7	48.0	32.7	10.5	1.7	1.5
209	ICG 14705	48.4	25.4	41.5	36.0	11.5	2.2	1.1
210	ICG 3746	46.3	21.1	48.8	31.4	10.1	0.6	1.6
211	ICG 4955	48.9	22.5	51.9	27.6	12.8	0.0	1.9
212	ICG 12879	54.1	20.5	46.5	34.1	11.0	1.8	1.4
213	ICG 5221	58.8	22.7	47.7	38.5	7.9	2.7	1.2
214	ICG 4543	47.9	22.6	44.2	35.1	11.3	1.0	1.3
215	ICG 1834	45.9	23.8	45.5	34.1	10.8	0.9	1.4
216	ICG 2106	48.5	22.5	45.1	34.8	10.9	1.0	1.3
217	ICG 9507	43.8	27.6	46.1	32.7	10.8	1.3	1.4
218	ICG 1973	48.3	22.2	46.1	33.7	10.8	1.0	1.4
219	ICG 3673	47.6	22.1	46.8	31.7	14.0	0.2	1.5

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
220	ICG 3584	48.5	22.9	45.2	35.1	10.9	1.1	1.3
221	ICG 442	49.0	21.9	49.1	30.0	13.5	0.2	1.7
222	ICGV 01464	43.1	26.0	44.0	32.7	12.2	1.4	1.4
223	ICGV 01478	43.6	24.6	40.5	37.3	11.7	1.5	1.1
224	ICGV 02251	47.1	21.9	45.9	34.2	11.0	0.8	1.4
225	ICGV 03136	43.7	23.9	43.8	34.0	11.3	2.0	1.3
226	ICGV 05198	43.8	26.0	50.4	28.1	10.9	1.4	1.8
227	ICGV 06234	47.0	28.0	49.5	29.6	10.8	2.2	1.7
228	ICGV 00346	48.0	25.3	36.5	41.2	12.7	2.0	0.9
229	ICGV 00362	48.8	28.4	42.0	35.6	11.6	2.4	1.2
230	ICGV 00371	48.1	24.0	33.4	43.7	12.7	2.2	0.8
231	ICGV 02287	48.3	26.8	41.8	37.1	11.6	1.9	1.1
232	ICGV 02298	44.7	24.2	49.1	30.3	10.4	1.9	1.6
233	ICGV 02317	50.0	24.4	36.3	41.3	12.5	1.7	0.9
234	ICGV 97232	47.0	23.6	45.2	34.7	11.0	0.8	1.3
235	ICGV 99051	53.4	24.3	36.0	41.4	12.4	2.8	0.9
236	ICGV 99052	54.9	24.8	32.8	43.8	13.3	2.7	0.7
237	ICGV 00246	52.2	26.7	34.5	42.6	12.8	2.5	0.8
238	ICGV 00248	55.8	24.3	34.6	43.7	12.4	2.8	0.8
239	ICGV 01361	50.0	23.9	36.3	41.8	12.4	1.3	0.9
240	ICGV 02434	49.5	22.8	38.1	38.1	12.6	2.3	1.0
241	ICGV 04087	53.0	25.3	34.5	41.5	13.4	2.4	0.8
242	ICGV 06175	47.7	23.3	36.9	39.3	12.5	1.9	0.9
243	ICGV 97116	44.8	22.6	45.5	33.3	11.0	1.6	1.4
244	ICGV 97128	54.6	23.5	35.2	42.0	13.0	2.7	0.8
245	ICGV 98184	49.1	24.7	37.8	40.4	12.6	1.9	0.9
246	ICGV 00068	46.4	25.8	38.4	38.5	12.1	2.0	1.0
247	ICGV 01495	48.1	24.7	42.4	35.9	11.7	1.9	1.2
248	ICGV 05057	50.4	24.1	33.0	43.4	13.7	1.8	0.8
249	ICGV 07168	47.1	24.2	42.6	35.3	11.2	2.3	1.2
250	ICGV 01265	48.1	25.2	38.5	38.2	12.6	2.3	1.0
251	ICGV 98105	49.6	26.2	35.6	41.6	13.1	1.6	0.8
252	ICGV 99160	48.3	26.4	37.8	39.1	13.2	1.7	1.0
253	ICGV 02323	50.3	25.7	38.2	38.7	13.0	1.8	1.0
254	ICGV 04115	49.8	24.3	37.3	41.3	12.5	1.8	0.9
255	ICGV 05036	48.5	25.7	36.4	39.5	13.7	1.6	0.9
256	ICGV 06042	49.8	24.4	34.7	41.1	13.0	1.8	0.8
257	ICGV 86564	45.4	25.2	45.3	32.9	10.8	2.9	1.4
258	ICGV 98432	46.7	27.6	50.1	29.1	11.0	2.1	1.7
259	BAU 13	45.3	24.2	46.0	32.5	11.2	1.9	1.4
260	ICGV 87846	47.6	25.7	37.2	39.2	12.8	2.0	0.9
261	ICR 48	46.7	23.1	46.1	32.4	10.7	2.1	1.4
262	ICGV 86699	53.6	22.4	49.1	32.3	13.1	1.2	1.5
263	ICGV 98373	47.7	26.6	39.9	38.3	11.8	1.7	1.0
264	ICGV 97115	46.9	22.7	41.0	36.4	11.8	1.8	1.1
265	ICGV 06040	51.0	26.8	32.7	44.0	13.5	2.4	0.7
266	ICGV 06099	49.9	24.1	36.5	40.4	12.7	2.2	0.9
267	CS 39	50.1	24.3	39.9	38.1	12.1	2.2	1.1
268	ICGV 05032	47.3	25.3	39.6	37.3	12.7	1.7	1.1
269	ICGV 05141	52.9	23.0	48.5	30.7	11.2	1.9	1.6
270	ICGV 07359	43.1	26.0	45.6	30.7	11.7	2.2	1.5
271	ICGV 07368	40.9	26.8	43.9	31.9	12.4	1.6	1.4
272	ICGV 06110	41.4	26.5	43.2	34.0	12.2	1.4	1.3
273	ICGV 06188	44.1	24.6	49.6	30.2	10.4	1.0	1.6
274	ICGV 00440	44.7	23.5	45.2	33.3	11.0	2.0	1.4
275	ICGV 86352	47.0	22.9	49.9	31.2	10.1	1.1	1.6

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
276	ICGV 09112	45.5	24.0	45.1	34.0	11.4	1.3	1.3
277	ICGV 93920	45.4	22.4	44.6	34.4	11.3	2.0	1.3
278	ICGV 93216	43.9	22.4	46.6	32.9	10.7	1.5	1.4
279	ICGV 88438	45.6	25.8	46.7	33.4	10.2	2.0	1.4
280	ICG 11337	50.6	22.3	51.9	29.2	12.9	1.0	1.8
281	49 x 37-90	48.0	23.4	41.3	38.5	11.5	2.1	1.1
282	49 M-2-2	44.9	25.7	46.0	31.6	11.6	1.2	1.5
283	49 M- 1-1	45.2	25.0	35.8	40.3	13.6	1.3	0.9
284	TG 19	49.9	24.4	38.5	40.9	11.7	1.7	1.0
285	TG 39	44.2	23.1	47.4	32.3	11.2	0.9	1.5
286	TG LPS 3	44.3	22.5	51.1	28.8	10.8	1.1	1.8
287	26 X M-223-1	44.4	25.6	45.6	32.0	11.4	1.3	1.4
288	SPS 2	54.2	22.2	50.0	31.2	12.8	1.3	1.6
289	SPS 3	48.8	22.7	47.9	32.6	10.6	1.1	1.5
290	SPS 6	47.7	23.0	47.1	33.8	10.4	1.3	1.4
291	SPS 7	52.7	22.7	52.0	28.8	12.5	1.3	1.8
292	SPS 8	53.4	23.4	49.3	31.4	12.8	1.3	1.6
293	SPS 11	55.2	26.9	39.6	38.8	12.7	2.8	1.1
294	SPS 15	52.4	23.6	51.9	29.0	12.8	1.1	1.8
295	SPS 20	51.8	24.5	51.0	29.8	13.1	1.4	1.8
296	SPS 21	54.1	21.2	50.2	30.1	13.3	1.4	1.7
297	ICGV 03128	50.2	26.3	34.4	41.7	13.2	2.0	0.8
298	TMV 2 NLM	47.4	24.8	41.8	37.3	11.5	1.0	1.1
299	ICG 1668	49.5	23.0	44.2	35.4	11.3	1.0	1.2
300	ICG 8285	45.4	23.3	41.9	35.7	11.7	1.2	1.2
301	ICG 11426	52.4	23.3	51.4	30.0	12.8	1.1	1.7
302	ICGV 02290	46.5	23.5	45.3	32.3	11.3	2.3	1.4
303	ICGV 02446	50.7	26.8	33.7	40.7	14.4	2.7	0.8
304	ICG 156	43.3	23.8	45.8	33.1	10.7	1.4	1.4
305	ICGS 76	48.8	25.7	38.6	39.1	12.5	2.1	1.0
306	ICG 5891	46.5	22.8	43.8	35.6	11.1	1.3	1.2
307	CSMG 84-1	43.7	24.3	47.1	31.8	11.3	0.7	1.5
308	ICG 111	46.3	26.6	38.9	37.2	13.1	1.5	1.0
309	ICG 14834	47.3	23.4	47.4	31.6	11.2	1.4	1.5
310	ICG 11322	44.4	25.9	37.2	40.7	12.3	1.5	0.9
311	ICG 532	46.0	23.7	49.1	31.2	10.6	1.2	1.6
312	ICG 12509	52.3	23.9	52.7	29.8	12.5	1.5	1.8
313	ICG 12672	53.6	20.8	45.5	34.4	14.1	1.1	1.3
314	ICG 10185	44.1	24.3	43.4	34.5	11.8	1.0	1.3
315	ICG 2773	41.1	24.3	43.5	34.4	11.6	0.6	1.3
316	ICG 3027	46.9	23.4	43.9	34.1	11.8	1.7	1.3
317	ICG 5745	43.8	22.7	49.9	29.0	10.5	1.4	1.7
318	ICG 14482	55.1	22.7	62.4	23.3	10.5	1.5	2.8
319	ICG 4527	45.9	25.7	39.3	39.3	11.5	1.8	1.0
320	ICG 4343	43.8	24.2	43.8	34.4	11.2	0.9	1.3
321	ICG 13895	41.9	23.8	47.2	31.3	10.9	0.7	1.5
322	ICG 5663	44.3	24.0	41.2	37.1	11.8	1.1	1.1
323	ICG 721	45.1	24.8	38.7	39.7	12.0	1.5	1.0
324	ICG 12276	44.8	22.9	55.4	23.4	12.0	1.3	2.4
325	ICG 875	43.0	25.0	43.9	33.2	11.8	1.4	1.3
326	ICG 14475	52.6	22.1	59.3	26.5	10.6	1.7	2.3
327	ICG 15190	44.7	25.1	40.5	37.8	11.8	1.1	1.1
328	ICG 12370	44.2	24.6	42.4	35.8	11.3	1.0	1.2
329	ICGV 86325	47.1	23.3	46.3	33.3	10.7	1.8	1.4
330	ICG 5662	46.1	23.1	44.7	35.1	10.6	1.8	1.3
331	ICG 9961	46.9	21.8	45.1	33.8	11.3	1.4	1.4

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
332	ICG 14466	45.2	23.0	44.0	33.5	11.7	1.5	1.3
333	ICG 3053	47.4	26.4	42.1	33.5	13.0	1.3	1.3
334	ICG 6766	44.3	24.4	45.8	32.5	10.9	1.6	1.4
335	ICG 2381	59.3	22.2	44.3	38.7	8.4	3.9	1.1
336	ICG 2857	43.8	24.2	46.3	32.4	11.1	1.1	1.4
337	ICGV 13238	43.8	24.7	45.7	34.0	10.9	0.4	1.4
338	ICGV 13241	47.7	22.7	43.6	36.6	10.7	1.0	1.2
339	ICGV 13242	46.8	24.2	45.4	35.1	11.0	1.0	1.3
340	ICGV 13245	48.4	22.4	46.4	33.2	11.0	1.0	1.4
Mean		**48.5**	**24.1**	**42.9**	**36.1**	**11.7**	**1.7**	**1.3**
CV (%)		**3.3**	**6.9**	**5.7**	**5.7**	**4.5**	**18.6**	**7.9**
LSD at 5 % level		**2.6**	**2.7**	**4.0**	**3.4**	**0.9**	**0.5**	**0.05**

Appendix VIII

Best linear unbiased prediction of mean for yield and its contributing traits of Genomic Selection Panel of groundnut evaluated at ICRISAT during post-rainy season 2015-16

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12
1	ICGV 06423	45.0	9.0	27.6	10.0	6.0	4.0	55.9	41.2	150.2	228.8	1525.0	27.3
2	ICGV 07246	46.0	10.0	22.2	22.0	10.7	5.7	54.9	28.8	148.0	417.8	2785.4	21.8
3	ICGV 07247	44.0	7.0	27.2	24.0	17.0	11.6	66.1	32.0	146.0	567.1	3780.9	30.7
4	ICGV 07268	43.0	7.0	21.8	14.0	10.5	7.1	67.7	35.7	148.0	405.0	2699.9	26.5
5	ICGV 01005	35.0	6.0	31.8	13.0	9.3	5.5	57.2	40.1	139.9	370.7	2471.5	22.3
6	ICGV 01060	44.0	6.0	15.4	10.0	5.7	3.8	67.4	31.7	144.5	207.3	1382.2	13.0
7	ICGV 01124	43.0	6.0	15.8	5.0	3.3	1.8	47.4	23.2	145.0	122.9	819.3	15.7
8	ICGV 02206	43.0	5.0	22.8	14.0	8.6	4.8	55.4	29.9	145.0	342.1	2280.4	15.3
9	ICGV 03397	47.0	8.0	20.8	6.0	2.9	1.9	62.9	23.8	148.0	104.2	694.4	31.3
10	ICGV 03398	48.0	8.0	22.2	6.0	3.0	1.5	50.8	23.3	148.0	119.0	793.1	22.8
11	ICGV 04044	42.0	8.0	25.3	15.0	9.2	5.9	59.4	33.1	143.9	343.3	2288.4	23.7
12	ICGV 06347	43.0	6.0	17.1	12.0	7.1	3.9	67.2	31.6	142.0	283.5	1890.1	24.9
13	ICGV 93280	46.0	6.0	22.6	16.0	9.4	6.8	69.8	35.9	145.1	374.8	2498.3	28.2
14	ICGV 95469	41.0	7.0	21.4	11.0	6.0	4.2	71.0	40.1	146.6	229.3	1528.5	20.6
15	ICGV 00387	44.0	6.0	29.9	19.0	10.1	5.0	54.3	31.4	146.2	410.5	2736.5	21.6
16	ICGV 01393	41.0	5.0	27.2	5.0	3.4	1.5	48.9	29.9	144.1	138.7	924.8	20.0
17	ICGV 02242	40.0	7.0	26.8	13.0	10.9	6.7	59.2	40.9	146.0	388.0	2586.9	20.9
18	ICGV 97058	48.0	5.0	26.8	11.0	11.5	6.7	58.5	36.3	148.0	461.1	3073.7	13.3
19	ICGV 99083	39.0	6.0	22.9	11.0	7.3	3.9	49.6	33.0	146.0	246.7	1644.6	24.7
20	ICGV 00343	43.0	5.0	17.9	9.0	8.2	4.5	61.3	42.3	142.9	326.3	2175.6	19.3
21	ICGV 00349	41.0	5.0	25.8	14.0	7.9	5.5	70.1	37.6	144.0	318.1	2120.9	15.3
22	ICGV 01263	41.0	5.0	20.2	8.0	6.7	3.5	55.3	36.5	143.0	243.1	1620.9	10.1
23	ICGV 03056	44.0	5.0	20.1	12.0	9.8	5.6	60.3	39.8	147.8	392.6	2617.6	16.6
24	ICGV 03064	42.0	8.0	20.3	14.0	5.9	3.4	53.2	18.3	150.0	235.2	1568.0	15.5
25	ICGV 05161	41.0	7.0	22.2	9.0	6.3	3.2	51.0	28.3	149.0	245.9	1639.5	21.1
26	ICGV 05163	42.0	6.0	20.3	11.0	6.4	3.7	55.6	29.0	149.0	260.9	1739.1	15.8
27	ICGV 06422	44.0	7.0	21.0	11.0	6.7	3.6	53.4	41.3	148.9	258.4	1722.9	24.9
28	ICGV 06431	37.0	5.0	27.2	16.0	11.7	7.7	66.3	39.5	123.9	445.2	2968.1	28.2
29	ICGV 07220	45.0	7.0	19.3	6.0	3.9	2.2	60.5	26.7	149.0	152.3	1015.5	23.1
30	ICGV 07223	46.0	9.0	20.0	20.0	10.0	6.5	64.2	31.6	146.0	371.9	2479.4	25.8
31	ICGV 07227	47.0	8.0	23.9	14.0	9.9	6.2	62.7	35.7	149.0	396.7	2644.5	27.2
32	ICGV 07235	45.0	7.0	22.9	14.0	7.6	5.0	68.1	40.5	148.0	291.0	1940.0	15.8
33	ICGV 99233	40.0	6.0	20.1	9.0	6.7	3.9	57.7	39.2	140.1	263.8	1758.6	9.8
34	ICGV 97165	42.0	6.0	19.8	4.0	2.2	1.9	49.4	26.9	148.2	71.2	474.7	31.8
35	ICGV 99029	42.0	5.0	22.2	12.0	6.0	3.1	57.1	30.5	149.9	221.8	1478.4	24.3
36	ICGV 00191	41.0	6.0	20.0	10.0	5.2	3.3	53.4	34.3	145.9	188.4	1255.9	25.5
37	ICGV 07120	43.0	9.0	24.9	12.0	9.2	6.0	66.1	41.0	147.9	355.3	2368.7	30.0
38	ICGV 97092	45.0	6.0	17.9	7.0	3.7	1.8	52.9	28.3	148.0	138.2	921.1	22.9
39	ICGV 97120	45.0	7.0	27.6	10.0	7.7	5.2	57.8	51.9	149.1	279.9	1865.9	23.7
40	ICGV 98163	41.0	7.0	23.5	8.0	4.0	2.6	68.0	35.7	148.0	129.7	864.7	19.5
41	ICGV 00005	40.0	7.0	24.1	13.0	8.8	5.5	62.3	35.8	147.9	341.6	2277.0	13.7
42	ICGV 01273	45.0	6.0	23.1	16.0	9.1	5.2	61.4	33.0	146.1	299.2	1994.7	35.9
43	ICGV 01274	42.0	7.0	17.1	12.0	5.3	3.2	58.8	30.8	148.0	213.7	1424.8	15.6
44	ICGV 02321	45.0	7.0	18.7	14.0	6.4	4.2	63.7	36.0	149.1	237.3	1581.8	19.3
45	ICGV 03043	44.0	8.0	21.4	15.0	7.0	4.2	59.9	32.5	148.0	274.2	1828.3	16.7
46	ICGV 04124	46.0	9.0	24.3	17.0	8.3	4.4	56.9	27.9	148.0	314.7	2098.0	24.8
47	ICGV 00290	42.0	5.0	16.6	13.0	7.0	3.9	57.8	28.3	148.9	237.8	1585.2	25.7
48	ICGV 00321	39.0	5.0	33.4	17.0	10.9	6.6	64.3	35.5	123.6	436.5	2910.2	9.8
49	ICGV 02125	38.0	5.0	22.2	19.0	9.5	6.1	63.9	25.0	125.9	378.2	2521.7	9.5
50	ICGV 02144	38.0	5.0	29.5	15.0	7.7	4.6	60.4	30.4	142.5	253.0	1686.9	12.4

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12
51	ICGV 03184	43.0	6.0	27.9	15.0	10.9	7.1	72.7	38.7	146.1	430.7	2871.2	25.9
52	ICGV 03207	40.0	5.0	21.2	8.0	4.4	2.8	61.4	32.7	129.1	176.6	1177.3	11.3
53	ICGV 04018	40.0	5.0	25.6	12.0	9.9	6.0	69.5	37.8	126.4	398.6	2657.1	12.0
54	ICGV 07210	40.0	5.0	21.4	12.0	7.6	4.8	62.3	27.2	132.5	306.7	2044.7	19.5
55	ICGV 07217	41.0	5.0	24.6	21.0	11.2	8.0	65.3	29.9	132.4	448.8	2991.7	16.2
56	ICGV 95290	39.0	5.0	21.3	9.0	5.6	3.5	69.8	45.9	136.9	224.6	1497.4	8.3
57	ICGV 97261	39.0	5.0	21.7	12.0	7.2	5.2	71.7	26.6	129.0	278.0	1853.2	12.1
58	ICGV 97262	45.0	5.0	16.1	6.0	3.5	1.8	51.4	25.3	142.8	139.1	927.6	11.4
59	ICGV 99181	39.0	5.0	19.7	12.0	6.3	3.8	60.6	31.4	135.0	251.7	1678.2	16.8
60	ICGV 99195	42.0	5.0	22.3	12.0	5.9	3.4	57.0	23.7	141.8	235.7	1571.3	11.5
61	ICGV 89104	42.0	5.0	24.9	14.0	5.6	3.5	62.8	22.8	135.5	204.9	1366.0	13.6
62	ICGS 11	41.0	6.0	19.3	12.0	6.1	4.1	67.1	43.3	144.1	218.0	1453.4	23.5
63	J 11	40.0	5.0	26.5	16.0	8.6	5.4	63.2	25.4	132.1	326.1	2174.3	17.3
64	ICGV 99085	40.0	5.0	20.2	10.0	5.0	3.3	66.3	32.7	142.0	199.5	1330.2	9.3
65	TKG 19A	42.0	5.0	36.1	12.0	5.6	3.5	59.4	31.9	147.1	205.2	1368.2	23.3
66	TPG 41	39.0	4.0	31.9	6.0	5.4	2.7	48.1	32.6	148.9	162.7	1084.8	27.2
67	ICGV 00350	42.0	6.0	20.4	10.0	8.2	5.3	65.5	41.6	143.1	325.7	2171.0	20.8
68	DH 86	41.0	7.0	20.8	13.0	6.0	2.9	48.0	34.5	148.1	205.7	1371.6	25.8
69	ICGV 95058	47.0	5.0	21.3	8.0	3.2	1.9	58.8	23.1	144.0	118.5	790.1	19.9
70	ICGV 95070	44.0	5.0	18.1	8.0	3.8	1.9	47.4	19.9	148.0	139.7	931.4	22.2
71	GPBD 4	38.0	5.0	25.8	13.0	7.4	4.5	62.0	25.8	142.1	272.9	1819.5	23.1
72	ICGV 91114	38.0	4.0	30.5	11.0	7.7	4.7	65.1	31.5	139.9	274.0	1826.4	15.2
73	TMV 2	41.0	6.0	20.6	10.0	9.1	4.5	58.3	31.4	148.0	317.5	2116.8	21.7
74	Faizpur 1-5	39.0	5.0	22.4	19.0	14.9	7.7	56.5	27.7	130.5	577.4	3849.6	11.6
75	Mutant 3	40.0	5.0	19.0	9.0	5.3	2.9	54.9	30.1	144.9	211.6	1410.4	12.8
76	ICGV 03042	45.0	6.0	19.7	11.0	5.9	3.2	51.9	27.0	149.1	207.9	1386.3	23.2
77	ICGV 05100	45.0	7.0	18.7	7.0	4.3	2.7	63.1	34.2	147.9	168.8	1125.3	18.8
78	ICGV 06049	38.0	5.0	20.7	11.0	6.8	4.4	66.0	35.5	135.8	270.7	1804.8	10.7
79	ICGV 06420	42.0	7.0	18.2	6.0	3.1	1.3	45.3	23.1	148.0	121.9	812.8	22.6
80	ICGV 06424	46.0	6.0	15.9	3.0	2.9	2.0	59.6	21.1	146.0	114.9	766.3	24.8
81	ICGV 07145	43.0	6.0	16.7	14.0	7.9	3.8	47.0	25.2	148.0	313.1	2087.5	32.8
82	ICGV 07148	37.0	5.0	22.1	10.0	5.7	4.1	69.3	34.1	132.4	228.0	1520.2	13.2
83	ICGV 07166	43.0	7.0	25.9	16.0	13.2	7.5	60.1	35.8	135.4	529.2	3527.8	21.6
84	ICGV 06142	44.0	7.0	15.7	5.0	4.1	2.7	66.2	27.0	148.0	161.7	1078.0	14.4
85	ICGV 91116	37.0	4.0	30.1	15.0	11.0	7.3	70.3	37.0	120.9	436.5	2909.8	13.0
86	ICGV 97045	43.0	5.0	18.2	10.0	5.9	3.9	58.2	35.2	149.1	175.8	1171.8	33.5
87	ICGV 94118	40.0	5.0	25.3	10.0	7.8	5.4	68.6	42.5	146.9	308.5	2056.5	23.7
88	ICGV 05176	41.0	6.0	27.5	9.0	7.8	5.5	58.2	51.6	145.9	266.1	1773.8	34.1
89	ICGV 04149	40.0	7.0	19.0	14.0	7.8	5.1	64.7	33.9	133.9	308.7	2058.1	8.4
90	ICGV 00351	41.0	8.0	16.0	12.0	8.7	5.6	64.9	53.1	140.9	346.8	2312.0	9.8
91	ICGV 92195	38.0	5.0	23.2	10.0	5.6	4.0	71.0	26.7	120.5	206.7	1377.9	11.0
92	ICGV 87187	45.0	8.0	16.2	11.0	5.2	2.8	56.1	28.8	146.9	206.5	1376.7	21.8
93	ICGV 86072	42.0	5.0	20.7	8.0	5.4	3.4	65.7	41.8	146.1	173.1	1153.7	27.3
94	ICGV 86015	41.0	5.0	15.0	15.0	7.2	4.2	60.5	28.6	146.0	254.9	1699.6	12.6
95	ICGV 93437	39.0	5.0	26.5	15.0	10.3	6.3	65.7	30.5	122.5	392.4	2616.1	11.0
96	ICGV 86143	41.0	6.0	16.0	7.0	3.9	2.2	55.1	31.3	148.9	157.1	1047.2	12.9
97	ICGV 90320	40.0	5.0	21.0	12.0	11.2	7.1	63.7	45.3	140.2	436.1	2907.3	14.6
98	ICGV 07273	40.0	5.0	22.3	10.0	5.9	4.1	68.8	36.0	123.9	219.2	1461.6	11.4
99	49 x 37-91	40.0	6.0	22.6	15.0	8.5	5.7	67.0	40.8	138.0	317.6	2117.1	15.8
100	49 x 37-134	39.0	5.0	28.0	8.0	6.0	4.0	66.9	46.9	147.5	242.1	1614.2	10.8
101	49 x 37-135	40.0	4.0	27.3	13.0	8.3	5.6	67.5	30.9	124.4	320.8	2138.7	16.0
102	49 x 37-97-1	44.0	6.0	16.4	3.0	2.1	1.2	67.9	48.6	149.1	61.4	409.0	20.7
103	49 x 37- 99(b) tall	45.0	5.0	16.1	4.0	3.7	2.1	49.9	27.5	148.1	110.4	735.8	22.6
104	39 x 49 -8	41.0	5.0	14.2	9.0	5.4	3.8	68.6	41.1	143.2	175.3	1168.9	11.2
105	39 x 49 -77	41.0	5.0	17.0	14.0	8.7	4.8	61.8	37.6	137.0	345.7	2304.6	11.4
106	49 x 39-20-2	40.0	6.0	24.8	8.0	6.1	3.5	56.8	39.2	146.0	227.8	1518.9	18.4

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12
107	49 x 39-21-2	42.0	5.0	22.2	9.0	3.8	1.9	47.4	35.8	144.0	113.4	756.1	13.7
108	49 x 39-8	41.0	5.0	19.3	7.0	5.9	4.0	67.0	43.5	135.5	218.9	1459.3	7.2
109	49 M-16	42.0	7.0	24.6	22.0	10.9	7.4	69.4	34.1	148.9	428.4	2855.8	20.8
110	49 x 27-19	45.0	5.0	16.8	16.0	10.3	5.3	53.7	43.9	148.0	411.2	2741.6	21.5
111	49 x 27-13 (ii)	40.0	5.0	24.2	11.0	7.7	3.9	51.9	33.1	146.1	260.1	1733.9	22.9
112	27 x 49- 16	42.0	5.0	37.9	15.0	9.5	4.4	47.3	33.1	146.0	340.9	2272.4	32.6
113	27 x 49- 12	37.0	5.0	15.3	7.0	4.4	3.0	67.8	34.8	130.5	158.7	1058.1	9.1
114	27 x 49- 14	42.0	6.0	20.3	10.0	7.3	4.6	64.5	45.0	149.1	236.0	1573.1	21.6
115	27 x 49- 27-1	38.0	6.0	17.9	13.0	8.1	4.9	60.4	46.0	144.5	325.9	2172.4	15.1
116	26 M 156-2	43.0	5.0	31.2	14.0	6.1	3.3	53.3	32.0	143.6	237.5	1583.2	18.0
117	26 M- 119-1	40.0	5.0	22.4	17.0	9.5	6.7	65.7	37.7	137.5	350.7	2338.3	11.6
118	24 M-86	44.0	8.0	19.4	7.0	5.0	2.4	53.8	34.9	149.9	179.1	1193.9	32.4
119	MN1-35	39.0	5.0	15.0	12.0	7.2	4.1	59.5	26.7	136.5	279.1	1860.9	9.7
120	M 110-14	45.0	6.0	20.8	4.0	3.0	1.3	46.9	21.4	147.9	102.0	679.7	17.4
121	M 28-2	47.0	6.0	19.5	7.0	3.2	1.7	51.9	20.8	143.9	121.4	809.0	13.3
122	Somnath	40.0	4.0	20.3	11.0	6.7	3.6	55.1	38.0	134.1	257.9	1719.1	15.0
123	TG 41	43.0	5.0	18.4	7.0	4.8	2.7	54.0	39.4	143.0	151.3	1008.4	11.4
124	TG 42	43.0	5.0	15.1	6.0	4.9	3.2	64.0	45.6	145.1	157.6	1050.7	21.7
125	TG 49	41.0	4.0	19.3	13.0	9.1	5.8	64.3	50.4	145.8	337.2	2248.2	21.2
126	TG LPS 4	43.0	5.0	18.0	5.0	2.7	2.9	68.6	28.1	146.1	91.5	609.8	17.7
127	TG LPS 7	43.0	7.0	18.8	6.0	3.5	1.8	50.3	25.9	146.0	127.6	850.6	14.3
128	24 x 37-2275	42.0	5.0	22.5	11.0	7.6	4.4	59.7	31.6	144.0	273.7	1824.4	22.3
129	24 x 39-31 MR	40.0	5.0	17.5	17.0	8.2	4.8	58.2	27.2	143.9	284.6	1897.4	13.4
130	26 X M-95-1 RI	37.0	5.0	13.0	15.0	9.1	6.3	69.0	43.6	122.0	363.5	2423.3	6.7
131	26 X 37-IV- 9IR	41.0	5.0	29.3	18.0	10.5	6.8	65.5	40.2	146.0	379.4	2529.6	23.7
132	26X 27-164	46.0	7.0	24.9	13.0	7.4	5.1	72.3	45.7	143.4	282.2	1881.2	23.1
133	49 X 39-21-1	43.0	4.0	15.2	9.0	4.6	2.8	61.6	24.6	126.4	136.6	910.4	27.2
134	49 X 39-21-2(a)	38.0	5.0	19.7	18.0	7.8	4.7	65.4	25.8	141.2	284.8	1898.8	14.5
135	49 x 39-74	41.0	6.0	15.2	14.0	8.4	6.2	75.5	35.7	124.4	332.9	2219.3	7.6
136	39x 49-81-1	40.0	5.0	15.7	12.0	7.0	4.7	67.1	37.7	126.6	277.5	1849.8	7.4
137	49 x 27-37	41.0	5.0	21.8	10.0	5.6	3.1	55.4	30.1	137.1	182.2	1214.9	22.1
138	TDG 10	41.0	5.0	17.7	12.0	5.7	3.3	55.2	28.9	125.0	219.5	1463.6	8.7
139	TDG 13	44.0	7.0	20.7	7.0	4.1	2.4	56.9	31.9	144.4	157.9	1053.0	14.3
140	TDG 14	40.0	6.0	18.1	7.0	4.7	2.5	52.4	41.1	144.1	145.4	969.6	11.7
141	DTG 3	44.0	7.0	20.8	18.0	9.5	5.6	62.2	30.5	141.0	358.0	2386.9	15.1
142	DTG 15	36.0	5.0	30.4	17.0	11.9	7.2	60.5	41.0	131.0	447.1	2980.5	17.3
143	M 28-2	44.0	7.0	29.7	11.0	6.9	3.6	52.6	31.3	148.0	227.9	1519.5	30.7
144	JL 24	38.0	5.0	29.1	11.0	5.9	4.3	72.1	32.4	122.9	215.0	1433.6	13.6
145	TAG 24	37.0	5.0	28.8	11.0	6.6	3.8	57.6	29.8	137.5	231.8	1545.5	14.6
146	SPS 1	43.0	5.0	29.2	11.0	7.8	4.9	62.1	31.5	122.5	280.9	1872.8	11.3
147	SPS 9	41.0	5.0	21.5	7.0	4.8	2.8	59.2	27.3	133.6	171.5	1143.2	12.8
148	SPS 10	41.0	5.0	19.4	7.0	5.4	3.4	68.5	32.1	136.0	215.2	1434.4	8.2
149	SPS 13	42.0	6.0	15.8	9.0	6.6	3.9	57.8	43.7	146.5	258.4	1722.9	13.2
150	SPS 14	42.0	5.0	13.3	8.0	4.2	2.3	55.1	26.7	127.5	141.1	940.4	4.8
151	SPS 17	43.0	6.0	23.7	9.0	7.9	4.0	49.3	37.9	144.6	280.8	1871.9	20.8
152	ICGV 02411	42.0	6.0	26.7	9.0	8.4	5.2	62.0	42.6	148.0	322.4	2149.1	19.5
153	ICGV 05155	40.0	7.0	21.5	18.0	7.8	4.0	50.9	27.0	148.0	310.5	2070.3	20.6
154	ICGV 06100	44.0	6.0	19.8	12.0	8.5	5.0	64.8	35.6	148.0	324.4	2162.3	28.1
155	ICGV 07023	39.0	5.0	32.2	13.0	8.8	5.6	60.8	38.6	127.0	323.0	2153.2	13.8
156	SunOleic 95R	41.0	5.0	16.9	5.0	2.8	1.4	49.8	29.5	144.0	103.1	687.5	16.6
157	ICG 434	41.0	5.0	26.1	14.0	6.1	3.9	60.8	30.0	145.0	202.2	1348.2	19.0
158	ICG 2031	40.0	4.0	22.8	13.0	6.8	4.8	70.7	30.2	122.9	269.4	1796.1	10.4
159	ICG 3102	39.0	4.0	21.0	11.0	7.4	4.7	62.7	34.7	140.0	277.3	1848.6	18.9
160	ICG 3140	39.0	5.0	31.0	13.0	9.0	5.5	58.4	31.3	125.9	351.1	2340.4	17.3
161	ICG 3343	42.0	4.0	24.7	7.0	4.4	2.7	60.6	35.9	142.9	151.8	1011.8	16.1
162	ICG 3421	40.0	5.0	22.2	17.0	8.3	4.9	67.1	24.9	133.5	335.3	2235.1	8.8

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12
163	ICG 4729	37.0	7.0	30.5	16.0	8.7	5.6	64.6	29.3	124.9	341.9	2279.1	21.8
164	ICG 6022	40.0	4.0	28.2	4.0	5.8	3.1	50.3	27.1	143.1	229.9	1532.7	14.4
165	ICG 6646	39.0	4.0	37.8	12.0	10.7	5.7	52.7	42.2	151.4	390.4	2602.6	22.9
166	ICG 8517	39.0	5.0	29.1	10.0	5.1	2.8	53.8	25.6	137.6	206.6	1377.6	13.0
167	ICG 8751	41.0	5.0	28.3	14.0	6.5	3.2	53.5	35.5	143.9	263.1	1754.3	20.2
168	ICG 9315	40.0	6.0	26.6	14.0	9.0	5.3	59.8	29.4	126.5	343.7	2291.4	14.6
169	ICG 10036	40.0	5.0	21.8	5.0	3.2	1.5	50.4	22.9	143.0	118.1	787.6	14.6
170	ICG 10053	39.0	5.0	29.3	7.0	6.9	3.6	51.6	43.6	143.5	266.7	1778.3	18.9
171	ICG 10701	40.0	6.0	18.8	14.0	10.2	6.2	60.2	41.5	128.1	369.1	2460.7	11.2
172	ICG 11088	41.0	5.0	21.7	8.0	8.0	4.3	55.0	34.0	127.7	298.1	1987.3	16.8
173	ICG 11651	38.0	5.0	24.4	19.0	12.2	7.1	57.3	33.2	138.1	494.7	3298.0	12.5
174	ICG 12625	41.0	5.0	23.1	10.0	7.6	4.1	53.8	35.4	135.5	302.0	2013.2	14.6
175	ICG 12991	41.0	5.0	19.8	10.0	5.4	3.6	64.1	33.5	136.0	214.3	1428.6	11.6
176	ICG 14985	43.0	6.0	24.0	6.0	4.6	2.8	57.1	35.7	143.9	172.2	1148.0	12.9
177	ICG 15415	42.0	5.0	21.8	6.0	4.0	2.0	50.4	28.9	136.9	141.3	941.9	16.0
178	ICG 15419	38.0	4.0	34.5	5.0	5.2	2.8	55.3	49.9	124.4	194.9	1299.4	33.3
179	ICGV 01232	40.0	5.0	30.0	13.0	10.8	6.8	63.3	44.3	139.0	391.4	2609.6	17.3
180	ICGV 01276	40.0	6.0	23.2	21.0	13.7	7.6	60.1	40.1	135.0	547.0	3646.6	17.1
181	ICGV 01328	42.0	5.0	19.0	13.0	8.4	5.6	67.8	27.7	140.9	315.4	2102.4	15.5
182	ICGV 02022	39.0	6.0	26.4	12.0	8.1	5.1	68.6	30.3	140.1	328.9	2192.7	8.9
183	ICGV 02038	40.0	5.0	25.3	11.0	6.9	5.0	71.6	35.8	132.5	276.7	1844.7	9.5
184	ICGV 02189	37.0	5.0	19.1	8.0	5.4	3.3	58.9	40.8	132.0	199.6	1330.7	8.9
185	ICGV 02194	40.0	5.0	26.7	13.0	7.3	4.7	64.1	28.6	140.9	285.9	1906.3	12.8
186	ICGV 02266	39.0	5.0	37.7	18.0	8.9	6.0	68.4	32.5	124.7	358.4	2389.1	15.4
187	ICGV 02271	41.0	5.0	19.5	12.0	8.8	5.7	64.8	39.1	148.1	347.9	2319.4	17.6
188	ICGV 02286	37.0	5.0	25.9	12.0	7.5	4.9	70.7	38.8	131.4	285.0	1900.0	17.3
189	ICGV 86011	38.0	5.0	37.6	14.0	9.8	6.6	67.5	32.6	127.0	386.7	2577.8	18.7
190	ICGV 86590	45.0	5.0	19.8	6.0	3.3	1.8	53.9	31.7	147.9	113.6	757.4	30.4
191	ICGV 87160	39.0	4.0	19.5	17.0	10.6	7.0	63.8	37.2	136.9	376.8	2512.2	7.4
192	ICGV 87354	40.0	5.0	19.0	7.0	4.3	1.8	49.2	22.7	142.3	160.7	1071.5	15.9
193	ICGV 87378	40.0	4.0	35.0	13.0	10.5	6.8	66.1	33.6	133.6	409.2	2728.1	14.9
194	ICGV 87921	38.0	5.0	26.5	13.0	10.9	6.0	54.3	38.6	134.0	434.2	2894.7	13.8
195	ICGV 88145	40.0	5.0	29.4	15.0	9.2	5.2	54.5	29.4	127.9	315.6	2104.2	22.0
196	ICGV 92267	40.0	6.0	29.4	13.0	9.7	6.2	63.5	40.3	131.4	362.0	2413.6	14.0
197	ICGV 93470	36.0	5.0	20.4	13.0	8.7	5.4	63.1	36.6	127.0	330.2	2201.2	11.8
198	ICGV 94169	44.0	5.0	26.7	11.0	7.0	3.7	56.6	39.7	141.9	266.9	1779.6	28.1
199	ICGV 94361	41.0	6.0	27.7	13.0	9.2	5.4	59.7	40.0	132.0	348.9	2325.8	22.7
200	ICGV 95377	39.0	4.0	23.6	11.0	9.9	5.5	71.1	42.3	146.4	339.9	2266.0	19.4
201	ICGV 96466	41.0	5.0	18.8	9.0	7.4	4.6	63.0	37.1	132.0	296.1	1974.2	9.8
202	ICGV 96468	39.0	7.0	23.5	12.0	9.7	5.9	64.5	40.5	130.8	388.2	2588.1	18.4
203	ICGV 97182	40.0	6.0	24.9	13.0	9.8	6.0	58.6	32.5	135.9	379.5	2530.2	16.1
204	ICGV 97183	40.0	5.0	22.5	11.0	7.6	4.1	54.6	33.7	145.1	228.3	1522.1	16.4
205	ICGV 98294	44.0	5.0	29.1	13.0	10.2	6.3	62.9	40.0	142.9	398.2	2654.4	18.8
206	Gangapuri	39.0	5.0	25.1	12.0	7.2	4.1	57.4	26.3	132.6	261.6	1743.8	12.3
207	ICGS 44	45.0	6.0	15.9	6.0	3.0	1.8	60.7	30.5	148.0	109.5	729.8	21.4
208	ICG 3312	40.0	5.0	18.5	8.0	5.7	3.9	69.4	29.3	126.9	225.7	1504.8	9.2
209	ICG 14705	39.0	6.0	24.8	10.0	7.2	4.9	69.3	37.3	143.1	277.3	1848.9	16.0
210	ICG 3746	38.0	5.0	26.5	14.0	7.4	5.2	71.2	26.1	124.6	250.8	1672.0	11.2
211	ICG 4955	39.0	5.0	35.3	16.0	10.2	7.8	69.9	37.7	131.0	398.2	2654.6	14.0
212	ICG 12879	42.0	5.0	18.9	11.0	5.5	3.5	62.7	29.0	125.0	217.6	1450.7	12.5
213	ICG 5221	41.0	5.0	28.5	8.0	2.8	1.5	49.9	23.1	144.0	92.5	616.7	16.9
214	ICG 4543	40.0	5.0	21.9	11.0	5.4	3.2	60.0	24.2	139.6	175.1	1167.6	13.2
215	ICG 1834	41.0	5.0	26.2	14.0	7.2	4.3	60.7	30.2	129.9	281.6	1877.1	16.0
216	ICG 2106	39.0	5.0	28.2	13.0	7.3	5.5	73.2	32.4	127.2	269.8	1798.9	12.4
217	ICG 9507	44.0	5.0	21.7	6.0	4.2	2.2	46.1	30.4	132.1	156.0	1040.1	12.0
218	ICG 1973	40.0	5.0	20.7	9.0	6.0	3.6	64.2	33.3	127.6	240.6	1604.2	11.4

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12
219	ICG 3673	41.0	5.0	27.3	11.0	7.3	5.1	67.3	34.8	136.0	263.2	1754.7	23.5
220	ICG 3584	38.0	5.0	28.8	17.0	9.3	6.7	73.3	30.6	126.5	322.9	2152.6	18.9
221	ICG 442	38.0	5.0	25.3	11.0	4.1	2.0	54.0	22.5	137.8	155.8	1038.8	14.7
222	ICGV 01464	41.0	6.0	20.3	4.0	3.0	1.6	48.0	31.5	147.9	90.2	601.0	32.8
223	ICGV 01478	44.0	4.0	18.0	4.0	2.6	1.6	58.2	58.5	149.1	81.8	545.1	26.9
224	ICGV 02251	39.0	5.0	26.6	13.0	8.0	5.4	69.9	35.8	125.6	291.4	1942.8	21.4
225	ICGV 03136	47.0	6.0	19.3	6.0	4.8	2.6	63.7	51.1	149.1	167.8	1118.9	26.8
226	ICGV 05198	40.0	6.0	28.3	11.0	10.9	5.8	57.7	48.7	145.9	372.9	2485.8	27.8
227	ICGV 06234	42.0	7.0	25.5	17.0	14.2	8.2	63.6	58.6	148.9	551.0	3673.5	29.2
228	ICGV 00346	43.0	7.0	27.0	16.0	10.1	5.9	59.3	44.0	151.8	403.0	2686.9	30.9
229	ICGV 00362	45.0	6.0	14.5	7.0	3.1	1.6	49.6	24.4	141.9	118.6	790.6	22.9
230	ICGV 00371	45.0	8.0	18.0	11.0	4.9	3.0	54.8	30.7	146.1	199.3	1328.4	13.9
231	ICGV 02287	47.0	7.0	18.0	6.0	2.8	1.5	49.5	34.5	147.9	107.1	714.1	15.5
232	ICGV 02298	44.0	6.0	18.8	8.0	4.3	2.4	59.6	34.9	145.1	144.8	965.0	23.7
233	ICGV 02317	43.0	7.0	21.8	10.0	6.2	3.8	66.7	39.2	149.0	247.0	1646.4	30.7
234	ICGV 97232	38.0	6.0	20.2	9.0	5.6	3.5	62.2	30.5	137.0	214.7	1431.3	10.6
235	ICGV 99051	45.0	6.0	28.2	10.0	6.9	4.1	58.7	29.5	147.9	250.4	1669.1	30.0
236	ICGV 99052	42.0	5.0	22.8	7.0	3.6	1.9	54.1	23.1	148.9	112.3	748.9	25.6
237	ICGV 00246	45.0	5.0	23.7	6.0	4.3	2.1	54.8	34.1	149.1	126.1	840.5	15.7
238	ICGV 00248	41.0	5.0	21.8	7.0	5.0	3.0	57.8	31.1	148.0	179.8	1198.4	19.8
239	ICGV 01361	44.0	8.0	26.5	14.0	9.6	6.0	61.1	25.2	147.9	364.7	2431.2	25.8
240	ICGV 02434	43.0	6.0	15.9	12.0	6.2	4.3	69.3	42.1	149.7	220.2	1468.2	22.4
241	ICGV 04087	43.0	7.0	29.4	16.0	9.2	4.9	56.7	29.2	148.1	368.0	2453.0	31.8
242	ICGV 06175	46.0	7.0	20.5	6.0	3.3	1.5	52.8	35.9	149.0	130.3	868.9	22.2
243	ICGV 97116	48.0	5.0	14.5	6.0	2.9	1.7	57.8	29.1	148.0	102.2	681.3	23.0
244	ICGV 97128	40.0	9.0	27.1	12.0	7.2	4.0	59.0	31.0	149.0	285.4	1902.8	24.1
245	ICGV 98184	41.0	7.0	26.0	13.0	9.2	5.5	60.3	38.3	146.0	358.3	2388.9	23.8
246	ICGV 00068	43.0	5.0	16.6	8.0	4.6	2.0	49.6	27.9	148.0	170.2	1134.4	23.8
247	ICGV 01495	42.0	9.0	28.3	16.0	14.2	8.0	61.3	46.8	143.0	548.3	3655.5	27.9
248	ICGV 05057	46.0	8.0	29.2	9.0	7.4	4.6	62.7	47.0	148.2	293.7	1958.2	26.3
249	ICGV 07168	44.0	6.0	21.7	5.0	3.5	1.8	53.5	21.7	148.0	117.0	780.1	24.2
250	ICGV 01265	45.0	7.0	17.5	7.0	3.7	1.9	50.5	32.3	145.6	126.3	842.1	25.4
251	ICGV 98105	43.0	7.0	21.2	16.0	9.0	5.6	61.7	41.7	146.0	346.8	2311.8	23.0
252	ICGV 99160	43.0	7.0	22.4	7.0	3.7	1.5	46.6	26.8	150.1	139.8	931.8	26.9
253	ICGV 02323	45.0	7.0	22.0	11.0	8.7	5.8	67.1	49.5	148.9	348.4	2323.0	18.2
254	ICGV 04115	42.0	7.0	19.0	7.0	5.8	3.6	62.4	41.0	139.1	231.6	1544.1	25.3
255	ICGV 05036	43.0	7.0	22.0	11.0	5.3	2.8	52.4	33.7	148.9	207.1	1380.5	35.9
256	ICGV 06042	45.0	6.0	17.1	10.0	5.6	3.3	55.5	29.2	149.1	202.6	1350.4	29.7
257	ICGV 86564	44.0	8.0	23.2	3.0	3.5	2.2	62.2	53.5	148.9	124.1	827.0	40.5
258	ICGV 98432	47.0	8.0	26.8	5.0	3.6	1.6	44.9	42.4	151.0	107.5	716.6	31.6
259	BAU 13	48.0	6.0	26.6	5.0	6.0	3.3	64.1	40.1	148.0	200.1	1334.1	30.9
260	ICGV 87846	43.0	6.0	24.9	9.0	6.7	3.8	61.4	39.0	148.1	235.2	1568.1	26.2
261	ICR 48	46.0	8.0	17.3	3.0	2.8	1.6	59.8	34.8	149.1	100.2	668.0	24.7
262	ICGV 86699	44.0	6.0	15.8	5.0	3.1	1.8	60.4	20.9	148.1	112.8	752.0	21.1
263	ICGV 98373	44.0	8.0	22.8	9.0	6.3	3.2	51.7	37.3	148.9	232.2	1547.9	18.1
264	ICGV 97115	49.0	5.0	14.6	6.0	2.5	1.3	46.4	27.0	148.0	85.8	571.9	20.8
265	ICGV 06040	47.0	6.0	21.7	9.0	4.8	2.9	60.5	42.5	150.1	188.5	1256.8	21.8
266	ICGV 06099	45.0	6.0	25.5	18.0	11.3	7.7	65.2	40.5	148.0	350.1	2334.2	23.3
267	CS 39	43.0	7.0	22.4	21.0	19.9	11.6	63.1	46.4	146.0	648.2	4321.2	29.9
268	ICGV 05032	40.0	7.0	24.0	18.0	11.8	6.2	52.4	40.3	149.0	424.6	2830.6	32.5
269	ICGV 05141	43.0	6.0	20.2	11.0	6.7	4.3	62.4	46.4	147.9	238.7	1591.2	29.7
270	ICGV 07359	46.0	6.0	35.9	12.0	9.1	5.5	58.6	52.7	149.0	315.8	2105.4	32.6
271	ICGV 07368	47.0	5.0	20.3	9.0	10.7	5.2	52.5	51.1	148.1	369.1	2460.9	30.7
272	ICGV 06110	43.0	8.0	22.0	11.0	4.6	2.0	52.0	37.1	148.0	161.2	1074.5	24.1
273	ICGV 06188	44.0	6.0	19.4	8.0	6.4	4.0	62.7	56.5	147.9	241.7	1611.6	15.7
274	ICGV 00440	45.0	7.0	26.9	6.0	5.6	2.8	49.1	42.5	145.9	184.6	1230.4	32.9

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12
275	ICGV 86352	39.0	5.0	22.9	8.0	5.8	3.2	55.8	34.4	134.0	229.4	1529.3	8.2
276	ICGV 09112	43.0	7.0	24.8	6.0	4.6	2.7	62.7	41.6	149.9	165.0	1099.8	32.8
277	ICGV 93920	45.0	6.0	20.4	18.0	9.5	5.2	61.2	27.7	144.0	379.4	2529.1	12.4
278	ICGV 93216	38.0	6.0	17.0	15.0	10.7	7.1	65.0	31.2	140.0	423.7	2825.0	15.3
279	ICGV 88438	49.0	6.0	14.6	3.0	1.9	0.9	49.6	25.0	149.0	61.7	411.4	27.1
280	ICG 11337	44.0	6.0	19.5	5.0	2.3	1.2	49.1	24.1	148.1	77.0	513.5	23.5
281	49 x 37-90	44.0	8.0	26.8	5.0	2.3	1.6	51.6	24.9	146.0	80.6	537.5	23.0
282	49 M-2-2	47.0	9.0	19.4	3.0	2.6	1.4	46.7	34.1	146.0	102.0	680.3	10.5
283	49 M- 1-1	47.0	5.0	24.9	5.0	4.0	2.0	54.5	46.7	148.0	146.8	978.4	22.7
284	TG 19	42.0	5.0	18.2	6.0	4.3	2.4	61.9	27.4	141.8	174.9	1166.1	16.6
285	TG 39	43.0	5.0	16.2	7.0	5.0	2.4	49.2	35.2	149.1	195.3	1302.2	16.6
286	TG LPS 3	45.0	8.0	18.8	10.0	7.8	5.2	66.1	43.5	143.9	279.9	1865.8	27.7
287	26 X M-223-1	49.0	5.0	16.0	7.0	3.1	1.8	56.6	42.6	148.0	95.3	635.6	18.3
288	SPS 2	44.0	8.0	19.6	7.0	3.9	2.3	60.1	27.2	147.9	129.3	862.1	30.7
289	SPS 3	37.0	5.0	18.0	11.0	5.7	3.8	65.8	27.4	132.4	222.1	1480.5	10.7
290	SPS 6	38.0	5.0	27.3	15.0	8.9	5.5	61.3	34.7	132.0	339.6	2264.3	16.7
291	SPS 7	45.0	7.0	23.3	8.0	4.7	2.7	55.6	35.5	150.1	162.2	1081.6	25.3
292	SPS 8	43.0	7.0	21.2	8.0	5.8	3.7	60.6	27.6	148.0	188.3	1255.4	26.1
293	SPS 11	44.0	7.0	20.7	9.0	6.6	4.5	67.6	30.7	144.1	265.5	1770.2	15.3
294	SPS 15	45.0	5.0	16.9	8.0	4.0	2.1	60.8	20.5	147.9	126.7	844.7	30.7
295	SPS 20	45.0	7.0	20.6	5.0	2.6	1.5	54.2	22.5	154.6	84.5	563.3	27.3
296	SPS 21	42.0	7.0	19.2	10.0	5.9	3.8	63.3	30.9	148.1	203.3	1355.4	22.2
297	ICGV 03128	45.0	6.0	29.9	19.0	14.3	9.1	65.9	37.9	146.1	545.5	3636.5	29.6
298	TMV 2 NLM	37.0	5.0	17.3	10.0	5.2	2.7	50.3	30.8	140.0	208.4	1389.6	10.3
299	ICG 1668	39.0	5.0	22.3	10.0	6.6	4.9	65.4	46.5	131.9	238.4	1589.4	17.3
300	ICG 8285	50.0	5.0	13.2	13.0	7.6	4.2	55.7	32.3	149.3	230.1	1533.8	28.7
301	ICG 11426	44.0	7.0	18.0	8.0	4.1	2.0	53.8	23.0	146.3	130.8	872.0	21.9
302	ICGV 02290	45.0	8.0	19.6	7.0	3.9	2.9	67.3	34.0	148.0	132.9	885.9	36.0
303	ICGV 02446	43.0	7.0	24.3	13.0	7.1	3.9	54.7	34.8	149.1	284.0	1893.3	32.4
304	ICG 156	45.0	6.0	20.9	11.0	9.8	5.8	65.8	37.7	146.0	325.8	2172.2	21.5
305	ICGS 76	45.0	9.0	22.6	13.0	6.7	3.7	54.8	33.8	143.5	269.1	1793.8	27.5
306	ICG 5891	50.0	5.0	16.0	4.0	3.1	1.6	50.9	29.8	149.0	97.4	649.4	17.3
307	CSMG 84-1	41.0	6.0	18.9	6.0	3.0	1.5	50.8	26.3	144.5	100.4	669.4	15.3
308	ICG 111	43.0	4.0	15.2	7.0	5.4	3.4	63.1	27.6	148.0	160.6	1070.7	17.7
309	ICG 14834	46.0	7.0	15.5	3.0	2.1	0.7	52.9	24.8	134.1	62.5	416.4	13.6
310	ICG 11322	44.0	6.0	16.4	5.0	3.8	2.3	62.2	24.2	147.9	148.7	991.1	19.6
311	ICG 532	47.0	5.0	14.6	5.0	2.4	1.3	58.4	20.6	149.1	70.9	472.9	23.2
312	ICG 12509	45.0	5.0	20.1	8.0	7.0	4.5	64.8	49.6	148.0	209.8	1398.9	14.7
313	ICG 12672	40.0	5.0	24.5	7.0	3.2	1.8	55.6	25.9	141.8	122.8	818.4	14.7
314	ICG 10185	47.0	7.0	27.9	7.0	5.8	2.8	52.9	27.0	145.9	173.0	1153.4	19.1
315	ICG 2773	50.0	4.0	12.9	4.0	2.5	1.3	45.2	31.4	148.0	73.9	492.7	15.6
316	ICG 3027	48.0	6.0	18.2	5.0	3.8	1.7	53.1	19.1	149.1	121.0	807.0	11.2
317	ICG 5745	47.0	6.0	18.6	11.0	7.4	4.1	54.1	36.4	146.1	291.1	1941.0	14.7
318	ICG 14482	44.0	6.0	15.5	4.0	3.0	1.5	51.0	33.0	149.1	96.0	639.9	18.9
319	ICG 4527	41.0	7.0	19.1	4.0	3.2	1.7	57.1	30.0	149.1	98.6	657.1	25.6
320	ICG 4343	45.0	7.0	14.8	4.0	3.7	2.0	52.6	22.6	148.0	119.7	797.9	12.6
321	ICG 13895	49.0	8.0	14.4	3.0	2.3	1.4	54.9	31.1	148.0	69.9	466.3	16.0
322	ICG 5663	46.0	5.0	17.9	3.0	2.1	1.2	53.9	24.3	149.0	75.5	503.2	22.0
323	ICG 721	47.0	5.0	16.9	14.0	6.0	3.7	55.1	24.5	146.5	199.7	1331.3	18.0
324	ICG 12276	39.0	5.0	18.6	10.0	6.0	4.0	54.9	21.6	149.1	197.2	1314.6	22.9
325	ICG 875	48.0	7.0	17.3	6.0	2.0	1.0	49.5	22.2	148.9	71.3	475.3	29.3
326	ICG 14475	43.0	4.0	15.8	7.0	2.8	1.3	47.0	32.6	151.0	80.9	539.2	34.8
327	ICG 15190	46.0	7.0	17.3	3.0	3.0	1.5	50.0	21.6	146.2	91.1	607.4	27.5
328	ICG 12370	48.0	5.0	14.7	4.0	3.4	2.0	50.5	24.3	145.9	115.5	769.8	23.9
329	ICGV 86325	45.0	7.0	20.0	6.0	5.5	3.3	59.2	31.5	145.9	179.9	1199.5	28.9
330	ICG 5662	48.0	5.0	20.0	3.0	1.9	1.2	65.1	34.5	147.9	76.4	509.1	23.2

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12
331	ICG 9961	53.0	5.0	15.8	4.0	2.4	0.9	66.3	28.0	148.0	82.8	551.7	17.3
332	ICG 14466	49.0	9.0	24.7	4.0	3.0	1.7	60.6	31.7	146.0	102.5	683.5	11.6
333	ICG 3053	43.0	6.0	16.2	11.0	5.8	3.0	51.1	22.9	146.1	199.1	1327.1	16.8
334	ICG 6766	49.0	5.0	16.4	4.0	3.0	1.6	51.1	25.9	148.0	89.5	596.7	21.5
335	ICG 2381	46.0	5.0	16.4	3.0	2.6	1.4	47.7	22.6	146.0	77.4	515.8	22.1
336	ICG 2857	52.0	4.0	17.2	5.0	2.9	2.0	58.4	25.2	148.0	110.5	736.9	15.1
337	ICGV 13238	38.0	5.0	21.3	10.0	6.4	4.4	68.3	40.0	127.1	256.3	1708.4	9.3
338	ICGV 13241	34.0	5.0	20.9	13.0	8.7	5.4	63.0	36.3	128.2	346.5	2309.9	14.1
339	ICGV 13242	37.0	5.0	20.1	14.0	7.3	4.4	59.8	36.0	126.4	250.1	1667.6	15.9
340	ICGV 13245	38.0	6.0	21.1	12.0	10.1	6.9	65.9	40.8	134.7	348.3	2321.7	13.8
Mean		**42.0**	**6.0**	**22.1**	**10.0**	**6.6**	**4.0**	**59.4**	**33.8**	**142.0**	**246.2**	**1641.4**	**19.4**
CV (%)		**3.5**	**7.2**	**7.6**	**20.0**	**20.6**	**22.1**	**4.4**	**6.3**	**1.3**	**22.6**	**22.6**	**13.5**
LSD at 5 % level		**2.4**	**0.1**	**2.8**	**3.4**	**2.2**	**1.4**	**4.3**	**3.5**	**3.1**	**91.9**	**612.5**	**0.7**

Appendix IX

Best linear unbiased prediction of mean for nutritional quality traits of Genomic Selection Panel of groundnut evaluated at ICRISAT during post-rainy 2015-16

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
1	ICGV 06423	49.5	27.6	42.9	35.5	12.7	2.4	1.2
2	ICGV 07246	47.5	27.2	41.1	35.8	13.1	2.0	1.2
3	ICGV 07247	51.5	25.0	38.2	38.8	13.8	2.3	1.0
4	ICGV 07268	50.1	24.4	38.8	39.6	12.4	2.6	1.0
5	ICGV 01005	44.9	31.2	44.1	34.2	11.9	1.8	1.3
6	ICGV 01060	49.7	27.7	41.9	36.9	11.9	2.8	1.1
7	ICGV 01124	49.9	26.8	54.7	26.5	11.1	2.6	2.1
8	ICGV 02206	48.6	26.3	42.6	36.5	12.8	2.4	1.2
9	ICGV 03397	46.8	27.5	35.5	40.6	14.5	2.1	0.9
10	ICGV 03398	46.0	30.2	38.3	38.8	14.0	2.3	1.0
11	ICGV 04044	49.0	25.5	42.1	36.0	13.4	2.7	1.2
12	ICGV 06347	48.7	25.0	38.6	39.1	13.6	2.0	1.0
13	ICGV 93280	50.3	22.7	38.4	38.5	13.6	2.3	1.0
14	ICGV 95469	49.7	26.5	37.7	39.9	13.7	2.1	1.0
15	ICGV 00387	48.6	26.5	41.1	36.7	13.3	2.3	1.2
16	ICGV 01393	48.5	27.6	46.8	32.7	11.2	2.5	1.5
17	ICGV 02242	44.3	28.4	45.6	32.2	12.5	2.5	1.4
18	ICGV 97058	47.6	26.9	45.2	32.2	12.4	2.2	1.4
19	ICGV 99083	48.1	26.0	40.2	36.1	14.1	2.2	1.1
20	ICGV 00343	53.6	26.4	40.0	37.6	14.4	3.3	1.1
21	ICGV 00349	52.2	26.5	44.8	34.2	12.8	2.4	1.3
22	ICGV 01263	48.7	27.6	51.6	27.9	11.2	2.5	1.9
23	ICGV 03056	51.7	25.2	45.0	32.8	12.5	2.6	1.4
24	ICGV 03064	51.5	21.7	48.7	31.9	11.6	3.0	1.6
25	ICGV 05161	50.5	24.0	43.8	35.0	12.3	2.8	1.3
26	ICGV 05163	48.6	26.9	38.9	39.0	13.2	2.5	1.0
27	ICGV 06422	48.6	26.9	44.4	33.6	12.6	2.8	1.3
28	ICGV 06431	48.9	28.1	38.2	39.5	12.4	2.1	1.0
29	ICGV 07220	54.0	23.0	54.2	27.6	12.6	1.5	2.0
30	ICGV 07223	47.6	26.4	42.7	34.7	12.9	2.3	1.2
31	ICGV 07227	51.9	26.2	42.8	34.6	13.6	2.6	1.2
32	ICGV 07235	49.1	24.9	36.0	41.6	13.6	2.1	0.9
33	ICGV 99233	48.0	28.4	36.5	41.3	12.4	2.1	0.9
34	ICGV 97165	49.2	27.0	45.4	32.7	13.1	2.4	1.5
35	ICGV 99029	46.5	27.3	38.0	37.5	14.1	2.8	1.0
36	ICGV 00191	48.0	25.2	40.3	36.7	13.6	2.9	1.1
37	ICGV 07120	49.1	25.7	41.2	36.6	13.0	2.4	1.1
38	ICGV 97092	48.2	26.7	40.2	38.0	14.2	2.6	1.1
39	ICGV 97120	51.4	27.3	55.6	26.7	12.4	1.9	2.1
40	ICGV 98163	50.4	26.4	37.5	38.5	14.4	2.5	1.0
41	ICGV 00005	52.2	24.5	38.2	37.1	14.1	2.6	1.1
42	ICGV 01273	49.5	25.3	37.6	39.6	13.6	2.3	1.0
43	ICGV 01274	46.1	29.2	40.2	38.0	12.7	2.0	1.1
44	ICGV 02321	49.9	27.6	41.0	35.5	13.7	2.5	1.2
45	ICGV 03043	50.7	26.6	40.3	38.3	13.3	2.1	1.0
46	ICGV 04124	48.1	29.4	39.4	38.3	13.6	2.2	1.0
47	ICGV 00290	46.3	28.4	41.7	37.1	12.4	1.9	1.1
48	ICGV 00321	45.9	31.0	40.6	37.2	12.4	2.2	1.1
49	ICGV 02125	48.1	26.8	47.4	32.8	11.5	1.6	1.5
50	ICGV 02144	47.3	30.1	50.4	29.5	11.0	2.3	1.8
51	ICGV 03184	52.0	22.9	45.0	32.0	12.9	2.7	1.4

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
52	ICGV 03207	49.2	28.0	45.3	34.4	11.8	2.0	1.3
53	ICGV 04018	51.1	28.0	44.1	35.0	11.9	2.9	1.3
54	ICGV 07210	48.7	25.5	46.2	33.4	12.0	2.4	1.4
55	ICGV 07217	47.7	26.5	40.0	38.5	12.6	1.9	1.0
56	ICGV 95290	44.0	33.1	39.6	36.7	12.4	2.3	1.1
57	ICGV 97261	50.4	27.3	46.4	33.5	11.7	2.3	1.4
58	ICGV 97262	46.1	32.1	40.6	35.7	13.1	3.1	1.2
59	ICGV 99181	50.0	26.5	44.4	35.7	11.8	2.4	1.3
60	ICGV 99195	45.3	31.6	38.8	39.1	13.3	2.2	1.0
61	ICGV 89104	49.0	28.9	47.0	31.6	12.1	2.6	1.5
62	ICGS 11	51.5	24.8	39.8	38.9	12.8	2.6	1.0
63	J 11	49.0	26.5	44.3	35.2	12.2	2.3	1.3
64	ICGV 99085	49.5	25.9	52.5	26.8	10.6	2.9	2.0
65	TKG 19A	44.7	29.0	40.3	37.6	12.2	2.0	1.1
66	TPG 41	46.7	28.1	43.8	34.2	12.5	2.7	1.3
67	ICGV 00350	52.3	25.5	33.2	44.2	13.7	2.4	0.8
68	DH 86	45.8	30.7	39.4	37.1	13.0	2.6	1.1
69	ICGV 95058	46.1	29.6	50.5	27.2	12.4	2.0	1.9
70	ICGV 95070	50.1	27.0	40.8	36.2	13.4	2.4	1.1
71	GPBD 4	53.1	22.9	51.0	29.6	10.4	2.5	1.7
72	ICGV 91114	48.5	28.7	41.5	37.0	12.4	2.3	1.1
73	TMV 2	46.7	26.4	50.2	28.7	10.6	2.2	1.7
74	Faizpur 1-5	44.1	34.6	39.5	38.0	13.4	2.4	1.0
75	Mutant 3	47.9	30.5	43.5	35.1	12.4	2.6	1.3
76	ICGV 03042	52.1	22.3	38.8	39.7	13.3	2.2	1.0
77	ICGV 05100	50.5	24.9	40.5	37.3	13.3	2.5	1.1
78	ICGV 06049	47.4	29.7	44.6	35.0	11.9	2.2	1.3
79	ICGV 06420	51.0	25.8	40.5	38.5	12.9	2.1	1.1
80	ICGV 06424	52.7	26.0	45.2	33.3	12.2	3.0	1.4
81	ICGV 07145	49.2	25.3	37.4	39.2	14.0	2.6	0.9
82	ICGV 07148	47.4	30.9	41.3	37.8	12.0	2.4	1.1
83	ICGV 07166	50.7	25.1	40.5	37.9	12.9	2.6	1.1
84	ICGV 06142	52.1	28.0	39.2	37.8	13.4	2.9	1.0
85	ICGV 91116	50.8	26.3	41.8	36.5	12.6	2.0	1.2
86	ICGV 97045	57.9	26.4	53.7	21.8	12.5	3.9	2.6
87	ICGV 94118	50.2	25.2	40.5	35.9	14.0	3.2	1.2
88	ICGV 05176	46.2	30.1	45.4	31.5	12.2	2.9	1.5
89	ICGV 04149	49.9	27.5	47.8	31.8	12.7	2.2	1.5
90	ICGV 00351	43.7	28.1	52.6	27.4	10.7	1.8	1.9
91	ICGV 92195	46.7	27.6	44.4	34.1	11.9	1.9	1.3
92	ICGV 87187	47.4	26.1	46.0	32.7	12.9	2.0	1.4
93	ICGV 86072	49.4	24.1	43.9	34.7	12.5	2.3	1.3
94	ICGV 86015	46.4	27.4	38.9	38.0	13.9	2.0	1.0
95	ICGV 93437	46.1	26.9	38.0	40.1	13.0	1.6	0.9
96	ICGV 86143	47.5	29.7	44.1	33.8	12.3	2.8	1.3
97	ICGV 90320	47.1	26.5	45.3	33.0	11.7	2.6	1.4
98	ICGV 07273	45.4	30.3	42.4	36.7	12.1	2.0	1.2
99	49 × 37-91	51.7	24.1	35.4	43.8	12.9	2.4	0.8
100	49 × 37-134	45.2	27.2	47.5	30.0	12.6	1.7	1.6
101	49 × 37-135	51.6	25.5	47.9	33.0	11.0	2.4	1.4
102	49 × 37-97-1	50.9	26.7	45.7	32.3	12.2	2.5	1.4
103	49 × 37- 99(b) tall	52.2	28.0	49.5	25.6	11.8	2.8	2.2
104	39 × 49 -8	49.1	24.2	46.4	32.6	11.8	1.9	1.4
105	39 × 49 -77	49.7	24.0	49.9	32.2	10.6	2.1	1.6
106	49 × 39-20-2	45.6	29.7	45.4	33.4	11.6	2.4	1.4
107	49 × 39-21-2	49.4	25.3	48.1	31.8	11.5	2.7	1.6

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
108	49 × 39-8	47.5	23.7	51.4	29.3	10.6	2.1	1.7
109	49 M-16	50.3	29.2	40.1	37.5	13.0	2.6	1.1
110	49 × 27-19	42.4	28.8	46.4	30.8	12.1	1.6	1.5
111	49 × 27-13 (ii)	45.1	25.6	48.2	30.8	12.8	1.7	1.6
112	27 × 49- 16	46.8	27.6	48.3	29.4	12.0	2.8	1.7
113	27 × 49- 12	48.8	28.7	42.2	37.2	12.0	2.2	1.1
114	27 × 49- 14	50.6	24.0	45.3	32.4	13.0	2.4	1.4
115	27 × 49- 27-1	46.2	25.6	46.9	31.7	12.3	1.6	1.5
116	26 M 156-2	48.0	25.1	45.7	33.1	12.5	2.0	1.4
117	26 M- 119-1	47.3	29.8	40.9	37.4	12.5	2.3	1.1
118	24 M-86	52.2	24.8	42.8	35.5	13.4	2.6	1.2
119	MN1-35	53.0	29.5	48.6	32.6	12.9	1.9	1.5
120	M 110-14	46.2	26.8	44.5	34.1	11.8	2.9	1.3
121	M 28-2	49.2	28.1	38.0	38.2	13.6	2.4	1.0
122	Somnath	47.1	30.5	41.5	37.7	11.7	2.8	1.1
123	TG 41	46.1	23.6	46.6	31.5	12.7	1.9	1.5
124	TG 42	45.1	28.2	42.4	34.3	13.2	1.8	1.3
125	TG 49	44.8	25.2	47.2	31.1	12.3	1.5	1.5
126	TG LPS 4	48.1	25.1	39.9	36.7	13.2	1.6	1.1
127	TG LPS 7	47.0	28.3	49.3	28.3	12.3	2.2	1.7
128	24 × 37-2275	49.7	25.3	46.4	32.3	12.0	2.3	1.4
129	24 × 39-31 MR	51.7	24.5	41.5	38.4	11.6	2.4	1.1
130	26 × M-95-1 RI	53.8	22.0	46.8	32.8	11.2	2.7	1.4
131	26 × 37-IV- 9IR	49.0	26.3	46.9	31.3	11.7	2.4	1.5
132	26× 27-164	44.6	26.3	36.9	39.6	13.5	1.7	0.9
133	49 × 39-21-1	51.0	21.5	46.5	34.9	11.3	1.8	1.3
134	49 × 39-21-2(a)	53.0	20.8	43.7	35.5	12.2	2.6	1.3
135	49 × 39-74	51.0	25.5	49.1	31.1	10.9	2.6	1.6
136	39× 49-81-1	48.5	25.9	43.9	34.9	11.9	2.3	1.3
137	49 × 27-37	47.0	30.4	41.7	37.1	11.9	2.4	1.1
138	TDG 10	47.4	27.4	43.9	36.2	11.7	2.2	1.2
139	TDG 13	53.3	24.5	37.7	40.8	13.3	2.7	0.9
140	TDG 14	44.6	28.6	46.1	33.6	11.5	2.5	1.4
141	DTG 3	46.1	23.8	48.4	30.6	12.4	1.3	1.6
142	DTG 15	49.2	25.5	45.2	34.9	11.8	2.1	1.3
143	M 28-2	52.8	25.2	39.4	38.1	13.3	2.8	1.1
144	JL 24	50.6	25.0	47.6	32.7	11.2	2.3	1.5
145	TAG 24	46.7	27.1	40.2	38.7	12.4	2.0	1.1
146	SPS 1	52.9	27.8	43.1	35.2	15.1	2.2	1.2
147	SPS 9	52.4	27.3	44.7	34.9	14.3	2.3	1.3
148	SPS 10	48.3	27.8	43.2	36.7	12.2	2.2	1.2
149	SPS 13	46.1	26.4	50.5	29.8	11.5	2.0	1.7
150	SPS 14	52.4	29.5	44.8	34.6	14.3	1.8	1.3
151	SPS 17	45.3	26.2	46.7	32.4	12.6	2.5	1.5
152	ICGV 02411	51.7	28.2	39.4	38.6	13.1	2.6	1.0
153	ICGV 05155	55.2	22.2	38.9	39.2	13.4	2.5	1.0
154	ICGV 06100	52.5	25.0	42.7	36.0	13.2	2.8	1.2
155	ICGV 07023	47.3	28.5	44.9	35.0	11.9	2.3	1.3
156	SunOleic 95R	49.3	26.4	76.1	4.6	7.1	2.0	16.5
157	ICG 434	49.9	29.1	37.8	39.1	13.2	2.7	1.0
158	ICG 2031	49.2	26.8	45.4	34.1	11.7	2.2	1.4
159	ICG 3102	49.8	27.3	39.7	39.1	12.9	2.2	1.0
160	ICG 3140	49.7	25.7	43.9	35.6	12.1	2.1	1.3
161	ICG 3343	48.6	25.5	42.7	35.6	13.2	2.2	1.2
162	ICG 3421	49.0	26.3	44.4	33.7	12.3	2.3	1.3
163	ICG 4729	51.9	25.6	49.0	31.8	10.8	2.6	1.5

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
164	ICG 6022	54.2	26.1	56.2	30.1	8.5	3.3	1.9
165	ICG 6646	49.2	26.5	47.9	34.0	11.1	2.6	1.5
166	ICG 8517	49.9	26.4	44.2	34.5	14.7	1.7	1.3
167	ICG 8751	43.9	28.2	40.1	37.4	12.5	2.0	1.1
168	ICG 9315	48.4	29.8	41.3	37.6	12.4	1.9	1.1
169	ICG 10036	44.8	27.2	41.9	37.4	11.7	2.6	1.1
170	ICG 10053	47.4	27.8	50.4	28.9	11.3	2.7	1.8
171	ICG 10701	45.7	24.0	40.8	38.2	11.6	1.8	1.1
172	ICG 11088	51.1	26.2	50.9	33.0	10.4	2.3	1.5
173	ICG 11651	46.7	25.6	38.9	38.3	12.4	1.6	1.0
174	ICG 12625	55.9	21.8	51.3	34.8	10.2	2.3	1.5
175	ICG 12991	48.1	27.5	46.9	33.8	11.3	2.0	1.4
176	ICG 14985	49.0	25.4	45.6	31.9	12.3	2.2	1.4
177	ICG 15415	46.5	26.1	39.6	39.6	11.8	2.8	1.0
178	ICG 15419	54.9	24.1	50.3	34.9	9.8	2.8	1.5
179	ICGV 01232	47.3	27.3	36.4	40.7	13.7	2.2	0.9
180	ICGV 01276	47.2	28.8	38.3	37.7	13.2	2.2	1.0
181	ICGV 01328	50.0	24.8	51.4	28.7	13.5	1.8	1.8
182	ICGV 02022	49.3	27.8	37.9	40.6	12.6	2.3	1.0
183	ICGV 02038	44.4	33.3	42.0	35.4	12.1	2.5	1.2
184	ICGV 02189	46.9	30.7	38.6	39.7	12.7	2.2	1.0
185	ICGV 02194	50.9	24.9	43.5	35.4	12.4	3.0	1.2
186	ICGV 02266	47.3	28.5	44.5	34.2	11.9	2.2	1.3
187	ICGV 02271	50.7	27.9	30.6	46.6	14.1	2.8	0.7
188	ICGV 02286	49.2	24.5	43.3	35.0	12.5	2.3	1.3
189	ICGV 86011	47.5	28.7	43.4	35.8	12.0	1.9	1.2
190	ICGV 86590	47.5	27.9	33.8	43.7	13.2	2.8	0.8
191	ICGV 87160	45.7	28.2	45.0	33.8	11.5	2.4	1.3
192	ICGV 87354	47.9	28.8	47.3	30.2	12.7	2.5	1.6
193	ICGV 87378	50.3	29.4	32.9	43.5	13.5	2.4	0.8
194	ICGV 87921	47.8	28.8	43.8	34.6	12.1	2.1	1.3
195	ICGV 88145	48.8	26.3	41.6	37.1	12.7	1.9	1.1
196	ICGV 92267	50.2	27.4	36.5	42.1	12.8	2.2	0.9
197	ICGV 93470	49.6	27.1	43.6	36.1	11.8	2.2	1.2
198	ICGV 94169	46.3	25.4	50.9	28.5	11.5	2.2	1.8
199	ICGV 94361	51.5	24.4	40.1	38.5	13.0	2.2	1.0
200	ICGV 95377	46.4	29.6	41.9	36.1	12.4	2.8	1.2
201	ICGV 96466	49.1	29.5	42.7	35.7	12.2	2.6	1.2
202	ICGV 96468	52.4	26.3	40.4	38.2	13.1	3.1	1.1
203	ICGV 97182	50.5	23.1	38.5	39.7	13.1	2.7	1.0
204	ICGV 97183	44.4	30.9	39.7	37.7	12.7	2.0	1.0
205	ICGV 98294	48.1	29.2	47.5	31.1	12.1	2.9	1.5
206	Gangapuri	47.3	26.3	44.3	34.3	14.5	1.0	1.4
207	ICGS 44	48.8	27.3	36.0	41.9	13.5	2.2	0.8
208	ICG 3312	48.1	29.3	45.1	33.6	11.9	2.4	1.3
209	ICG 14705	51.6	25.3	41.4	35.4	13.0	2.8	1.2
210	ICG 3746	50.2	26.0	44.6	35.4	11.7	2.0	1.3
211	ICG 4955	51.1	24.5	46.2	32.7	13.8	0.8	1.4
212	ICG 12879	51.3	24.6	45.7	34.3	11.4	2.0	1.3
213	ICG 5221	54.5	26.5	54.8	30.3	9.1	3.0	1.8
214	ICG 4543	49.0	27.8	46.3	33.2	11.8	2.0	1.4
215	ICG 1834	50.7	26.9	39.9	38.7	12.5	2.1	1.0
216	ICG 2106	49.3	27.4	42.7	35.9	12.1	2.4	1.2
217	ICG 9507	48.7	30.9	44.5	33.2	12.9	2.5	1.4
218	ICG 1973	48.0	29.2	46.2	32.9	11.4	2.3	1.4
219	ICG 3673	54.2	23.4	44.2	35.4	14.4	1.0	1.3

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
220	ICG 3584	49.0	25.5	38.5	39.5	13.1	1.9	1.0
221	ICG 442	51.2	25.2	53.5	26.7	13.5	1.1	2.0
222	ICGV 01464	48.9	24.8	45.6	32.7	13.2	2.5	1.4
223	ICGV 01478	47.0	28.7	40.5	37.4	13.1	2.5	1.1
224	ICGV 02251	51.0	24.3	41.2	38.0	12.1	2.1	1.1
225	ICGV 03136	45.3	28.8	45.0	31.6	11.9	3.1	1.4
226	ICGV 05198	45.7	26.3	47.6	30.3	12.4	1.9	1.6
227	ICGV 06234	49.7	24.0	47.9	30.9	11.5	2.2	1.5
228	ICGV 00346	48.9	24.6	40.6	37.1	13.1	2.4	1.1
229	ICGV 00362	48.0	27.0	46.3	32.4	11.7	2.6	1.5
230	ICGV 00371	49.6	24.3	38.2	40.0	13.0	2.6	1.0
231	ICGV 02287	48.7	27.1	46.0	32.4	12.1	3.1	1.4
232	ICGV 02298	46.5	26.4	47.5	31.9	11.6	2.2	1.5
233	ICGV 02317	51.6	24.7	33.2	43.8	13.9	2.0	0.8
234	ICGV 97232	47.3	28.3	43.6	35.2	12.2	2.1	1.3
235	ICGV 99051	49.6	26.5	36.5	40.8	13.6	2.4	0.9
236	ICGV 99052	51.1	25.6	41.4	35.8	13.0	2.6	1.2
237	ICGV 00246	49.9	27.2	40.2	36.1	13.6	2.9	1.1
238	ICGV 00248	48.7	27.3	37.9	38.1	13.7	2.5	1.0
239	ICGV 01361	48.5	24.7	37.5	38.5	13.7	2.1	1.0
240	ICGV 02434	46.6	29.4	39.1	37.4	13.0	2.6	1.0
241	ICGV 04087	51.5	24.6	35.2	41.5	14.1	2.3	0.8
242	ICGV 06175	51.4	25.3	42.5	35.6	13.1	2.6	1.2
243	ICGV 97116	51.3	20.4	49.7	31.8	10.7	2.5	1.6
244	ICGV 97128	53.8	23.4	36.9	40.9	13.6	2.5	1.0
245	ICGV 98184	47.7	26.5	38.8	39.6	13.4	2.4	1.0
246	ICGV 00068	47.3	27.7	43.2	34.5	12.3	2.4	1.3
247	ICGV 01495	49.0	25.7	43.2	33.4	13.3	2.4	1.3
248	ICGV 05057	47.9	26.4	34.9	41.3	14.1	2.3	0.8
249	ICGV 07168	48.1	28.6	45.0	32.5	13.5	2.7	1.4
250	ICGV 01265	49.0	24.3	46.4	32.5	13.5	2.5	1.5
251	ICGV 98105	51.9	26.5	30.3	46.4	14.3	2.3	0.6
252	ICGV 99160	49.4	25.9	41.2	37.8	13.0	2.0	1.1
253	ICGV 02323	48.3	28.1	38.2	39.3	12.9	2.1	1.0
254	ICGV 04115	49.8	27.3	33.0	43.8	13.1	2.4	0.8
255	ICGV 05036	49.7	24.4	36.4	41.6	13.7	1.7	0.9
256	ICGV 06042	48.1	27.8	42.2	33.7	13.6	2.6	1.3
257	ICGV 86564	48.9	28.2	50.4	28.3	11.3	3.6	1.8
258	ICGV 98432	52.6	22.0	48.9	32.3	10.6	2.5	1.5
259	BAU 13	50.4	24.6	46.5	32.3	12.6	2.8	1.5
260	ICGV 87846	48.3	27.6	40.2	37.0	13.3	2.5	1.1
261	ICR 48	46.7	27.9	47.5	31.1	11.4	2.7	1.5
262	ICGV 86699	52.7	24.9	58.5	24.7	11.6	2.0	2.4
263	ICGV 98373	46.4	27.4	41.9	36.5	11.9	2.1	1.2
264	ICGV 97115	49.4	25.4	42.4	34.4	13.0	2.8	1.2
265	ICGV 06040	51.2	26.3	38.6	38.8	13.7	2.6	1.0
266	ICGV 06099	50.5	25.8	40.4	37.2	13.4	2.3	1.1
267	CS 39	48.0	25.8	40.0	37.3	13.4	2.4	1.1
268	ICGV 05032	49.8	25.4	45.1	33.6	12.5	2.1	1.4
269	ICGV 05141	51.2	26.8	46.6	31.4	13.1	2.7	1.5
270	ICGV 07359	45.4	28.8	49.5	27.5	12.3	2.4	1.8
271	ICGV 07368	45.7	28.9	43.1	34.1	12.6	2.4	1.3
272	ICGV 06110	46.2	30.8	46.3	31.2	13.3	2.1	1.5
273	ICGV 06188	45.1	31.0	48.7	29.5	11.9	2.1	1.6
274	ICGV 00440	49.6	25.4	46.2	32.1	11.8	3.1	1.5
275	ICGV 86352	48.7	26.4	43.4	37.1	11.8	1.9	1.2

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
276	ICGV 09112	49.2	28.0	41.5	36.0	12.8	2.3	1.2
277	ICGV 93920	42.0	28.4	46.3	31.9	11.9	1.9	1.5
278	ICGV 93216	43.6	28.7	46.5	33.0	11.3	2.4	1.4
279	ICGV 88438	53.3	24.2	51.7	29.0	10.3	2.7	1.8
280	ICG 11337	49.7	27.5	57.2	24.2	12.2	2.1	2.4
281	49 × 37-90	51.1	25.6	41.5	38.2	12.7	2.1	1.1
282	49 M-2-2	48.5	29.6	44.7	34.4	11.7	2.5	1.3
283	49 M- 1-1	42.8	28.6	38.8	35.5	14.1	1.5	1.1
284	TG 19	49.4	30.0	41.7	36.0	12.8	2.6	1.2
285	TG 39	43.6	28.8	46.3	31.5	12.6	1.9	1.5
286	TG LPS 3	46.2	25.1	46.7	31.6	12.2	1.9	1.5
287	26 × M-223-1	52.3	23.3	35.8	40.6	13.1	2.4	0.9
288	SPS 2	52.4	22.7	55.2	26.5	12.7	1.5	2.1
289	SPS 3	46.1	27.5	44.3	34.7	12.1	2.0	1.3
290	SPS 6	48.0	26.8	43.9	35.9	11.9	2.2	1.2
291	SPS 7	51.7	24.6	51.6	30.9	12.4	1.5	1.7
292	SPS 8	53.9	26.0	51.1	30.5	13.2	1.8	1.8
293	SPS 11	50.6	29.2	41.3	36.9	12.4	3.0	1.1
294	SPS 15	53.5	24.3	56.1	27.1	12.2	2.0	2.2
295	SPS 20	52.7	25.3	55.7	27.5	12.1	1.7	2.0
296	SPS 21	55.0	19.6	48.3	32.9	12.8	1.7	1.5
297	ICGV 03128	50.2	27.7	44.5	33.4	12.2	2.2	1.4
298	TMV 2 NLM	46.8	28.8	44.1	35.1	12.4	2.0	1.3
299	ICG 1668	47.4	27.5	43.9	35.2	12.8	2.2	1.3
300	ICG 8285	46.7	28.3	41.2	35.8	12.8	2.2	1.2
301	ICG 11426	48.8	26.2	53.1	26.7	13.0	1.8	2.0
302	ICGV 02290	48.1	26.1	47.1	30.9	12.6	2.5	1.5
303	ICGV 02446	49.5	26.8	39.0	36.3	13.9	3.1	1.1
304	ICG 156	48.9	25.5	48.0	29.8	11.6	2.8	1.6
305	ICGS 76	48.6	23.4	41.1	36.1	13.3	2.1	1.2
306	ICG 5891	47.6	27.7	42.4	35.9	12.3	2.1	1.2
307	CSMG 84-1	45.0	26.4	44.5	33.8	12.6	1.7	1.3
308	ICG 111	49.5	27.5	42.9	35.5	12.7	2.4	1.2
309	ICG 14834	48.6	26.1	46.2	32.2	11.3	2.7	1.4
310	ICG 11322	48.1	27.8	36.8	40.7	13.5	2.2	0.9
311	ICG 532	50.6	25.0	44.3	31.6	13.2	2.6	1.4
312	ICG 12509	50.8	29.7	48.2	31.0	13.9	2.9	1.6
313	ICG 12672	47.6	30.1	47.1	31.3	14.6	0.9	1.5
314	ICG 10185	50.8	26.0	45.9	32.3	11.6	2.9	1.4
315	ICG 2773	53.2	24.8	45.1	29.6	12.4	3.4	1.7
316	ICG 3027	51.7	28.8	47.4	29.2	12.9	2.8	1.8
317	ICG 5745	47.7	26.2	52.1	26.6	11.3	2.7	2.0
318	ICG 14482	55.3	22.6	53.2	29.3	11.7	2.2	1.8
319	ICG 4527	49.2	29.3	49.6	31.0	11.3	2.3	1.6
320	ICG 4343	48.0	26.3	44.4	32.5	12.9	1.9	1.4
321	ICG 13895	51.3	26.9	40.6	38.5	12.1	2.8	1.1
322	ICG 5663	51.5	25.3	49.8	29.8	12.6	2.1	1.8
323	ICG 721	49.0	26.1	39.0	40.6	12.6	2.5	1.0
324	ICG 12276	53.8	27.6	44.0	29.4	13.1	3.4	1.5
325	ICG 875	49.3	23.1	45.2	32.7	12.8	2.2	1.4
326	ICG 14475	56.4	27.0	54.5	30.6	10.4	2.5	1.8
327	ICG 15190	47.8	26.4	47.6	30.3	12.7	2.2	1.6
328	ICG 12370	49.4	26.6	43.9	33.8	12.4	2.3	1.3
329	ICGV 86325	50.0	24.7	49.6	30.9	12.1	1.9	1.6
330	ICG 5662	50.8	26.9	42.4	35.8	13.0	2.6	1.2
331	ICG 9961	50.0	23.0	47.0	31.8	11.6	2.4	1.5

S. No.	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
332	ICG 14466	48.5	29.0	47.9	30.5	12.4	2.3	1.6
333	ICG 3053	47.0	27.1	43.9	35.6	11.7	2.3	1.2
334	ICG 6766	52.7	24.6	42.8	34.0	13.3	2.8	1.3
335	ICG 2381	60.6	23.5	54.7	31.8	8.2	4.8	1.9
336	ICG 2857	43.2	34.1	44.0	31.6	12.8	2.0	1.4
337	ICGV 13238	46.3	30.5	41.2	36.9	11.9	2.3	1.1
338	ICGV 13241	49.6	27.5	40.2	38.9	12.0	2.0	1.0
339	ICGV 13242	46.0	27.2	40.6	38.1	12.2	1.9	1.1
340	ICGV 13245	45.5	29.3	45.3	34.8	11.9	1.5	1.3
Mean		**49.1**	**26.7**	**43.9**	**34.7**	**12.5**	**2.3**	**1.4**
CV (%)		**4.0**	**7.4**	**8.2**	**8.4**	**5.0**	**14.0**	**17.9**
LSD at 5 % level		**3.2**	**3.3**	**5.9**	**4.8**	**1.0**	**0.5**	**0.4**

Appendix X

Pooled BLUPs for yield and its contributing traits of Genomic Selection Panel of groundnut evaluated across four environments

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
1	ICGV 06423	36.0	1.7	3.7	6.0	1.3	2.7	4.3	37.1	7.1	19.0	12.9	7.8	58.3	32.2	131.5	2516.4	23.8
2	ICGV 07246	36.0	1.3	4.0	6.0	1.0	3.3	5.3	31.9	7.8	21.1	13.8	8.4	59.5	34.3	120.5	2827.2	20.0
3	ICGV 07247	34.0	1.3	4.7	6.7	1.0	3.0	5.3	31.8	7.8	25.4	17.3	11.2	64.1	34.4	120.0	3202.9	24.7
4	ICGV 07268	33.0	2.7	5.7	8.0	2.7	5.3	7.3	31.9	6.2	15.4	13.0	8.9	68.2	39.1	121.5	2164.1	20.1
5	ICGV 01005	31.0	3.0	5.3	7.7	3.0	6.3	7.7	45.8	5.0	11.3	8.4	5.0	59.8	34.9	119.6	1527.8	19.6
6	ICGV 01060	33.0	1.7	4.0	6.3	1.3	4.0	5.7	35.1	5.4	14.8	9.7	6.2	65.3	30.9	122.4	1477.9	13.5
7	ICGV 01124	33.0	2.7	5.0	7.0	1.7	4.0	6.0	33.2	6.5	13.2	8.0	4.7	56.0	28.2	118.8	1236.3	17.4
8	ICGV 02206	34.0	2.7	5.3	7.3	2.3	4.3	6.3	37.0	5.3	15.1	10.2	6.6	61.7	34.1	123.8	1835.9	14.0
9	ICGV 03397	37.0	2.0	5.0	6.7	1.7	3.7	6.0	29.3	6.9	13.3	6.7	4.2	62.3	25.4	117.0	1139.9	23.0
10	ICGV 03398	36.0	2.7	6.0	8.0	1.3	4.7	6.7	33.6	7.3	16.8	10.9	6.7	58.3	27.1	118.8	1488.4	18.4
11	ICGV 04044	33.0	1.7	5.0	6.3	1.7	4.0	6.0	33.7	6.2	17.7	11.6	6.3	53.6	33.6	120.5	2082.0	21.1
12	ICGV 06347	34.0	2.3	5.3	6.7	2.0	6.0	7.3	30.5	5.7	15.5	10.4	6.5	64.5	32.7	118.8	2048.0	17.9
13	ICGV 93280	34.0	2.0	5.0	7.7	1.3	3.7	6.3	32.8	5.6	20.3	11.6	7.3	62.8	30.4	120.0	2025.8	20.4
14	ICGV 95469	31.0	2.3	5.3	6.7	2.0	4.7	6.0	33.7	5.5	18.2	11.4	7.8	69.5	34.0	115.5	1758.8	17.5
15	ICGV 00387	34.0	2.0	5.7	7.0	2.0	5.0	6.7	40.2	5.7	15.1	10.2	5.1	52.2	29.4	121.0	2235.9	17.6
16	ICGV 01393	32.0	2.3	5.0	6.7	2.3	4.3	6.3	38.1	5.0	8.7	7.5	4.0	53.4	44.3	127.5	1335.4	18.4
17	ICGV 02242	31.0	2.7	4.7	7.0	2.0	3.3	7.3	38.4	5.2	13.7	13.2	7.4	55.8	40.6	123.3	2396.5	16.7
18	ICGV 97058	35.0	2.3	5.0	6.3	1.7	4.7	6.3	37.8	4.7	11.5	10.4	6.0	59.0	38.2	126.3	2210.9	12.9
19	ICGV 99083	30.0	2.7	6.0	7.7	2.7	5.0	7.0	37.3	5.8	10.5	8.0	3.8	47.5	36.7	122.6	1360.7	18.7
20	ICGV 00343	34.0	2.3	5.7	8.0	2.7	5.7	7.0	34.7	4.8	10.7	9.3	5.3	58.7	37.6	120.1	1664.7	18.6
21	ICGV 00349	33.0	3.0	6.7	8.3	3.0	6.0	7.3	30.0	4.8	14.5	9.0	5.6	62.7	29.6	120.0	1456.6	12.6
22	ICGV 01263	32.0	2.7	5.3	7.0	2.3	5.0	6.0	40.2	4.3	15.6	14.5	8.3	59.0	39.3	118.3	1772.6	13.3
23	ICGV 03056	33.0	1.7	5.0	7.0	1.3	4.0	6.0	35.3	6.1	16.7	12.5	6.7	59.2	32.1	117.5	2898.6	16.5
24	ICGV 03064	33.0	1.7	4.0	6.7	1.3	3.0	5.3	35.6	6.6	17.8	14.6	8.2	55.2	32.8	122.9	3040.7	16.6
25	ICGV 05161	33.0	1.7	4.7	7.0	1.3	3.7	6.0	36.6	6.1	15.3	12.9	7.3	57.4	33.8	126.5	2538.0	17.0
26	ICGV 05163	33.0	1.3	3.0	6.3	1.3	3.0	5.3	35.3	6.3	21.6	16.8	9.7	57.0	35.5	121.0	2978.0	18.2
27	ICGV 06422	34.0	1.3	3.7	5.7	1.3	2.3	3.7	36.7	6.9	21.1	13.2	8.0	58.9	34.9	132.9	2460.7	20.8
28	ICGV 06431	29.0	3.0	6.0	7.7	3.0	6.3	7.7	37.7	4.8	16.8	11.8	7.0	60.0	33.0	112.1	1837.8	23.3
29	ICGV 07220	35.0	1.0	3.3	5.3	1.0	3.0	4.7	32.7	6.8	15.9	9.8	5.3	56.0	28.2	131.9	1274.6	23.6
30	ICGV 07223	35.0	1.3	4.0	6.3	1.3	2.3	5.0	30.0	7.3	19.8	13.0	8.2	61.9	34.3	120.6	2747.2	19.4
31	ICGV 07227	34.0	2.0	5.0	7.0	1.3	3.0	5.3	33.1	7.5	16.7	10.4	6.3	61.0	32.1	119.4	2207.0	21.3
32	ICGV 07235	36.0	1.3	3.0	6.0	1.3	2.3	5.0	30.4	7.6	20.2	13.6	8.4	63.3	35.5	126.3	2667.9	15.3

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
33	ICGV 99233	31.0	2.0	5.3	7.0	1.7	4.0	5.7	35.5	5.0	15.9	10.8	6.1	56.4	32.9	117.1	1497.4	11.6
34	ICGV 97165	33.0	1.3	4.3	6.3	1.7	3.3	5.0	39.3	5.2	7.3	6.4	3.5	50.5	25.4	117.8	998.5	23.5
35	ICGV 99029	31.0	1.3	3.7	5.0	1.0	3.0	4.0	37.1	5.2	17.7	11.2	6.4	57.6	32.5	132.8	1992.6	26.0
36	ICGV 00191	31.0	1.3	3.7	5.0	1.0	3.0	4.0	37.1	5.3	18.1	11.6	7.1	59.1	33.0	131.5	2003.7	21.4
37	ICGV 07120	35.0	1.3	3.3	4.3	1.0	2.7	4.0	35.1	7.0	18.9	13.6	8.6	64.4	37.6	132.4	2602.1	27.6
38	ICGV 97092	33.0	2.3	5.0	7.3	1.3	4.3	6.3	34.1	6.1	15.4	9.7	5.5	56.1	29.3	117.8	1873.6	19.6
39	ICGV 97120	34.0	2.0	4.7	7.3	1.7	3.3	6.0	37.2	5.5	11.5	9.7	5.7	57.4	40.8	120.8	2033.7	19.3
40	ICGV 98163	33.0	2.0	4.7	7.0	1.7	4.3	6.0	38.0	6.9	17.9	10.8	6.6	62.5	31.5	117.5	1833.3	17.0
41	ICGV 00005	33.0	1.7	4.0	6.3	1.3	3.0	5.0	34.5	6.7	19.1	12.5	7.7	59.2	30.4	117.5	2053.5	12.8
42	ICGV 01273	34.0	1.3	3.3	6.3	1.0	2.7	5.0	31.3	6.4	21.2	13.2	8.2	63.3	32.6	115.0	2499.7	24.6
43	ICGV 01274	35.0	1.3	3.0	5.0	1.3	2.7	5.0	29.7	6.6	18.9	13.7	8.5	61.1	32.7	117.9	2677.7	14.5
44	ICGV 02321	35.0	1.7	4.7	6.7	1.3	3.3	5.7	31.7	6.7	19.3	11.6	7.4	62.0	31.8	118.3	2178.1	16.7
45	ICGV 03043	34.0	1.7	3.0	4.3	2.0	2.7	3.0	33.0	6.9	20.4	14.6	8.6	59.7	36.4	131.5	2547.3	15.8
46	ICGV 04124	33.0	3.0	5.3	7.0	3.0	4.3	6.3	32.4	6.1	15.6	9.6	5.6	59.3	31.4	118.0	1538.1	19.5
47	ICGV 00290	34.0	2.3	4.3	6.3	2.3	3.3	4.7	31.5	5.6	17.3	12.3	7.5	58.6	34.1	117.1	2049.2	24.3
48	ICGV 00321	30.0	2.7	6.3	8.0	2.7	6.0	7.7	36.7	4.8	14.3	10.9	6.9	63.3	34.8	115.1	2256.1	11.8
49	ICGV 02125	31.0	2.3	6.0	7.3	2.7	5.3	7.0	32.4	4.7	13.8	7.7	5.0	64.1	24.4	111.4	1857.0	12.3
50	ICGV 02144	31.0	2.7	5.7	7.3	3.0	6.0	7.7	37.0	5.5	15.1	9.8	5.8	59.7	29.7	116.8	1659.3	12.4
51	ICGV 03184	31.0	2.7	5.3	7.3	2.7	5.7	6.7	49.1	5.3	14.8	10.5	6.7	67.0	34.5	120.4	1900.6	21.4
52	ICGV 03207	32.0	2.7	5.7	6.7	2.0	5.0	7.0	34.1	4.8	17.6	10.9	6.9	62.2	27.4	119.0	1306.5	10.8
53	ICGV 04018	30.0	2.3	5.7	7.0	3.0	5.7	7.0	44.3	4.7	12.8	9.9	6.5	66.6	38.1	112.0	1533.3	15.9
54	ICGV 07210	30.0	2.7	5.3	7.0	1.7	4.3	6.7	32.3	4.6	17.7	9.1	6.3	64.8	27.0	113.4	1645.9	15.0
55	ICGV 07217	32.0	2.0	6.3	7.7	2.7	6.0	6.7	32.2	4.6	17.0	8.8	5.8	65.5	26.1	111.8	1464.7	12.6
56	ICGV 95290	30.0	2.3	5.7	7.7	2.7	5.7	7.0	32.3	4.7	15.6	10.1	6.7	67.8	38.0	117.0	1324.6	10.3
57	ICGV 97261	30.0	2.7	6.0	7.7	3.0	5.7	7.3	33.6	4.5	15.8	8.9	5.8	66.6	27.8	112.9	1463.7	13.4
58	ICGV 97262	33.0	2.7	6.3	7.7	3.0	5.7	7.0	32.1	5.0	15.2	9.8	6.4	62.9	27.4	116.5	1254.1	11.2
59	ICGV 99181	29.0	2.7	6.3	8.0	2.7	6.7	8.0	31.7	4.3	14.1	9.4	5.9	62.6	30.2	114.3	1579.6	15.8
60	ICGV 99195	31.0	3.0	6.0	7.7	2.0	5.0	7.3	33.7	4.9	13.0	8.7	5.4	61.6	31.3	115.6	1373.9	11.1
61	ICGV 89104	33.0	2.7	6.0	7.3	3.0	6.0	7.3	34.4	4.9	11.6	5.8	3.4	57.2	21.8	118.0	873.0	12.3
62	ICGS 11	31.0	2.7	6.0	7.0	3.0	6.0	7.7	31.1	5.6	13.1	7.7	4.8	62.8	32.6	120.4	1355.3	17.6
63	J 11	32.0	3.0	6.3	7.3	3.3	6.3	7.7	36.4	4.4	17.5	9.9	6.1	62.0	24.5	113.5	1421.3	16.5
64	ICGV 99085	32.0	1.3	3.7	5.7	1.3	3.0	5.3	36.0	5.5	16.5	8.8	5.2	61.8	30.2	129.6	1434.2	13.7
65	TKG 19A	31.0	1.7	5.0	7.0	2.3	5.3	6.7	42.9	5.1	13.4	7.8	4.6	58.3	29.5	117.5	1416.7	19.4
66	TPG 41	32.0	2.0	5.0	6.7	2.3	6.0	7.7	43.2	4.2	9.6	9.0	4.7	50.0	45.5	125.4	1361.2	22.7
67	ICGV 00350	34.0	1.7	4.0	7.0	2.0	4.7	7.3	33.1	5.2	16.5	11.3	6.9	63.4	32.1	119.1	2165.9	19.2

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
68	DH 86	33.0	2.3	5.0	6.7	1.7	4.3	6.0	31.9	7.1	16.9	11.6	7.6	60.4	35.4	117.9	2104.7	19.1
69	ICGV 95058	35.0	2.0	4.7	6.7	2.3	5.3	7.3	32.3	5.0	12.7	8.2	5.3	63.5	28.2	118.9	1321.7	17.1
70	ICGV 95070	33.0	2.7	6.0	8.0	2.7	6.3	7.7	29.4	5.3	18.1	9.8	5.7	56.4	26.1	121.4	1408.8	18.0
71	GPBD 4	30.0	1.3	2.3	4.0	1.3	2.3	3.3	38.1	4.8	17.0	9.2	5.8	62.0	27.3	130.4	1647.3	22.0
72	ICGV 91114	30.0	2.7	6.0	7.3	3.0	6.3	7.3	37.2	4.6	11.1	7.6	4.8	64.1	29.4	116.8	1534.4	16.7
73	TMV 2	33.0	2.0	7.0	8.3	3.7	6.7	8.3	33.4	5.1	7.7	7.9	3.9	53.1	30.1	116.8	1420.8	12.1
74	Faizpur 1-5	30.0	2.7	5.7	7.0	3.0	6.7	8.3	35.6	4.7	15.4	10.7	6.3	61.4	29.9	113.4	2115.9	10.7
75	Mutant 3	31.0	2.7	6.0	7.7	3.0	6.3	8.0	36.2	4.9	11.4	7.1	4.1	58.8	29.2	120.8	1185.3	14.4
76	ICGV 03042	34.0	1.3	3.3	6.0	1.0	2.7	5.0	31.0	5.7	18.8	14.0	8.3	58.2	33.4	121.0	2622.1	20.4
77	ICGV 05100	35.0	1.3	3.0	5.0	1.3	2.3	4.0	30.4	6.6	17.5	11.5	5.9	59.0	33.0	131.5	1784.3	20.0
78	ICGV 06049	29.0	2.7	5.7	6.7	3.3	5.7	7.0	33.7	4.8	13.1	8.4	5.3	60.8	31.6	119.8	1254.8	12.5
79	ICGV 06420	33.0	1.7	4.3	6.3	1.3	3.3	5.0	32.8	6.6	18.0	11.7	6.9	56.3	28.6	130.9	2279.7	20.9
80	ICGV 06424	35.0	1.7	4.0	5.7	1.7	2.7	4.3	28.9	5.9	17.5	10.9	6.6	59.2	25.4	114.1	1766.4	25.0
81	ICGV 07145	33.0	1.7	4.0	6.3	1.0	2.7	5.3	32.2	6.1	18.0	11.9	6.1	50.4	29.9	130.9	1818.5	23.7
82	ICGV 07148	31.0	1.7	4.7	5.3	2.0	4.0	5.3	35.3	5.1	13.6	8.5	4.9	57.5	30.8	113.3	1523.7	12.6
83	ICGV 07166	33.0	1.3	4.0	6.0	1.0	3.7	6.3	32.8	6.3	19.7	13.4	7.6	57.3	35.1	116.6	2464.0	19.0
84	ICGV 06142	34.0	1.3	2.7	4.7	1.0	2.3	4.3	34.4	6.6	20.5	15.2	9.0	61.9	29.6	132.9	2677.3	18.5
85	ICGV 91116	29.0	3.0	6.7	8.0	3.3	6.0	7.3	43.8	4.4	16.7	11.6	7.4	65.7	30.2	111.9	1689.8	14.4
86	ICGV 97045	32.0	1.7	5.0	6.7	2.0	5.0	6.7	35.3	4.8	9.6	8.9	5.0	55.3	42.6	132.6	1437.6	27.5
87	ICGV 94118	32.0	1.7	4.3	6.3	1.0	3.3	5.0	38.7	5.3	11.6	8.9	5.5	63.0	38.1	120.4	1635.3	20.4
88	ICGV 05176	33.0	2.0	5.3	7.3	2.3	4.7	7.0	39.7	5.9	9.2	10.8	6.9	60.6	49.9	125.9	1595.7	26.9
89	ICGV 04149	29.0	2.7	6.0	7.7	3.3	6.7	8.3	30.0	4.9	17.1	10.7	6.2	62.1	30.1	120.9	1681.6	10.0
90	ICGV 00351	32.0	1.7	4.7	6.7	1.7	4.0	6.0	32.9	5.4	15.8	10.7	7.0	62.1	36.6	116.3	2390.8	10.4
91	ICGV 92195	31.0	2.0	5.7	8.0	3.0	6.0	8.0	37.7	5.0	13.7	6.5	4.0	60.8	23.2	107.4	989.2	15.6
92	ICGV 87187	33.0	2.0	5.0	6.3	2.0	5.0	6.3	34.2	6.6	15.0	8.3	5.2	61.8	32.9	121.4	1252.0	20.4
93	ICGV 86072	33.0	2.7	6.0	7.7	3.0	6.0	7.7	34.5	5.5	13.9	10.4	6.1	60.0	36.2	121.3	1487.9	21.4
94	ICGV 86015	31.0	2.0	5.3	7.7	2.3	5.7	7.3	27.5	5.5	13.6	8.4	5.1	62.0	28.5	118.3	1472.4	15.7
95	ICGV 93437	31.0	2.3	5.3	7.3	2.7	6.0	7.3	38.8	4.6	15.3	9.5	5.9	64.9	27.2	114.8	1559.3	13.7
96	ICGV 86143	33.0	2.7	5.7	6.7	2.7	5.3	6.3	33.6	6.3	10.8	7.8	5.0	63.6	30.5	118.0	1159.6	13.1
97	ICGV 90320	31.0	2.0	4.3	7.3	2.0	4.7	6.3	30.5	4.6	15.4	12.5	7.3	58.6	36.2	116.3	2391.4	13.6
98	ICGV 07273	33.0	2.7	6.3	8.0	2.3	5.7	7.3	33.5	4.8	14.4	8.3	5.5	66.0	29.4	115.4	1191.9	13.2
99	49 × 37-91	31.0	2.7	6.7	8.3	3.0	7.0	8.3	28.3	5.0	14.9	9.7	5.8	60.6	39.9	124.1	1825.2	11.7
100	49 × 37-134	32.0	2.0	3.7	6.3	1.7	3.3	6.3	38.2	4.6	13.4	8.7	4.8	56.8	42.4	119.6	1200.4	12.9
101	49 × 37-135	32.0	2.3	6.0	7.7	3.0	6.3	8.0	35.3	4.7	13.5	8.2	5.0	62.8	24.8	115.5	1103.2	14.4
102	49 × 37-97-1	35.0	2.3	5.7	7.0	3.3	6.0	8.0	27.7	5.1	8.5	7.9	4.2	56.9	49.2	126.4	994.5	16.0

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
103	49 × 37- 99(b) tall	34.0	2.3	5.7	7.7	3.0	6.3	8.0	27.9	5.7	9.5	9.8	5.4	53.2	45.2	126.5	1046.9	18.0
104	39 × 49 -8	33.0	1.3	4.3	6.3	1.3	3.3	5.7	27.8	5.3	14.0	10.1	5.8	58.5	44.7	118.0	1624.0	11.0
105	39 × 49 -77	31.0	1.7	4.0	6.3	1.3	4.0	6.0	27.6	4.9	15.8	10.7	5.2	50.5	39.7	117.3	1861.1	11.8
106	49 × 39-20-2	31.0	2.3	6.3	8.0	2.7	6.0	7.7	27.4	4.9	11.5	9.3	5.0	53.5	38.6	123.3	1564.3	14.8
107	49 × 39-21-2	32.0	2.3	4.7	6.3	2.3	4.3	5.7	34.0	5.2	13.6	7.1	3.5	46.4	32.4	131.0	894.4	13.6
108	49 × 39-8	32.0	1.3	3.7	6.3	1.3	4.0	6.3	27.2	5.0	11.7	8.3	4.9	59.4	35.2	114.5	1469.1	9.3
109	49 M-16	35.0	1.0	3.0	5.0	1.0	2.3	4.0	35.6	7.1	23.2	13.7	8.6	62.6	31.5	132.0	2525.9	19.4
110	49 × 27-19	33.0	2.3	5.7	6.7	2.3	5.3	7.0	31.6	4.6	14.4	9.7	4.9	51.8	39.1	122.5	1545.9	18.7
111	49 × 27-13 (ii)	32.0	2.7	6.3	7.7	3.0	5.7	8.0	35.3	4.8	10.8	10.0	5.1	51.7	41.8	126.6	1573.3	19.7
112	27 × 49- 16	33.0	1.7	4.7	7.0	2.0	5.3	6.7	46.8	5.2	10.9	8.0	4.4	54.9	39.2	122.1	1480.3	24.2
113	27 × 49- 12	30.0	1.7	4.0	6.3	1.7	4.0	6.3	29.8	4.5	15.7	9.8	5.8	61.4	33.4	117.8	1044.9	10.9
114	27 × 49- 14	32.0	2.0	4.3	7.3	2.0	5.0	7.0	34.5	5.1	10.7	8.4	4.6	56.4	43.0	122.5	1186.8	17.6
115	27 × 49- 27-1	30.0	2.0	5.7	8.0	2.3	6.0	7.3	24.0	4.9	13.8	9.8	5.4	55.9	47.9	122.9	1512.1	12.1
116	26 M 156-2	34.0	1.7	4.3	7.0	2.0	5.3	7.7	36.2	4.5	14.4	8.2	4.0	51.9	32.4	116.4	1496.5	17.7
117	26 M- 119-1	32.0	3.0	6.0	8.0	3.3	6.0	7.7	32.8	4.8	15.1	9.9	6.5	66.6	31.5	115.1	1340.0	13.0
118	24 M-86	33.0	1.3	3.3	4.7	1.7	3.7	5.7	31.0	6.9	10.0	7.4	3.9	54.4	33.5	132.3	939.5	22.8
119	MN1-35	31.0	2.0	5.0	6.7	1.3	4.0	5.7	30.0	4.9	8.8	5.6	2.7	48.7	20.3	114.9	1656.0	13.7
120	M 110-14	34.0	1.3	4.0	6.3	1.3	4.0	6.0	29.0	6.1	10.6	8.6	5.0	53.9	33.9	127.3	939.1	17.5
121	M 28-2	35.0	1.7	3.3	6.0	1.7	4.0	6.3	25.8	5.3	13.6	10.5	5.8	53.9	31.3	115.4	1542.2	12.3
122	Somnath	32.0	2.3	5.0	7.0	3.0	5.3	6.7	41.0	4.7	15.4	9.2	5.4	58.5	30.7	116.1	1311.6	15.5
123	TG 41	33.0	2.0	5.7	7.3	2.3	6.3	8.0	32.3	4.7	12.4	9.5	5.3	54.8	49.7	120.8	1428.0	11.2
124	TG 42	33.0	2.0	5.3	7.3	2.3	5.0	7.0	27.6	5.3	9.9	8.3	5.0	60.8	52.1	119.3	1436.0	16.5
125	TG 49	30.0	2.3	6.0	8.0	2.7	6.0	7.7	25.8	4.7	13.7	10.7	6.3	59.0	41.9	116.5	1681.0	14.7
126	TG LPS 4	32.0	2.3	5.7	7.0	2.3	5.0	7.3	32.3	4.8	11.8	9.2	5.8	61.5	38.9	117.5	1194.0	15.3
127	TG LPS 7	31.0	2.3	5.7	7.0	2.7	6.3	7.7	31.2	4.9	9.3	6.2	3.5	56.4	36.0	119.5	1058.5	12.1
128	24 × 37-2275	32.0	2.0	5.3	6.7	1.7	4.7	7.0	31.3	4.5	14.1	10.6	6.0	57.4	31.1	121.4	1569.8	16.8
129	24 × 39-31 MR	31.0	1.7	3.7	6.0	1.3	3.3	5.0	32.4	5.1	14.0	7.6	3.8	49.8	26.9	128.9	1585.7	16.1
130	26 × M-95-1 RI	29.0	2.0	4.0	6.7	1.7	4.0	5.0	25.7	5.3	17.3	9.6	5.7	60.1	33.6	107.8	1977.2	11.5
131	26 × 37-IV- 9IR	33.0	1.7	4.7	6.7	2.0	5.3	7.0	37.2	4.8	18.4	11.6	7.4	63.5	32.5	119.5	1990.2	21.7
132	26 × 27-164	35.0	2.3	5.3	7.3	2.7	5.7	7.3	38.5	6.0	13.3	9.2	6.1	67.1	36.8	114.3	1770.7	18.0
133	49 × 39-21-1	33.0	2.0	4.7	6.3	1.7	3.7	6.7	32.3	4.4	12.6	7.7	4.6	60.9	28.3	114.3	1154.7	20.0
134	49 × 39-21-2(a)	31.0	2.0	5.0	7.7	1.3	4.7	7.7	28.7	5.0	22.5	13.3	7.8	60.9	29.8	113.9	1531.2	10.9
135	49 × 39-74	33.0	1.3	3.7	6.0	1.3	3.0	6.3	29.7	5.3	22.2	10.7	6.8	65.0	29.0	111.0	1711.2	8.6
136	39 × 49-81-1	31.0	1.0	3.3	5.3	1.3	3.0	6.0	29.4	4.7	18.9	12.1	7.1	59.6	32.7	108.8	1877.5	9.9
137	49 × 27-37	32.0	1.7	4.3	6.7	1.7	4.7	7.0	29.9	4.8	15.5	9.4	5.0	53.1	29.7	112.8	1136.8	19.0

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
138	TDG 10	32.0	2.3	5.3	7.3	2.3	6.3	8.0	31.1	4.9	14.6	8.7	5.1	57.7	29.2	114.3	1420.4	9.4
139	TDG 13	32.0	1.7	5.0	6.7	2.0	4.7	6.0	30.4	5.4	13.0	8.3	4.9	59.6	31.9	119.1	1376.1	13.2
140	TDG 14	30.0	2.0	4.7	6.3	2.0	4.7	5.7	29.2	5.4	13.6	9.6	5.7	58.0	39.0	119.1	1328.9	12.4
141	DTG 3	34.0	2.3	5.3	6.7	2.7	6.0	6.3	30.5	5.9	16.5	9.6	5.9	62.1	29.2	120.1	1840.5	12.1
142	DTG 15	29.0	2.3	6.3	8.0	2.7	6.0	7.7	34.5	5.1	16.8	10.9	6.8	62.8	31.2	116.8	1664.3	17.3
143	M 28-2	35.0	1.3	3.0	6.3	2.0	4.0	6.0	30.0	5.4	14.6	8.1	4.4	55.5	33.8	118.0	1094.0	20.5
144	JL 24	31.0	3.0	6.0	7.7	3.0	6.0	8.0	41.5	4.9	15.0	8.4	5.5	65.5	28.1	111.5	1144.8	14.5
145	TAG 24	29.0	3.0	6.3	8.3	3.3	5.7	7.3	37.3	5.0	11.6	6.8	4.0	60.5	27.3	115.5	1034.5	14.1
146	SPS 1	32.0	1.3	3.7	5.0	1.7	3.7	5.7	37.1	4.8	15.3	9.7	6.0	61.8	28.1	111.9	1647.4	20.4
147	SPS 9	32.0	1.7	3.3	5.0	2.0	3.7	5.0	34.4	5.1	11.3	7.4	3.9	52.5	23.8	113.4	1142.1	16.1
148	SPS 10	31.0	3.3	5.3	7.0	4.0	6.3	8.0	33.6	5.1	10.8	6.8	3.8	60.2	27.1	113.3	1589.6	14.2
149	SPS 13	32.0	2.0	5.3	7.0	2.7	5.3	7.3	24.2	4.9	12.9	11.5	6.1	53.5	45.9	117.6	1511.1	11.2
150	SPS 14	32.0	1.7	3.3	5.0	1.7	3.3	5.0	23.2	5.1	9.1	5.1	3.2	59.5	23.0	125.9	724.5	8.5
151	SPS 17	32.0	3.0	5.3	7.3	2.7	4.7	7.0	35.1	5.2	9.2	8.5	4.4	52.0	40.9	120.3	1598.7	19.1
152	ICGV 02411	32.0	1.3	2.7	4.3	1.0	2.3	4.0	39.7	6.2	17.7	14.6	8.5	58.5	37.1	130.6	2561.6	23.0
153	ICGV 05155	33.0	1.3	3.7	5.7	1.3	2.3	4.7	34.3	6.1	21.1	13.8	8.2	59.1	33.5	115.3	2952.5	18.7
154	ICGV 06100	33.0	2.3	5.0	7.7	1.3	3.7	6.0	36.0	6.6	19.4	16.2	9.3	60.4	38.9	124.5	2981.1	22.2
155	ICGV 07023	30.0	3.0	6.0	8.0	3.3	6.0	7.7	40.3	4.8	11.5	7.6	4.5	60.2	32.8	115.3	1340.1	15.3
156	SunOleic 95R	31.0	2.3	5.7	7.3	2.7	5.3	6.7	28.3	5.2	10.7	6.9	4.1	57.9	29.1	115.6	1001.7	16.0
157	ICG 434	31.0	3.0	6.0	7.3	3.3	6.7	8.0	36.6	4.7	12.0	6.6	3.9	60.6	28.4	122.1	1020.1	15.2
158	ICG 2031	32.0	2.7	6.3	7.7	2.7	5.7	7.7	37.2	4.9	14.5	7.1	4.3	63.7	25.6	110.5	1275.5	10.9
159	ICG 3102	29.0	2.7	6.0	8.0	3.0	6.0	7.3	37.2	4.5	12.8	8.5	5.1	59.8	31.9	120.8	1375.2	16.6
160	ICG 3140	31.0	2.7	5.3	6.7	3.3	6.0	7.0	39.7	5.0	11.2	7.1	4.2	56.9	29.6	115.8	1261.3	14.5
161	ICG 3343	31.0	2.7	6.3	7.7	3.0	5.7	7.3	38.1	4.5	14.2	9.4	5.5	57.2	28.9	119.3	1054.4	15.7
162	ICG 3421	32.0	2.7	6.0	7.7	3.3	6.3	8.0	36.3	4.7	14.1	7.4	4.5	63.2	24.0	111.4	1285.7	9.9
163	ICG 4729	30.0	2.7	7.0	8.0	3.7	7.0	8.3	42.2	5.1	16.5	9.4	6.0	65.3	25.8	114.5	1235.2	17.4
164	ICG 6022	30.0	1.3	3.0	5.7	1.7	3.7	5.7	53.6	3.8	7.2	9.6	4.9	51.8	32.3	116.3	1138.4	18.5
165	ICG 6646	31.0	1.7	4.3	6.7	2.3	4.3	6.7	49.8	4.2	7.5	8.0	4.1	51.5	31.9	121.1	1227.0	23.6
166	ICG 8517	32.0	2.7	5.7	7.7	2.7	6.0	7.7	41.2	4.5	8.6	6.7	3.8	57.0	27.0	116.6	1061.5	13.1
167	ICG 8751	32.0	2.0	4.7	6.7	1.7	3.0	6.0	47.1	4.0	11.2	9.3	5.0	54.2	31.4	117.4	1655.7	22.2
168	ICG 9315	33.0	2.0	6.3	8.0	2.7	6.7	7.7	37.4	4.9	14.6	8.8	5.0	58.6	27.4	116.9	1474.8	15.9
169	ICG 10036	32.0	2.0	4.7	6.0	1.3	3.7	5.7	40.3	4.3	10.0	8.6	4.5	51.2	23.8	117.8	1049.0	13.8
170	ICG 10053	31.0	2.3	4.3	6.0	2.0	4.7	6.3	38.6	5.0	12.0	11.2	6.5	55.3	40.0	116.6	1472.3	17.0
171	ICG 10701	30.0	2.7	6.0	8.0	3.3	6.3	7.7	27.3	5.2	14.6	9.9	6.1	60.0	35.2	117.8	1569.2	9.3
172	ICG 11088	33.0	2.3	5.3	7.7	2.0	4.7	7.0	38.5	4.4	9.7	8.5	5.0	58.6	28.9	113.9	1445.0	15.9

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
173	ICG 11651	31.0	2.7	5.3	6.7	3.0	5.3	6.7	31.8	4.7	13.5	10.0	5.6	54.8	32.6	115.4	2038.9	12.1
174	ICG 12625	33.0	1.3	3.7	5.3	1.7	3.7	5.0	38.0	4.1	9.5	7.0	3.7	53.6	31.5	130.5	1273.3	15.8
175	ICG 12991	30.0	3.0	6.3	7.3	3.7	6.0	7.7	36.1	5.0	16.0	8.8	5.8	64.9	26.5	116.3	1011.6	11.9
176	ICG 14985	31.0	2.7	6.0	7.7	3.0	6.7	8.3	32.8	5.6	11.2	8.4	4.8	57.4	33.5	119.5	1437.5	14.0
177	ICG 15415	30.0	2.0	5.0	7.3	1.3	4.0	6.3	36.8	4.4	12.6	8.8	5.1	56.1	26.3	115.3	1284.3	14.6
178	ICG 15419	30.0	2.0	4.3	6.0	2.0	4.0	5.7	56.2	4.1	5.7	7.3	3.8	52.9	39.3	115.4	1308.5	26.6
179	ICGV 01232	32.0	3.0	6.3	8.0	3.0	6.0	7.0	42.5	5.3	13.7	12.9	7.2	55.9	40.9	117.0	2004.6	18.5
180	ICGV 01276	32.0	2.0	3.7	6.0	2.0	2.7	5.3	33.7	6.6	24.5	17.3	10.6	61.7	36.2	129.5	2923.8	17.6
181	ICGV 01328	32.0	1.3	2.7	4.7	1.7	4.0	5.3	27.7	5.0	13.2	8.8	5.5	62.8	26.6	129.0	1750.7	18.0
182	ICGV 02022	30.0	2.0	5.3	7.3	2.7	5.7	6.3	38.2	5.5	14.1	8.9	5.5	63.6	28.0	120.3	1537.5	10.3
183	ICGV 02038	31.0	3.0	6.7	8.0	3.7	6.0	7.7	39.6	4.7	12.2	7.4	5.0	67.9	32.0	114.4	1071.1	12.5
184	ICGV 02189	29.0	3.3	5.0	7.7	3.3	5.7	7.3	32.8	4.8	13.7	9.5	5.9	61.8	32.3	114.5	1255.9	13.1
185	ICGV 02194	33.0	2.7	6.3	7.7	2.0	5.0	7.3	39.3	4.7	14.8	8.0	4.9	60.7	25.9	116.4	1552.0	15.6
186	ICGV 02266	32.0	2.0	5.7	7.0	2.0	4.7	6.0	40.2	5.4	16.1	10.0	6.2	62.1	34.9	111.4	1894.1	17.6
187	ICGV 02271	31.0	2.0	5.7	7.3	2.3	5.3	7.3	32.6	5.1	14.9	10.6	6.7	62.3	34.4	118.0	1894.0	15.1
188	ICGV 02286	32.0	1.3	4.3	7.0	2.0	4.7	6.3	41.2	4.7	18.7	12.4	8.2	65.5	33.0	112.5	1897.7	17.6
189	ICGV 86011	30.0	2.3	6.0	7.3	2.7	6.0	8.0	43.0	5.1	18.6	11.7	7.1	61.4	29.5	111.0	1672.1	17.4
190	ICGV 86590	34.0	2.0	3.7	5.3	1.3	3.0	4.3	37.8	4.6	12.8	9.9	5.5	55.1	33.9	120.8	1541.3	22.7
191	ICGV 87160	31.0	2.0	5.0	7.3	2.7	5.3	7.0	31.0	4.6	13.6	7.8	4.7	59.2	28.1	113.6	1123.4	8.5
192	ICGV 87354	34.0	2.7	5.7	7.0	3.0	5.3	7.3	32.0	5.0	8.8	5.5	2.3	49.9	20.7	113.4	770.0	14.1
193	ICGV 87378	29.0	3.0	6.0	7.0	3.3	5.7	7.3	42.0	4.3	14.7	11.7	7.3	63.2	29.2	119.1	1665.7	15.6
194	ICGV 87921	31.0	2.3	5.3	7.3	1.7	3.3	6.0	38.4	5.2	17.3	13.1	7.1	54.0	36.8	112.5	2468.9	15.3
195	ICGV 88145	30.0	3.0	6.0	8.0	3.0	5.7	7.3	45.8	5.0	15.9	11.0	6.4	57.2	30.6	118.4	1537.0	21.9
196	ICGV 92267	33.0	3.0	6.0	7.7	3.0	5.7	7.7	40.7	5.5	14.6	10.9	6.3	61.2	35.4	111.8	1875.1	14.4
197	ICGV 93470	29.0	2.7	7.0	8.3	3.3	6.3	8.0	34.2	4.7	15.5	9.9	6.0	61.5	31.6	111.1	1718.7	14.3
198	ICGV 94169	33.0	2.0	5.3	7.0	2.3	5.7	7.7	36.4	5.6	14.8	12.4	7.3	59.3	40.6	121.0	1930.6	23.3
199	ICGV 94361	31.0	2.7	6.0	7.7	3.0	5.7	6.7	35.2	5.0	13.3	8.7	5.4	61.6	33.9	112.0	1549.0	17.0
200	ICGV 95377	32.0	2.0	5.3	6.7	2.3	5.7	7.3	40.0	4.9	11.3	9.5	5.7	64.5	41.4	115.5	1579.9	16.9
201	ICGV 96466	33.0	2.3	6.7	7.7	2.7	5.0	7.0	30.4	4.8	12.4	8.3	5.2	63.1	34.5	111.5	1365.3	13.2
202	ICGV 96468	30.0	3.0	6.0	7.7	3.3	6.7	7.7	40.7	5.4	12.3	10.3	6.0	58.9	39.3	112.5	2145.8	17.0
203	ICGV 97182	33.0	2.0	5.0	6.0	1.7	4.0	5.7	36.4	5.7	17.0	11.4	6.7	58.2	30.0	118.0	1823.3	16.5
204	ICGV 97183	33.0	2.3	5.3	7.7	3.3	5.7	7.3	32.0	4.7	11.1	8.5	4.9	58.0	35.1	115.4	1414.2	14.4
205	ICGV 98294	35.0	2.3	6.0	7.7	2.0	5.0	6.7	36.5	5.2	14.5	12.1	7.2	60.0	38.1	115.9	2372.6	15.6
206	Gangapuri	30.0	2.0	5.0	7.3	2.7	5.3	7.0	37.4	5.2	9.7	7.2	4.2	59.2	27.9	112.9	1138.9	15.9
207	ICGS 44	35.0	2.3	6.0	8.0	2.3	5.7	7.3	27.8	6.0	12.2	8.7	5.2	61.7	29.9	120.3	980.8	16.3

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
208	ICG 3312	32.0	2.7	6.7	8.0	3.0	5.3	7.0	31.7	4.7	14.0	7.2	4.6	64.1	27.0	112.0	1078.6	10.6
209	ICG 14705	31.0	2.3	5.0	6.7	2.7	5.3	6.7	31.1	5.1	11.3	8.0	5.2	65.3	35.3	116.5	1446.8	13.1
210	ICG 3746	31.0	3.0	5.7	7.7	3.7	6.0	7.7	43.3	4.8	16.1	7.9	5.3	66.2	22.8	119.5	1050.8	12.4
211	ICG 4955	30.0	2.7	6.0	6.7	3.0	5.7	7.0	42.5	4.8	16.1	9.7	6.5	66.9	31.2	113.3	1493.1	15.6
212	ICG 12879	31.0	2.3	6.3	7.7	2.7	6.0	7.3	33.0	4.5	15.1	8.1	5.1	61.3	25.9	116.0	1197.8	12.7
213	ICG 5221	31.0	3.0	5.0	6.7	3.0	5.3	7.0	43.6	4.7	9.7	7.4	4.2	54.6	29.4	118.1	829.5	18.3
214	ICG 4543	30.0	3.7	6.3	7.7	3.3	6.0	7.3	38.4	4.8	14.9	7.1	4.3	59.6	24.1	115.1	942.3	13.3
215	ICG 1834	34.0	2.3	5.3	7.3	3.0	6.3	7.7	32.3	4.9	13.6	8.6	5.5	62.9	26.6	113.6	1169.8	14.7
216	ICG 2106	30.0	3.3	5.7	7.3	3.7	5.7	7.0	37.4	4.9	17.4	9.6	6.5	67.7	28.0	112.6	997.4	12.2
217	ICG 9507	33.0	2.7	7.0	7.7	3.3	5.7	7.3	34.0	4.8	9.1	6.3	3.8	57.7	29.6	117.9	1157.7	13.1
218	ICG 1973	30.0	2.7	6.3	8.0	3.3	6.3	8.3	37.7	4.7	14.9	8.0	5.0	63.2	26.6	116.5	1111.8	13.7
219	ICG 3673	31.0	2.3	6.3	7.7	3.0	6.0	8.0	39.4	4.6	9.8	6.1	4.1	61.3	29.4	124.6	1201.3	20.8
220	ICG 3584	29.0	3.0	7.0	8.3	3.7	6.3	8.0	39.3	4.8	16.7	9.9	5.9	59.3	28.6	115.9	1577.4	15.9
221	ICG 442	30.0	2.7	6.3	7.7	3.3	6.3	8.0	39.9	4.7	11.6	6.0	3.6	60.7	24.0	119.3	804.1	14.6
222	ICGV 01464	34.0	2.0	4.7	6.7	1.3	2.7	4.7	35.8	5.7	8.1	7.8	3.7	46.7	38.6	132.9	1243.3	30.4
223	ICGV 01478	36.0	1.7	6.0	7.7	2.0	4.7	6.3	30.1	6.2	11.3	12.2	6.7	55.9	48.0	126.4	1549.3	23.5
224	ICGV 02251	31.0	2.3	6.0	7.7	2.7	5.7	7.3	34.1	4.8	13.3	8.1	5.1	65.8	32.0	120.5	1228.8	17.8
225	ICGV 03136	36.0	2.0	5.0	7.3	2.3	4.0	6.0	30.9	7.0	8.4	9.2	4.9	56.5	45.7	120.5	1188.1	22.2
226	ICGV 05198	33.0	3.0	6.0	7.0	2.3	4.7	6.0	37.7	5.0	11.5	14.7	8.1	55.4	52.4	122.9	2142.1	21.3
227	ICGV 06234	34.0	2.7	5.7	7.3	2.0	5.3	7.0	34.2	5.5	11.4	10.0	5.8	59.9	48.8	126.9	1838.6	22.9
228	ICGV 00346	35.0	1.3	4.0	6.0	1.3	2.7	4.3	36.9	6.6	13.2	10.0	5.5	59.2	40.1	119.6	1986.2	26.0
229	ICGV 00362	36.0	1.3	3.0	5.0	1.3	2.3	3.3	32.9	5.7	15.0	9.4	5.3	54.3	26.7	119.1	1470.2	23.7
230	ICGV 00371	36.0	2.0	4.7	7.0	2.3	5.7	7.3	32.9	6.0	14.2	7.6	4.1	53.1	27.7	119.3	1187.6	15.5
231	ICGV 02287	35.0	2.0	4.7	6.0	1.7	3.7	5.7	33.5	6.7	14.3	10.6	6.2	58.3	35.6	118.0	1398.8	17.5
232	ICGV 02298	36.0	2.7	5.7	7.0	3.0	5.7	6.7	30.9	6.8	13.7	9.9	6.0	60.2	35.0	121.1	1101.6	18.3
233	ICGV 02317	34.0	1.3	4.0	5.7	1.3	3.0	5.0	33.3	6.5	15.7	10.5	5.3	56.3	35.3	121.4	1944.7	26.0
234	ICGV 97232	31.0	2.7	6.0	7.3	3.0	6.0	7.3	31.4	4.9	12.8	7.8	4.9	62.6	27.9	121.8	1371.4	12.8
235	ICGV 99051	36.0	1.3	2.7	4.7	1.0	2.3	4.0	40.4	5.9	19.6	14.7	8.4	57.5	34.3	131.9	1839.0	25.7
236	ICGV 99052	34.0	1.3	3.0	3.7	1.0	2.0	3.7	40.8	6.5	17.3	12.5	7.0	56.0	31.5	132.1	1821.8	25.7
237	ICGV 00246	36.0	1.0	2.7	4.0	1.0	2.3	3.3	40.5	5.8	10.0	8.5	5.0	57.1	34.4	132.5	1315.8	21.8
238	ICGV 00248	33.0	1.3	2.3	4.0	1.3	2.3	3.7	37.5	6.1	12.8	9.4	5.3	57.8	31.0	131.9	1818.9	20.7
239	ICGV 01361	35.0	1.3	3.3	4.7	1.3	2.3	4.0	34.4	7.8	15.0	11.7	7.2	61.9	30.2	131.9	2326.4	20.9
240	ICGV 02434	33.0	1.7	4.3	5.7	1.7	3.3	5.3	29.6	6.1	14.7	8.6	5.0	57.9	34.7	117.9	1453.3	19.2
241	ICGV 04087	34.0	1.3	3.0	5.0	1.3	2.7	3.3	40.1	7.0	20.5	14.1	7.7	56.3	29.9	131.8	2145.9	27.5
242	ICGV 06175	35.0	2.0	4.0	5.7	1.3	3.0	4.7	31.6	6.1	14.6	9.8	5.5	55.8	32.3	123.6	1316.6	20.7

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
243	ICGV 97116	37.0	1.7	4.3	6.3	2.3	4.7	6.7	30.7	6.0	9.8	6.3	3.9	61.0	31.7	121.8	981.6	18.6
244	ICGV 97128	34.0	1.0	4.0	6.0	1.0	2.7	4.3	35.8	7.4	17.7	12.0	7.0	58.2	31.9	131.9	2122.2	21.1
245	ICGV 98184	34.0	1.7	4.7	6.3	1.3	3.7	5.0	33.5	5.8	16.5	10.5	5.7	53.9	35.1	131.9	1888.1	20.2
246	ICGV 00068	35.0	1.3	2.7	4.0	1.0	2.7	4.0	30.4	5.9	15.6	11.4	6.0	53.5	28.6	131.6	1713.7	19.3
247	ICGV 01495	34.0	2.0	4.0	6.3	2.0	4.0	6.7	36.2	7.0	16.9	16.2	9.7	60.3	45.2	122.5	2821.5	20.9
248	ICGV 05057	34.0	1.3	4.0	5.7	1.3	2.7	4.3	32.0	7.4	14.8	12.1	7.3	60.1	38.8	131.3	1973.0	21.2
249	ICGV 07168	35.0	2.0	5.0	5.7	2.0	4.7	6.0	30.8	5.8	11.5	8.0	4.8	60.7	31.1	121.3	1194.6	21.7
250	ICGV 01265	35.0	1.7	4.0	5.0	1.3	2.7	5.3	30.8	7.0	16.3	9.9	5.6	53.6	35.6	120.5	1509.1	25.1
251	ICGV 98105	34.0	1.3	3.7	5.3	2.0	3.0	5.7	31.6	6.2	18.5	12.9	7.6	59.4	38.0	131.4	2360.0	23.5
252	ICGV 99160	34.0	1.3	3.0	5.0	1.7	2.3	4.7	36.4	6.0	15.5	12.6	7.2	55.8	35.2	132.3	2075.1	24.0
253	ICGV 02323	34.0	1.3	3.0	5.0	1.3	2.3	4.7	31.9	7.1	22.0	16.3	10.5	64.9	39.5	133.0	2620.7	17.6
254	ICGV 04115	34.0	1.7	4.3	6.0	1.7	3.7	5.0	28.2	6.9	13.7	10.3	6.2	59.2	35.2	115.4	1298.5	23.4
255	ICGV 05036	33.0	1.3	2.7	5.3	1.0	2.7	4.0	35.0	6.7	17.7	13.3	7.5	55.6	36.6	131.5	2277.0	27.6
256	ICGV 06042	35.0	1.7	4.0	6.0	1.3	3.7	5.7	34.0	6.7	17.9	11.2	6.9	60.5	30.3	118.1	2186.7	20.8
257	ICGV 86564	37.0	2.0	5.3	7.3	2.0	4.0	6.7	34.2	7.1	7.3	7.7	4.6	56.9	47.0	129.5	1073.9	28.5
258	ICGV 98432	35.0	2.0	4.3	6.7	2.0	4.0	5.7	35.5	6.9	11.3	9.8	5.6	55.8	40.3	129.0	975.0	23.9
259	BAU 13	37.0	2.0	4.3	6.0	1.7	4.3	5.3	40.6	6.6	9.5	11.0	6.6	62.0	46.5	132.3	1430.2	24.1
260	ICGV 87846	35.0	1.3	3.7	4.7	1.3	2.3	3.3	35.3	6.1	14.0	10.8	5.9	57.7	37.9	132.1	2041.5	24.8
261	ICR 48	36.0	2.0	4.7	7.7	2.3	5.3	7.3	30.1	7.3	12.9	9.7	6.2	63.0	33.6	122.1	1320.4	19.6
262	ICGV 86699	35.0	1.0	2.0	4.0	1.0	2.3	4.0	33.3	6.5	14.3	8.7	5.1	57.6	27.0	114.1	1010.1	20.4
263	ICGV 98373	35.0	1.7	4.7	6.7	1.3	3.0	5.0	33.6	6.1	14.1	9.6	5.2	51.6	38.2	128.0	1523.0	18.7
264	ICGV 97115	36.0	2.0	4.3	6.3	1.7	3.7	5.7	30.4	5.8	14.4	9.4	5.3	53.3	29.4	118.9	1139.3	18.4
265	ICGV 06040	35.0	2.0	4.3	6.0	1.3	4.0	5.0	33.7	6.5	16.1	11.5	6.5	57.7	41.2	123.0	2353.4	20.9
266	ICGV 06099	35.0	1.7	5.0	7.0	1.3	3.7	6.0	35.9	6.6	20.2	16.2	10.3	62.8	40.7	125.4	2610.8	20.0
267	CS 39	35.0	1.7	4.0	7.0	1.3	3.0	6.3	29.7	6.4	15.0	11.8	6.8	57.2	38.2	124.6	2174.6	26.2
268	ICGV 05032	32.0	1.3	3.3	5.3	1.3	2.3	3.3	33.5	6.9	16.4	12.0	6.2	51.1	37.3	131.8	2429.4	24.4
269	ICGV 05141	35.0	1.3	2.7	4.3	1.0	2.7	3.7	33.0	6.9	16.3	12.6	7.8	61.7	38.7	130.9	2163.2	24.9
270	ICGV 07359	36.0	2.3	5.3	7.0	2.7	5.3	6.3	42.5	6.6	12.0	9.9	5.4	55.7	46.8	127.0	1611.2	27.1
271	ICGV 07368	37.0	2.3	4.7	6.7	2.3	5.0	6.7	36.3	5.5	9.2	9.6	5.5	58.7	48.7	131.0	1677.3	25.9
272	ICGV 06110	34.0	2.3	5.0	7.0	2.7	6.3	7.7	30.9	7.4	10.6	10.2	5.3	52.2	43.8	129.3	1486.3	19.2
273	ICGV 06188	33.0	2.3	4.3	6.3	1.7	4.0	6.0	32.3	5.6	10.5	11.0	6.8	60.4	51.5	123.6	1799.6	14.1
274	ICGV 00440	36.0	2.3	5.3	7.3	2.3	4.7	7.0	36.7	7.2	9.3	10.1	5.4	53.3	51.0	121.6	1678.7	24.5
275	ICGV 86352	32.0	2.7	5.3	7.3	2.7	5.7	7.3	35.9	4.8	12.0	8.1	4.7	58.7	31.5	113.8	1290.3	13.7
276	ICGV 09112	34.0	2.3	5.7	8.0	2.7	5.3	7.0	35.2	7.4	12.6	7.3	4.4	61.0	33.1	122.8	1119.5	24.1
277	ICGV 93920	34.0	1.7	4.3	6.3	1.7	3.3	6.0	31.5	6.4	18.7	10.6	6.2	59.7	28.7	116.5	2072.2	12.8

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
278	ICGV 93216	31.0	1.3	5.0	7.0	1.7	4.3	6.3	31.2	5.6	17.5	10.9	6.8	61.3	29.0	120.0	1956.1	12.8
279	ICGV 88438	37.0	1.7	5.3	6.7	1.7	5.0	5.7	26.3	6.6	8.2	6.2	3.3	52.8	32.5	126.4	902.1	21.6
280	ICG 11337	34.0	1.3	2.7	4.7	1.0	2.7	4.7	35.5	6.0	9.3	6.8	3.7	52.3	30.9	131.4	815.8	23.5
281	49 × 37-90	34.0	2.3	4.0	6.7	2.3	4.0	6.7	31.0	6.5	11.2	7.9	4.8	58.3	30.1	116.4	1325.8	20.4
282	49 M-2-2	34.0	1.3	4.3	6.3	2.0	4.0	5.7	33.4	8.4	11.1	9.3	4.9	56.1	36.7	130.9	1129.0	16.1
283	49 M- 1-1	35.0	1.3	3.0	5.7	1.3	2.7	5.0	26.0	5.0	12.7	10.9	6.4	60.3	45.8	130.9	1150.0	19.4
284	TG 19	33.0	2.7	6.0	7.7	3.0	7.0	8.0	28.6	4.6	13.5	9.1	5.8	63.3	27.9	115.6	1222.7	13.4
285	TG 39	34.0	2.3	6.0	8.0	2.7	6.0	8.0	23.3	5.4	11.0	7.8	4.0	52.3	42.6	121.9	1459.6	13.6
286	TG LPS 3	35.0	2.0	5.7	7.7	2.7	5.7	7.7	26.3	6.3	12.4	11.3	6.8	60.7	47.2	119.1	1658.0	23.8
287	26 × M-223-1	33.0	1.7	4.7	7.0	2.0	4.7	6.7	28.5	5.7	14.4	7.7	3.9	54.2	32.9	114.3	1211.6	14.3
288	SPS 2	36.0	1.3	2.7	4.3	1.3	2.3	4.3	32.2	7.4	12.3	8.1	4.6	57.2	31.6	120.9	1394.0	27.4
289	SPS 3	29.0	2.7	6.0	8.0	3.3	5.7	7.0	39.6	5.0	12.5	8.3	5.4	63.3	30.1	112.8	1210.6	13.7
290	SPS 6	30.0	2.7	6.0	7.7	3.0	5.7	7.0	36.3	4.4	15.5	10.3	6.6	64.4	29.3	113.5	1426.0	14.9
291	SPS 7	35.0	1.0	3.3	4.3	1.0	2.3	4.0	32.7	7.4	15.2	10.3	6.5	61.6	35.8	117.6	1567.2	24.2
292	SPS 8	35.0	1.0	2.7	4.0	1.0	2.7	4.0	33.8	7.1	13.4	8.7	4.7	58.8	28.7	119.8	1433.1	25.3
293	SPS 11	35.0	1.3	2.7	5.0	1.0	2.3	4.0	36.7	7.3	22.3	16.3	10.1	62.4	30.7	130.9	3129.5	16.2
294	SPS 15	35.0	1.7	3.3	4.7	1.0	4.0	5.7	34.6	5.8	11.0	7.6	4.3	58.2	29.9	131.8	1261.2	23.0
295	SPS 20	35.0	1.0	2.3	4.7	1.0	2.0	3.3	30.4	6.5	14.0	8.7	5.2	59.1	28.0	133.6	923.2	24.2
296	SPS 21	34.0	1.3	3.7	4.0	1.0	2.3	4.0	32.7	6.7	13.0	8.8	5.3	59.9	27.3	131.5	1046.5	25.2
297	ICGV 03128	36.0	1.3	4.3	6.7	1.3	3.7	6.0	32.5	6.5	20.5	14.8	9.4	66.7	34.1	121.5	2783.6	20.4
298	TMV 2 NLM	29.0	3.0	6.0	7.7	3.3	5.7	7.0	33.5	5.1	15.0	8.7	5.4	60.0	29.4	119.1	1155.6	14.5
299	ICG 1668	30.0	3.0	5.3	7.3	3.3	5.7	7.0	33.1	5.0	11.8	7.5	5.0	64.1	33.0	118.5	1345.6	18.1
300	ICG 8285	38.0	2.0	4.3	6.3	2.3	4.7	6.0	29.4	6.5	12.8	8.1	4.7	57.3	32.0	122.1	874.5	22.2
301	ICG 11426	35.0	1.3	3.7	6.0	1.3	2.7	4.7	29.0	5.7	11.1	7.1	4.1	56.1	29.0	120.9	936.0	19.2
302	ICGV 02290	35.0	2.0	5.0	7.3	2.3	5.0	6.3	31.8	7.0	10.6	7.5	4.9	64.5	34.2	124.5	1098.1	26.1
303	ICGV 02446	35.0	1.3	3.0	4.3	1.0	2.3	4.0	33.0	6.1	13.2	9.4	5.3	55.5	32.9	131.4	1405.9	24.0
304	ICG 156 (M 13)	35.0	1.7	4.3	6.7	2.0	5.3	6.3	28.2	5.9	12.5	7.7	4.8	65.0	39.0	121.4	1428.6	17.5
305	ICGS 76	36.0	1.3	4.3	6.0	1.3	3.3	6.0	31.6	7.0	13.9	10.4	5.8	54.9	34.7	115.9	1509.0	23.8
306	ICG 5891	38.0	2.3	5.0	7.0	2.7	5.3	6.3	28.0	6.3	11.3	7.5	4.3	57.4	28.7	121.8	764.5	14.8
307	CSMG 84-1	31.0	2.0	4.3	5.7	2.0	4.7	5.7	32.4	6.2	13.8	8.9	4.8	56.5	28.6	114.0	1257.7	15.6
308	ICG 111	36.0	2.0	5.3	6.7	2.3	5.0	6.3	28.0	5.9	11.5	8.9	5.1	58.2	28.5	123.5	751.5	17.1
309	ICG 14834	36.0	2.0	4.3	6.7	2.0	4.3	6.0	29.5	6.5	9.0	5.9	3.4	56.3	29.9	116.1	909.5	14.7
310	ICG 11322	35.0	2.0	4.7	7.3	2.3	5.7	7.0	26.9	6.2	10.9	6.7	4.0	61.9	27.2	121.8	1034.8	16.3
311	ICG 532	37.0	2.0	4.7	7.0	2.0	4.3	6.0	26.3	6.5	9.4	6.0	3.5	58.1	30.7	118.3	678.7	18.9
312	ICG 12509	35.0	2.0	4.7	7.0	1.7	5.0	6.7	34.9	6.0	8.5	6.0	3.6	60.0	38.0	122.6	1009.5	16.6

S. No.	Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
313	ICG 12672	32.0	2.3	5.3	7.3	2.7	5.3	7.3	41.2	4.5	14.0	7.7	4.5	56.9	24.3	116.0	847.0	15.7
314	ICG 10185	36.0	2.3	5.0	7.0	2.3	5.3	6.7	38.9	6.6	9.0	6.2	3.4	56.6	33.2	121.3	768.4	19.2
315	ICG 2773	36.0	2.0	5.0	7.0	2.0	4.3	6.0	25.5	6.0	6.3	4.2	2.6	54.1	25.0	123.4	478.3	14.9
316	ICG 3027	37.0	2.0	5.3	7.0	2.0	4.7	6.0	33.8	6.5	8.5	5.7	3.2	56.1	29.0	121.3	798.7	15.9
317	ICG 5745	36.0	2.3	5.0	7.3	2.7	5.0	6.7	28.3	6.1	10.1	7.7	4.6	61.4	39.3	123.4	1317.7	14.0
318	ICG 14482	37.0	1.7	4.3	5.7	2.0	4.7	6.3	31.7	6.7	7.6	6.6	3.7	56.0	34.0	123.3	939.6	23.7
319	ICG 4527	34.0	2.0	4.3	6.3	2.0	5.0	6.0	33.5	7.0	9.4	7.0	4.2	59.4	33.0	117.4	769.6	24.3
320	ICG 4343	36.0	2.3	4.7	6.3	2.3	4.7	6.3	27.9	5.8	6.8	5.2	3.1	59.0	27.0	119.4	709.9	14.0
321	ICG 13895	37.0	2.3	4.3	6.3	2.3	4.7	6.7	28.4	7.0	5.7	3.9	2.1	55.9	29.2	119.3	611.8	13.3
322	ICG 5663	34.0	2.0	5.3	7.7	2.0	5.7	7.0	36.1	5.8	6.9	5.2	3.1	57.9	32.2	124.3	575.1	18.8
323	ICG 721	38.0	2.3	4.7	6.7	2.7	5.3	6.7	34.4	6.2	14.3	9.4	5.6	56.9	30.8	122.3	881.2	18.3
324	ICG 12276	34.0	1.7	4.3	6.0	1.3	4.0	5.3	37.1	4.8	8.0	5.2	3.0	52.2	24.7	131.3	747.3	22.7
325	ICG 875	37.0	2.3	5.0	6.3	2.3	5.0	7.3	29.4	6.7	9.1	5.4	3.1	54.8	28.6	121.0	498.1	24.0
326	ICG 14475	36.0	1.3	4.0	6.3	2.3	4.7	6.0	33.0	5.5	10.5	6.2	3.2	52.3	31.3	122.3	1200.8	29.0
327	ICG 15190	36.0	2.3	5.3	5.7	1.7	4.0	5.0	33.2	7.0	7.7	4.6	2.7	56.5	30.0	127.4	582.9	22.3
328	ICG 12370	36.0	1.3	3.7	6.7	1.7	3.3	4.7	31.9	5.7	8.2	5.1	2.8	52.0	25.5	119.0	567.1	20.8
329	ICGV 86325	34.0	1.3	4.3	6.3	2.0	4.3	7.0	32.7	7.0	14.7	9.0	5.6	61.8	32.6	119.1	1407.5	23.3
330	ICG 5662	37.0	2.0	4.0	6.3	2.3	4.3	6.0	31.8	6.1	6.1	6.5	2.7	48.9	37.7	120.8	998.9	20.7
331	ICG 9961	38.0	2.0	5.0	7.0	2.0	5.3	6.3	31.2	6.2	12.1	6.7	4.0	62.7	28.6	124.1	878.4	14.9
332	ICG 14466	37.0	2.0	5.0	5.3	2.3	4.7	6.0	34.5	6.8	8.5	4.9	3.0	59.0	28.6	122.0	1194.2	18.2
333	ICG 3053	35.0	2.0	5.3	6.7	1.7	4.7	5.3	30.2	5.7	9.5	6.6	3.7	55.9	30.7	131.4	793.0	16.6
334	ICG 6766	37.0	1.7	4.0	5.3	1.7	3.7	5.7	32.7	5.6	4.9	4.8	2.8	56.5	34.3	119.0	536.1	20.3
335	ICG 2381	36.0	1.7	4.0	6.3	2.0	3.3	6.0	34.6	6.5	7.9	5.6	3.0	51.2	29.1	118.3	1436.5	20.0
336	ICG 2857	38.0	2.0	4.0	6.3	2.0	3.7	5.3	30.7	5.8	9.1	6.4	3.6	54.2	27.1	123.0	702.5	14.1
337	ICGV 13238	29.0	2.3	5.7	7.3	2.7	6.0	7.7	32.3	4.7	12.5	8.0	5.1	63.7	30.1	112.3	1296.1	11.6
338	ICGV 13241	29.0	3.0	6.0	7.7	3.3	5.0	7.0	31.5	4.7	12.3	8.1	4.7	59.2	30.6	116.5	1285.7	15.9
339	ICGV 13242	30.0	3.7	6.3	7.7	3.0	6.0	7.3	33.2	5.7	14.6	9.6	5.9	59.4	30.2	109.0	1361.2	15.6
340	ICGV 13245	30.0	3.0	6.0	7.7	3.0	5.7	7.3	35.0	7.0	12.7	8.9	5.7	63.3	31.5	111.9	1426.4	16.9
Mean		**33.0**	**2.1**	**4.9**	**6.7**	**2.1**	**4.6**	**6.3**	**34.2**	**5.6**	**13.8**	**9.6**	**5.6**	**58.9**	**33.1**	**120.4**	**1549.9**	**17.8**
CV (%)		**4.6**	**13.5**	**7.5**	**6.7**	**13.5**	**9.4**	**9.8**	**7.0**	**7.2**	**19.1**	**17.0**	**18.3**	**5.5**	**7.8**	**1.5**	**19.5**	**15.9**
LSD at 5 % level		**2.1**	**0.1**	**0.1**	**0.1**	**0.1**	**0.1**	**0.1**	**3.3**	**0.1**	**3.9**	**2.8**	**1.8**	**4.5**	**3.6**	**2.5**	**461.1**	**3.9**

X1= Days to 50% flowering; **X2, X3, X4=** Disease score of late leaf spot at 75, 90 and 105 days after sowing, respectively; **X5, X6, X7=** Disease score of rust at 75, 90 and 105 days after sowing, respectively; **X8=** Number of primary branches per plant; **X9=** Plant height (cm); **X10=** Number of pods per plant; **X11=** Pod yield per plant (g); **X12=** Seed yield per plant (g); **X13=** Shelling percent; **X14=** Hundred seed weight (g); **X15=** Days to maturity; **X16=** Yield per hectare (Kg); **X17=** Haulm yield per plant (g)

Appendix XI

Pooled BLUPs for nutritional quality traits of Genomic Selection Panel of groundnut evaluated across four environments

Entry No	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
1	ICGV 06423	53.47	21.77	36.36	43.19	12.67	2.01	0.87
2	ICGV 07246	51.36	23.92	38.31	40.87	12.51	2.14	0.96
3	ICGV 07247	52.62	23.73	36.14	42.81	12.93	2.19	0.86
4	ICGV 07268	50.59	20.81	39.79	40.12	11.47	2.35	1.00
5	ICGV 01005	50.27	23.47	45.50	35.81	10.98	1.77	1.28
6	ICGV 01060	53.83	23.33	37.46	42.50	11.85	2.84	0.90
7	ICGV 01124	51.29	22.98	47.35	33.29	11.63	2.12	1.50
8	ICGV 02206	53.32	21.93	38.17	42.18	12.51	2.47	0.93
9	ICGV 03397	50.46	24.09	33.76	44.58	13.51	2.25	0.77
10	ICGV 03398	47.81	26.32	36.19	42.24	13.31	2.26	0.88
11	ICGV 04044	51.55	21.96	36.41	43.52	12.90	2.46	0.85
12	ICGV 06347	49.78	22.74	33.41	45.23	13.20	1.83	0.76
13	ICGV 93280	52.44	21.01	36.13	42.44	13.05	2.24	0.87
14	ICGV 95469	51.11	22.30	32.74	45.51	13.46	2.06	0.75
15	ICGV 00387	49.55	21.63	35.43	43.21	13.14	1.98	0.85
16	ICGV 01393	49.20	22.59	45.98	35.68	10.64	1.87	1.33
17	ICGV 02242	48.02	23.86	44.39	35.54	11.54	2.49	1.28
18	ICGV 97058	50.12	21.78	46.26	34.10	11.34	2.22	1.37
19	ICGV 99083	49.82	23.36	41.46	38.42	12.23	2.06	1.09
20	ICGV 00343	51.18	23.87	38.52	41.06	12.56	2.67	0.95
21	ICGV 00349	53.11	23.01	39.35	40.50	12.34	2.27	1.00
22	ICGV 01263	50.46	24.50	47.54	33.37	10.97	2.28	1.47
23	ICGV 03056	54.25	20.84	39.63	40.25	12.42	2.25	1.01
24	ICGV 03064	53.24	21.48	42.13	38.97	11.62	2.57	1.12
25	ICGV 05161	53.53	21.24	39.50	41.07	12.12	2.52	0.99
26	ICGV 05163	55.03	20.42	35.18	44.89	12.66	2.27	0.80
27	ICGV 06422	53.71	21.64	36.90	42.94	12.41	2.35	0.90
28	ICGV 06431	52.47	21.11	42.04	38.93	11.36	1.95	1.12
29	ICGV 07220	55.30	21.00	50.45	32.24	12.72	1.29	1.60
30	ICGV 07223	52.78	22.55	37.84	41.94	12.39	2.13	0.93
31	ICGV 07227	53.60	23.37	36.28	41.61	13.56	2.40	0.91
32	ICGV 07235	52.10	23.40	35.12	44.18	12.72	2.12	0.82
33	ICGV 99233	53.37	22.91	37.66	42.85	11.95	2.39	0.89
34	ICGV 97165	49.88	22.51	38.11	39.97	13.06	2.17	1.01
35	ICGV 99029	50.70	23.71	37.57	39.70	13.36	2.83	0.96
36	ICGV 00191	52.43	22.29	36.85	41.01	13.40	2.85	0.92
37	ICGV 07120	51.63	21.57	36.66	41.51	13.04	2.24	0.90
38	ICGV 97092	49.02	22.63	35.53	42.66	13.31	2.06	0.85
39	ICGV 97120	52.78	23.36	54.19	29.32	12.58	1.51	1.86
40	ICGV 98163	53.65	23.59	34.39	43.02	13.61	2.41	0.82
41	ICGV 00005	54.32	23.56	34.75	42.29	13.43	2.58	0.85
42	ICGV 01273	52.96	22.83	34.12	44.01	13.26	2.35	0.79
43	ICGV 01274	50.34	23.93	37.84	41.44	12.40	1.81	0.93
44	ICGV 02321	52.79	24.24	36.03	41.39	13.34	2.36	0.89
45	ICGV 03043	54.40	21.54	35.30	44.10	13.20	1.99	0.81
46	ICGV 04124	50.91	22.53	38.15	41.98	12.02	1.91	0.93
47	ICGV 00290	51.24	23.52	37.31	42.32	12.12	2.04	0.90
48	ICGV 00321	48.52	26.67	41.25	38.01	11.64	2.06	1.10
49	ICGV 02125	51.60	22.46	42.32	38.45	11.54	1.69	1.13
50	ICGV 02144	50.16	24.37	47.19	33.96	10.82	1.92	1.43
51	ICGV 03184	49.72	24.33	41.69	36.84	11.92	2.25	1.15
52	ICGV 03207	52.51	22.77	43.98	37.28	11.39	1.98	1.20

Entry No	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
53	ICGV 04018	51.68	24.96	41.48	38.00	11.77	2.65	1.12
54	ICGV 07210	53.36	22.03	44.04	37.20	11.47	2.37	1.20
55	ICGV 07217	52.80	20.64	38.64	42.32	12.08	1.98	0.93
56	ICGV 95290	49.76	25.65	38.09	40.85	12.21	2.23	0.94
57	ICGV 97261	52.89	22.86	42.75	38.10	11.59	2.02	1.15
58	ICGV 97262	51.05	24.73	40.75	38.34	12.08	2.64	1.08
59	ICGV 99181	53.90	21.37	40.96	40.13	11.68	2.44	1.04
60	ICGV 99195	50.87	25.53	33.13	45.95	13.18	2.27	0.75
61	ICGV 89104	51.43	22.31	44.19	36.15	11.45	1.88	1.25
62	ICGS 11	49.35	23.20	36.93	42.72	12.26	1.92	0.87
63	J 11	52.56	22.45	39.62	40.84	12.10	1.96	1.00
64	ICGV 99085	57.99	21.02	50.70	31.05	10.15	3.24	1.68
65	TKG 19A	50.88	22.39	37.85	42.18	11.73	2.30	0.91
66	TPG 41	49.15	23.54	43.38	36.76	11.22	2.55	1.21
67	ICGV 00350	53.35	20.78	33.97	45.22	12.83	2.06	0.76
68	DH 86	49.43	25.28	37.69	41.18	12.18	2.24	0.94
69	ICGV 95058	49.14	22.88	46.99	32.51	11.64	1.91	1.48
70	ICGV 95070	52.10	19.98	38.64	40.98	12.27	2.03	0.96
71	GPBD 4	57.83	20.39	50.37	32.08	10.07	2.83	1.60
72	ICGV 91114	51.66	21.64	46.74	34.86	10.87	1.96	1.35
73	TMV 2	45.92	26.99	47.84	31.16	10.68	2.18	1.56
74	Faizpur 1-5	48.38	27.66	36.80	42.23	12.81	2.41	0.89
75	Mutant 3	51.83	22.32	41.36	38.83	11.91	1.94	1.10
76	ICGV 03042	55.63	20.28	32.83	47.06	13.23	1.99	0.71
77	ICGV 05100	54.50	21.12	36.37	43.30	13.03	1.97	0.87
78	ICGV 06049	51.06	22.87	42.59	38.64	11.55	1.82	1.13
79	ICGV 06420	56.60	20.57	34.45	45.43	12.97	2.15	0.80
80	ICGV 06424	55.03	20.77	39.99	40.12	12.10	2.39	1.04
81	ICGV 07145	51.08	22.59	36.42	42.97	12.77	2.37	0.86
82	ICGV 07148	51.01	22.52	39.64	40.62	12.10	1.93	1.01
83	ICGV 07166	51.99	22.02	38.71	41.55	12.26	2.38	0.96
84	ICGV 06142	56.10	24.13	37.89	41.51	12.53	2.95	0.93
85	ICGV 91116	50.25	23.90	39.74	39.08	12.29	1.89	1.04
86	ICGV 97045	52.19	22.32	45.13	33.79	12.30	2.72	1.51
87	ICGV 94118	52.13	22.86	39.28	39.05	13.14	2.74	1.03
88	ICGV 05176	48.59	26.29	43.47	35.33	11.57	2.67	1.25
89	ICGV 04149	53.96	21.41	44.32	37.02	11.77	2.16	1.23
90	ICGV 00351	51.57	22.59	37.42	42.04	12.20	2.28	1.05
91	ICGV 92195	48.92	22.34	44.64	35.56	11.32	1.55	1.27
92	ICGV 87187	48.52	22.82	45.30	35.25	11.58	1.76	1.30
93	ICGV 86072	49.29	20.22	45.27	34.72	11.71	1.75	1.33
94	ICGV 86015	48.11	24.03	36.73	41.41	13.07	1.82	0.89
95	ICGV 93437	49.75	22.90	37.08	42.52	12.47	1.61	0.88
96	ICGV 86143	49.00	24.46	45.22	34.89	11.47	2.14	1.31
97	ICGV 90320	50.35	20.25	41.67	38.56	11.48	2.22	1.11
98	ICGV 07273	49.52	23.72	43.55	37.06	11.48	1.62	1.21
99	49 × 37-91	50.61	21.73	44.14	36.20	11.43	1.87	1.29
100	49 × 37-134	50.45	22.19	46.17	34.74	11.08	1.79	1.37
101	49 × 37-135	50.87	20.93	45.76	35.64	10.86	1.74	1.29
102	49 × 37-97-1	47.25	23.92	46.67	33.12	11.28	1.64	1.44
103	49 × 37- 99(b) tall	49.27	23.17	48.12	31.16	11.13	1.86	1.64
104	39 × 49 -8	50.23	22.96	44.15	36.58	11.03	1.90	1.24
105	39 × 49 -77	53.57	22.13	42.60	39.48	11.04	2.37	1.11
106	49 × 39-20-2	48.06	23.68	43.82	36.34	11.13	1.89	1.23
107	49 × 39-21-2	49.50	22.62	46.52	34.18	10.96	2.29	1.41
108	49 × 39-8	51.05	20.22	50.48	31.84	10.31	1.76	1.61

Entry No	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
109	49 M-16	55.30	24.38	37.43	42.40	12.46	2.63	0.91
110	49 × 27-19	46.01	24.39	44.46	34.82	11.15	1.53	1.30
111	49 × 27-13 (ii)	44.91	24.31	46.67	33.45	11.57	1.60	1.44
112	27 × 49- 16	47.89	25.23	44.98	34.24	11.27	2.37	1.35
113	27 × 49- 12	52.95	21.53	43.14	38.47	11.38	1.98	1.16
114	27 × 49- 14	51.01	21.88	44.38	35.47	12.01	1.75	1.27
115	27 × 49- 27-1	47.66	22.69	44.37	36.73	11.31	1.45	1.24
116	26 M 156-2	51.35	22.10	42.57	38.00	11.68	2.12	1.14
117	26 M- 119-1	49.77	23.83	41.57	38.81	11.58	1.85	1.08
118	24 M-86	51.26	24.35	38.66	40.33	12.89	2.38	0.97
119	MN1-35	54.08	23.28	47.10	34.83	12.78	1.41	1.40
120	M 110-14	51.47	23.00	39.02	39.99	12.35	2.72	1.00
121	M 28-2	53.26	22.76	37.98	40.95	12.88	2.65	0.95
122	Somnath	51.72	23.41	36.77	43.53	11.89	2.44	0.86
123	TG 41	48.32	22.77	43.98	35.78	12.09	1.58	1.25
124	TG 42	47.94	22.77	40.11	38.83	12.48	1.47	1.05
125	TG 49	46.64	23.17	45.31	34.98	11.36	1.58	1.31
126	TG LPS 4	48.22	23.12	41.38	37.27	12.21	1.56	1.12
127	TG LPS 7	48.81	22.83	42.64	36.95	11.87	1.69	1.21
128	24 × 37-2275	50.00	22.37	49.81	31.47	10.43	2.04	1.61
129	24 × 39-31 MR	53.20	22.94	40.60	39.79	11.56	2.55	1.03
130	26 × M-95-1 RI	54.53	21.53	46.02	35.66	10.57	2.56	1.35
131	26 × 37-IV- 9IR	48.60	20.14	44.68	35.92	11.31	1.54	1.27
132	26 × 27-164	45.96	21.99	34.90	43.52	12.96	1.33	0.82
133	49 × 39-21-1	51.99	20.27	43.59	38.33	11.38	1.77	1.16
134	49 × 39-21-2(a)	54.49	20.59	43.99	37.06	11.25	2.77	1.20
135	49 × 39-74	53.72	19.65	47.69	34.43	10.58	2.11	1.41
136	39 × 49-81-1	52.15	20.52	44.29	36.67	11.02	2.20	1.23
137	49 × 27-37	50.08	23.43	38.02	41.62	11.93	2.11	0.93
138	TDG 10	49.78	22.83	40.76	40.60	11.41	2.09	1.02
139	TDG 13	53.74	21.57	39.57	40.59	12.03	2.29	0.98
140	TDG 14	48.64	25.11	42.39	38.02	11.48	2.14	1.14
141	DTG 3	46.74	19.98	45.06	35.32	11.48	1.11	1.31
142	DTG 15	51.23	21.43	43.84	37.43	11.30	1.74	1.19
143	M 28-2	53.63	22.76	39.33	40.03	12.46	2.86	1.02
144	JL 24	51.09	20.27	46.61	35.05	10.70	1.59	1.35
145	TAG 24	49.14	23.05	42.66	37.70	11.54	1.54	1.16
146	SPS 1	54.80	23.69	41.13	38.53	14.36	1.98	1.10
147	SPS 9	55.41	22.00	41.65	38.29	14.41	1.80	1.10
148	SPS 10	50.08	22.93	42.89	37.82	11.48	1.68	1.14
149	SPS 13	49.33	22.46	46.39	34.86	11.60	1.42	1.38
150	SPS 14	54.97	22.65	43.75	36.92	13.56	1.85	1.20
151	SPS 17	45.89	24.18	45.96	34.14	11.45	1.75	1.36
152	ICGV 02411	55.09	23.20	36.42	42.81	12.82	2.65	0.86
153	ICGV 05155	57.65	18.50	38.13	42.71	12.27	2.25	0.90
154	ICGV 06100	55.09	22.87	35.30	43.42	13.35	2.59	0.85
155	ICGV 07023	49.95	23.83	44.29	36.59	11.23	1.87	1.24
156	SunOleic 95R	50.60	22.99	78.83	5.61	7.63	1.86	14.09
157	ICG 434	51.80	25.00	36.75	42.22	12.64	2.31	0.89
158	ICG 2031	51.88	21.10	44.17	36.77	11.20	1.84	1.24
159	ICG 3102	51.96	22.60	40.66	39.38	12.15	1.82	1.04
160	ICG 3140	48.87	22.61	43.79	36.26	11.47	1.62	1.23
161	ICG 3343	49.34	22.64	41.71	37.93	12.06	1.53	1.12
162	ICG 3421	51.88	20.82	45.01	35.71	11.16	1.84	1.28
163	ICG 4729	51.76	20.63	45.13	35.81	10.90	1.79	1.29
164	ICG 6022	58.27	20.35	51.11	37.34	8.35	3.19	1.42

Entry No	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
165	ICG 6646	51.92	20.48	46.43	37.34	9.98	2.56	1.27
166	ICG 8517	51.48	23.04	43.67	36.79	14.20	1.32	1.21
167	ICG 8751	48.15	21.18	37.24	41.67	12.23	1.94	0.90
168	ICG 9315	51.63	22.94	41.51	39.64	11.75	1.79	1.05
169	ICG 10036	46.39	22.30	39.68	40.50	11.39	2.30	0.99
170	ICG 10053	49.95	24.49	47.37	33.39	10.93	2.35	1.44
171	ICG 10701	48.54	22.43	40.27	39.97	11.85	1.81	1.03
172	ICG 11088	53.82	20.86	49.22	35.40	10.27	2.14	1.42
173	ICG 11651	48.64	23.54	37.47	41.81	11.88	1.63	0.91
174	ICG 12625	58.29	19.86	50.96	38.22	8.55	2.55	1.38
175	ICG 12991	50.22	21.00	45.51	35.66	10.98	1.48	1.29
176	ICG 14985	46.32	24.31	43.37	35.18	12.02	1.69	1.29
177	ICG 15415	49.17	21.76	38.32	42.19	11.69	2.71	0.92
178	ICG 15419	59.18	21.36	49.06	39.55	8.00	3.36	1.28
179	ICGV 01232	50.67	22.69	35.58	44.03	12.55	2.06	0.82
180	ICGV 01276	50.81	25.46	33.61	44.49	13.14	2.09	0.77
181	ICGV 01328	53.84	21.63	47.88	32.86	13.96	1.33	1.52
182	ICGV 02022	50.37	23.63	39.18	41.29	11.78	1.92	0.97
183	ICGV 02038	47.77	27.38	38.26	40.11	12.21	2.22	0.98
184	ICGV 02189	49.65	24.20	41.64	39.08	11.68	1.62	1.08
185	ICGV 02194	53.02	21.85	39.83	40.11	12.16	2.49	1.02
186	ICGV 02266	49.76	24.12	42.54	36.76	11.91	2.05	1.17
187	ICGV 02271	52.93	25.07	31.21	47.60	13.19	2.81	0.66
188	ICGV 02286	52.36	21.10	36.22	43.18	12.55	2.24	0.87
189	ICGV 86011	50.64	22.12	46.37	34.89	10.89	1.83	1.34
190	ICGV 86590	49.29	23.36	34.76	44.76	12.26	2.46	0.78
191	ICGV 87160	49.19	23.47	45.07	35.61	11.16	2.10	1.27
192	ICGV 87354	49.79	23.45	44.70	34.91	11.62	1.85	1.30
193	ICGV 87378	51.27	23.39	38.73	41.27	11.98	2.17	0.96
194	ICGV 87921	52.28	22.02	39.47	41.27	11.82	2.18	0.99
195	ICGV 88145	51.25	22.47	43.82	37.24	11.33	1.85	1.20
196	ICGV 92267	52.74	23.17	40.03	40.62	11.77	2.32	0.99
197	ICGV 93470	50.63	23.04	42.12	38.41	11.67	1.72	1.12
198	ICGV 94169	50.01	21.12	47.23	33.58	11.21	2.02	1.44
199	ICGV 94361	53.03	22.07	36.31	43.56	12.64	2.10	0.86
200	ICGV 95377	50.50	24.62	41.05	39.49	11.65	2.62	1.05
201	ICGV 96466	51.62	24.05	40.92	39.01	11.81	2.34	1.06
202	ICGV 96468	51.73	22.65	36.55	42.92	12.62	2.41	0.88
203	ICGV 97182	52.04	21.78	36.04	43.19	12.80	2.46	0.85
204	ICGV 97183	48.97	24.60	42.59	37.41	11.63	1.86	1.16
205	ICGV 98294	51.70	25.91	40.18	39.56	11.93	3.12	1.05
206	Gangapuri	49.45	21.88	43.10	36.67	14.13	1.15	1.20
207	ICGS 44	48.59	23.20	35.46	43.66	12.58	1.84	0.82
208	ICG 3312	52.69	20.92	45.80	35.39	11.07	2.16	1.31
209	ICG 14705	51.89	23.37	40.03	38.71	12.11	2.55	1.05
210	ICG 3746	50.93	21.02	45.55	35.46	10.88	1.54	1.30
211	ICG 4955	51.78	21.05	49.40	31.55	13.06	0.42	1.59
212	ICG 12879	53.30	20.46	45.89	35.44	10.97	1.88	1.31
213	ICG 5221	58.61	22.38	48.34	38.64	8.32	2.91	1.30
214	ICG 4543	51.86	20.93	44.85	36.20	11.42	1.77	1.26
215	ICG 1834	50.78	23.30	43.55	36.15	11.36	1.88	1.27
216	ICG 2106	50.94	21.26	44.65	36.12	11.14	1.69	1.25
217	ICG 9507	48.45	26.40	40.79	38.31	12.00	2.00	1.11
218	ICG 1973	50.92	21.78	46.31	34.75	10.83	1.84	1.35
219	ICG 3673	53.00	20.57	43.72	37.05	13.72	0.97	1.24
220	ICG 3584	52.02	20.38	43.44	37.45	11.39	1.77	1.17

Entry No	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
221	ICG 442	53.12	20.65	45.02	35.43	13.28	1.02	1.37
222	ICGV 01464	47.73	23.56	43.12	35.15	12.41	1.88	1.25
223	ICGV 01478	47.31	24.44	41.37	38.15	11.79	2.28	1.09
224	ICGV 02251	51.58	21.68	42.20	38.69	11.54	1.82	1.12
225	ICGV 03136	48.60	23.51	40.60	38.09	11.90	2.32	1.11
226	ICGV 05198	46.77	24.74	49.10	31.20	11.02	1.74	1.60
227	ICGV 06234	51.08	23.79	49.08	31.62	10.72	2.34	1.56
228	ICGV 00346	51.57	21.73	36.36	42.67	12.81	2.19	0.87
229	ICGV 00362	51.27	25.12	44.01	35.58	11.22	2.71	1.26
230	ICGV 00371	51.14	21.05	33.55	45.52	12.71	2.37	0.76
231	ICGV 02287	51.00	24.39	43.20	36.88	11.79	2.33	1.20
232	ICGV 02298	47.92	22.56	47.40	33.28	10.64	1.99	1.44
233	ICGV 02317	53.71	21.33	34.67	43.94	13.00	2.06	0.80
234	ICGV 97232	49.21	24.49	42.45	38.04	11.49	1.69	1.14
235	ICGV 99051	54.16	22.23	34.16	44.61	12.95	2.51	0.79
236	ICGV 99052	54.87	22.68	35.13	42.94	13.12	2.56	0.84
237	ICGV 00246	54.53	23.01	34.33	44.09	13.15	2.57	0.80
238	ICGV 00248	56.32	21.38	34.34	44.95	12.88	2.74	0.78
239	ICGV 01361	51.03	21.58	36.81	41.50	12.74	1.72	0.90
240	ICGV 02434	50.14	23.29	37.79	40.02	12.46	2.30	0.96
241	ICGV 04087	54.16	22.74	32.46	44.81	13.56	2.44	0.74
242	ICGV 06175	50.45	22.38	38.33	39.70	12.68	2.19	0.99
243	ICGV 97116	50.04	20.75	45.86	34.79	10.79	2.15	1.34
244	ICGV 97128	56.99	20.08	33.57	45.53	13.17	2.63	0.76
245	ICGV 98184	51.12	21.99	37.14	42.74	12.80	2.13	0.88
246	ICGV 00068	50.02	23.85	39.73	39.86	11.79	2.20	1.02
247	ICGV 01495	52.05	21.93	41.10	38.07	12.19	2.32	1.10
248	ICGV 05057	51.75	22.10	33.92	44.03	13.50	2.10	0.77
249	ICGV 07168	49.84	23.51	42.61	36.39	11.84	2.46	1.19
250	ICGV 01265	50.82	22.16	40.79	37.78	12.93	2.42	1.10
251	ICGV 98105	54.43	21.32	32.09	46.76	13.48	1.91	0.69
252	ICGV 99160	51.97	23.24	35.95	43.57	13.00	1.85	0.84
253	ICGV 02323	50.53	24.21	36.59	42.12	12.82	1.80	0.89
254	ICGV 04115	51.62	22.88	36.44	42.80	12.48	2.03	0.87
255	ICGV 05036	51.68	23.09	35.36	43.60	13.21	1.75	0.82
256	ICGV 06042	51.88	23.93	37.04	40.23	13.12	2.23	0.94
257	ICGV 86564	48.94	23.99	46.57	33.30	10.81	3.19	1.41
258	ICGV 98432	50.51	22.18	47.30	34.47	10.62	2.22	1.41
259	BAU 13	48.66	22.91	44.80	34.71	11.53	2.33	1.31
260	ICGV 87846	50.87	23.38	35.99	42.34	13.03	2.26	0.87
261	ICR 48	48.22	23.71	46.28	33.33	10.86	2.31	1.43
262	ICGV 86699	54.84	22.12	50.60	32.55	12.59	1.37	1.64
263	ICGV 98373	48.68	24.13	38.48	40.50	11.98	1.87	0.96
264	ICGV 97115	50.26	21.36	40.51	37.73	12.45	2.25	1.09
265	ICGV 06040	54.78	24.21	33.89	44.61	13.49	2.69	0.78
266	ICGV 06099	54.72	22.08	36.56	42.52	13.12	2.60	0.89
267	CS 39	50.63	23.45	39.88	38.99	12.28	2.31	1.04
268	ICGV 05032	52.03	21.67	39.08	40.25	12.72	1.97	1.03
269	ICGV 05141	54.72	21.24	45.64	34.64	11.94	2.32	1.35
270	ICGV 07359	46.72	25.09	43.30	34.33	12.29	2.35	1.32
271	ICGV 07368	44.89	25.48	42.56	35.28	12.33	2.00	1.23
272	ICGV 06110	44.58	26.25	43.75	34.37	12.51	1.80	1.30
273	ICGV 06188	47.51	25.14	48.07	32.65	10.76	1.70	1.49
274	ICGV 00440	48.31	22.85	43.91	35.34	11.41	2.65	1.27
275	ICGV 86352	50.06	22.81	44.80	36.51	11.10	1.86	1.27
276	ICGV 09112	48.34	22.65	44.96	35.24	11.60	1.68	1.28

Entry No	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
277	ICGV 93920	46.97	22.89	42.75	36.71	11.67	2.00	1.21
278	ICGV 93216	46.36	22.34	44.75	35.59	10.95	1.95	1.28
279	ICGV 88438	50.94	21.91	47.07	34.48	10.61	2.14	1.41
280	ICG 11337	54.23	21.40	51.62	31.67	12.54	1.49	1.72
281	49 × 37-90	53.69	20.55	40.87	40.42	11.98	2.42	1.03
282	49 M-2-2	48.99	23.99	44.44	35.61	11.36	1.84	1.27
283	49 M- 1-1	48.04	23.94	36.70	40.85	13.30	1.83	0.92
284	TG 19	53.66	23.27	40.01	40.10	11.88	2.42	1.01
285	TG 39	47.12	23.22	46.27	34.45	11.37	1.49	1.36
286	TG LPS 3	47.59	23.55	46.34	34.30	11.33	1.54	1.38
287	26 × M-223-1	50.71	23.91	38.58	40.24	12.31	2.18	0.99
288	SPS 2	54.77	21.36	50.65	32.39	12.54	1.29	1.62
289	SPS 3	50.74	22.16	44.76	36.46	11.20	1.82	1.24
290	SPS 6	49.78	22.63	44.00	37.22	11.11	1.72	1.19
291	SPS 7	54.02	22.09	48.95	33.86	12.33	1.49	1.49
292	SPS 8	54.85	21.95	49.22	33.91	12.68	1.40	1.50
293	SPS 11	55.45	24.38	38.49	40.78	12.44	2.88	0.98
294	SPS 15	54.67	20.81	50.74	32.66	12.22	1.62	1.63
295	SPS 20	54.21	22.96	51.97	31.40	12.42	1.37	1.71
296	SPS 21	56.58	18.91	48.63	34.23	12.83	1.45	1.44
297	ICGV 03128	53.30	24.10	37.20	40.94	12.91	2.38	0.94
298	TMV 2 NLM	49.70	24.02	40.75	39.38	11.87	1.77	1.06
299	ICG 1668	52.04	21.93	42.65	37.90	11.73	2.00	1.15
300	ICG 8285	48.84	22.89	41.83	36.71	12.08	1.92	1.15
301	ICG 11426	53.96	22.19	52.43	29.96	12.44	1.53	1.76
302	ICGV 02290	49.97	22.69	43.24	35.79	11.99	2.26	1.28
303	ICGV 02446	53.02	23.64	37.46	40.07	12.74	2.84	0.95
304	ICG 156 (M 13)	47.34	22.63	47.09	33.04	10.62	1.99	1.44
305	ICGS 76	50.92	22.18	39.79	39.61	12.29	2.07	1.03
306	ICG 5891	50.90	21.44	43.30	36.92	11.49	2.01	1.20
307	CSMG 84-1	46.95	22.32	45.14	34.56	11.59	1.40	1.32
308	ICG 111	49.85	23.66	40.77	38.29	12.31	2.12	1.07
309	ICG 14834	49.57	22.58	45.07	34.63	11.36	1.89	1.33
310	ICG 11322	48.10	23.06	36.79	42.51	12.43	1.74	0.88
311	ICG 532	50.36	21.30	44.89	34.84	11.62	1.83	1.33
312	ICG 12509	54.07	23.90	49.54	32.76	12.06	2.13	1.60
313	ICG 12672	53.49	22.25	45.24	36.24	13.67	1.09	1.29
314	ICG 10185	49.75	22.51	43.93	35.57	11.51	2.00	1.24
315	ICG 2773	48.61	21.85	43.23	35.61	11.72	1.73	1.28
316	ICG 3027	50.84	22.71	40.01	38.26	12.74	2.00	1.17
317	ICG 5745	47.38	21.50	49.10	31.07	10.65	2.00	1.64
318	ICG 14482	58.50	20.98	57.40	28.64	10.84	1.97	2.11
319	ICG 4527	49.58	23.92	40.37	39.93	11.53	2.10	1.06
320	ICG 4343	48.31	22.74	43.22	35.54	11.83	1.58	1.24
321	ICG 13895	49.06	23.63	40.61	38.44	12.08	1.92	1.10
322	ICG 5663	50.16	22.45	42.53	37.38	11.95	1.85	1.20
323	ICG 721	49.25	22.13	40.26	39.55	11.77	1.98	1.02
324	ICG 12276	51.17	22.47	53.74	26.11	11.44	2.16	2.13
325	ICG 875	48.11	22.67	42.06	36.51	12.26	1.95	1.17
326	ICG 14475	56.03	21.84	54.22	32.18	10.66	2.03	1.73
327	ICG 15190	49.02	22.47	42.19	36.88	12.21	1.82	1.16
328	ICG 12370	48.72	23.23	41.31	37.39	11.80	1.72	1.13
329	ICGV 86325	50.74	20.97	45.52	35.19	11.46	1.97	1.31
330	ICG 5662	51.48	20.84	41.10	39.27	11.64	2.16	1.08
331	ICG 9961	50.13	20.79	46.44	33.79	11.24	1.81	1.38
332	ICG 14466	48.73	23.19	43.39	35.62	12.03	1.84	1.25

Entry No	Genotype	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)	Palmitic acid (%)	Stearic acid (%)	O/L ratio
333	ICG 3053	50.24	22.82	41.56	37.24	12.15	1.85	1.15
334	ICG 6766	49.39	22.73	43.22	35.76	11.89	2.08	1.23
335	ICG 2381	58.97	21.13	44.09	40.11	8.28	3.97	1.20
336	ICG 2857	47.06	25.02	44.47	34.78	11.61	1.72	1.29
337	ICGV 13238	49.69	22.40	42.82	37.75	11.46	1.59	1.14
338	ICGV 13241	50.56	22.33	42.14	38.45	11.50	1.71	1.10
339	ICGV 13242	49.66	23.26	42.43	38.26	11.66	1.58	1.13
340	ICGV 13245	49.93	22.16	44.15	36.79	11.48	1.56	1.21
Mean		**51.18**	**22.67**	**41.91**	**38.21**	**11.95**	**2.07**	**1.17**
CV (%)		**1.99**	**4.39**	**3.98**	**3.72**	**2.59**	**16.44**	**8.56**
LSD at 5 % level		**2.83**	**2.69**	**4.57**	**3.90**	**0.84**	**0.46**	**0.06**

APPENDIX XII

Weekly weather data during the crop season recorded at ICRISAT, Patancheru during rainy and post rainy season 2015-16

Latitude: 17º53’N **Longitude: 78º27 ’E** **Altitude: 545 MSL**

Week No.	Month	Rainfall (mm)	Temperature(ºC)		Relative humidity (%)	
			Min	Max	At 07:17 hrs.	At 14:17 hrs.
Rainy 2015						
25	June	16.80	22.26	30.46	87.56	63.28
26	June	15.00	23.78	33.28	79.70	52.28
27	July	0.00	24.03	34.84	75.29	43.57
28	July	29.60	24.53	34.89	76.14	44.42
29	July	15.00	22.82	32.22	84.29	58.42
30	July	1.19	22.48	32.74	83.14	53.14
31	August	2.60	22.57	32.60	83.14	51.71
32	August	25.60	22.48	31.30	89.56	64.85
33	August	45.39	22.14	29.28	92.29	71.56
34	August	38.60	21.94	30.62	91.43	64.56
35	August	27.19	22.28	30.17	88.43	70.29
36	September	32.00	22.19	32.49	90.29	56.71
37	September	95.20	21.41	29.26	95.43	75.85
38	September	44.79	21.57	30.62	92.29	67.56
39	September	1.00	21.94	32.06	91.14	56.14
40	October	13.59	21.05	31.91	92.56	54.57
41	October	40.00	19.92	32.67	83.43	38.14
42	October	0.00	19.51	32.53	91.14	45.14
43	October	0.00	17.80	32.49	90.56	40.00
44	November	10.00	19.73	31.51	92.14	48.57
45	November	0.00	17.05	31.53	86.43	38.00
46	November	0.00	14.50	30.80	88.56	36.85
47	November	0.30	18.37	29.76	84.85	54.28
48	November	2.20	17.62	30.80	89.29	42.42
49	December	0.00	14.57	29.94	90.00	44.00
50	December	0.00	17.03	32.71	91.56	36.42
51	December	0.00	16.39	32.68	91.85	32.57
52	December	0.00	9.63	30.48	83.87	28.75
Total/Mean		**456.05**	**20.06**	**31.67**	**87.73**	**51.22**
Post-rainy 2015-2016						
1	January	0.00	11.42	30.91	91.43	37.28
2	January	0.00	11.10	29.76	87.00	39.14
3	January	0.20	16.53	29.89	80.56	40.71
4	January	0.00	14.40	29.94	78.14	38.85
5	January	0.00	12.50	34.20	77.56	27.42
6	February	0.00	16.73	33.53	80.70	29.71
7	February	0.00	18.10	33.57	77.14	29.00
8	February	0.00	18.00	36.29	73.56	28.14
9	February	0.00	20.85	33.89	79.87	39.63
10	March	0.00	20.30	35.82	68.85	32.00
11	March	0.00	21.94	37.28	71.56	24.00
12	March	0.00	20.14	38.67	65.43	19.42
13	March	4.40	21.62	38.17	69.29	22.28
14	April	0.00	24.08	39.50	58.14	20.28
15	April	0.00	24.85	40.09	54.42	19.00
16	April	0.40	26.69	40.89	63.00	19.57

Week No.	Month	Rainfall (mm)	Temperature(ºC)		Relative humidity (%)	
			Min	Max	At 07:17 hrs.	At 14:17 hrs.
17	April	5.70	25.23	41.24	51.28	26.57
18	May	76.79	23.91	39.86	66.85	26.57
19	May	69.20	22.46	35.99	78.14	36.14
20	May	20.19	24.33	36.60	79.43	40.71
21	May	25.80	25.71	39.36	65.70	30.71
22	May	36.20	24.71	37.39	75.43	38.28
23	June	40.79	21.60	32.53	90.85	57.28
24	June	8.19	23.57	33.82	78.70	49.57
25	June	10.40	21.82	31.26	89.70	63.85
Total/Mean		**298.26**	**20.76**	**34.59**	**76.77**	**39.82**

APPENDIX XIII

Daily weather data during the crop season recorded at Jalgoan during rainy season 2015

Latitude: 21^{0}03 ‘N **Longitude: 75^{0}34 ‘E** **Altitude: 201 MSL**

Week No.	Month	Rainfall (mm)	Temperature (^{0}C)		Relative Humidity (%)	
			Min	Max	At 07:17 hrs.	At 14:17 hrs.
22	June	0.00	27.83	42.90	68.71	30.57
23	June	0.00	27.31	40.70	63.29	32.43
24	June	40.70	25.06	34.50	82.00	63.43
25	June	38.80	25.06	34.09	81.00	64.86
26	June	5.60	25.26	35.57	78.00	47.86
27	July	0.00	25.94	37.50	72.29	41.57
28	July	0.00	26.34	36.50	69.57	43.57
29	July	4.90	25.37	33.90	78.29	62.71
30	July	47.10	24.49	32.60	84.43	66.14
31	August	66.00	24.47	32.09	84.86	66.71
32	August	19.40	24.06	31.40	87.00	75.14
33	August	23.00	24.07	31.90	85.86	72.71
34	August	0.00	23.11	34.30	80.43	63.14
35	August	26.30	22.94	33.40	85.00	68.00
36	September	0.00	23.90	35.00	76.00	50.00
37	September	23.00	23.56	34.31	83.43	63.29
38	September	125.40	23.69	32.44	82.57	64.29
39	September	0.00	22.50	34.10	79.00	51.00
40	October	0.00	23.00	36.00	73.00	46.00
41	October	3.80	22.20	37.30	76.00	36.00
42	October	0.00	21.31	37.04	73.86	37.43
43	October	1.00	22.31	36.19	74.71	42.00
44	November	3.00	19.71	33.31	70.86	44.14
45	November	0.00	19.14	34.37	65.00	43.57
46	November	0.00	16.91	34.04	65.00	39.00
47	November	0.60	17.53	31.83	62.00	42.86
48	December	0.00	17.51	33.87	63.14	40.43
49	December	0.00	14.20	32.67	59.00	37.14
50	December	0.00	15.03	31.59	56.57	40.43
51	December	0.00	12.89	30.69	59.29	44.29
52	December	0.00	9.60	29.80	70.00	37.86
Total/mean		**428.60**	**21.82**	**34.38**	**73.88**	**50.28**

APPENDIX XIV

Daily weather data during the crop season recorded at Aliyarnagar during rainy season 2015

Latitude: 10^{0}29 ‘N **Longitude: 76^{0}56 ‘E** **Altitude: 288 MSL**

Weak No.	Month	Rainfall (mm)	Temperature (^{0}C)		Relative humidity (%)	
			Min	Max	At 7.20 am	At 2.20 pm
23	June	0.00	22.67	35.33	83.00	53.67
24	June	62.40	21.93	34.29	86.86	58.00
25	June	13.40	22.36	34.07	88.86	54.43
26	June	30.20	22.79	31.14	77.14	48.86
27	July	56.20	22.00	33.46	81.75	60.75
28	July	0.00	22.71	33.86	80.57	50.57
29	July	5.20	21.64	34.07	84.71	53.00
30	July	55.20	21.07	31.86	85.43	57.57
31	August	10.20	20.42	33.17	84.00	63.50
32	August	0.00	21.50	34.70	89.80	59.20
33	August	10.40	20.64	33.50	88.14	65.00
34	August	54.80	20.21	32.36	89.71	68.29
35	August	26.51	20.25	33.33	85.33	68.33
36	September	0.00	20.50	34.00	87.00	74.50
37	September	40.90	19.43	32.50	91.00	86.71
38	September	3.00	19.93	33.86	91.00	81.00
39	September	1.00	21.75	33.50	93.83	75.83
40	October	4.60	21.33	34.25	90.00	76.00
41	October	36.00	20.79	32.14	90.14	72.71
42	October	4.20	19.79	33.79	90.00	77.43
43	October	0.00	20.08	34.25	90.00	73.67
44	November	21.20	20.33	33.17	88.50	64.00
45	November	28.80	19.38	29.63	94.25	86.50
46	November	49.20	19.14	30.36	91.86	79.71
47	November	33.20	19.50	29.67	89.00	70.67
48	November	132.80	19.75	29.00	91.67	62.33
49	December	4.00	17.75	30.00	91.00	78.50
50	December	106.63	19.00	27.29	92.29	83.57
51	December	15.40	18.92	28.17	94.83	67.00
52	December	0.00	15.25	31.42	87.17	70.67
Total/Mean		**805.44**	**20.43**	**32.40**	**88.29**	**68.07**

VITAE

Name of author:	**Sunil Chaudhari**
Date of birth:	**09/07/1988**
Place:	**Khargone, Madhya Pradesh**

Academic background

Course	School/college	Board/ University	Year of passing
Ph.D. Genetics and Plant Breeding	College of Agriculture, Jabalpur	J.N.K.V.V., Jabalpur (M.P.)	Pursuing (2013-17)
M.Sc. (Ag.) Genetics and Plant Breeding	R. A. K. College Of Agriculture, Sehore	R.V.S.K.V.V., Gwalior	2013
B.Sc. (Ag)	College Of Agricultural Indore	R.V.S.K.V.V., Gwalior (M.P.)	2011
Higher secondary	Govt. H.S. School Bedia (M.P.)	M.P. Board of Education, Bhopal (M.P.)	2006
High School	Prabhat Convent School, Bedia (M.P.)	M.P. Board, Bhopal (M.P.)	2004

Publications

Sunil Chaudhari, Khare D, Sundravadana S, Singh SM, Murali TV and Janila P. 2017. Genetic analysis of foliar disease resistance, yield and nutritional quality traits in groundnut. Electronic Journal of Plant Breeding (Accepted).

Sunil Chaudhari, Khare D, Sundravadana S, Singh SM, Murali TV. 2017. Capturing genetic diversity in genomic selection panel of groundnut for foliar disease resistance, yield and nutritional quality traits. International Journal of Genetics. 9(5):278-283

Sunil Chaudhari, Tikle AN, Uttamchand, Saxena KB and Rathore A. 2015. Stability of male sterility and fertility restoration in pigeonpea. Journal of Crop Improvement. 29: 269-280

Sunil Chaudhari, Tikle AN and Saxena KB. 2014. Effect of temperature on expression of male sterility in CMS lines of pigeonpea. Progressive Research 9: 69-71.

Achievements

- Completed Master and Doctoral thesis research at International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Hyderabad, India.
- Awarded with Best Research Scholar Award by Indian Academic Researchers Association, Tamil Nadu, India in 2016.
- Qualified National Eligibility Test (ASRB-NET) in 2014.