

**Research Article****Genetic analysis of foliar disease resistance, yield and nutritional quality traits in groundnut****Sunil Chaudhari^{1,2}, D. Khare², S. Sundravada³, Murali T. Variath¹, Surendra S. Manohar¹ and P. Janila¹**¹International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Hyderabad, Telangana, India²Jawaharlal Nehru Krishi Vishwa Vidyalaya (JNKVV), Jabalpur, India³Coconut Research Station, Tamil Nadu Agricultural University (TNAU), Aliyarnagar, Tamil Nadu, India**E-mail:** schoudhary612@gmail.com

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Abstract

A set of 340 diverse groundnut genotypes included in Genomic Selection Panel (GSP) was used to evaluate genetic parameters and trait associations for resistance to rust and late leaf spot (LLS) along with yield and nutritional quality traits. The findings revealed high genetic variability coupled with high heritability and genetic advance as percent of mean (GAM) for resistance to both the diseases and yield traits, whereas low variability for nutritional quality traits with high heritability and low GAM. Disease severity scores for rust and LLS at 90 days after sowing (DAS) were negatively associated with yield, indicating pod yield penalty, thus deploying host-resistance for rust and LLS is a good strategy to plug the pod yield losses and reduce the input cost. It is possible to simultaneously improve the number of pods per plant and hundred kernel mass that contribute to pod yield as no trade-offs were detected between them. The association of oil and protein content with pod yield showed no tradeoffs, suggesting the possibility of simultaneous improvement of pod yield either with high oil or protein content. In breeding programs that target development of groundnut varieties to meet two distinct end-uses, oil milling, and food and confectionery, selection for either high oil (for oil purpose) or high protein and low oil (food/confections) will be efficient, as an inverse association between oil and protein content was observed. The use of disease score at 90 DAS for rust and LLS is effective and optimizes resources to make selection decisions in breeding as positive association among disease severity scores at different periods (75, 90 and 105 DAS) was observed.

Key words

Groundnut, Heritability, Variability, Correlation coefficient, Foliar disease resistance

Introduction

The cultivated groundnut (*Arachis hypogaea* L.; Family Leguminosae), native to Brazil in South America is one of the most important oilseeds and food crop of the world. It is cultivated in more than 100 countries on 26.54 m hectare area with an annual production of 43.91 m tonnes and productivity of 1654 kg/ha (FAOSTAT, 2014). In India, groundnut is grown on 4.68 m hectare area with the production of 6.55 m tonnes (FAOSTAT, 2014). The productivity of groundnut in India is low (1399 kg/ha) compared to Israel (7389 kg/ha), USA (4397 kg/ha), China (3492 kg/ha) and Argentina (2848 kg/ha) (FAOSTAT, 2014). Groundnut kernels are regarded as healthy foods as their nutrient profile is balanced (Arya *et al.*, 2016). The kernels contain 48-50% oil, 10-20% carbohydrates, and 25-28% easily digestible protein, and provides 564 kcal of energy for every 100 g of kernels (Arya *et al.*, 2016). In addition, groundnut is a rich source of several micronutrients and health-enhancing components, including minerals, antioxidants, and vitamins along with some biologically active polyphenols, flavonoids, and isoflavones (Janila *et al.*, 2013, Arya *et al.*, 2016). Groundnut kernels with high Oleic/linoleic (O/L) acid ratio have extended shelf life and command a premium price in domestic and international markets. For oil purpose, cultivars with high oil content are preferred, whereas, for confectionary and food purposes

cultivars with low oil and high protein content are preferred.

Notwithstanding the narrow genetic base owing to its evolutionary origin from a single hybridization event, substantial progress has been made through conventional breeding approaches to improve the pod yield potential in groundnut cultivars, and tolerance to biotic and abiotic stresses. However, a wide gap exists between the genetic potential of the modern cultivars and realized yield and several factors other than the genetics of varieties contribute to the observed yield gap. Losses caused by biotic and abiotic stresses are the most important factors contributing to yield gap. Among the biotic stresses, foliar fungal diseases, late leaf spot (LLS) (caused by *Phaeoisariopsis personata* Berk and Curt) and rust (caused by *Puccinia arachidis* Speg.) are widespread and are major production constraints in groundnut growing regions. They together are responsible for the reduction of 50 to 70% pod yield depending on severity of the infection besides having an adverse effect on seed quality (Subrahmanyam *et al.*, 1984, McDonald *et al.*, 1985). Development of LLS and rust resistant groundnut cultivars is a major breeding objective in groundnut to sustain the pod yield in rainfed ecologies of Africa and Asia and reduce the input cost.

Genetic information of target traits and their association with other traits including

environmental factors has been quite useful in breeding varieties with improved yield, nutritional quality and resistance/tolerance to biotic and abiotic stresses in groundnut. Genetic studies on nutritional parameters in groundnut are limited. Presence of extensive variation among the genotypes for the trait of interest is a critical aspect of such studies. Earlier studies have reported on genetic variation and heritability for traits like LLS and rust (Narasimhulu *et al.*, 2013), yield (Shridevi *et al.*, 2014) and nutritional quality traits (Sarvamangla *et al.*, 2010). Association between the different traits was also reported (John *et al.*, 2009). However, the number of genotypes involved in these studies was limited and in most cases, the genotypes differed only for one or few traits. Genetic studies carried out on a set of genotypes that have been selected for different important target traits, disease resistance, drought tolerance, different maturity groups, bold-seeded types and nutritional quality trait can provide more reliable and comprehensive information due to diversity in the genetic background, which allows for more complex interactions between genes and also with the environment. Hence, in the present study, a genomic selection panel (GSP) comprising a set of 340 diverse groundnut genotypes was used to estimate genetic parameters including heritability in broad sense and genetic advance for resistance to rust and LLS, nutritional quality, pod yield and its contributing traits in groundnut. Trait associations between important target traits were also studied.

Materials and methods

A collection of 340 diverse groundnut genotypes included in GSP, belonging to 21 geographically diverse countries and representing diversity for important target traits such as foliar disease resistance, drought tolerance, maturity duration, seed size, and pod, seed and plant morphological traits. The GSP includes genotypes from all six varieties of cultivated groundnut *viz.*, *vulgaris* (212), *fastigiata* (10), *peruviana* (4), *aequatoriana* (1), *hypogaea* (111), *hirsuta* (1) and a single genotype of unknown botanical group. These genotypes were evaluated at experimental field of Coconut Research Station, Aliyarnagar, Tamil Nadu, India (10°29' N, 76° 58' E, 288 m MSL) for two major foliar fungal diseases i.e. rust and LLS, yield and nutritional quality traits during rainy season of 2015. The trial was planted in Alpha Lattice Design (incomplete block design) with two replications; each replication was divided into 20 equal sized blocks with 17 genotypes in each to reduce intra-block variation and maintain homogeneity in the experimental field. Each entry was planted in a single row of 4 m length with inter- and intra-row spacing of 30 and 10 cm, respectively. Aliyarnagar is disease hot spot location, however, to further ensure inoculum load screening was conducted in disease screening

nursery. Infector rows of a highly susceptible cultivar, TMV 2 were planted around the experimental plot, and in between the blocks to maintain the disease pressure during crop growth stage. The genotypes were evaluated for LLS and rust through visual observation and a modified 1 to 9 point scale as given by Subrahmanyam *et al.* (1995). A disease score of 1 indicates resistance with no or very little infection, while a score of 9 represents >80% leaves severely infected and defoliated in case of LLS, whereas burning like appearance in case of rust. Scoring of the genotypes for rust and LLS was carried out at three different times during crop growth *viz.*, 75, 90 and 105 days after sowing (DAS). Observations were also recorded for days to 50% flowering, plant height, number of primary branches, number of mature pods per plant, pod and seed yield per plant, shelling percent, hundred seed weight, days to maturity and pod yield per hectare. Nutritional quality traits such as oil and protein content along with four major fatty acids *i.e.*, oleic, linoleic, palmitic and stearic acid were estimated using near infrared reflectance spectroscopy (NIRS). Standard agronomic management practices were followed to raise a good crop with optimum plant population. The experimental field received 60 kg phosphorus pentoxide (P₂O₅) per hectare as a basal, pre-emergence application of pendimethalin @ 1 kg active ingredient per ha and irrigation soon after planting and subsequently when needed. Gypsum @ 400 kg/ha was applied to the experimental field at peak flowering stage. Chemical spraying was done to prevent damage from insects as and when required whereas no preventive measures were used to control foliar fungal diseases.

Analysis of variance was done using general linear mixed model (GLM) through proc glm function of SAS version 9.2 (SAS Institute Inc, 2013) and genetic parameters such as genotypic and phenotypic coefficient of variation (GCV & PCV), heritability and genetic advance were calculated using partitioned variance component from ANOVA in Microsoft Excel. Best linear unbiased predictions (BLUPs) or adjusted means were estimated for each genotype for all the traits, except disease severity scores of rust and LLS, because higher severity score among both the replications was considered as the final score of genotype. Genotypic and phenotypic association among disease resistance, yield, and nutritional quality traits was done using META-R version 5.0.

Results and discussion

ANOVA revealed significant differences among genotypes for disease scores of rust and LLS at 75, 90 and 105 DAS, agronomic traits, yield and nutritional quality traits (Table 1) indicating substantial variability in the population in part, attributed to diverse pedigree of the advanced breeding lines, botanical types, and collection of

genotypes from 21 different geographical locations that were involved in the constitution of the GSP. 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, Narasimhulu *et al.*, 2013), yield and its contributing traits (Shridevi *et al.*, 2014), and nutritional quality traits (Sarvamangla *et al.*, 2010, Channayya *et al.*, 2011).

Genetic variability and heritability, the key parameters that determine the response to selection or genetic gain in a breeding program are assessed in the GSP. The genotypic and phenotypic coefficient of variation (GCV and PCV), heritability in broad sense (h^2) and genetic advance as percent of mean (GAM) for all the traits are summarized in Table 1. The GCV and PCV values for resistance to LLS (7.54 & 10.40%) and rust (9.96 & 12.05%) were low to moderate at 105 DAS, moderate to high at 90 DAS (15.14 & 16.53% for LLS and 19.67 & 21.22% for rust) and moderate to high at 75 DAS (17.06 & 23.65% for LLS and 26.43 & 30.66% for rust). Higher PCV values compared to GCV for resistance to LLS and rust indicate the influence of environment on disease scores. Heritability in broad sense ranged from 68.3 to 85.9% for rust, and from 52.0 to 83.9% for LLS, while the GAM was 16.9 to 46.9% for rust and 11.3 to 28.5% for LLS. High heritability along with moderate to high GAM at 90 DAS indicated a strong response to selection governing resistance to these two diseases as was reported earlier (Narasimhulu *et al.*, 2013).

Among the yield and its associated traits, higher GCV and PCV values were observed for number of mature pods per plant (31.83 & 36.67%), pod yield per plant (32.30 & 37.65%), seed yield per plant (33.30 & 38.92%), hundred seed weight (22.68 & 23.51%) and pod yield per hectare (43.92 & 49.71%). Higher PCV values than GCV values for the yield traits suggest the influence of environment on these traits. Heritability was high for all the yield traits and ranged from 65.2 to 93.0% while the GAM ranged from as low as 8.4% for days to maturity to 79.9% for yield. High heritability for yield and its associated traits was observed earlier in different sets of populations (Hariprasanna *et al.*, 2008, Shridevi *et al.*, 2014).

Range of variation was observed among the genotypes for days to 50% flowering (26-35 days), number of primary branches per plant (3-8), shelling percent (39-71%), days to maturity (101-121 days) and nutritional quality traits such as, oil content (45-64%), protein content (16-28%), oleic acid (29-74%), linoleic acid (5-51%) and palmitic acid (7-15%) but the GCV and PCV values of these traits were generally low (Table 1). This 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. Heritability for the nutritional quality traits ranged from 40.5% for protein content to 68.7% for palmitic acid content but the GAM values were low (3.83-27.69%) which indicated that selection may not be effective for these traits. Genetic variability for nutritional quality traits in groundnut was also reported by others (Dwivedi *et al.*, 1993, Sarvamangala *et al.*, 2010, Channayya *et al.*, 2011). Dwivedi *et al.*, (1993), however, targeted breeding efforts to improve nutritional quality are limited. High heritability coupled with low GAM was earlier reported for oil and protein content along with oil quality traits (Channayya *et al.*, 2011).

The present study identified disease resistant genotypes with disease severity score of <3 at 90 DAS for LLS and rust; 67 genotypes were resistant to LLS, 87 were resistant to rust, and 50 were resistant to rust and LLS (Figure 1). The GSP includes 36 advanced breeding lines (ICGVs) from ICRISAT, bred for foliar fungal disease resistance, and all these lines were resistant to rust and LLS in the present study. Further confirmation of the disease reaction over the environments and seasons, and evaluation for pod yield will enable the use of disease resistant genotypes in breeding and/or for cultivation. The genotypes ICGV 02038, TG LPS 3, Faizpur 1-5, and ICGV 01276 recorded high protein content of 26-28% among the GSP. Significant effect of environment and genotype \times environment interactions for protein content in groundnut (Dwivedi *et al.*, 1993, Upadhyaya *et al.*, 2012) indicated the need to test the performance of the genotypes in different growing environments before using in breeding programs. One genotype in the GSP, SunOleic 95R, an introduction from the USA recorded high oleic acid content of 74%, indicating a strong need to breed high oleic groundnut lines.

Genotypic and phenotypic correlation between traits: Genotypic and phenotypic correlations between some important pairwise traits are given in Table 2. Pod yield per hectare had significant positive genotypic and phenotypic association with other yield component traits like number of pods per plant ($r_g=0.49$ & $r_p=0.40$), pod yield per plant ($r_g=0.60$ & $r_p=0.49$) and seed yield per plant ($r_g=0.57$ & $r_p=0.47$). Positive association of yield with number of mature pods per plant and hundred kernel weight was reported John *et al.* (2009). Thus, improvement in pod yield can be expected through selection for number of mature pods per plant and size of the kernels, and the selection can

be simultaneous as the number of pods per plant and hundred kernel mass are not associated.

Disease severity scores of both LLS and rust at 90 DAS had a significant negative association with yield ($r_g=-0.45$ & $r_p=-0.37$ with LLS and $r_g=-0.58$ & $r_p=-0.47$ with rust), which was also reported by others (Narasimhulu *et al.*, 2013, Sudini *et al.*, 2015). The pod yield of resistant cultivars with a disease score for rust and LLS of ≤ 3 varied from 747 to 3809 kg/ha, whereas in susceptible cultivars with disease score of ≥ 7 for both the diseases, it varied from 436 to 1247 kg/ha. Yield penalty due to the incidence of rust and LLS is common for rainy season crop, and the extent of loss is determined by the severity of the disease. Thus, host-resistance is critical to improve pod yield potential of cultivated groundnut by plugging the loss and reduce the input cost. Recently, near isogenic lines of groundnut for rust and LLS were developed at ICRISAT using marker assisted backcrossing program and these lines recorded 39-79% improved pod yield over the recurrent parents (Janila *et al.*, 2016a).

Resistance to rust and LLS showed a strong positive association with each other ($r_g=0.84$ & $r_p=0.73$) indicating that resistance to both the disease can be incorporated by single breeding effort. A significant positive association among LLS and rust scores (0.48 to 0.60) was also reported by Anderson *et al.* (1990). 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). Significant positive association was also observed between disease severity scores of LLS at 90 DAS with 75 DAS ($r_g=0.93$ & $r_p=0.69$), and 105 DAS ($r_g=0.87$ & $r_p=0.66$). Similarly, disease scores of rust at 90 DAS also had positive association with rust scores at 75 ($r_g=0.95$ & $r_p=0.82$), and 105 DAS ($r_g=0.90$ & $r_p=0.79$). 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 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 three observations at 75, 90 and 105 DAS.

Negative significant association was observed between severity scores of both the diseases and days to maturity but the extent of association was low (~ 0.4). High level of resistance to foliar fungal diseases is required in groundnut varieties belonging to all maturity groups. For pod yield per hectare, association with oil content is positive ($r_g=0.20$ & $r_p=0.14$), 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. Oil content had significant negative association with protein content ($r_g=-0.61$ & $r_p=-0.54$) indicating that simultaneous improvement for both these traits is not possible in groundnut. In groundnut breeding program selections are carried out either for high oil (for oil milling) or high protein and low oil (for food and confectionary uses) to meet two distinct end-uses. Similar observations were also reported by others (Dwivedi *et al.*, 1990, Sarvamangla *et al.*, 2010). Hundred seed weight had significant negative association with oil content ($r_g=-0.34$ & $r_p=-0.20$), and significant positive association with protein content ($r_g=0.36$ & $r_p=0.20$). However, the magnitude of association is low which offers an opportunity to develop cultivars that combine high hundred seed 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).

Among the oil quality traits, high oleic acid content is important as it enhances the shelf-life of oil and food products made from high oleic groundnuts (Bachlava *et al.*, 2008). A strong negative association was observed between oleic acid and two other major fatty acids *viz.*, linoleic ($r_g=-0.95$ & $r_p=-0.95$) and palmitic ($r_g=-0.73$ & $r_p=-0.73$) 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 Oleic acid. The negative association between oleic and palmitic acid represents an increased rate of palmitic acid elongation to stearic acid, with rapid desaturation to oleic acid *via* $\Delta 9$ desaturase (Groff *et al.*, 1996).

Conclusions

The genetic variability for resistance to foliar fungal diseases, rust and LLS, and yield and nutritional quality parameters in the large GSP collection is a potential source to identify suitable genotypes for cultivation that combine high pod

yield potential with resistance to both the diseases, as well as select elite parents for recycling in the breeding programs to enhance genetic gains. From the collection of GSP, 50 genotypes were found to be resistant with disease score of <3 for rust and LLS at 90 DAS, of which 36 were advanced breeding were from ICRISAT suggesting the contribution of foliar fungal disease resistance breeding program at ICRISAT. Trait association studies generated information that would facilitate breeders in the process of selection decisions. Pod yield improvement can be targeted by simultaneous selection for higher number of pods per plant and large kernels. Absence of tradeoffs suggests simultaneous improvement of pod yield with either high oil content (for oil milling purpose) or low oil and high protein content (for food and confectionary purposes) to meet the need of targeted end-use. Disease severity scores recorded at 90 DAS is efficient to make selection decisions, and optimizes resources. The study revealed the need to breed for new high oleic groundnut varieties.

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Table 1. Analysis of variance, mean, range and genetic parameters for foliar disease resistance, yield and nutritional quality traits in a collection of 340 genotypes of GSP evaluated at Aliyarnagar, Tamil Nadu during 2015 rainy season

Traits	Analysis of Variance				Mean ± SE	Range	GCV (%)	PCV (%)	h ² (%)	GAM (%)
	Replication	Block(Rep)	Genotypes	Residual						
Degrees of freedom	1	38	339	301						
Foliar Disease resistance										
LLS 75	0.289**	0.006	0.015**	0.005	1.67±0.004	1.00-3.04	17.06	23.65	52.00	25.34
LLS 90	0.205**	0.004	0.025**	0.003	4.26±0.006	1.52-7.14	15.14	16.53	83.86	28.55
LLS 105	0.003	0.005	0.013**	0.004	6.49±0.004	2.93-8.52	7.54	10.40	52.64	11.27
Rust 75	0.239**	0.006	0.036**	0.006	2.09±0.007	1.00-4.56	26.43	30.66	74.29	46.93
Rust 90	0.118**	0.005	0.043**	0.004	4.48±0.008	1.00-7.53	19.67	21.22	85.95	37.57
Rust 105	0.045*	0.005	0.018**	0.004	6.41±0.005	1.42-9.05	9.96	12.05	68.26	16.95
Yield and its contributing traits										
Days to 50% flowering	21.18**	4.58**	8.56**	1.04	30.03±0.105	26-35	6.45	7.29	78.40	11.77
Plant height (cm)	735.86**	22.77**	60.41**	4.13	36.70±0.288	25.17-67.34	14.47	15.49	87.21	27.83
Number of primary branches	0.094**	0.008**	0.009**	0.002	4.93±0.038	3-8	8.82	10.92	65.22	14.68
Number of pods per plant	33.55	16.10**	50.78**	7.14	14.66±0.253	3-35	31.83	36.67	75.36	56.92
Pod yield per plant (g)	98.39	10.70	29.14**	4.43	10.88±0.191	3.61-29.03	32.30	37.65	73.60	57.08
Seed yield per plant (g)	21.41	3.90*	11.36**	1.76	6.57±0.119	2.15-17.21	33.30	38.92	73.18	58.68
Shelling percent	202.71**	9.47	57.06**	7.24	60.56±0.271	38-71	8.23	9.35	77.47	14.92
Hundred seed weight (g)	37.65	2.82	47.34**	3.14	32.60±0.400	19.64-66.22	22.68	23.51	93.05	45.06
Days to maturity	20.67	8.98*	113.05**	4.07	108±0.255	101-121	4.34	4.64	87.56	8.37
Yield (kg ha ⁻¹)	4965700.3**	138719.9	858484.8**	105842.7	1392.08±33.26	386-3809	43.92	49.71	78.05	79.92
Nutritional quality traits										
Oil content (%)	0.222	0.042	0.095**	0.03	53.47±0.146	44.99-64.22	2.51	3.38	54.93	3.83
Protein content (%)	0.01	0.11	0.13**	0.06	20.21±0.092	16.00-28.44	4.20	6.60	40.55	5.51
Oleic acid (%)	0.57	0.09	0.36**	0.08	42.06±0.267	29.38-74.38	5.80	7.19	65.11	9.64
Linoleic acid (%)	0.32	0.07	0.28**	0.06	39.68±0.216	5.30-51.25	5.22	6.49	64.56	8.63
Palmitic acid (%)	0.09	0.02	0.05**	0.01	11.65±0.051	7.50-14.88	4.07	4.91	68.66	6.94
Stearic acid (%)	0.19*	0.02	0.05**	0.02	2.18±0.021	0.68-3.61	9.11	11.89	58.61	14.36
O/L ratio	0.008	0.01	0.01**	0.01	1.11±0.017	0.58-14.03	16.28	19.72	68.15	27.69

*, ** Significant at 5 and 1 per cent level, respectively; GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; h²: heritability in broad sense; GAM: Genetic advance as per cent of mean; 75, 90, 105: Disease severity scores of rust and late leaf spot (LLS) at 75, 90 and 105 days after sowing (DAS)

Table 2. Genotypic and phenotypic association among important traits in 340 genotypes of Genomic Selection Panel (GSP) evaluated at Aliyarnagar, Tamil Nadu during 2015 rainy season

Traits	Trait associate with	r value	
		r_g	r_p
Pod yield per hectare (Kg/ha)	Disease severity score of Rust at 90 DAS	-0.58**	-0.47**
	Disease severity score of LLS at 90 DAS	-0.45**	-0.37**
	Number of mature pods per plant	0.49**	0.40**
	Pod yield per plant	0.60**	0.49**
	Seed yield per plant	0.57**	0.47**
	Oil content	0.20**	0.14**
	Protein content	0.03	0.02
Number of mature pods per plant	Pod yield per plant	0.81**	0.81**
	Seed yield per plant (g)	0.81**	0.80**
	Hundred seed weight	-0.11	-0.06
Pod yield per plant	Seed yield per plant (g)	0.97**	0.97**
	Protein content	-0.61**	-0.54**
Oil content (%)	Disease severity score of LLS at 90 DAS	-0.41**	-0.26**
	Disease severity score of Rust at 90 DAS	-0.36**	-0.26**
	Hundred seed weight (g)	-0.34**	-0.20**
Protein content (%)	Hundred seed weight	0.36**	0.20**
	Linoleic acid	-0.95**	-0.95**
Oleic acid content (%)	Palmitic acid	-0.73**	-0.73**
	O/L ratio	0.97**	0.97**
	Palmitic acid	0.61**	0.62**
Linoleic acid content (%)	O/L ratio	-0.99**	-0.99**
	Palmitic acid content (%)	O/L ratio	-0.66**
Stearic acid content (%)	Disease severity score of LLS at 90 DAS	-0.52**	-0.45**
	Disease severity score of Rust at 90 DAS	-0.57**	-0.52**
	Disease severity score of LLS at 75 DAS	0.93**	0.69**
Disease severity score of LLS at 90 DAS (1 to 9 scale)	Disease severity score of LLS at 105 DAS	0.87**	0.67**
	Disease severity score of Rust at 90 DAS	0.84**	0.73**
	Days to maturity	-0.45**	-0.39**
Disease severity score of Rust at 90 DAS (1 to 9 scale)	Disease severity score of Rust at 75 DAS	0.95**	0.82**
	Disease severity score of Rust at 105 DAS	0.90**	0.79**
	Days to maturity	-0.44**	-0.38**

** represents significant at <0.001 probability level; r_g = Genotypic correlation coefficient; r_p = Phenotypic correlation coefficient; LLS =late leaf spot; DAS= Days after sowing

Fig. 1. Frequency distribution of genotypes of Genomic Selection Panel for disease severity scores of late leaf spot and rust on a 9-point scale given by Subrahmanyam *et al.*, (1995)

