Genetic Resources of Pulse Crops – Present Status and Future Plans

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Abstract

Plant genetic resources (PGR) are essential for a sound and successful crop improvement programme and insurance against nature's vagaries. India has been considered a primary centre of diversity for urdbean, mothbean and pigeonpea; a secondary centre of diversity for cowpea, and regional (Asiatic) centre of diversity for crops like chickpea and mungbean. Several exploration missions have been undertaken for collection of available indigenous diversity in different legume crops especially in chickpea, pigeonpea, urdbean, mungbean, cowpea, peas, lentil, lathyrus, mothbean, horsegram and cowpea. About 42,425 accessions representing 26 pulse crops are stored at -20°C in long-term repository of National Gene Bank of NBPGR. Evaluation of germplasm has led to the release of more than 60% of total pulse varieties as direct selection from the germplasm in India. PGRs are also being used in hybridization programmes for genetic upgradation of cultivars as well as creation of new varieties. So far, 434 varieties have been developed in different pulse crops following this approach. However, due to rapid agro-ecological changes, many species, old and primitive cultivars, land races and their wild relatives are being eroded. Hence, concerted and systematic efforts for collection, conservation, evaluation, and utilization of germplasm need to be undertaken.

1. Introduction

Plant genetic resources (PGR) are required for a sound and successful crop improvement programme and insurance against nature's vagaries. Pulses are one of the important components of Indian farming system. They provide protein rich food; restore and maintain the soil fertility and also fit well in different cropping patterns. The important pulse crops grown in India are chickpea (*Cicer arietinum* L.), pigeonpea (*Cajanus cajan* L. Millsp.), mungbean (*Vigna radiata* L. Wilczek), urdbean (*Vigna mungo* L. Hepper), lentil (*Lens culinaris* Med.), pea (*Pisum sativum* L.), lathyrus (*Lathyrus sativus* L.), cowpea (*Vigna unguiculata* L. Walp.), mothbean (*Vigna aconitifolia* (Jacq.) Marechal), and frenchbean (*Phaseolus vulgaris* L.). Other pulse crops of minor importance grown in India are ricebean (*Vigna umbellata* (Thunb.) Ohwi and Ohashi), horsegram (*Macrotyloma uniflorum* (Lamb.) Verdc.), fababean (*Vicia faba* L.), and lablab bean (*Lablab purpureus* (L.) Sweet).

2. Pulse Crop Diversity

Pulses are widely distributed in different agro-ecological regions of the world. Among pulse crops, *Vigna* is the largest genera comprising seven subgenera and 150 species, which are naturally distributed across Africa and Asia. Subgenus *Ceratotropis* is mostly referred to as Asiatic *Vigna*. Lathyrus is also a large genus with 150 species followed by *Vicia* with 140 species. Primary centers of diversity of pulse crops are presented in Table 1.

Table 1: Number of species in different genera of pulses

Tribe	Genus	No. of species	Origin and primary centre of diversity
Phaseoleae DC	*Vigna*	150	Africa, Asia
	Dolichos	60	Africa, East Asia
	Phaseolus	50	America
	Cajanus	32	South Africa, South East Asia, and East Africa
	Macrotyloma	24	Tropical Africa and Asia
Cicereae Alef	*Cicer*	43	Central Asia, South West Asia and Mediterranean countries and Himalayas
Vicieae	*Lathyrus*	150	Europe, Asia and North America
(Adans.) DC	*Vicia*	140	Europe, Asia and North America
	Lens	5	Mediterranean countries and Ethiopia
	Pisum	2	Southern Europe, Mediterranean region and West Asia

Source: Van der Maesen and Somaatmadja (1989)

India is one of the 12 mega gene centres/regions of diversity of crop plants in the world (Zeven and Zhukovsky, 1975). Pulses are grown for diversified uses from time immemorial. *Pisum arvense, Lens* and *Lathyrus* were domesticated in India in Neolithic and Chalcolithic periods (Vishnu-Mittrre, 1974). India has been considered a primary centre of diversity for urdbean, mothbean and pigeonpea; a secondary centre of diversity for cowpea, and regional (Asiatic) centre of diversity for crops like chickpea and mungbean (Arora, 1988). The regions which are rich in pulse crops diversity in India are North-eastern region (Frenchbean, pigeonpea, ricebean, urdbean and winged bean); Gangetic Plains (chickpea, cowpea and mungbean); Indus Plains (chickpea, clusterbean, mothbean, and urdbean); western Himalayas including cold arid tracts (Frenchbean, lentil, peas and urdbean); eastern Himalayas (Frenchbean,

cowpea, peas and urdbean); eastern Peninsular region/eastern Ghats/Deccan (cowpea, horsegram, pigeonpea, mungbean and ricebean); and western Peninsular region/western Ghats/ Malabar (cowpea, horsegram, mungbean, pigeonpea and urdbean). The legume diversity in wild relative and related types of cultivated plants in India is estimated to about 31 species (Arora and Nayar, 1984). The ancient travellers, invaders and religious missionaries have also contributed significantly towards enriching the Indian gene centre by introduction of crops like Frenchbean and pea.

Though India is rich in genetic resources, there is severe threat to genetic diversity because of population explosion resulting in increased pressure on land for food and shelter. Due to rapid agro-ecological changes in many parts of the world, many species, old and primitive cultivars, landraces and their wild relatives endowed with superior genes are being rapidly eroded. Therefore, collection, conservation, evaluation, and utilization of PGR assume considerable significance, especially in view of the rapid environmental degradation and exploitation of the available genetic wealth all over the world.

3. Historical Perspective

For collection of pulse crops, sporadic surveys were undertaken during the initial phase (Shaw and Khan, 1931; Shaw *et al.,* 1933). Systematic plant explorations and collection were initiated in India with the establishment of central agency for this purpose in 1946 in the Division of Botany, Empirical Agricultural Research Institute, New Delhi and the late Dr. Harbhajan Singh referred as "Indian Vavilov" initiated strengthening of germplasm programme through collection and introduction. Later on, All India Coordinated Pulse Improvement Project (AICPIP) was launched in 1966-67 under the aegis of Indian Council of Agricultural Research (ICAR). Under this project, large number of collections consisting of local landraces, traditional varieties, and primitive types were assembled. The first international effort to improve this crop was initiated in 1962, when the Regional Pulse Improvement Project (RPIP) was taken up in India and Iran. In 1972, International Crops Research Institute for Semi-Arid Tropics (ICRISAT) came into existence in Andhra Pradesh at Hyderabad (India). It assumed the responsibilities as the Word repository for genetic resources of chickpea and pigeonpea. In view of the far reaching importance of genetic resources activities, the Plant Introduction Division of Indian Agricultural Research Institute (IARI) was elevated as National Bureau of Plant Genetic Resources (NBPGR) in 1976. Now, NBPGR with its 11 regional stations located in various agro-climatic regions of the country and 42 national active germplasm sites (NAGS) cater to the requirement of the National Plant Genetic System. The Indian Institute of Pulse Research, Kanpur (IIPR), has been identified as NAGS for pulses in India.

4. Research Accomplishments

4.1 Exploration and Collection

Several exploration missions have been undertaken in the country for collection of available indigenous diversity in different legume crops especially chickpea, pigeonpea, urdbean, mungbean, cowpea, peas, lentil, lathyrus, mothbean, horsegram and cowpea besides vegetable types such as cluster bean, Frenchbean, winged bean, *etc.* The programme on grain and forage legumes germplasm collection was also supported by PL 480 Scheme (9868 collections).

After the inception of Bureau in 1976, systematic explorations, both crop specific and region specific, were conducted to augment the pulse genetic resources in the country. Crop specific explorations for pulse crops were carried out in collaboration with ICAR Institutes, ICRISAT, and State Agricultural Universities. Area surveyed and collections made in different parts of country by NBPGR and collaborative institutes are presented in Table 2. A mega project namely "Jai Vigyan National Science and Technology Mission on Conservation of Agro-biodiversity (Plant Genetic Resources)" under NATP was started in 1999 with NBPGR as lead center. A large number of explorations were conducted in various diversity rich areas. As a result, wild species of *Vigna viz., V. bourneae, V. capensis, V. dalzelliana, V. grandis, V. hainiana, V. minima, V. mungo, V. mungo* var. *sylvestris, V. radiata, V. radiata* var *sublobata, V. unguiculata, V. unguiculata* var. *sesquipedalis,* and *V. vexillata* were collected from western and eastern Ghats, North western plains, central plateau region and northern Himalayas. Dana (1998) also collected wild species of *Vigna viz., V. aconitifolia* var. *silvestris, V. dalzelliana, V. hainiana, V. khandalensis, V. mungo* var. *silvestris, V. radiata* var. *setulosa, V. radiata* var. *sublobata,* and *V. trilobata* from seven states of the country, namely Gujarat, Rajasthan, Maharashtra, Madhya Pradesh, Bihar, Orissa and West Bengal between 1974 and 1994.

ICRISAT has made extensive efforts to assemble large number of accessions of chickpea (17258) from 44 countries and pigeonpea (13548) from 74 countries (FAO, 1998). ICARDA also assembled germplasm accessions of *kabuli* chickpea (9,974), lentil (7911), and fababean (9703) from various countries of the world (FAO, 1998). NBPGR has also collected large number of pulse crops from Russia, Mali, Nigeria, Malawi and Zambia.

4.2 Introduction

Over 60,000 accessions of pulse crops were introduced by NBPGR from more than 56 countries under strict quarantine measures. However, most of the introduced materials were in the form of international screening nurseries and yield trials. Some

Table 2: Germplasm collection of pulse crops and area surveyed

Crop	Accessions (no.)	Area of collection
Chickpea	3830	Gangetic plains, North western plains and arid region, eastern and western peninsular region, central India and higher tracts of North western Himalayas
Pigeonpea	2147	North-western plains and arid region, eastern and western peninsular region
Mungbean	2420	North-western plains and arid region, eastern and western peninsular region, central India
Urdbean	2827	Gangetic plains, North-western plains and arid region, eastern and western peninsular region, central India, North eastern region
Lentil	1379	Gangetic plains, western Himalayas, central India
Pea	700	Gangetic plains, North-western plains and arid region, sporadic surveys in peninsular region, central India and western Himalayas
Cowpea	4338	North-western plains and arid region, eastern and western peninsular region, central India, North-eastern Himalayas and Lakshdeep
Lathyrus	507	Gangetic plains, North Himalayas, parts of eastern and western peninsular region, central India
Mothbean	1827	North-western plain and arid region, western peninsular region, parts of central India
French bean	1284	Eastern and western Himalayas and central India, North-eastern region
Ricebean	307	Eastern and western Himalayas and North-eastern region
Horsegram	975	Arid zone, and eastern and western peninsular region
Fababean	74	Gangetic Plains and North-eastern region
Vigna sp.	199	Arid areas, eastern and western peninsular region, Khasi hills, H.P. hills, J&K and North eastern region

of the useful exotic germplasm of pulse crops include accessions with low neurotoxin contents, disease resistant, insect–pest resistant, cold tolerant, drought resistant, widely adapted to different agro climatic conditions, *etc.* Main contributors of pulse germplasm are International Centre for Agricultural Research in the Dry Areas (ICARDA), Asian Vegetable Research and Development Centre (AVRDC), United States Department of Agriculture (USDA), and International Institute of Tropical Agriculture (IITA). An emphasis was also given on the introduction of wild and related species with useful gene/genes especially of *Cicer, Lens, Lathyrus, Pisum, Vigna* and *Cajanus* species. The introduced materials have been utilized in various crop improvement programmes in the country.

4.3 Germplasm Conservation

A total of 42,425 accessions representing 26 pulse crops are stored at -20°C in long-term repository of National Gene Bank of NBPGR (Table 3). Besides, 2523

Table 3: Base collections of pulse crops in National Gene Bank at NBPGR, New Delhi

Crop	Accessions (No.)	Crop	Accessions (No.)
Adzukibean	194	Limabean	19
Urdbean	610	Mothbean	702
Chickpea	14566	Ricebean	1081
Cluster bean	2623	Velvet bean	28
Cowpea	2499	Winged bean	81
Mungbean	2789	Scarlet runner bean	51
Horsegram	1733	Swordbean	57
Lathyrus	2702	*Atylosia* species	7
Lentil	2212	*Flemingia* species	1
Pea	2721	Parkia	3
Pigeonpea	5454	Rhyncosia	9
Fababean	232	Dolichos bean	15
Frenchbean	1084	*Vigna* species	164
Lablab bean	788		

accessions of pigeonpea and its wild relatives and 7712 accessions of lentil have been conserved as safety duplicate sets of ICRISAT and ICARDA, respectively. Active or working collections of pulses are stored under medium term storage conditions (5°C temperature and 40% humidity) at NBPGR and its regional stations namely, Akola, Amravati, Bhowali Cuttack, Hyderabad, Jodhpur, Ranchi, Shillong, Shimla and Thrissur. Indian Institute of Pulses Research (IIPR), Kanpur has been identified as National site for maintenance of active/ working collection of pulses. Global collections of major pulse crops are maintained at national and international centres (Table 4).

4.4 Characterization and Evaluation

A large number of accessions have been characterized and evaluated for various agro- morphological traits at NBPGR, ICAR institutes, State Agricultural Universities (SAUs), and at International Agricultural Research Institutes (IARC), namely, ICRISAT, ICARDA, IITA and CIAT. A large number of chickpea accessions were evaluated for different agro-morphological characters and some of the promising accessions for

Table 4 : World's collection of major pulse crops maintained at national and international centers

Crop	Total world's collection (No.)	National and international centers	
		Name	Accessions (No.)
Chickpea	69736	ICRISAT (India)	17258
		ICARDA (Syria)	9981
Pigeonpea	24938	ICRISAT (India)	13548
Lentil	27424	ICARDA (Syria)	8193
Pea	75288	IPSR (UK)	5000
Common beans	268369	CIAT (Columbia)	54906
Cowpea	85543	IITA (Nigeria)	16654
Fababean	31831	ICARDA (Syria)	15489

Source: www.SINGER.cgiar.org

different traits were identified (Patel *et al.*, 1995; Asthana and Chandra, 1997; Pundir *et al.*, 1988). A large number of germplasm accessions were also evaluated for different biotic stresses and some of the germplasm accessions were found to be resistance to wilt (Dandnaik and Zote, 1988; Karki *et al.*, 1988; Pawar *et al.*, 1992; Asthana and Chandra, 1995), ascochyta blight (Shukla and Pandya, 1988; Pal and Singh, 1990; Reddy and Singh, 1992) and viruses (Mali, 1988). Some of the lines have resistance to more than one isolates/strains and also to more than one disease (Nene, 1988; Sandhu *et al.*, 1988; Asthana and Chandra, 1995). A few lines have been identified with resistance to *Helicoverpa* pod borer (Lateef *et al.*, 1985; Asthana and Chandra 1995) and root knot nematode (Darekar and Jagdale, 1987; Sharma *et al.*, 1988; Mishra and Gaur, 1989). A small number of the germplasm accessions were also reported to be tolerant to drought (Saxena *et al.*, 1993) and salinity (Asthana and Chandra, 1995). The wild relatives of *Cicer viz., C. judaicum* have been reported as resistant to botrytis gray mold (Meeta and Bedi, 1987), fusarium wilt (Nene and Haware, 1980) and have high methionine content. *C. pinnatifidum* also possesses resistance to botrytis gray mold and has high tryptophane content.

In pigeonpea, many lines with desirable agronomical characters such as earliness, more branches, and long and profuse pod setting have been identified from germplasm collections (Patel *et al.*, 1995; Asthana and Chandra, 1997). Two varieties of pigeonpea and seven other species related to pigeonpea were studied for their usefulness in pigeonpea improvement. The study revealed that five wild species can be easily crossed with pigeonpea indicating the scope of utilizing the alien genes in pigeonpea

improvement (Pundir and Singh, 1987). A large number of accessions were also evaluated for biotic stresses and resistance lines for sterility mosaic virus (Nene *et al.*, 1989; Reddy and Raju, 1997); Fusarium wilt (Das and Gupta, 1992; Amin *et al.*, 1993b; Pawar *et al.*, 1993; Reddy *et al.*, 1995a, 1995b); phyllosticta leaf spot (Gupta *et al.*, 1989); and phytophthora blight (Amin *et al.*, 1993a) were identified. A few lines have been found to be resistant to pod borer and pod fly (Borad *et al.*, 1991), cyst nematode (Sharma *et al.*, 1993) and cold (Singh *et al.*, 1997). Identification of lines with genetic male sterility gene has facilitated hybrid breeding and some of the sources of male sterile lines, MS 3A found in ICP 1555, and MS 4A in ICP 1596, are the field collections from India (Reddy *et al.*, 1978).

Several workers (Malik and Singh, 1991; Reddy *et al.*, 1991; Kawalkar *et al.*, 1996; Sharma *et al.*, 1997; Chen *et al.*, 1998) have reported wide variability for various agro-morphological characters in mungbean. Sources of disease resistance have been identified for mungbean yellow mosaic virus (MYMV) (Shukla and Pandya, 1985; Patel and Srivastava, 1990; Mohanty *et al.*, 1998), bacterial leaf spot (Muhammad *et al.*, 1988; Sandhu *et al.*, 1996; Deshmukh *et al.*, 1999), powdery mildew (Agarwal and Nema, 1989; Venu *et al.*, 1997) and *Rhizoctonia solani* (Singh *et al.*, 1989). A few lines were identified as resistant to cyst nematode (Toida *et al.*, 1991; Das *et al.*, 1988); bruchids (Tomooka *et al.*, 1992) and thrips (Chhabra and Malik, 1992; Chhabra and Kooner, 1994). The wild progenitor of mungbean *(V. radiata var. sublobata)* had at least one of the genes for resistant to yellow mosaic virus different than in cultivated types (Singh and Sharma, 1983). TC 1966 of *V. radiata* var. *sublobata* was identified to carry bruchid tolerance gene (Tomooka *et al.*, 1992).

A wide range of variability was reported for various traits in the germplasm collections of urdbean (Acharya *et al.*,1993; Sirohi *et al.*, 1994; Kasundra *et al.*, 1995; Patil and Narkhede, 1995; Nautiyal and Shukla,1999; Singh *et al.*, 2000). A local landrace namely 'Quaudhari mash' has been observed to be drought tolerant (Ashraf and Karim, 1991). A large number of germplasm lines were screened and some of the lines were found to be resistant to MYMV (Singh *et al.*, 1991; Sirohi *et al.*, 1994; Asthana and Chandra, 1995), powdery mildew (Kaushal and Singh, 1989; Asthana and Chandra, 1995), macrophomina blight (Gurha, 1981), cercospora leaf spot (Asthana and Chandra, 1997; Basandrai *et al.*, 1999), leaf blight (Singh and Shukla , 1986), leaf spot (Kaushal and Singh,1989), leaf crinkle (Iqbal *et al.*, 1990; Prasad *et al.*, 1998; Patel *et al.*, 1999) and cyst nematode (Siddiqui *et al.*, 1999). Some of the lines also showed resistance to more than one disease (Singh *et al.*, 2000). A few accessions of wild progenitor *V. mungo* var. *silvestris* are reported as resistant to MYMV (Reddy, 1986).

Genetic stocks having resistance to wilt (Saxena and Khare, 1988; Singh, 1991; Khare *et al.,* 1993), collar rot (Mohammad and Kumar, 1986), rust (Singh and Sandhu, 1988; Singh and Singh, 1990), blight (Kapoor *et al.,* 1990; Iqbal *et al.,* 1990; Sugha *et al.,* 1991), and wilt as well as rust (Singh and Singh, 1993) have been identified in lentil. A few lines were reported to be resistant to bruchids (Chopra and Rajni, 1987) and aphids (Sharma and Yadav, 1993). Some of the germplasm lines were also identified tolerant to drought (Hamdi and Erskine, 1996), salt (Ashraf and Waheed, 1990) and terminal heat (Chandra and Asthana, 1993).

A large number of pea germplasm accessions were evaluated and wide genetic diversity has been reported (Joshi *et al.,* 1992; Partap *et al.,* 1992; Singh, 1995). At NBPGR, a number of germplasm accessions were evaluated for different agro-morphological traits and wide variations were recorded in respect to qualitative and quantitative traits (Sardana *et al.,* 1998; Sardana and Suneja, 2000). Many promising accessions have been found resistant to powdery mildew (Gupta and Katiyar, 1991), ascochyta leaf and pod spot (Ondrej, 1994), and rust (Asthana and Chandra, 1997).

In Cowpea a large number of accessions were evaluated for different agro-morphological and nutritional traits and for reaction to diseases and insect pests (Nielsen *et al.,* 1993; Aghora *et al.,*1994; Fotso *et al.,* 1994; Muhammad *et al.,*1996; Backiyarani and Nadarajan,1996; Sreekumar and Nair, 1996; Singh *et al.,* 1999; Sardana *et al.,* 2000). Aghora *et al.* (1994) reported some of the accessions with high protein value. Pandey *et al.* (1995) evaluated 49 germplasm lines for their multiple resistances against economically important insect pests (gllerucid beetle, semilooper), diseases (bacterial blight, cowpea mosaic virus) and nematode (root knot nematode), and identified some of the resistant accessions. Asthana and Chandra (1997) also reported accessions resistant to multiple diseases.

A total of 2604 germplasm collections of *Lathyrus* were analyzed for neurotoxin compound b -N-Oxaly-L-μ, diaminopropionic acid (ODAP) (Pandey *et al.,* 1998). The results revealed that low ODAP concentration was recorded in *L. odoratus, L. aphaca* and *L. cicera* species, which also possessed resistance to pod borer.

4.5 Documentation

Documentation and information dissemination are an integral part of genetic resources management. A catalogue with appropriate documentation of evaluation descriptors serves as a fast, reliable and efficient means of disseminating pertinent information to enhance utilization.

NBPGR has published 23 catalogues describing over 78,000 accessions of 11 crops. It has also published a monograph on ricebean (Chandel *et al.,* 1988). ICAR

Research Complex for NEH Region published a research bulletin on ricebean germplasm (Sarma *et al.,* 1995).

The first catalogue on world's collection on chickpea was published by ICRISAT (Pundir *et al.,* 1988) followed by IIPR (Singh and Kumar, 2004). A catalogue on world's collection of pigeonpea was published by ICRISAT (Remanandan *et al.,* 1988). ICARDA has published four catalogues, two on *kabuli* chickpea (Singh *et al.,* 1983) and one each on lentil (Erskine and Witcombe, 1984) and fababean (Robertson and Sherbeeny, 1988). Germplasm catalogue of mungbean was published by AVRDC (Tay *et al.,* 1989), urdbean by Commonwealth Scientific and Industrial Research Organization (Imrie *et al.,* 1981) and IIPR (Gupta *et al.,* 2003) and cowpea by IITA, Nigeria (IITA, 1974).

5. Utilization of Germplasm in Crop Improvement

Evaluation of germplasm has led to the release of more than 60% of total pulse varieties as direct selection from the germplasm in India. Many germplasm lines with desirable agronomic characters have been used in hybridization programmes to develop varieties with high yield and desirable plant types. A large number of germplasm lines have also been utilized as sources for transferring resistance to diseases. The utilization of desirable germplasm either for direct selections or in hybridization and mutation breeding has led to release of a large number of varieties in pigeonpea (103); chickpea (90); mungbean (93); urdbean (66); lentil (34); fieldpea (26); French bean (21) and lathyrus (4) in India.

A large number of short duration varieties of different pulse crops are available which may fit well in already existing cropping sequence as a catch crop. Some of the germplasm lines of Indian origin were also utilized to release the varieties in other countries (Sethi and Rheenen, 1994). Germplasm lines have also been used to generate information on the inheritance of traits and also in elucidating phylogeny relationships

6. Future Plans

It is a need of the hour to give more emphasis on new emerging concepts for better utilization of germplasm. This requires proper reorientation of research priorities in the country as briefly described below:

6.1 Pre-breeding and Germplasm Enhancement

The genetic base of pulses is quite narrow and, therefore, a quantum jump in yield has not been achieved so far. It is, therefore, important to broaden the genetic base of these crops. Wild relatives of pulses are known as valuable sources for

resistance to several biotic and abiotic stresses besides yield components. Pre-breeding and germplasm enhancement involving diverse germplasm and closely related wild species need to be adequately utilized in comprehensive and elaborate breeding programmes. Further refinement in embryo rescue technique is required to bring tertiary gene pool under the gambit of hybridization. To make use of wild species, there is need to integrate biotechnological tools with active breeding programme to unravel the useful genes for various desirable traits difficult to manage by conventional breeding approach.

6.2 Development of Core Collections

The establishment of *ex situ* germplasm collections has been the result of several decades of efforts to conserve plant biodiversity. The need of plant breeding for large variability and concern about potential loss of this variability, and non-availability of low cost tools to identify similarities and differences among accessions have led gene banks to hold large germplasm collections of various crops. This has resulted from the belief that the representativeness of collections can be achieved through large collection sizes (Frankel and Bennett, 1970). As collections rapidly grew beyond easily manageable sizes, the task of quantifying diversity became daunting. Also, with increase in size of collections the realization that they are little used by breeders also grew (Duvick, 1984). The large variability within the gene bank, rather than prompting its enhanced utilization, creates the "problem of plenty" *i.e.,* not knowing what germplasm to begin with, in the genetic enhancement of crop breeding pool(s). Frankel (1984) proposed that the collections could be pruned to a manageable sample or core collection. The core subset should be designed to minimize repetitiveness within collection and it should represent the rich genetic diversity of crop. The core collection should serve as a working collection, which should be extensively examined, and the accessions, which are not included in the core collection, should be designated as reserve collection (Frankel, 1984). Frankel and brown (1984) and Brown (1989a, b) developed the core collection proposal further and described methods to select core subsets using information on the origin, and characteristics of the accessions.

For efficient management and utilization of large number of collections, research priority should be to develop core collections. NBPGR has developed a core subset of 152 accessions from 1532 accessions in mungbean (Bisht *et al.,* 1998). Recently, core sets of chickpea (Upadhyaya *et al.,* 2001) and pigeonpea (Reddy, 2003, pers. Comm.) have been developed from the global collections at ICRISAT. Upadhyaya *et al.* (2001) used data on geographic origin and 13 quantitative traits on 16,991 accessions from 44 countries and developed a representative core of 1956 accessions. In pigeonpea data, origin and 14 qualitative morphological descriptors on 12,153 accessions from 56

countries were utilized to develop a core subset of 1290 accessions. The future efforts should be to develop representative core subsets of remaining pulse crops for their better management and efficient utilization.

6.3 Mini Core Collection

The main purpose of a core collection is to improve the use of genetic resources in crop improvement programmes. In many crops the number of accessions contained in the gene bank are several thousands and a core subset consisting of 10% of total accessions would be an unwisely proposition. For example, chickpea core collection developed at ICRISAT consists 1956 entries. Recognizing this, Upadhyaya and Ortiz (2001) suggested a two-stage strategy to select mini core collection, consisting of only about 1% of the entire collection held in the gene banks. The mini core collection subset still represents the diversity of the entire core collection. Of the two stages, the first stage involves developing a representative core subset (about 10%) from the entire collection using all the available information on origin, geographical distribution, and characterization and evaluation data of accessions. The second stage involves evaluation of the core subset for various morphological, agronomic, and quality traits, and selecting a further subset of about 10% accessions from the core subset. They suggest that at both stages standard clustering procedure should be used to separate groups of similar accessions. A mini core subset consisting 211 chickpea accessions from 1956 core collection accessions (entire collection 16991 accessions), using data on 22 morphological and agronomic traits was selected. The mini core subsets due to their drastically reduced size will prove a point of entry to the proper exploitation of chickpea genetic resources (Upadhyaya and Ortiz, 2001).

6.4 Evaluation of Core Collections

The main purpose of developing core and mini core collection is to select useful parents for use in the crop improvement programmes. The core collection of lentil comprising 287 accessions has been evaluated for variation in phenological, morphological, biomass and seed yield, which indicated significant variation to warrant their use in the breeding programme (Tullu *et al.*, 2001). Upadhyaya *et al.* (2002) evaluated chickpea core collection consisting 1956 entries for 7 morphological descriptors and 15 agronomic characteristics in the 1999/2000 post rainy season at ICRISAT to estimate phenotypic diversity. All the three groups differed significantly for flower colour, plant colour, dots on seed testa, seed testa texture, plant width, days to maturity, pods per plant, 100-seed weight and plot yield. They have identified useful parents for important agronomic and economic traits like early maturity and large seed size in chickpea. Early maturity is one of the most important traits for enhancing adaptation

of crop but only a few sources are available to the breeders. About 13 new diverse sources of early maturity in chickpea that mature as early as the earliest maturing germplasm Harigantas (85-90 days) but produce up to 70% more yield have been identified. The large seeded characteristic is a premium trait for *kabuli* type of chickpea. At ICRISAT, 16 diverse germplasm lines that have 100-seed weight up to 55 g have been identified. Extensive multilocation evaluation of core and mini core collections should be undertaken.

6.5 Registration of Germplasm

Registration of useful germplasm is one of the important activities in context to conflicts arising due to Intellectual Propriety Rights (IPR). The NBPGR has been identified as a nodal agency for implementation of Plant Germplasm Registration. Two accessions of chickpea namely, INGR 98008 (salt tolerance) and INGR 99016 (multipinnate leaf, with shorter internodes); 9 germplasm accessions of pigeonpea, INGR 99028 (male sterile mutant); INGR 00012, INGR 01025-30 (stable cytoplasmic male sterile) and INGR 01015 (multiple disease resistant); 2 accessions of mungbean INGR 97003 (pentafoliate) and INGR 00011 (high seed weight, long pods and high protein); 2 germplasm accessions of Lathyrus, namely, INGR 98023 and INGR 99029 (low ODAP and high yield) and a germplasm accession of mothbean, INGR 01024 (erect, early, high- yielding, higher uptake and nutrient utilization) have been registered as genetic stocks at NBPGR. ICRISAT has also registered a good number of useful germplasm of chickpea and pigeonpea with the Society of Crop Improvement. However, there is urgent need to register all the genetic stocks held with the breeders.

6.6 Use of Biotechnology

In recent years, isozymes, amplified fragment length polymorphism (AFLP), random amplified polymorphic DNA (RAPD) and sequence tagged microsatellite (STMS) markers have helped to enhance the development of pulse genome maps. Molecular markers based genetic diversity will help to identify duplicates/redundant accessions and select and utilize the genetically diverse germplasm in the pulse improvement programme. This will also help in validating the core and mini core collections.

6.7 Value Addition

There is tremendous scope to initiate targeted activity, leading to the production of high quality pulses. Recent advances in biosynthetic pathway engineering have opened up new vistas for quality improvement in pulses. The knowledge about heritable variation for anti-nutritional factors among germplasm accessions in Lathyrus makes

it possible to develop varieties with low ODAP (b-N-Oxaly-L-a, b-diaminopropionic acid). The germplasm with low levels of ODAP needs to be selected for use in the breeding programmes.

6.8 Uncovering Genetic Mechanisms

To improve the efficiency, predictability, and effectiveness, efforts should be intensified for identification and proper nomenclature of genes and genetic stocks of pulses. Efforts should be made to develop molecular linkage maps of crops. These maps should be exhaustive, precise and evenly distributed to elucidate the genetic basis of several important traits. Molecular markers linked with agronomic importance in pulses like pea, chickpea and lentil have been identified and preliminary molecular maps have been developed. The ability to use marker-assisted selection to pyramid genes will be of great help to pulse breeders.

7. Future Thrusts

- The areas, which have not been explored so far, should be surveyed for collection of germplasm. For chickpea germplasm, the areas to be surveyed include drier tracts of Uttar Pradesh, central and northern Karnataka, adjoining areas of Maharashtra and parts of Haryana. The major areas yet to be surveyed for pigeonpea are North Karnataka and parts of Bihar and Maharashtra. For *Vigna* species, further surveys need to be made in Western Ghats starting from Mount Abu to Nilgiri Mountains. Mothbean germplasm needs to be collected from parts of Tamil Nadu, Kerala and Karnataka. Hilly areas in Manipur, Himachal Pradesh, northern West Bengal, parts of Uttar Pradesh and Madhya Pradesh should be surveyed for collection of fieldpea. Local landraces of lathyrus are to be collected from Bundelkhand region of Uttar Pradesh, northern Bihar, Chhattisgarh and West Bengal. More genetic diversity in common bean should be collected from Maharashtra, Himachal Pradesh, Uttaranchal and Northeastern region. For horsegram, parts of Madhya Pradesh, Maharashtra, Orissa and drier parts of Uttar Pradesh are yet to be surveyed.
- Concerted efforts are required for identification and introduction of trait specific germplasm. A thorough search of the literature should be made to identify the target countries and an effective interaction with the plant breeders should take place in AICRP workshops and Germplasm Field Days.
- Germplasm accessions will have to be additionally screened for response to fertilizers, resistance to lodging, biotic and abiotic stresses, early seedling vigour and for low light interceptions.

- To facilitate effective utilization of pulse germplasm in breeding programme, multilocation evaluation of core and mini core collections and trait specific germplasm and, identification of promising diverse accessions for various agronomic traits, resistance/tolerance to biotic and abiotic stresses is needed. Documentation of the useful germplasm identified in various evaluation programmes should be taken up on priority.
- Quick screening techniques should be developed for screening of genetic resources against biotic and abiotic stresses.
- The existing germplasm accessions available at different centers should be pooled and duplicates should be identified.
- Core collections for all the pulse crops should be developed.
- Registration of promising genetic stocks should be encouraged on priority.
- Pre-breeding/genetic enhancement programme should be taken up to foster germplasm utilization including wild species. Biotechnologists and molecular biologists should work in a team with plant breeders for speedy transfer of desirable genes. Biotechnological tools need to be utilized for germplasm characterization. In view of emerging Intellectual Property Rights (IPR) issues, there is a need to develop database of entire germplasm in the country.
- Development and use of viable farmers participatory genetic resources management should be initiated in areas of rich genetic diversity for enhanced productivity, stability and value addition while conserving on-farm genetic diversity.
- Multidisciplinary and inter-institutional collaborations are urgently needed to evaluate the usefulness of the conserved germplasm.

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