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Use of Core Collection Approach to Enhance Germplasm Utilization in Chickpea and Pigeonpea

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The utility of plant materials for the benefit of human being increased dramatically in the past century. It is only about 12,000 years ago that human beings started growing food of their choice, rather than merely gathering it from the wild state. Domesticated plants were freely moved from one part of the world to another along with people's migration. It was in fact a golden era because so much of the plant diversity was created mainly due to introduction. Following the Mendelian discovery of inheritance in plants in early 20th century, scientific plant breeding replaced the simple procedure of selection practiced by the farmers for many generations. Improved crop varieties started to replace the prevalent landraces and local cultivars. However, the process was not rapid. By 1960, the development and spread of high yielding varieties of wheat and other crops started replacing the local cultivars very rapidly. This could be called the beginning era of plant diversity erosion. This loss of native crop landraces and cultivars prompted the international organizations such as the Food and Agriculture Organization (FAO) and the World Bank to create new institutional structures for the collection and preservation of these valuable plant genetic resources in the ex-situ genebanks. Since the last four decades, this program has continued and achieved spectacular success. Over six million germplasm accessions have been collected and/or assembled in 1308 genebanks world over (FAO, 1998).

One of the objectives of the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT – one of the 15 CGIAR centers) is to assemble, collect, and conserve the genetic resources of five mandate crops and six small millets and their wild relatives including

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chickpea and pigeonpea. We present in this paper a brief account of establishing the chickpea and pigeonpea collections, assessment of diversity in them and their utilization. Subsequently, we describe the core and mini-core collection approach as a means to further enhance the utilization of germplasm in crop improvement.

1. Germplasm collection in ICRISAT genebank

Historically, the assembly of chickpea and pigeonpea germplasm work was initiated by the former Regional Pulse Improvement Project (RPIP), a joint project of the Indian Agricultural Research Institute (IARI), the United States Department of Agriculture (USDA), and Karaj Agricultural University in Iran during 1964 to 1970. Germplasm that was held by the various institutes in India and Iran were assembled, and fresh collections were made. This resulted in assembly of over 10,000 accessions of chickpea and pigeonpea. These numbers were designated with acronym 'P'. Sets of the RPIP collections were donated to ICRISAT in 1973. Besides this, several other institutes in India, Turkey, Chile, and Mexico and other countries donated their collections of chickpea and pigeonpea to ICRISAT.

ICRISAT also initiated programs to add new germplasm from the priority regions. Special efforts were made to collect landraces and wild relatives from areas threatened by genetic erosion or from the areas of significant genetic diversity. Sixty-six collection missions for chickpea and 99 for pigeonpea were launched in various countries during 1974 and 1997 securing 4228 and 3873 germplasm samples, respectively. Of these missions, about half were organized mainly to collect chickpea or pigeonpea whereas the remaining half were arranged to collect other crops, chickpea, and pigeonpea too were collected. Presently, ICRISAT genebank (named as Rajendra S. Paroda Genebank in 2002) is holding 17,123 accessions of cultivated chickpea from 45 countries and 13,632 of cultivated pigeonpea representing 74 countries (Table 1).

Table 1. Chickpea and pigeonpea germplasm accessions in ICRISAT genebank by region, September 2005

Region	Number of accessions		
	Chickpea	Pigeonpea	Total
India	7,216	10,820	18,036
Asia (less India)	6,965	575	7,540
Africa	1,479	1,310	2,789
Americas	622	747	1,369
Europe	794	30	824
Oceania	3	139	142
Unknown	179	11	190
Total	17,258	13,632	30,890

2. Diversity in chickpea and pigeonpea collections

2.1. Chickpea: The phenotypic diversity of 16,820 chickpea accessions for seven morphological and 13 agronomic traits analyzed over 11 regions indicated that the variances for all the traits among regions were heterogeneous. South Asia contained maximum range of variation for all the traits. Seed color and days to 50% flowering showed the highest pooled diversity index. Principal component analysis (PCA) using 13 traits and clustering of the first three PC scores delineated two regional clusters: Africa, South Asia, and Southeast Asia in the first cluster; and the Americas, Europe, West Asia, Mediterranean region, and East Asia in the second cluster (Upadhyaya, 2003). An earlier study of chickpea germplasm data at ICRISAT (Pundir *et al.*, 1988) revealed that in general, Indian accessions were highest yielding and the accessions from Chile had higher plant height and greater seed mass. The accessions from Spain and Syria had longer flowering duration and the accessions from Greece and Russia were rich for erect growth habit. Resistance to fusarium wilt was more common in accessions from Bangladesh than from other countries.

2.2. Pigeonpea: We analyzed the patterns of variation for 14 qualitative and 12 quantitative traits in 11,402 pigeonpea germplasm accessions from 54 countries, which were grouped into 11 regions. Semi-spreading growth habit, green stem color, indeterminate flowering pattern, and yellow flower color were predominant among qualitative traits. The germplasm accessions from Oceania were conspicuous by short growth duration, short height, fewer branches, pods with fewer seeds, smaller seed size, and lower seed yields. The accessions from Africa were of longer duration, taller, with multiseeded pods, and larger seeds. The germplasm diversity indicated by Shannon-Weaver diversity index (H') pooled over all traits, was highest for Africa (0.464 ± 0.039) and lowest for Oceania (0.337 ± 0.037). The cluster analysis based on three principal component scores using 12 quantitative traits revealed formation of three clusters: cluster 1 includes accessions from Oceania; cluster 2 from India and adjacent countries, and cluster 3 from Indonesia, Thailand, The Philippines, Europe, Africa, America and the Caribbean countries (Upadhyaya *et al.*, 2005).

3. Current trend of germplasm utilization

Germplasm supply to bonafide researchers is one of the main responsibilities that ICRISAT genebank performs. Healthy and viable seeds of germplasm resources are supplied to researchers on request. During 1973 to 2004, a sum of 187,156 germplasm samples of chickpea and pigeonpea were supplied. These samples were drawn from over 95% of the entire chickpea and 78% of the entire pigeonpea unique accessions. On an average, ICRISAT genebank has been supplying 6037 germplasm samples of chickpea and pigeonpea annually (mean from 1974 to 2004). This figure indicates satisfactory germplasm distribution service of the genebank (Marshall, 1989). However, the use of basic germplasm in breeding programs is scanty. For example, in the ICRISAT chickpea-breeding program (1978-2004), 12,887 parents (586 unique parents) were used in developing 3548 breeding lines, which included only 91 unique germplasm accessions of chickpea and five of wild *Cicer* species. Similarly in pigeonpea, 1256 parents were used to develop 527 advanced lines that involved only 54 unique accessions. There are similar experiences from groundnut breeding work at ICRISAT

(Upadhyaya *et al.*, 2003) and also from China (Jiang and Duan, 1998) and USA (Knauft and Gorbet, 1989).

4. Core and mini-core approach to enhance germplasm utilization

4.1. Core collection: The vast collection of germplasm will be of limited use unless the individual accessions are characterized for relevant traits and data is available in user-friendly manner. Some of the traits are highly influenced by genotype x environments interactions, and require replicated multilocational evaluations. This is a very costly and resource-demanding task owing to the large size of the germplasm collection. To overcome this, our research now focuses on studying the diversity of germplasm collection and developing "core collections," which are about 10% of the entire collection, but represent almost full diversity of the species. From the germplasm collection in the ICRISAT genebank, we have already developed core collection of chickpea (1,956 accessions, Upadhyaya *et al.*, 2001) and pigeonpea (1,290 accessions, Reddy *et al.*, 2005).

4.2. Mini-core collection: When the size of entire collection is large, even a core collection becomes unwieldy for evaluation by breeders. To overcome this, ICRISAT scientists developed a two-stage seminal strategy to develop a mini-core collection, which consists of 10% accessions of the core collection (only 1% of the entire collection) (Upadhyaya and Ortiz, 2001). This mini-core subset still represents the diversity of the entire core collection. 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. At both stages standard clustering procedure should be used to separate groups of similar accessions. At ICRISAT, we have already developed mini-core collections of chickpea consisting of 211 accessions (Upadhyaya and Ortiz, 2001) and pigeonpea consisting of 146 accessions (unpublished data).

5. Identification of sources for traits of economic importance for use in crop improvement program

Due to the reduced size, the core collection can be evaluated extensively to identify the useful parents for crop improvement. By evaluating core collection of chickpea, we identified new sources of important traits, namely, early maturity (29 accessions), and large seeded kabuli (16 accessions) types. These accessions were not only new source of economic traits, but also were diverse from the check cultivars. The core collection was evaluated for agronomic traits through the yield trials conducted during 1999/2000 and 2000/01 seasons at ICRISAT, Patancheru along with two control cultivars, Annigeri and L 550. The controls were the released cultivars adapted to Patancheru conditions. We found that seven chickpea accessions (ICCs 6122, 8324, 12197,13124, 14230, 16862, and 16934) were superior in respect to the four important yield traits (days to flowering, pod number, plot grain yield and 100 seed weight) compared to control Annegeri. Similarly nine kabuli accessions (ICCs

3410, 5644, 6160, 6246, 7200, 8042, 10755, 10783, and 15763) were superior in respect to the above said four yield traits compared to the control, L 550 (Table 2).

Table 2. Chickpea accessions found superior compared to respective desi and kabuli type controls in core collection of chickpea, mean of 1999/2000 and 2000/01 seasons, Patancheru, India.

Accession	Country of origin	Biological status	Days to 50% flowering	Pods/ plant (kg h^{-1})	Seed yield	100-seed weight (g)
Desi						
ICC 6122	India	Landrace	40	64	1832	34.6
ICC 8324	India	Landrace	46	72	2251	21.7
ICC 12197	India	Breeding line	44	72	2178	28.6
ICC 13124	India	Landrace	48	53	2188	33.8
ICC 14230	India	Landrace	49	55	2166	33.6
ICC 16862	India	Landrace	45	74	2288	25.2
ICC 16934	India	Landrace	48	72	2212	23.1
Kabuli						
ICC 3410	Iran	Landrace	54	65	2138	21.8
ICC 5644	India	Landrace	61	60	2138	23.3
ICC 6160	Syria	Landrace	59	66	1996	40.5
ICC 6246	Tunisia	Landrace	63	68	1898	21.8
ICC 7200	Egypt	Breeding line	62	59	2171	21.5
ICC 8042	Iran	Landrace	59	55	2075	30.8
ICC 10755	Turkey	Landrace	61	58	2014	31.4
ICC 10783	Turkey	Landrace	61	60	2167	35.6
ICC 15763	Morocco	Landrace	59	69	1886	26.0
Control						
Annigeri (Desi)	India	Cultivar	50	70	2057	21.3
L550 (Kabuli)	India	Cultivar	63	64	1858	19.9

The core collection of pigeonpea was also evaluated during 2004 rainy season at ICRISAT, Patancheru along with four control cultivars, each one of them representing the four maturity groups (extra early, early, medium and late) in pigeonpea. In extra early group, six accessions (ICPs 10905, 14421, 14426, 14828, 14946, and 15066) were significantly higher yielder than the control, ICP 11543. The six accessions were also superior in respect to the other three traits (days to flowering, harvest index and shelling percentage). In the early group, although none of the accessions yielded on par with the control, (ICP 6971), three accessions (ICPs 8754, 9696, and 13647) were superior in respect to the above said three traits. In medium group, only one accession, ICP 10720 was significantly higher yielding compared to the control, ICP 8863 and also superior in respect to the above said three traits. In the late maturity group, seven accessions (ICPs 1615, 4519, 9378, 10009, 10478, 11722, and 14722 were significantly higher yielding compared to the control, ICP 7221. They were also superior in respect to the above said three traits (Table 3).

Table 3. Pigeonpea germplasm accessions found superior for 3-4 traits compared to respective controls in core collection of pigeonpea, 2004 rainy season, Patancheru, India[1]

ICP	Days to flowering	Harvest index (%)	Shelling	Yield kg ha^{-1}
Extra early				
10905	64	22.46	62.57	645
14421	71	20.68	60.66	724
14426	67	18.96	57.61	633
14828	67	25.37	62.63	724
14946	66	17.91	54.98	634
15066	71	18.86	57.7	656
Control-11543	73± 4.3	17.14± 4.36	51.7± 6.79	219± 355.25
Early				
8754	102	23.79	69.39	1245
9696	96	23.33	64.81	1064
13647	91	26.49	64.82	1267
Control-6971	103± 4.3	22.66± 4.36	64.44± 6.79	1600± 355.25
Medium				
0720	106	25.69	69.04	2241
Control-8863	110± 4.3	24.79± 4.36	65.2± 6.79	1870± 355.25
Late				
1615	116	28.83	65.63	2851

4519	117	25.45	64.4	2829
9378	120	30.29	64.54	2648
10009	115	29.18	62.59	3032
10478	118	28	65.71	2693
11722	119	26.2	64.85	2557
14722	120	26.69	65.35	2784
Control-7221	125± 4.3	25.39± 4.36	68.43± 6.79	2201± 355.25

1 = accessions were significantly superior for yield in all classes except the early group.

To gain benefits, the mini-core collection of chickpea has been evaluated and diverse sources for useful traits have been identified. From the chickpea mini-core, 10 accessions having traits related to drought tolerance (Kashiwagi *et al.*, 2005) and 29 accessions tolerant to soil salinity (Serraj *et al.*, 2004) have been identified. Similarly, Pande et al. (2005) screened the mini-core collection for resistance to various diseases and identified 67 accessions resistant/highly resistant to fusarium wilt, moderate resistance to ascochyta blight in 3 accessions, botrytis grey mold in 55 accessions, and to dry root rot in 6 accessions. ICC 11284 was the only accession moderately resistant to both the foliar diseases (ascochyta blight and botrytis grey mold). Four accessions were found with combined resistance to dry root rot and fusarium wilt, and 15 accessions to fusarium wilt and botrytis grey mold.

6. Future outlook

In future, our focus will be on further characterization and assessment of the germplasm for their usefulness for crop improvement. The core and mini-core subsets of the germplasm will be evaluated at diverse locations to identify trait specific diverse parents. Molecular characterization of mini-core collection, and establishing trait specific germplasm sets will be enhanced to add value to the germplasm accessions. We have initiated developing composite sets of ICRISAT mandate crops under the Generation Challenge Program. Phenotypic and genotypic characterization of these sets will provide vast scope for identifying useful and unique germplasm resources for utilization in the crop improvement.

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