

Biodiversity and Crop Improvement: An Integrated Approach to Enhance use of Plant Genetic Resources for Sustainable Food Production

CLL Gowda, HD Upadhyaya and SL Dwivedi

International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, 502 324, India
e-mail: c.gowda@cgiar.org

Plant genetic resources are the basic materials for future genetic progress and an insurance against unforeseen threats to agricultural production. Use of germplasm in crop improvement is one of the ways to conserve valuable genetic resources, protect the natural ecosystems, and simultaneously enhance agricultural production and food security.

Plant Genetic Resources at ICRISAT Genebank, Patancheru, India

- 118,882 accessions of its five mandate crops and six small millets from 144 countries
- 80% landraces, 16% advanced breeding lines/cultivars, 2% wild relatives
- 87% accessions preserved under long-term storage (-20°C)
- Continue to acquire new germplasm not represented in collection
- Developing marker-aided introgression lines as a resource for the discovery and exploitation of unused genetic variability
- Identifying novel alleles from wild relatives associated with agronomic traits.

Phenotypic variability in germplasm collection.



Crop improvement programs globally benefited from the genebank accessions

- Distributed 0.694 million seed samples to researchers in 144 countries and 0.651 million seed samples to researchers at ICRISAT
- Sixty-six germplasm lines released directly as cultivars in 44 countries contributing to food security
- Using ICRISAT-bred breeding lines, 77 countries have released 545 varieties and hybrids for cultivation by farming communities.

Core and mini core to enhance utilization of germplasm in crop improvement

- Core (10% of entire collection) and mini core (1% of entire collection) are cost-effective approaches to identify accessions with desirable agronomic traits
- Core and/or mini core subsets developed for chickpea, pigeonpea, groundnut, pearl millet, sorghum, finger millet and foxtail millet collections
- Trait-specific germplasm identified by NARS after evaluating core/mini core collections
 - 35 groundnut accessions in China, Thailand and Vietnam
 - 52 chickpea and 19 finger millet accessions in India

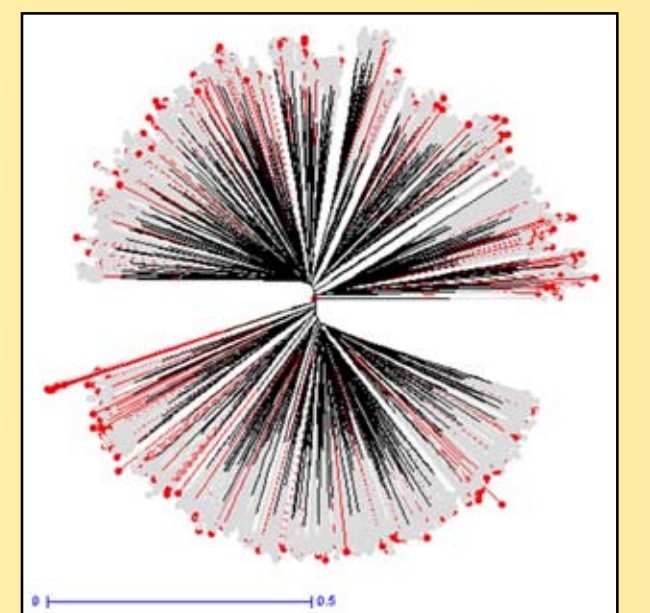
- Germplasm with specific agronomic attributes identified from evaluating core/mini core collections at ICRISAT
 - 5 Helicoverpa tolerant accessions in chickpea
 - 7 pigeonpea accessions resistant to sterility mosaic
 - 31 chickpea accessions with multiple resistance to diseases
 - 20-28 early maturing accessions in chickpea, groundnut and pigeonpea
 - 39 kabuli chickpea accessions with early maturity, high yield and large-seeded traits
 - 25 accessions with high seed yield and early maturity in both finger millet and foxtail millet
 - 54 pigeonpea accessions with high yield, large-seed size, and high harvest index.

Table 1. Entire, core, mini core, composite collections and reference sets established at ICRISAT

Crop	Number of accessions					
	Entire collection	Used in core development	Core collection	Mini core collection	Composite collection	Reference set
Sorghum	37,904	22,474	2,247	242	3,367	384
Pearl millet	21,594	20,844	2,094	238	1,000	300
Chickpea	20,140	16,991	1,956	211	3,000	300
Pigeonpea	13,632	12,153	1,290	146	1,000	300
Groundnut	15,419	14,310	1,704	184	1,000	300
Finger millet	5,949	5,940	622	65	1,000	300
Foxtail millet	1,535	1,474	155	-	500	200

Studying population structure and diversity in composite collection and reference set

- Composite collections developed for chickpea, groundnut, pigeonpea, pearl millet, sorghum, finger millet and foxtail millet
- Reference sets developed for chickpea, groundnut, pigeonpea, sorghum, finger millet and foxtail millet representing over 78% allelic variation from composite collections
- Reference sets as a resource for whole genome scanning and marker-trait association.



Global warming impacting biodiversity and world food production

- Significant decline in yields predicted for most crops, although cooler regions might benefit
- Expected are more frequent drought, flood, temperature extremes, and rise in salinity
- Identifying new sources of variation for crop breeding is essential to make crops adapted to these extremes
- Climate change is threatening biodiversity that must be preserved for humankind.

New sources identified for drought, salinity and high temperature tolerance

- 18 drought, 12 salinity and 5 high temperature tolerant chickpea lines
- 18 drought, 12 salinity and 158 low temperature tolerant groundnut lines
- 16 salinity tolerant pigeonpea lines
- 7 sorghum and 22 pearl millet salinity tolerant lines.

Salinity tolerance.



Conclusions

- Core and mini core collection and genotype-based reference sets are in demand by NARS for evaluation
- Tolerance to drought and salinity identified for use in crop improvement
- Genetically diverse and agronomically superior germplasm with beneficial agronomic traits identified
- Trait-specific germplasm identified by NARS
- Mini core collections and reference sets available for genomics studies.