Conservation and Use of Agrobiodiversity in Semi-Arid Tropic Regions

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Plant genetic resources are basic for future genetic progress and are an insurance against unforeseen threats to agricultural production. Conservation and enhanced use of germplasm in crop improvement increases agricultural production and food security, and protects agroecosystems.

Plant Genetic Resources at ICRISAT Genebank, Patancheru, India

- 119,739 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.

Phenotypic variability in germplasm collection

37,949 sorghum accessions.

22,211 pearl millet accessions.

10,235 small millets accessions.

20,267 chickpea accessions.

13,632 pigeonpea accessions.

15,445 groundnut accessions.

ICRISAT genebank at Patancheru.

Regeneration of wild Arachis *species.*

Crop improvement programs globally benefited from the genebank accessions

- Distributed 1.4 million seed samples to researchers in 144 countries
- Seventy-five germplasm lines released directly as cultivars in 58 countries contributing to food security
- Using ICRISAT-bred lines, 657 varieties and hybrids have been released in 78 countries 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 traits
- Core and mini core collections developed for chickpea, pigeonpea, groundnut, pearl millet, sorghum, finger millet and foxtail millet
- 115 sets of core/mini core collections supplied to scientists in 22 countries
- Trait-specific germplasm identified by ICRISAT and NARS after evaluating core/mini core collections.

Germplasm with specific traits identified from core/mini core collections

- 5 chickpea accessions with high protein content, 18 with multiple resistance to diseases, and 39 with early maturity, high yield and large seeds
- 54 pigeonpea accessions with high yield, large seed size, and high harvest index, and 7 resistant to sterility mosaic
- 20-28 early maturing accessions in chickpea, groundnut and pigeonpea
- 20 accessions with high seed yield and early maturity in both finger millet and foxtail millet
- 5 large-seeded groundnut accessions each in China and Thailand, 5 groundnut accessions for high shelling percentage each in China, Thailand and Vietnam
- 4 groundnut accessions with high oleic/linoleic ratio in China, and 11 in Dharwad, India
- 7 groundnut accessions with high oil content identified in China, 10 in Vietnam, 5 in Thailand, 7 in Raichur (India), 6 in Kawadimatti (India) and 5 in Dharwad (India)
- 50 sorghum accessions with resistance to grain mold, 6 to downy mildew, 6 to anthracnose, and 1 with multiple resistance to five diseases (downy mildew, anthracnose, leaf blight, rust and grain mold).

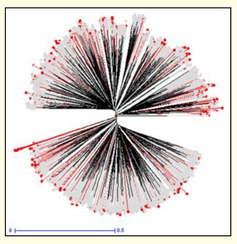
Table 1. Core and mini core collections at ICRISAT.

Crop	Number of accessions			
	Entire collection	Used in core development	Core collection	Mini core collection
Sorghum	37,949	22,474	2,247	242
Pearl millet	22,211	20,766	2,094	238
Chickpea	20,267	16,991	1,956	211
Pigeonpea	13,632	12,153	1,290	146
Groundnut	15,445	14,310	1,704	184
Finger millet	5,957	5,940	622	80
Foxtail millet	1,542	1,474	155	-

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, pearl millet, sorghum, finger millet and foxtail millet representing over 78% allelic variation from composite collections
- Mini core collections and reference sets as a resource for genome scanning and marker-trait association.

Genetic diversity in chickpea germplasm: pod number and maturity.



Chickpea composite collection (2,915 accessions) representing reference set (300 accessions).

Agrobiodiversity and SAT

- Frequent droughts, temperature extremes, and rise in salinity are expected to occur frequently in the semi-arid tropics (SAT) due to climate change
- Identifying new sources of variation for crop breeding is essential to adapt crops to climate change and variability
- Identifying novel alleles from wild relatives associated with agronomic traits assists in adapting crops to future climate change
- Developing marker-aided introgression lines as a resource for the discovery and exploitation of unused genetic variability.

New sources identified for drought, salinity, water logging 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- and 24 water logging-tolerant pigeonpea lines.

Salinity tolerance

(Left) Tolerant and (right) susceptible chickpea.

(Left) Tolerant and (right) susceptible groundnut.

Conclusions

- Mini core collections are in demand by partners for evaluation and development of trait-specific and genetically diverse parents for crop improvement
- Tolerance to drought and salinity and resistance to diseases identified for use in crop improvement
- Genetically diverse and agronomically superior germplasm with beneficial agronomic traits identified
- Mini core collections available for genomics studies and use in crop improvement.

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Science with a human face

International Crops Research Institute for the Semi-Arid Tropics

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