

Large-scale Characterization for Management and Utilization of Indian National Genebank Collections

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Globally, plant genetic resources (PGR) are the key biological resources having great potential to meet the challenges of food and nutritional security. ICAR-National Bureau of Plant Genetic Resources (NBPGR) has been working with a network of 10 regional stations located in different agro-climatic zones of India for the management of genetic resources. The linkages established with CGIAR centres, national crop-based institutes and state agricultural universities are the backbones of PGR utilization. NBPGR characterizes and evaluates germplasm conserved in the Indian national genebank for different traits and provides material to breeders. The effective utilization of PGR in crop improvement programmes depends mainly on their systematic characterization and evaluation, and identification of potentially useful germplasm. To date, we have characterized more than 2.35 lakh accessions of different agri-horticultural crops and developed core collections for the effective management of a large number of accessions. Presently, our focus is on the large-scale characterization of entire germplasm conserved in the Indian National Genebank and detailed evaluation of prioritized crops; identification of reference sets and core sets for enhanced utilization.

Key Words: Crop wild relatives, Characterization, Evaluation, Genebanks, Germplasm

Introduction

Plant genetic resources (PGR) are the genetic material of plants having immense value as a resource for mankind of present and future generations. The ICAR-NBPGR acts as a nodal institute at a national level for the management of PGR under the national agricultural research system. The Bureau's activities include PGR exploration, collection, exchange, characterization, evaluation, conservation and documentation. Genebanks houses pools of germplasm variability containing vital genes that play a crucial role in breeding programs for sustainable crop production. Efficient and effective use of germplasm in crop improvement depends upon a thorough understanding of the existing genetic variability, and knowledge of the traits and genes present in individual accession, which depends on the comprehensive characterization and evaluation. Without the information on the traits of the accessions conserved in genebanks, they become museums of plant accessions or living herbaria. To identify novel accessions corresponding to the genes with desired traits, it is prudent to characterize the germplasm collections conserved in the genebanks. Thus, the need for characterization and evaluation for sustainable use of agro-biodiversity has been felt universally. However, the characterization of large collections by plant breeders is time- and resource-consuming, therefore genebank

curators have developed a concept of a core set (~10% of the entire collection) from entire collections that are characterized at once to identify the targeted germplasm and use it efficiently (Frankel and Brown, 1984). The core set refers to a minimum set of germplasm that captures the entire range of genetic variability of any crop, with minimum repetitiveness. Being smaller in size and diverse in nature, the core set can be efficiently used as a kickoff point to enhance genetic gains, including the use of phenomics and genomics tools in less time. Further, depending on the number of collections it can be minimized to a mini core set that is ~1% of the entire collection. Also, trait-specific reference set can be identified for introgression, gene discovery and genomics studies.

Therefore, it is essential to use genetic diversity conserved in genebanks and identify novel germplasm, core sets and reference sets for their use in trait-specific breeding programs to enhance cultivar productivity and resilience to climate change.

Status and Strategies of Characterization, Evaluation and Utilization

To date, more than 2.35 lakhs accessions of different crops at ICAR-NBPGR have been characterized and evaluated (Singh *et al.*, 2020). The year-wise information

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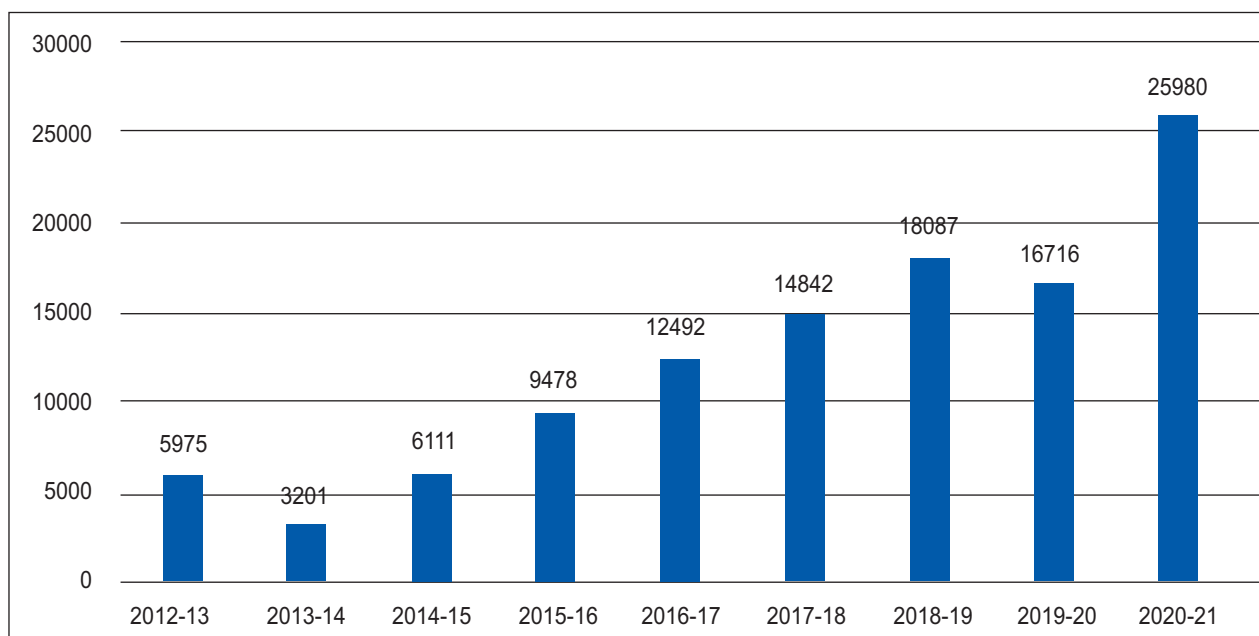


Fig. 1. Characterization of agri-horticultural crops (2012-2022)

on characterized accessions at ICAR- NBPGR have been depicted in Fig. 1.

To characterize the entire accessions conserved in the Indian national genebank (INGB), the mega programme on characterization and evaluation of germplasm was initiated in 2011-12 in which 22,416 accessions of wheat were characterized. Similarly, 18,775 accessions of chickpea were also characterized in 2012-13. These mega-characterization programmes paved the way for other prioritized crops conserved in INGB. Under a focused strategy for enhancing germplasm utilization, ICAR-NBPGR has shifted from piecemeal work to a complete characterization approach in recent years where entire accessions of prioritized crops were characterized in one go using a comprehensive strategic plan (Fig. 2). The large-scale characterization is being carried out under institute projects, Consortium Research Platform on agrobiodiversity and other network projects. The network project on minor pulses, minor oilseeds, rice, wheat and chickpea have been initiated under the mission mode programme supported by the Department of Biotechnology, Government of India. To facilitate germplasm management and utilization, core sets have been developed in different crops at ICAR-NBPGR (Table 1). Moreover, core sets have been developed for cowpea, mungbean, urdbean and horsegram are under evaluation and validation stage. Besides this, trait-specific germplasm (TSG) has been also identified from

large-scale characterization and evaluation programs which are becoming the material of choice for crop breeders nationally. Some trait-specific germplasm has been identified and validated which are mentioned in Table 2.

Future Perspectives

Global interdependence for PGR requirements is a matter of utmost importance to satisfy the needs of countries. There is a need to collaborate at local, national and global levels for the evaluation and utilization of the germplasm. Genebank researchers should work on the strategy of linking every accession conserved in genebanks with traits. Completely characterized genebank collections will facilitate their management and utilization. New tools of phenotyping including drones and digital data loggers need to be deployed to accelerate the phenotyping of the large number of accessions. Further, the characterization and evaluation activity requires substantial inputs and a decentralized evaluation network with the collaboration of NARS partners. Also, there is a need to modify the descriptors for evaluation accordingly and make the search for the desired characteristics in the database as quick and efficient as possible. The core collection concept is a more structured and efficient approach to identifying limited sets of diverse germplasm and utilising the same more effectively. The use of crop wild relatives (CWR) is needed to incorporate novel traits related to

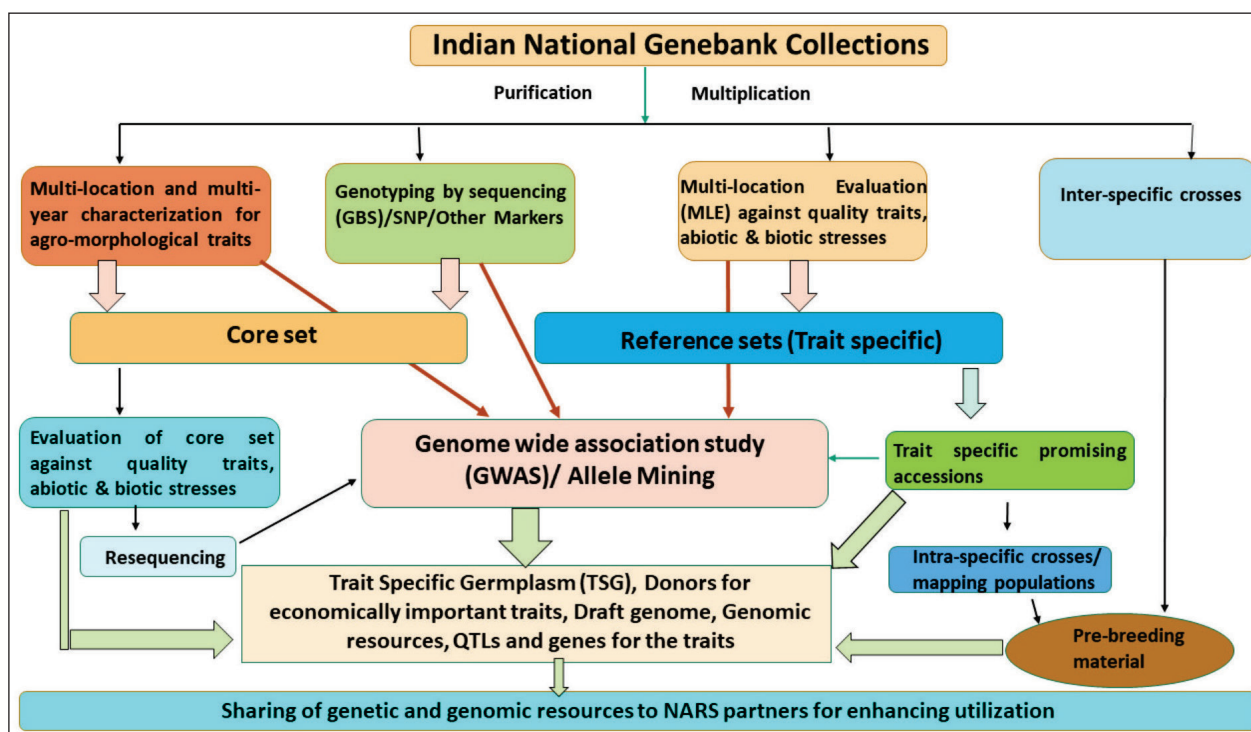


Fig. 2. Flowchart depicting strategies adopted by ICAR-NBPGR for germplasm utilization

Table 1. Large-scale characterization and core sets developed at ICAR-NBPGR during the last decade

Crop	No. of Acc. Characterized/ Descriptors	No. of Acc. in core collection	Reference
Wheat	22,464/34	2,226	Phogat <i>et al.</i> , 2020
Chickpea	14,651/21	1,103	Archak <i>et al.</i> , 2016
Barley	6,778/19	688	Kaur <i>et al.</i> , 2022
Lentil	2,324/26	170	Tripathi <i>et al.</i> , 2022
Wild lentil	405/18	96	Singh <i>et al.</i> , 2014
Cowpea	3,720	425	Under validation
Mungbean	4,100	400	Under validation
Urdbean	2,266	218	Under validation
Horsegram	2,186	300	Under validation

abiotic and biotic stresses, and nutritional quality to bring enhanced levels of productivity and stability of performance, and to provide food and nutritional security.

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Table 2. Glimpses of trait-specific germplasm identified by ICAR-NBPGR

Lentil, IC317520 (INGR 19072) Trait: Extended funiculus (Tripathi <i>et al.</i> , 2019)	
Lentil, IC241473 (INGR21223) Trait: Multi-podding germplasm (Tripathi <i>et al.</i> , 2022)	
Pearl millet, IC283734 (INGR 13056) Trait: High popping yield (Kumari <i>et al.</i> , 2016)	
Wheat, IC529962 (INGR19044) Trait: Highly resistant to spot blotch (Kumari <i>et al.</i> , 2018)	
Chickpea, EC267301(INGR 21137) Trait: Resistant to Ascochyta blight (Gayacharan <i>et al.</i> , 2020)	

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