Indian J. Plant Genet. Resour. 29(3): 261-264 (2016)
DOI 10.5958/0976-1926.2016.00040.1

Germplasm Management for Enhanced Genetic Gains

Hari D Upadhyaya

RS Paroda Genebank, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Telangana–502324, India

Challenges to Global Agriculture

Feeding 9.3 billion population by middle of 21st century the safe and nutritious food is the greatest challenge to the humanity. Agriculture is vulnerable to global warming and depletion of natural resources. Biodiversity loss, risk of change in pest dynamics, declining food quality and greater risk to food contamination (mycotoxins) are other adverse impact of global warming (Dwivedi *et al*., 2013). South Asia and sub-Saharan Africa are predicted to be worst affected due to climate change and variability effects and it is in these regions that ICRISAT mandate crops (chickpea, pigeonpea, groundnut, pearl millet, sorghum, and finger millet) are largely grown and consumed (FAO, 2014). More importantly, the risk absorbing capacity of the farmers in these regions is low and therefore, developing climate-resilient technologies including improved and nutritious seeds together with judicious management of natural resources is the way forward to address food and nutritional security.

Yield Increase and Genetic Gains

Globally, following adoption of improved technologies including seed, productivity of maize, rice and wheat has been drastically increased, while such a dramatic increase was not observed in coarse grains and legumes (Fig. 1) (FAO, 2014). Of recent, the yield in many crops either stagnated, declined or showed only marginal increase (Fig. 1). Genetic gain is defined as the annual increase in yield realized through crop breeding. A review of literature reveals <1.0 year^{-1} genetic gains through breeding in many crops, for example, from 0.65% year^{-1} to 0.74% year^{-1} in wheat (Zhou *et al*., 2007; Sharma *et al*., 2012), 0.85% year^{-1} in sorghum (Woldesemayat *et al*., 2015), and from 0.43% year^{-1} to 1.89% year^{-1} in groundnut (Hagos *et al*., 2012; Haro *et al*., 2013). There is therefore a need to double the genetic gains in most crops to increase food and nutritional security to growing world population.

Plant Genetic Resources (PGR) for Enhanced Genetic Gains

PGR are the basic raw materials to power current and future progress in crop improvement programmes. Globally, 7.4 million accessions are conserved in more than 1,750 genebanks (FAO, 2010). RS Paroda genebank at ICRISAT, Patancheru, India has the largest collection (1,24,305 accessions) of its mandate crops from 144 countries (www.icrisat.org), conserved as active (4°C temperature and 30% relative humidity in medium-term storage) and (116,491 accessions) in base (-20°C temperature in long-term storage) collections.

Low use of germplasm is a major concern as only less than 1% of assembled germplasm has been used in breeding programmes globally (Upadhyaya *et*

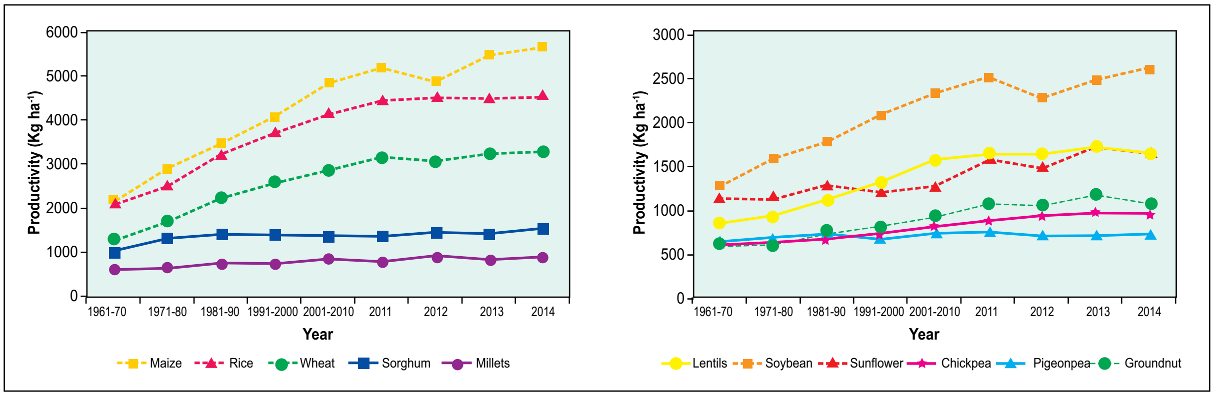

Fig. 1. Trends in productivity of important cereals and legume crops during 1961-2014.

**Author for Correspondence: Email- h.upadhyaya@cgiar.org* *al*., 2006) leading to a narrow genetic base in most crop cultivars. For example, 50% of wheat, 75% of potato, 50% of soybean cultivars grown in USA trace back to 9, 4 and 6 genotypes in their pedigrees, respectively (World Conservation Monitoring Centre, 1992). Enhanced use of germplasm can be achieved through developing representative core (10% of entire collection) and mini-core (10% of core or 1% of entire collection) collections facilitating extensive evaluation of germplasm and identification of genetically diverse accessions with agronomically beneficial traits for use in breeding programmes.

Forming Core and Mini-core Collections

Large size of collections and lack of reliable data on traits of economic importance, which show high genotype × environment interaction are considered as the main reasons for low use of genetic resources. To overcome this core and mini-core (Upadhyaya and Ortiz, 2001) collections, based on passport, characterisation and evaluation data and reference set based on genotyping information are now available in ICRISAT mandate crops and small millets (Upadhyaya, 2015, www.generationcp.org). Due to its reduced size and representativeness of species diversity, the mini-core collections are an ideal genetic resources for an in depth characterisation of its biological diversity and use in crop improvement programmes (Fig. 2). So far, the Genebank has provided 274 sets of mini-core collections of different crops to scientists in 36 countries and 114 sets to scientists at ICRISAT.

Identifying New Sources of Variations using Mini-core Collections

Systematic evaluation of core/mini-core collections resulted in identification of a number of germplasm lines with agronomically and nutritionally beneficial traits in addition to resistance/tolerance to abiotic and biotic stresses. For example, multiple stress resistance in chickpea (Upadhyaya *et al*., 2013); multiple stress resistance and nutrient dense (oil, protein, Fe, Zn, oleic acid) in groundnut (Upadhyaya *et al*., 2014a); high sugar stalk sorghum germplasm (Upadhyaya *et al*., 2014b); downy mildew resistant pearl millet (Sharma *et al*., 2015) or nutrient dense finger and foxtail millets (Upadhyaya *et al*., 2011 a, b).

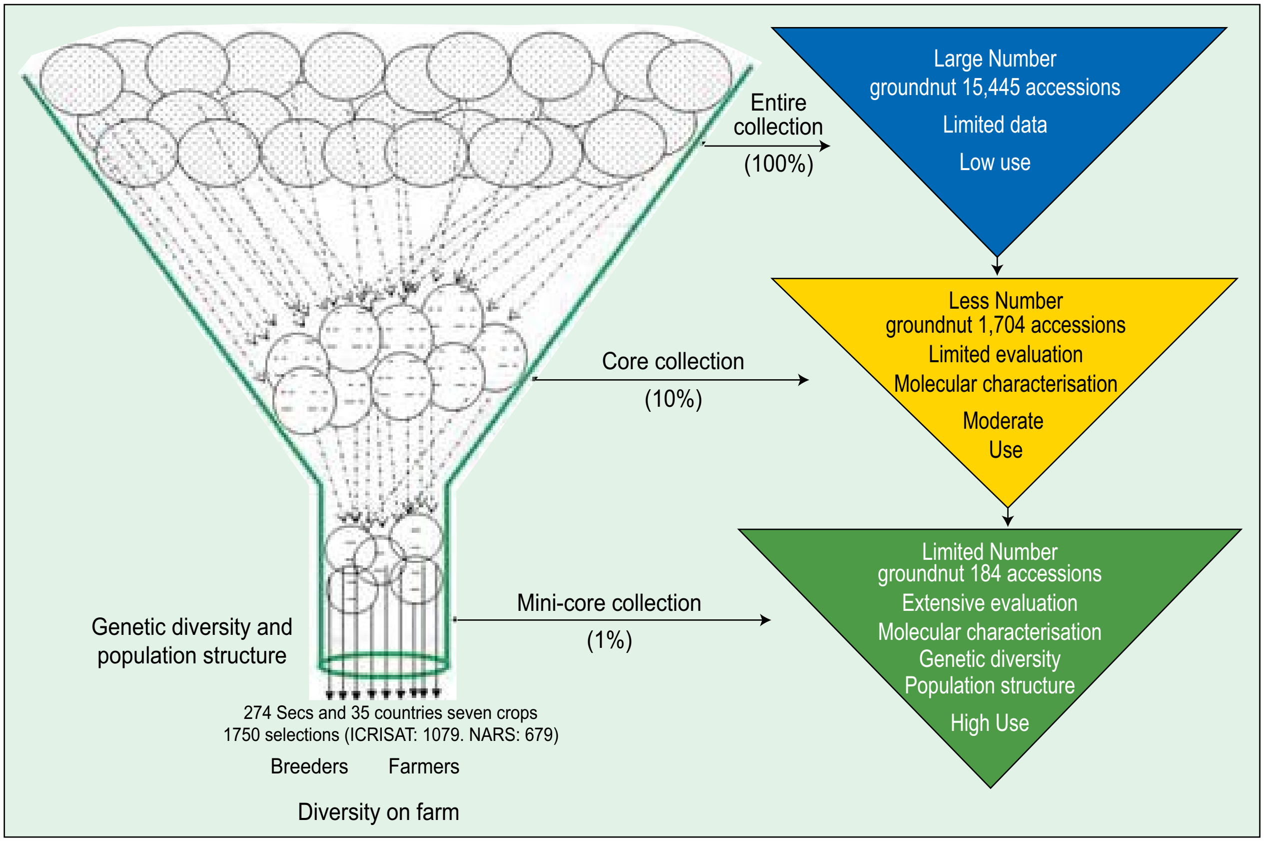

Fig. 2. Mini-core collections for enhanced use of germplasm

Enhanced Uptake of Germplasm in Crop Breeding

An analysis of the uptake of germplasm in crop improvement programmes at ICRISAT showed that germplasm use has increased since the formation of the mini-core collections in some crops. For example, 30% stresses tolerant accessions used in breeding during 2005-2009 were from mini-core, while in 2010-2014, more emphasis (17%) was given to those germplasm possessing yield and seed nutritional traits. The emphasis in groundnut during 2005-2009 was on stress tolerance (37% from mini-core), which during 2010-2014 changed to involving both stress tolerance (54%) and yield and quality (52%) traits in breeding.

Germplasm Released as Cultivars

To date, 109 germplasm lines supplied by RS Paroda genebank were directly released as 146 cultivars in 51 countries, few lines in more than three countries. For example, a chickpea landrace ICC 11879 was released in eight Mediterranean countries; a vegetable type pigeonpea landrace ICP 7035 in Fiji, India, China, Nepal and Philippines or a groundnut accession ICG 7827 in nine countries. Over 800 cultivars were released in 79 countries utilising germplasm and breeding lines from ICRISAT.

Economic Impact of PGR Use in Cultivar Development

The PGR contribute to development of breeding populations or direct release of germplasm as cultivars. PGR has been particularly useful in adding disease resistance through hybridization or when a resistant PGR has been released as cultivar. This has significant economic impact on farmers. For example, a wilt resistant pigeonpea landrace ICP 8863 released as 'Maruti' in India in 1986 benefited US$75 million by 1996. Similarly, in case of groundnut a single germplasm line PI 203396, resistant to tomato spotted wilt virus has contributed >200 million US $ annually in the USA.

Crop Wild Relatives (CWR) for Enhancing Cultigen Genepools

CWR harbour genes for stress tolerance, seed yield and nutritional traits (Rao *et al*., 2003; Upadhyaya, 2008). RS Paroda genebank conserves a total of 2,876 accessions of wild relatives. Several promising sources were identified for agronomic and nutritional traits and abiotic and biotic stress resistances in all mandate crops. ICRISAT made systematic efforts to infuse diversity from wild relatives to enhance resistance to pod borer in chickpea and pigeonpea, and to rust and leaf spots in groundnut (Upadhyaya, 2015). In groundnut wild species through amphidiploid has been successfully used to enhance 100-seed weight, pod yield (Upadhyaya, 2008) and traits related to drought tolerance such as specific leaf area and SPAD value using chlorophyll meter.

Accelerating Genetic Gain through Use of Genetic and Genomic Resources

ICRISAT mandate crops are no more orphan but genetic (germplasm representative subsets, stress tolerant and nutritionally dense seed, genetic mapping populations) and genomics (DNA markers, high density genetic maps, reference genomes) resources rich crops. Researchers are now using high throughput phenotyping and genotyping platforms (including genotyping by sequencing) to dissect the genetic and physiological basis of trait expression and deployment to accelerate genetic gains in crop breeding. In addition, researchers are now sequencing genomes of diversity panels (for example, 300-chickpea or groundnut genomes) and its comparison with reference genome is expected to associate sequence difference with agronomically beneficial traits.

The judicious use of these genetic and genomic resources have enabled researchers identify significant marker-trait associations or candidate genes associated with agronomic traits, for example, stress tolerance and agronomic traits in sorghum, chickpea and groundnut. In addition, the use of groundnut germplasm lines identified from mini-core collection have resulted in developing exceptionally high oil (up to 63%, compared to ~48% in control cultivar) and high-yielding breeding lines, indicating that new germplasm sources contribute to enhancing genetic gains.

In conclusion, plant genetic resources play an important role in developing cultivars with high genetic gains to meet the adverse effects of climate change on global agriculture. Use of representative subsets such as mini-core collections serves as an ideal diversity panels for trait discovery. The availability of high throughput genotyping and phenotyping facility at ICRISAT has opened the gateway to accelerate understanding of the genetic control of the trait expression and subsequently to rapid genetic gains in crop breeding.

References

Dwivedi S, KL Sahrawat, HD Upadhyaya and R Ortiz (2013) Food, nutrition and agrobiodiversity under climate change. *Adv. Agron*. **120**: 1-128.

FAO (2010) Food and Agriculture Organization. The second report on the state of the world's plant genetic resources for food and agriculture. Rome, Italy.

FAO (2014) Food and Agriculture Organization. http://www/FAO.ORG/FAOSTAT database.

Hagos F, H Zeleke and B Woyossa (2012) Genetic gain in yield and yield related traits of groundnut [*Arachis hypogea* (L.)] in Central Rift Valley of Ethiopia. *East African J Sci*. **6(2)**: 125-136.

Haro RJ, J Baldessari and ME Otegui (2013) Genetic improvement of peanut in Argentina between 1948 and 2004: Seed yield and its components. *Field Crops Res.* **149(1):** 76-83

Rao NK, LJ Reddy and PJ Bramel (2003) Potential of wild species for genetic enhancement of some semi-arid food crops. *Genet. Resour. Crop Evol*. **50**: 707-721.

Sharma RC, J Crossa, G Velu, J Huerta-Espino, M Vargas, TS Payne and RP Singh (2012) Genetic gains for grain yield in CIMMYT spring bread wheat across international environments. *Crop Sci.* **52**: 1522-1533

Sharma R, HD Upadhyaya, S Sharma, VL Gate and C Raj (2015) Identification of new sources of resistance to multiple pathotypes of *Sclerospora graminicola* in the pearl millet mini-core germplasm collection. *Crop Sci*. **55**: 1-10. doi:10.2135/cropsci2014.12.0822

Upadhyaya HD (2008) Crop Germplasm and wild relatives: a source of novel variation for crop improvement. *Korean J Crop Sci.* **53**: 12-17.

Upadhyaya HD (2015) Establishing core collections for enhanced use of germplasm in crop improvement. *J. Crop Breed. Gen.* **1-1**: 1-12.

Upadhyaya HD, N Dronavalli, SL Dwivedi, K Kashiwagi, L Krishnamurthy, S Pande, HC Sharma, V Vadez, S Singh, RK Varshney and CLL Gowda (2013) Mini-core collection as a resource to identify new sources of variation. *Crop Sci*. **53**: 2506-2517.

Upadhyaya HD, SL Dwivedi, V Vadez, F Hamidou, S Singh, RK Varshney and B Liao (2014a) Multiple resistant and nutritionally dense germplasm identified from mini-core collection in peanut. *Crop Sci*. **54**: 679-693.

Upadhyaya HD, SL Dwivedi, P Ramu, SK Singh and S Singh (2014b) Genetic variability and effect of post-flowering drought on stalk sugar content in sorghum mini-core collection. *Crop Sci.* **54**: 2120-2130.

Upadhyaya HD, CLL Gowda, HK Buhariwalla and JH Crouch (2006) Efficient use of crop germplasm resources: identifying useful germplasm for crop improvement through core and mini-core collections and molecular marker approaches. *Plant Genet. Resour.* **4**: 25-35.

Upadhyaya HD, S Ramesh, S Sharma, SK Singh, SK Varshney, NDRK Sharma, CR Ravishanker, Y Narasimhudu, VG Reddy, KL Sahrawat, TN Dhanalakshmi, MA Mgonja, HK Parzies, CLL Gowda and S Singh (2011a). Genetic diversity for grain nutrients contents in a core collection of finger millet [*Eleusine coracana* (L.) Gaertn.] germplasm. *Field Crops Res*. **121**: 42-52.

Upadhyaya HD, and R Ortiz. (2001) A mini-core subset for capturing diversity and promoting utilisation of chickpea genetic resources in crop improvement. Theor. App. Genet. **102**:1292-1298.

Upadhyaya HD, CR Ravishankar, Y Narasimhudu, NDRK Sarma, SK Singh, SK Varshney, VG Reddy, S Singh, HK Parzies, SL Dwivedi, HL Nadaf, KL Sahrawat and CLL Gowda (2011b). Identification of trait-specific germplasm and developing a mini-core collection for efficient use of foxtail millet genetic resources in crop improvement. *Field Crops Res*. **124**: 459-467.

Woldesemayat MY, F Mekbib and S Gebeyehu (2015) Genetic gain in lowland sorghum [*Sorghum bicolor* (L.) Moench] varieties in Ethiopia. *Int. J. Hort. Pl. Breed. Sci.* **2(1):** 1-13.

World Conservation Monitoring Centre (1992) *In:* Global biodiversity: status of the earth's living resources (Groombridge, B ed.), Chapman & Hall.

Zhou Y, HZ Zhu, SB Cai, ZH He, XK Zhang, XC Xia and GS Zhang (2007) Genetic improvement of grain yield and associated traits in the Southern China winter wheat region: 1949 to 2000. *Euphytica* **157(3):** 465-473.