

Enhancement of the use and impact of germplasm in crop improvement

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Abstract

Plant genetic resources are raw materials and their use in breeding is one of the most sustainable ways to conserve biodiversity. The ICRISAT has over 120,000 accessions of its five mandate crops and six small millets. The management and utilization of such large diversity are greatest challenges to germplasm curators and crop breeders. New sources of variations have been discovered using core and minicore collections developed at the ICRISAT. About 1.4 million seed samples have been distributed; some accessions with specific attributes have been requested more frequently. The advances in genomics have led researchers to dissect population structure and diversity and mine allelic variations associated with agronomically beneficial traits. Genome-wide association mapping in sorghum has revealed significant marker–trait associations for many agronomically beneficial traits. Wild relatives harbour genes for resistance to diseases and insect pests. Resistance to pod borer in chickpea and pigeonpea and resistance to rust and late leaf spot in groundnut have been successfully introgressed into a cultivated genetic background. Synthetics in groundnut are available to broaden the cultigen's gene pool. ICRISAT has notified the release of 266 varieties/cultivars, germplasm, and elite genetic stocks with unique traits, with some having a significant impact on breeding programs. Seventy-five germplasm lines have been directly released for cultivation in 39 countries.

Keywords: association genetics; core and minicore collections; population structure and diversity; impact on breeding; plant genetic resources

Introduction

Worldwide, 3993 million tonnes are annually contributed to food production by cereals, legumes, oilseeds, roots and tubers, and plantains and bananas (<http://faostat.fao.org>, data accessed on July 10, 2013), among which cereals contribute predominantly (64.6%). The contribution of legumes to the world food basket is only about 2%. However, legumes are rich sources of dietary protein to millions of people, more so in the developing countries. Global food production should be doubled to feed nine billion people in 2050, and to achieve this, the

annual yield should increase at the rate of 2.4% per year. The yields in many crops are either stagnated or much below that projected to double the production by 2050 (Ray *et al.*, 2013). Sustaining and increasing crop yields, through technological innovations, is the way forward to increase global food production to meet the growing food demand (McCouch *et al.*, 2013).

Why low use of germplasm in breeding

Reasons for the underutilization of germplasm include the following: (1) non-availability of reliable information on traits of economic importance; (2) linkage load of undesirable genes and assumed risks; (3) restricted access to germplasm collections and regulations

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governing international exchange; (4) enhanced role of non-additive genetic variations when diverse germplasm collections are used by the breeders; (5) lack of robust, cost-effective tools to facilitate the efficient utilization of exotic germplasm in crop breeding; and (6) limited exposure to available germplasm and re-circulation of the same genotypes in breeding (Duvick, 1995; Dwivedi *et al.*, 2009; Upadhyaya *et al.*, 2011a).

Developing representative sets as a means to discover new sources of variation

Core (Frankel, 1984) and minicore (Upadhyaya and Ortiz, 2001) collections, which represent diversity of the entire collection of a given species, have been suggested as a gateway to enhance the utilization of germplasm in crop breeding. These subsets are available in chickpea (Upadhyaya and Ortiz, 2001; Upadhyaya *et al.*, 2001), groundnut (Upadhyaya *et al.*, 2002, 2003), pigeonpea (Reddy *et al.*, 2005; Upadhyaya *et al.*, 2006b), pearl millet (Upadhyaya *et al.*, 2009a, 2011e), sorghum (Grenier *et al.*, 2001; Upadhyaya *et al.*, 2009b), finger millet (Upadhyaya *et al.*, 2006a, 2010), foxtail millet (Upadhyaya *et al.*, 2008b, 2011c) and proso millet (Upadhyaya *et al.*, 2011d).

Research carried out to date suggests these subsets to be useful for finding germplasm with agronomically beneficial traits, e.g. resistance to abiotic and/or biotic stress in chickpea (Upadhyaya *et al.*, 2013a), finger millet (Kiran Babu *et al.*, 2013), groundnut (Upadhyaya *et al.*, 2014), pigeonpea (Krishnamurthy *et al.*, 2012; Sharma *et al.*, 2012a), pearl millet (Sharma *et al.*, 2013a) and sorghum (Sharma *et al.*, 2010, 2012b; Vadez *et al.*, 2011). Genetically diverse and nutritionally dense germplasm accessions have also been reported in finger millet (Upadhyaya *et al.*, 2011b), foxtail millet (Upadhyaya *et al.*, 2011c) and groundnut (Upadhyaya *et al.*, 2012a, b).

Population structure, diversity, allele mining and association genetics

Understanding how diversity is structured to unlock its potential for crop improvement is an emerging area made possible by rapid advances in the scale, robustness and reliability of marker technologies and the sharp fall in the unit costs of their deployment. The genomes of several food crops including chickpea, foxtail millet, pigeonpea and sorghum have been sequenced (Hamilton and Buell, 2012; Varshney *et al.*, 2012, 2013), while groundnut genome sequences will be available soon (<http://www.peanutbioscience.com>). Furthermore, resequencing of

diverse germplasm collections may provide researchers opportunities to associate sequence differences with trait variations (Lai *et al.*, 2010; Zheng *et al.*, 2011).

Genotyping of representative subsets has revealed abundant allelic diversity to differentiate wild relatives from cultivated types and grouped the germplasm into distinct clusters, with many of the alleles being found to be unique to particular accessions in each crop (Upadhyaya *et al.*, 2008a; Billot *et al.*, 2013; www.generation.cp.org), which may be further explored to associate allelic diversity with temporal and eco-geographical diversity.

Genome-wide association mapping in sorghum has revealed significant marker-trait associations, with many of the identified markers being co-mapped on the same linkage groups previously reported to be harboring quantitative trait loci or candidate genes associated with anthracnose, leaf rust, and grain mold resistance, tillering, and plant height and maturity (Upadhyaya *et al.*, 2012c, d; Wang *et al.*, 2012; Upadhyaya *et al.*, 2013c, d).

Pre-breeding to accelerate cultivar development

Pre-breeding, the development of semi-finished products, provides a unique opportunity through introgression of desirable gene(s) from exotic germplasm into genetic backgrounds readily used by the breeders with minimum linkage drag (Sharma *et al.*, 2013b). Resistance to pod borer has been introgressed using wild relatives from secondary and tertiary gene pools in pigeonpea, with most of these lines exhibiting variability for agronomic traits in addition to resistance to phytophthora blight, bruchid and pod fly (Mallikarjuna *et al.*, 2011; Jadhav *et al.*, 2012; Ramgopal *et al.*, 2013). Wild *Cicer* species have been used to introgress resistance to pod borer, nematodes, phytophthora root rot, ascochyta blight and botrytis gray mold in chickpea (Ramgopal *et al.*, 2013). Amphidiploids, originating from interspecific crosses, have been found to exhibit resistance to late leaf spot and peanut bud necrosis in groundnut (Mallikarjuna *et al.*, 2012; Shilpa *et al.*, 2012).

Chromosome segment substitution lines (CSSLs) provide additional useful genetic resources to broaden a cultigen's gene pool (Dwivedi *et al.*, 2008). CSSLs have been developed in groundnut, which may be used for deciphering the molecular basis of trait variations (Fonceka *et al.*, 2012).

Research carried out to date suggests that wild relatives have not only contributed genes for resistance to biotic stress, but also variations to yield and quality traits (Dwivedi *et al.*, 2008; Imai *et al.*, 2013). Preliminary research carried out at the ICRISAT has revealed that

some cryptic introgressed lines, originating from TMV 2 and TxAG-6 cross, are phenotypically similar to TMV 2, but produce large seeds and exhibit higher pod yield (Upadhyaya *et al.*, 2013b). TxAG-6 is a synthetic amphidiploid (Simpson *et al.*, 1993), while TMV 2 is a medium-maturing cultivar, adapted to peninsular India (ICRISAT, 2009).

Germplasm use and impact

To date, 75 unique germplasm accessions have been released for cultivation in 39 countries. Some of these have been widely used in breeding programmes or grown widely, e.g. an early-maturing *Iniadi* pearl millet landrace from West Africa (Andrews and Kumar, 1996), a sorghum landrace (IS 33844) from Maharashtra, India (Reddy *et al.*, 2007), early-maturing and rosette-resistant groundnut landraces ICG 12991 and ICG 12988 in Uganda (Subrahmanyam *et al.*, 2000; Deom *et al.*, 2006), and a vegetable pigeonpea landrace (ICP 7035) with large seed size and resistance to sterility mosaic in many Asian countries (Shiferaw *et al.*, 2004). The ICRISAT has notified the release of its 266 varieties/cultivars, germplasm, and elite genetic stocks with specific traits, mostly published as registration articles in *Crop Science* for worldwide information dissemination.

Outlook

In the context of advances in genomics, especially next-generation sequencing technologies, genomics-based germplasm science is coming up now. Although understanding diversity in germplasm collections for a few traits based on phenotyping or genotyping based on a few markers was a challenging task in the past, now it is possible to understand genome-wide diversity in germplasm collections by resequencing at least in those species where reference or draft genome sequences are available. Such datasets are also accelerating efforts made to identify marker–trait associations as well as superior lines based on genome-wide association studies. Genomics-based germplasm analysis is expected to enhance the use of germplasm and have an impact on breeding programmes in the future.

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