



GENETIC AND GENOMIC RESOURCES FOR GRAIN CEREALS IMPROVEMENT

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Introduction

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Grain cereals, including rice, wheat, maize, barley, oat, sorghum, and millets (pearl millet, finger millet, foxtail millet, proso millet, barnyard millet, little millet, and kodo millet), are members of the grass family and occupy a considerable area under commercial cultivation worldwide. These cereals are also used to produce animal feed, oils, starch, flour, sugar, and processed foods including malts and alcoholic beverages. The increasing human population and enhanced standard of living are placing greater demands on food-related requirements in terms of quality, quantity, as well as genetic variability. As a base material for future crop improvement, genetic resources are the key to future food and nutritional security. An excellent performance has been obtained by applying contemporary approaches for germplasm characterization and evaluation to manage the crop genetic resources effectively and efficiently. Use of genomic resources and specialized germplasm sets, such as minicore collection and reference sets, will facilitate identification of trait-specific germplasm, trait mapping, and allele mining for resistance to major prevailing biotic and abiotic stresses and also for useful agronomic traits of interest. Here we conclude brief details on the genetic and genomic resources research on important grain cereals.

1 Rice

Rice is the staple food crop of more than half the world's population. Asia accounts for more than 90% of the world's total rice production and the balance is divided almost equally between Africa and Latin America, where the demand for rice is increasing. Rice has been cultivated in Asia since ancient times, and for generations farmers have maintained thousands of different local landraces for their subsistence agriculture (Jackson, 1995). Most countries in Asia maintain rice germplasm collections, and the largest are in China, India, Thailand, and Japan (FAO, 2013). The International Rice Research Institute (IRRI) holds the largest collection and is also the most genetically diverse and complete world rice collection. Africa contains a diversity of both cultivated and wild/weedy rice species. The region has 8 species representing 6 of the 10 known genome types. Genetic resources of these species are conserved in various global germplasm repositories, but they remain under collected and hence underrepresented in germplasm collections. The lack of *in situ* germplasm conservation programs further exposes them to possible genetic erosion or extinction. In order to obtain maximum benefits from these resources, it is imperative that they are collected,

efficiently preserved, and optimally utilized. High-throughput molecular approaches, such as genome sequencing, could be employed to study their genetic diversity and precise value and thereby enhance their use in rice genetic improvement.

2 Wheat

Wheat is the most important grain cereal for ensuring food security worldwide. Total demand for wheat has been growing with the increasing human population pressure globally. The production of wheat has increased substantially from 218.5 million tons in 1961 to 732 million tons in 2013 (www.fao.org) primarily due to the adoption of semidwarf high-yielding and input-responsive cultivars. Likewise, wheat genetic resources have played a pivotal role in genetic improvement by contributing potential gene sources for yield, wider adaptation, short stature plant height, improved grain quality, and resistance/tolerance to major prevailing biotic and abiotic stresses. In view of climate change and genetic erosion associated with many natural and anthropogenic factors as well as rapid expansion and domination of mega wheat cultivars across the major wheat agroecologies, efforts have been made to collect and preserve wheat genetic resources in *ex situ* collection. The center of genetic diversity for wild wheat relatives includes Egypt, Israel, Jordan, Lebanon, Syria, Turkey, Armenia, Azerbaijan, Iraq, Iran, Afghanistan, and the Turkic Republics of Central Asia. The range of distribution of wheat relatives occurs from the Canary Islands to western China and from southern Russia to northern Pakistan and India. To-date more than 900,000 wheat accessions (wild/weedy relatives, landraces, synthetic wheats, advance breeding lines, genetic stocks) are conserved in different gene banks worldwide. The wheat genetic resource center (WGRC) maintains 2500 wheat accessions including cytogenetic stocks, developed by wheat researchers across the globe. Genes for host-plant resistance to viral, bacterial, fungal, and insect pests and major abiotic stresses have been identified and introgressed into agronomically elite genetic backgrounds. Effective utilization of a large number of genetic resources, however, is a big challenge. Application of modern tools and techniques, such as focused identification of germplasm strategy (FIGS), effective gene introgression methods, and genomics, are essential in improving genetic resource utilization and improving breeding efficiency.

3 Barley

Barley belongs to the genus *Hordeum*, and all species have the basic chromosome number of $n = x = 7$. Furthermore, cultivated barley, *Hordeum vulgare* ssp. *vulgare*, and its immediate wild progenitor *H. vulgare* ssp. *spontaneous* (K. Koch.) Asch. & Graebn. are true diploid species with $2n = 2x = 14$ chromosome numbers. Likewise, other *Hordeum* species are diploid, tetraploid ($2n = 4x = 28$), or hexaploid ($2n = 6x = 42$). According to Harlan's gene pool concept, all barley species have been classified into three different gene pools. The primary gene pool includes elite breeding materials,

commercial cultivars, landraces, and the wild ancestor of cultivated barley. The secondary gene pool includes only one species, *Hordeum bulbosum* L., which shares the basic *Hordeum* genome. The tertiary gene pool of barley is very large and comprises all other remaining wild species (Bothmer et al., 1991). Genetic diversity of any crop species is defined as genetic variation within and between populations, landraces, and cultivars, arising due to recombination, mutations, and introgression. The use of highly diverse germplasm increases the chances for success in developing wider populations through introgression. Globally, more than 400,000 barley accessions are available for research and breeding purposes at different gene banks. Total gene bank collections represent landraces (44%), breeding lines (17%), crop wild relatives (CWR) (15%), commercial cultivars (15%), and other genetic stocks (9%).

4 Oat

Oat is one of the minor cereals used as feed, food, and industrial feedstock purposes. Common oat (*Avena sativa*) is the cultivated species grown under diverse agroecologic conditions. Globally, germplasm collection of *Avena* species consist of approximately 131,000 accessions preserved by more than 63 countries. Further distribution of total germplasm holding revealed that only 14 countries held more than 80% genetic resources. The largest collections are held in Canada (~40,000), the United States (~22,000), and Russia (~12,000). In Canada and Russia, cultivated species and several wild species are preserved, while in the United States emphasis was placed on *A. sativa* and its wild relatives from the primary gene pool. The genetic reserve conservation is defined as management and monitoring of genetic diversity of natural populations of CWR in specific areas for the long-term preservation. *On-farm* conservation is focused on cultivated species and in particular on landraces and traditional cultivars, and consists of agrobiodiversity preservation in a dynamic agroecosystem that is self-supporting and favoring evolutionary processes. The issue of *in situ* conservation of genetic resources in the genus *Avena* has been specifically targeted at the framework of the European project (Frese et al., 2013). It is aimed at the creation of conservation strategies for CWR and landraces and to transfer them into elite backgrounds.

5 Sorghum

Worldwide, a quarter million sorghum accessions have been collected and maintained by several national and international gene banks and the biggest sorghum germplasm holders are the US Department of Agriculture (USDA) and the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), India. The majority of collections in the United States gene bank are from Ethiopia, Sudan, Yemen, Mali, India, and the United States (http://www.ars-grin.gov/cgi-bin/npgs/html/tax_stat.pl). About 16% of the world collection of sorghum (235,711 accessions) is conserved in ICRISAT's

gene bank in India (FAO, 2009). This collection of 37,949 accessions from 92 countries comprises 32,578 landraces, 4,814 advanced breeding lines, 99 cultivars, and 458 wild and weedy relatives (Upadhyaya et al., 2014). Most of the accessions were characterized and evaluated for several traits of interest including trait-specific germplasm. Sorghum researchers can access these useful germplasm accessions to meet their research needs. More importantly, core and minicore collections or genotype-based reference sets, representing diversity available in the whole germplasm have been formed and using these subsets new sources of variations have been identified for use in sorghum genetic improvement. Furthermore, the ICRISAT collection is divided into active and base collections (Upadhyaya et al., 2014). More than 30,000 sorghum accessions have also been conserved in the Svalbard Global Seed Vault, Norway (Upadhyaya et al., 2014). Furthermore, molecular-marker development, genome mapping, and tagging of agronomically important traits have been taken well into consideration. A large number of single-nucleotide polymorphisms were identified through whole genome resequencing (Morris et al., 2013; Mace et al., 2013).

6 Pearl millet

Pearl millet is an important staple crop in the semi-arid tracts of Asia and Africa. Globally, 66,682 accessions of pearl millet are conserved in 97 gene banks, in which, ICRISAT has the largest collection. Tremendous genetic diversity has been observed in the cultivated gene pool for morphoagronomic traits and resistance to abiotic and biotic stresses, including nutritional traits. Core and minicore collections developed at ICRISAT would facilitate extensive evaluation and identification of trait-specific diverse germplasm accessions. Interspecific crosses were also developed within the primary gene pool for widening the genetic base of elite genetic background. A large number of germplasm accessions have been characterized at ICRISAT for several morphoagronomic traits using pearl millet descriptor states (IBPGR and ICRISAT, 1993). These accessions showed large phenotypic diversity for almost all qualitative and quantitative traits. Substantial variation was also reported for morphologic traits among landraces and wild relatives from India, west and central Africa, Cameroon, Yemen, and Ghana (Dwivedi et al., 2012). Among abiotic stresses, high-temperature stress at seedling and reproductive stages has an impact on crop establishment and yield of pearl millet. Genetic variation has been observed for heat tolerance at seedling and reproductive stage among germplasm. A recent finding for reproductive stage heat tolerance over 3–4 years could identify tolerant breeding and germplasm lines (Gupta et al., 2015). Low-temperature stress at vegetative stage causes increased basal tillering and grain yield; at elongation stage, it leads to reduced spikelet fertility, inflorescence length, and decreased grain yield; at grain development stage, it leads to increase in grain yield (Fussell et al., 1980). Pearl millet germplasm tolerant to salinity have also been reported. At ICRISAT, characterization and evaluation of a large number of germplasm accessions has led to the identification of resistant/tolerant gene sources for downy mildew, smut, ergot, and rust (Upadhyaya et al., 2007). Several

germplasms with multiple disease resistance to major prevailing diseases have also been identified (Dwivedi et al., 2012). Enormous variability has been reported in pearl millet germplasm collection for protein (up to 24.3%) among 260 accessions and micronutrient concentrations among 191 accessions (Rai et al., 2015). Genomic resources are expected to increase with pearl millet genome sequence due for release and faster developments in next-generation sequencing technologies, which would enhance germplasm management and crop improvement.

7 Finger and foxtail millets

Finger and foxtail millets are important ancient crops of dry-land agriculture and the climate-resilient crops for food and nutritional security. Assessing genetic variability of germplasm collections, development and use of genetic and genomic resources for breeding high-yielding cultivars, developing crop production and processing technologies, value addition for improving consumption, public–private partnerships, and policy recommendations are needed to upscale these crops to make them more remunerative to the farming community.

These crops are highly nutritious with diverse usage, well adapted to marginal lands, and mostly grown by resource-poor farmers. Worldwide more than 46,000 foxtail millet and about 37,000 finger millet germplasm accessions have been preserved and the largest collections of finger and foxtail millets are in India and China, respectively. Considerable variation exists for various biotic and abiotic stresses, and for quality including important agronomic traits. Entire genetic diversity of these crops has been captured in the form of core and minicore collections and is being used in genetic and genomic studies for identification of new sources of variation. Genomic resources are available in foxtail millet, while in finger millet these resources are being developed. Furthermore, use of genetic and genomic resources need to be accelerated to assist in developing improved cultivars of these crops.

8 Proso, barnyard, little, and kodo millets

Proso, barnyard, little, and kodo millets are highly nutritious crops and have climate-resilient traits. Globally, about 50,000 germplasm accessions of these crops have been conserved, and the largest collections of proso millet are in the Russian Federation and China, barnyard millet in Japan, and kodo millet and little millet in India. These crops have larger variation for yield and its component traits including stress tolerance related characters. Core collections representing diversity of entire collections of these crops have been developed for identification of new sources of variation for major prevailing biotic and abiotic stresses, and for quality as well as important agronomic traits. Globally, more than 29,000 accessions of proso millet, 8,000 accessions each of barnyard and kodo millet, and more than 3,000 accessions of little millet have been conserved. The ICRISAT gene bank in India conserves 849 accessions of proso millet,

749 accessions of barnyard millet, 665 accessions of kodo millet, and 473 accessions of little millet under medium- and long-term storage. Limited research works have been done on germplasm characterization and evaluation of various agronomic traits, nutritional traits, and biotic and abiotic stresses. A few studies on germplasm characterization and evaluation were conducted by Upadhyaya et al. (2011) and identified important gene sources including trait-specific germplasm in these crops. Genomic resources are limited and efforts to develop such resources through high-throughput genotyping are in progress.

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