

Plant Genetic Resources: Effective Utilization for Sustainability



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Abstract

The very basis of any crop improvement programme is the extent of variability available for different economically important traits in the germ plasm. The germplasm exploration and collection have resulted in accumulation of enormous genetic diversity of crop plants in the gene banks. Therefore, concerted efforts need to be focussed for identification of valuable alleles in the germplasm especially from unexplored/'exotic' germplasm using high throughput phenol typing, multi-location evaluation and modern genomic tools. Once identified, these alleles can be effectively utilized in crop improvement programmes through targeted introgression using molecular marker assisted/genomic assisted breeding. Further, development of core and mini core sets along with the reference sets for trait of interest, focused identification of germplasm strategy, pre-breeding, gene prospecting and allele mining are essentially required for effective utilization of genetic resources.

Introduction

Plant genetic resources are the basic foundation block of sustainable agriculture on which global food and nutritional security depends. They comprise diversity of genetic material contained in landraces, varieties (obsolete and in use), genetic stocks, wild progenitors and breeding lines. Genetic diversity provides farmers and plant breeders with options to develop, through selection and breeding, new and more productive crop varieties, that are resistant to virulent pests and diseases and adapted to changing environments. Selections from diverse landrace populations can reveal high yielding genotypes, which can be used directly or in breeding programmes. In the 20th century, half of the increase in food production globally can be attributed to genetic improvement, whose benefits also include reduced reliance on environmentally harmful inputs, more stable yield, higher nutritional value. Human population is increasing at an alarming rate and is expected to increase from 6.9 billion to 9 billion by 2050.

To feed the world population, we need to increase the food production by 60% up to 2050 with the limited land and water resources [1] and plant genetic resources will play a major role in boosting crop production by utilizing trait specific germplasm through introgression into elite lines, allele mining, wide crossing, molecular marker assisted breeding etc. For effective utilization of germplasm in crop improvement

programme substantial knowledge of full genetic potential of the germ plasm, their availability with desired traits and proper database with interactive retrieval system are essentially required. Therefore, proper evaluation of available germplasm is an important activity for promotion of germplasm utilization. Since most of the agronomic traits show large genotype x environment interaction, therefore, require the evaluation over environments/locations. Evaluation of germplasm for biotic and abiotic stresses require hot spot locations and evaluation of quality traits is also important keeping in view the changing dietary and nutritional demands of the consumer.

Gene banks serve as repositories of genetic variation present in the entire gamut of germplasm comprising primitive varieties, landraces, wild relatives of crop species and modern varieties etc. Currently, more than 1,750 individual gene banks are in place across the globe, and about 130 of which hold more than 10,000 accessions each. The total number of accessions conserved by *ex situ* methods worldwide has increased by approximately 20 per cent since 1996, reaching 7.4 million [2]. A total of 2,802,770 accessions are being conserved world-wide by 446 organizations represented in Genesys. Indian National Gene bank holds more than 4 lakhs accessions comprising wild relatives and landraces of about 2000 crop species. Till date over 2.35 lakhs accession of different agri-horticultural crops have been characterized and evaluated [3].

Utilization of Germplasm

Surprisingly, in spite of large collections available across the world, only limited number of germplasm accessions (<1%) have been utilized in crop improvement programs such as in wheat, maize, spring barley, soybean and other grain legumes [4] leading to a narrow genetic base. The major factor responsible for low utilization of plant genetic resources worldwide is the unavailability of evaluation and characterization data as the primary thrust so far has been mainly on characterization and regeneration of gene bank material and the value of PGR was not known. Characterization and evaluation of plant genetic resources for different morpho-physiological, biotic and abiotic stress and quality related traits etc. is essentially required for their efficient utilization in breeding programmes.

Further, the major bottleneck for limited use of germplasm in crop improvement programme is the large size of germplasm collections. Enhanced use of germplasm can be achieved through developing representative core (10% of entire collection) and minicore (10% of core or 1 % of entire collection) collections facilitating extensive evaluation of germplasm and identification of genetically diverse accessions with agronomic ally beneficial traits. Core collections have been developed by different countries and organizations for wheat, rice, maize, barley, beans, cassava, sweet potato, soybean, oats, brinjal, chickpea, wild lens etc. So far, gene banks have provided 274 sets of minicore collection of different crops in 36 countries [5].

Recently, In India, ICAR-National Bureau of Plant Genetic Resources (NBPGR) along with national partners has taken up initiatives to characterize gene bank material for prioritized crops for various economically important traits and also for identification and isolation of novel genes/alleles under various programs like National Initiative on Climate Resilient Agriculture and Consortium Research Platform. The entire set of around 22,000 wheat accessions were characterized for 34 agro-morphological traits, terminal heat tolerance using 18 morpho-physiological traits like canopy temperature, leaf rolling, heat susceptibility index etc. and biotic stresses including leaf, stem and stripe rusts and spot blotch diseases so that useful germplasm lines can be identified and used in crop improvement program. Also about 16,000 chickpea accessions were characterized for agronomic traits. Core sets has been developed in wheat for extensive evaluation and identification of traits specific germplasm [6].

New sources of resistance to rust and spot blotch diseases have been identified in wheat after evaluation under hot-spot locations and epiphytotic condition [7]. Under multi-location evaluation programme at ICAR-NBPGR trait specific germplasm has been identified in ten prioritized crops rice, wheat, maize, chickpea, pigeon pea, lentil, brassica, okra, brinjal and giloe. The information on identification of trait specific germplasm is available on NBPGR website. Also link of PGR portal comprising

all the passport as well as characterization data are available for the researchers.

Alternative Search for Genes: FIGS

Many plant genotypes are potential sources of novel genes that can improve drought tolerance, disease resistance and other traits. Since 1990s, geographic information system (GIS) has been specifically applied to the genetic resources conservation which is a database management system that can simultaneously handle digital spatial data and attached non-spatial attribute data [8]. Focused Identification of Germplasm Strategy (FIGS) combines agro-ecological information with data on plant traits and characteristics and identify sets of genotypes from large number of collections with a higher probability of containing specific 'target' traits. This strategy allows gene bank managers and agricultural researchers worldwide to screen large plant genetic resource collections more rapidly and accurately. It has helped identify sources of resistance to biotic stresses in wheat such as powdery mildew, Russian wheat aphid, stem rust, net blotch disease resistance in barley and abiotic stress tolerance such as drought tolerance in *Vicia faba* [9].

Utilization of wild species

Wild species are the reservoir of many useful genes/alleles as they have evolved under natural selection to survive climate extremes. In pulses, wild species of *Cicer*, *Cajanus*, and *Arachis* have been extensively screened and several of them were reported to have very high level of resistance/tolerance to various stresses. Among wild *Cicer* species, *C. bijugum*, *C. judaicum*, and *C. pinnatifidum* are the most important sources having the highest levels of resistance/tolerance to multiple stresses [4]. The dwarfing genes in wheat *Rht1* and *Rht2* were derived from a Japanese land race "Shiro Daruma" and in rice *sd1* was from "Dee-gee-woogen". Some other successful examples of germplasm utilization include, the only source of resistance to grassy stunt virus in rice, *Oryza nivara* [10], chickpea variety Pusa 1103 using *Cicer reticulatum*. The emerging threat to global crop production is climate variability, leading to frequent droughts as a result of erratic rainfall, prevalence of high temperature, water-logging, increased soil salinity, and emergence of new insect-pests and diseases. Due to climate change, several areas are now becoming unsuitable for cultivation of traditional crops. To cope with this situation, there is a need to breed new crop cultivars with a broad genetic base capable of withstanding frequent climatic fluctuations and wider adaptability due to co-adapted gene complex.

During the past decade, pre-breeding was recognized as an important tool to broaden the genetic base of the crops in Brazil, Cuba, Tajakistan, Ethiopia and The Russian Federation. However the major bottlenecks in using wild species are the compatibility in wide crossing and the linkage drag associated with the utilization of crop wild relatives. Further breaking the undesirable linkage drag through pre-breeding makes

the breeding program more time taking and cumbersome [4]. In wheat, the discovery of the Ph1/ph1 locus which regulates pairing and recombination between homoeologous (as opposed to homologous) chromosomes in wheat has been a very important finding [11,12]. Ph1 has been used widely and successfully in wheat to induce homoeologous recombination and the introgressed genome segments can be trimmed repeatedly to eliminate most of the linked undesirable alleles and/or genes.

Molecular Marker Assisted Utilization

The potential impact of molecular genetics on plant breeding is enormous and not so surprising given the explosion of new molecular technology and applications developed during the last decade. Progress in DNA markers became particularly important with the development of reliable polymerized chain reaction (PCR) based markers, such as microsatellites and amplified fragment length polymorphism (AFLP), Single Nucleotide Polymorphism (SNP), Genotype based sequencing (GBS) etc. Genotyping by sequencing, or next-generation sequencing, an ultimate MAS tool and a cost-effective technique, has been successfully used in implementing genome-wide association study (GWAS), genomic diversity study, genetic linkage analysis, molecular marker discovery and genomic selection under a large scale of plant breeding programs [13].

Furthermore, DNA markers are now used extensively to characterize germplasm (fingerprinting), to evaluate the genetic distance among accessions (genetic diversity) and to provide important supportive information to the fields of ecology, population genetics and also evolution. Till now 2300 varieties of > 35 crops have been fingerprinted to safeguard against biopiracy. Molecular markers are now a days used in identification, characterization and tagging of genes of economic interest. In rice, bacterial blight resistance genes Xa21, Xa23, Xa38(t) Xa27, Xa29 and Xa32(t) have been identified and transferred from related wild species, *O.longistaminata*, *O.rufipogon*, *O.nivara*, *O.minuta*, *O.officinalis* and *O.australiensis* respectively. Some of the genes have been transferred into cultivated crop species and varieties have also been released using Marker Assisted Selection based breeding approach e.g., Xa21 and Xa38 (*Oryza nivara*). In addition to this genes for grassy stunt virus, blast resistance, brown plant hopper, cytoplasmic male sterility, sheath blight and tungro virus have been transferred from wild species into the cultivated lines. In wheat, genes like Lr9 (*Aegilopes umbellulata*), Lr21 (*Ae. tauschii*), Lr25 (*Secale cereale*), Sr2 (*Triticum turgidum*), Sr36 (*T. timopheevi*), Sr38 (*Ae. ventricosa*), Yr15 (*T. dicoccoides*) and Pm8 (*Secale cereale*) have been transferred from wild species for resistance to leaf rust, stem rust, stripe rust and powdery mildew resistance [14].

Development of superior variety by accumulation of beneficial alleles from vast plant genetic resources is a major challenge. Enormous progress has been made in the last 15 years

in depositing an exponential amount of sequence information into Gene Bank. Based on gene and genome sequences, polymerase chain reaction (PCR) strategies are devised to isolate useful alleles of genes from a wide range of species. This capability enables direct access to key alleles conferring resistance to biotic and abiotic stresses, greater nutrient use efficiency, enhanced yield and improved quality. Using novel genomic tools, similar alleles responsible for a given trait and their variants in other genotypes can be identified through 'allele mining'. Identification of allelic variants from germplasm collections not only provides new germplasm for delivering novel alleles to targeted trait improvement but also categorizes the germplasm entries for their conservation.

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