



Exploring the Wild Germplasm for Crop Improvement

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Crop improvement needs selection of alleles for economic traits and one way is to explore the wild germplasm available in the nature. Such germplasm possess distinct agronomic traits which can be employed in breeding programmes. This is aptly called distant hybridization. The incorporation of allele/s from distant relative into the elite cultivar of crop provides an impetus to enhance peculiar trait. Concomitantly, it plays crucial role in evolution and speciation of species. It is imperative to carefully choose sources of desirable attributes depending on the degree of relationships, ploidy level, stability and inheritance of desirable traits. The wild germplasm should be increasingly exploited through surveys and from collections in seed banks for the search of new alleles.

Introduction

Selection methods in plant breeding has its roots in agriculture since long back, wherein humans preferred and selected high yielding, phenotypically superior crop varieties for cultivation. Subsequently, continued selection of alleles from the gene pool over years has brought a plateau in genetic diversity with narrow genetic base. The process in which genome of one distant species is transferred to another for combining diverged genomes into one nucleus is termed as distant/wide hybridization (DH). Hybridization carried between individuals of same genus is called inter-specific (*Triticum turanicum* x *Triticum timopheevi*) and that belonging to different genus is called inter-generic (*Triticum aestivum* x *Aegilops cylindrical*). Distant/wide hybridization breaks what is known as the species barrier for gene transfer and thus makes it possible to transfer the genome of one species to another, resulting in genotypic and phenotypic changes in the progenies. This is very important for species evolution and speciation since chromosome doubling of wide hybrids is responsible for the origin of many allopolyploid species. Repeated backcrossing of wide hybrids to their parental species has also contributed to the evolution and speciation of some species by gene introgression, i.e., the infiltration of chromosomes or chromosome fragments from one species into another through repeated

backcrossing of wide hybrids to their parental species. Distant hybridization and resulting wide hybrids have been widely used as an important tool of chromosome manipulation (also referred to as chromosome engineering) for crop improvement (Obok *et al.*, 2012; Ishii *et al.*, 2010).

Barriers in Distant Hybridization

There are certain barriers affecting the success of DH, with their scale broadly reflecting the evolutionary distance between the species involved the morphology and physiology of plants. Difficulties in hybridization could occur at crossing level, pre-embryonic, embryonic and post-embryonic level.

Techniques in Distant Hybridization and Detection of Hybrids

There are various techniques to accomplish DH for the generation of F₁ hybrid (Chowdhury and Kalloo, 1992). These are as follows: i) Chromosomal manipulation or engineering (chromosome behaviors of wide hybrids and the resulting chromosome constitutions in their progenies and includes amphidiploids, alien substitution lines and translocation lines), ii) Advanced backcross QTL/AB-QTL (involves combining QTL analysis with variety development), iii) *In vitro* embryo rescue technique (for recovery of F₁ embryo between distant relative and elite cultivar), iv) Somatic hybridization (involves fusion of two different plant protoplasts to form hybrid), v) Mentor pollen (uses small amount of pollen that is highly compatible with seed parent mixed with a large amount of pollen from intended pollen parent), vi) Application of hormones or nutrient solution provides impetus to embryo development/seed set respectively, vii) Inter-specific hybridization between wild relative and cultivar followed by backcrossing the F₁ with recurrent parent provides a way for introgression of alleles from wild relative.

The genomic regions introgressed from wild relatives can be tracked cytogenetically (Fluorescence *in situ* hybridization / Genomic *in situ* hybridization), by determining genome size and ploidy level analysis (flow cytometry) and through molecular markers like simple sequence repeat marker (SSR) (Liu *et al.*, 2011). Distant hybridization has been remarkable in cereals (rice, wheat, oat, pearl millet), pulses (peas, bitter melon, bitter melon, chilli, brinjal, momordica, ladies finger, capsicum, brassica spp), vegetables bitter melon, chilli, brinjal, momordica, ladies finger, capsicum, fruit crops papaya, grape, annona, cash crops (cotton, lily), oilseed crops (Jatropha, brassica spp.) and forage crops (napier grass). Several important genes from wild species have been utilized in breeding for improving economic agronomic traits like abiotic stress, biotic stress, quality parameters, yield and nutritional improvement of cultivated species. To cite, several QTLs from wild relatives of rice like *Oryza nivara*, *O. rufipogon*, *O. australiensis*, *O. glaberrima*, *O. glumaepatula*, *O. longistaminata*, *O. minuta*, *O. meyeriana* have been transferred to donor accessions for improving traits (Shakiba and Eizenga, 2014). In wheat, several traits have been transferred from wild species to cultivars, for eg: an alien chromosome segment (7DL) introgressed from a wild wheat relative species, *Agropyron elongatum* conferred drought adaptive response in cultivated wheat *Triticum aestivum* (Placido *et al.*, 2013).

Moreover, there are certain points crucial to successful hybridization like linkage drag, determination of QTLs affecting hybrid vigour or fitness, estimation of the contribution of each parent to the performance of the offspring, monitoring specific genomic blocks in different generations after hybridization, role of the genomic locations of genes, role of epistasis, genotype by environment interaction on the fitness or vigour of the hybrids.

However, there is a need to reduce linkage drag, which is associated with desirable trait from distant relative in distant hybridization. Synthetic mapping populations and genetic linkage maps can be combined simultaneously for studying the introgression process of distant species in cultivars. Pre-breeding could be employed for effective utilization of wild taxa. Collaborative work/projects should be framed for exploiting the extensive and rich reservoir of wild germplasm between institutes involved in conserving germplasm and crop improvement.

Conclusion

Exploitation of wild relatives serves as a source of novel alleles and broadens the genetic base by incorporating economic traits in crop improvement. Distant hybridization provides an efficient tool for genetic gain and furnishes new variation/diversity by incorporating economic traits like quality, biotic stress resistance, and abiotic stress tolerance from wild relatives into elite cultivars. Combination of *in vitro* and breeding techniques aids the survival and growth of the hybrid derived from cross between wild and cultivated genotype. The production of double haploids, amphidiploids and various introgression lines provides a source of mapping population and new varieties respectively. Advanced breeding strategies like marker-assisted selection along with advanced backcross QTL techniques can be employed for tracking segments of genes introgressed from wild relative for varietal enhancement.

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