

Mini Review

## Broadening gene pool of rice for resistance to biotic stresses through wide hybridization

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### Abstract

Variability in the cultivated germplasm for economic traits such as resistance to rice tungro virus, sheath blight, yellow stem borer, drought and salt tolerance is limited. This necessitated search for the genes in secondary and tertiary gene pool of genus *Oryza*. Fortunately, wild species are an important reservoir of useful genes for resistance to major disease, pests and tolerance to abiotic stresses. Wide hybridization in *Oryza* is normally difficult to achieve because many wild species of genus *Oryza* are difficult to cross with cultivated rice because of difference in chromosome number or genetic constitution. Fertilization may occur, but the embryo is aborted. Embryo rescue is used to maintain the hybrid embryos and  $F_1$ s through several cycles of back crosses until fertility is restored. Interspecific hybridization has been attempted by a number of workers and resulting hybrids and progenies have been used for taxonomic and phylogenetic analysis with limited efforts to transfer desirable traits from wild species to cultivated rice. Transfer of grassy stunt virus resistance from one accession of *O. nivara* has been achieved successfully. Another species belonging to the AA genome, *O. longistaminata* has been exploited for transfer bacterial blight resistance gene to cultivated rice. Wild species with genomes non-homologous to the AA genome of *O. sativa* such as *O. officinalis* (CC), *O. australiensis* (EE) and *O. minuta* (BBCC) possessing resistance to brown planthopper, white backed planthopper, bacterial blight and blast have been used to transfer these desirable alien traits to cultivated rice. Therefore, wide hybridization is one of the key components in programme aiming at transferring alien genes from diverse sources surmounting sexual barriers. Advances in embryo res-

cue, anther culture, chromosome engineering and genetics have facilitated in the transfer of genes and in precise monitoring and characterization of alien introgression from different genomes of *Oryza* into cultivated rice. Integrating conventional breeding with advanced methods of alien introgression offers great potent to develop disease and insect resistant varieties.

**Keywords:** *Oryza sativa*; Wide hybridization; Amphidiploidy, Aneuploidy; Cytoplasmic male sterility

### INTRODUCTION

Integrated Pest Management is a broad ecological pest control approach aiming at best mix of all known pest population below economic threshold level. It is a dynamic concept and sustainable system of crop protection that leads to maximum productivity with the least possible adverse impact on the total environment. Improvements in plant breeding techniques in present century have resulted in increased yield and solve many problems associated with diseases, insects, harvest and quality. The plant breeders have, historically, utilized the variability in land races for selection and improvement of crops. The variability and germplasm resources available for many cultivated varieties are becoming extremely limited (Harlan, 1976). As additional genetic resources are required to enrich the germplasm, unique and imaginative procedures are required to exploit fully the potential of our crop plants. Utilization of wild species (Sen *et al.*, 2005; Nayak *et al.*, 1996; Sahu *et al.*, 1994; Bose *et al.*, 1990), therefore, is one method designed to introduce additional germplasm into cultivated varieties (Stalker, 1980).

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**Why wide hybridization:** During last few decades, considerable attention has centered round the importance of wild species in plant breeding. The interest in wild species and primitive cultivars has been strengthened through FAO's pioneer work on genetic resources of crop plants, as well as, by the concerted efforts of many national and international crop research centers in promoting gene bank activities. It is also due, in no small measures, to breeders clear needs for a wider genetic base from wild germplasm to help and solve problems of resistance to diseases, pests and a greater range of environmental adaptation, better yields and better nutritional and economic characters in the plants concerned.

**Wild species of *Oryza* and its Importance:** The genus *Oryza* consists of about twenty wild (Sampath, 1961; Tateoka, 1964; Vaughan, 1989) and two cultivated species. The common cultivated rice *Oryza sativa* is distributed world wide while the African cultivated rice *Oryza glaberrima* is confined to West Africa only. Most of the wild species have similar genomes (AA) as that of *O. sativa* and *O. glaberrima*, other distantly related species have BB, CC, BBCC, CCDD, EE, FF, GG, HHJJ and HHKK genomes (Khush, 2004).

Comprehensive list of potential wild species available in the genus *Oryza*, their genome, distribution along with their reaction to biotic and abiotic stresses are presented to reinstate the genetic diversity of the species into the rice-breeding program (Table 1).

Several pre and post-fertilization barriers to crossability are known to limit the production of hybrids between distantly related species. Different approaches have been explored to overcome pre-fertilization barriers and also recent studies have pointed out the potential application of embryo, ovule and ovary culture to obtain fertile hybrids (Sen *et al.*, 2005; Jena and Khush, 1989). Although considerable work has been done to produce wide hybrids for taxonomic and phylogenetic analysis (Nezu *et al.*, 1960; Wu *et al.*, 1963, Chu *et al.*, 1969; Tateoka, 1964; Vaughan *et al.*, 1989; Sitch, 1990), limited effort has been made to transfer desirable traits from wild species to cultivated rice. *O. sativa f. spontanea* source of the wild abortive (WA) male sterile cytoplasm, which, is successfully exploited for hybrid rice production in China and in other hybrid rice breeding programs (Lin and Yuan, 1980). Two notable examples include the transfer of a gene for resistance to grassy stunt virus from *O. nivara* (Khush *et al.*, 1977) and the transfer of a gene for

**Table 1.** Taxa in the genus *Oryza*: genome and useful traits.

Wild Species	Genome	Distribution	Useful Traits
<i>O. sativa</i>	AA	World wide	Cultigen
<i>O. glaberrima</i>	A <sup>g</sup> A <sup>g</sup>	Primarily West Africa	Cultigen
<i>O. nivara</i>	AA	Tropical Asia	Resistance to grassy stunt virus and blast
<i>O. rufipogon</i>	AA	Tropical Asia and Australia	Tolerance of acid sulphate soils and stagnant flooding, source of CMS
<i>O. barthii</i>	A <sup>g</sup> A <sup>g</sup>	Tropical Africa	Resistance to bacterial leaf blight
<i>O. longistaminata</i>	A <sup>1</sup> A <sup>1</sup>	Tropical Africa	Floral characteristics for out crossing
<i>O. glumaepatula</i>	A <sup>cu</sup> A <sup>cu</sup>	Central and South America	Deep water rice
<i>O. meridionalis</i>	A <sup>m</sup> A <sup>m</sup>	Tropical Australia	Drought avoidance
<i>O. punctata</i>	BB, BBCC	Tropical Africa	Multiple pest resistance
<i>O. officinalis</i>	CC	Tropical Asia, Papua New Guinea	Resistance to BPH, GLH and WBPH
<i>O. rhizomatis</i>	CC	Sri Lanka	Drought resistance
<i>O. eichingeri</i>	CC	Sri Lanka, Tropical Africa	Resistance to BPH, GLH and WBPH
<i>O. minuta</i>	BBCC	Philippines	Resistance to BPH, GLH and WBPH, blast and Bacterial leaf blight
<i>O. latifolia</i>	CCDD	Central and South America	High biomass production
<i>O. grandiglumis</i>	CCDD	Central and South America	High biomass production
<i>O. australiensis</i>	EE	Tropical Australia	Resistance to BPH and drought
<i>O. brachyantha</i>	FF	Papua New Guinea, Tropical Africa	Resistance to stem borer and rice whorl maggot
<i>O. ridleyi</i>	HHJJ	South East Asia, Papua New Guinea	Resistance to rice whorl maggot, bacterial leaf blight and blast
<i>O. longiglumis</i>	HHJJ	Indonesia, Papua New Guinea	Resistance to bacterial leaf blight and blast
<i>O. granulata</i>	GG	Tropical Asia	Shade tolerance
<i>Porteresia</i>	HHKK	Tropical Asia	Tolerance to salinity
<i>coarctata</i>			

**BPH:** Brown planthopper, **GLH:** Green leaf hopper, **WBPH:** White backed planthopper, **CMS:** Cytoplasmic male sterility

Source: Khush GS (2004), FAO Rice conference, Rome, Italy, 12-13 Feb. 2004.

**Table 2.** Successful transfer of alien genes in rice through MAALS/Back crossing.

Introgression lines through	Donor species used With accession No.	Recipient cultivar	Genes for	Reference
MAALS	<i>O. australiensis</i> (100882)	IR 31917-45-3-2	BPH, BB	Jena & Khush, 1990
MAALS	<i>O. officinalis</i> (100896)	IR 31917-45-3-2	BPH, WBPH	Multani <i>et al.</i> , 1994
MAALS	<i>O. punctata</i> (W 1514)	Nipponbare	-	Yasui & Iwata, 1991
Back crossing	<i>O. nivara</i> (101508)	IR 24	GSV	Khush & Ling, 1974
Back crossing	<i>O. longistaminata</i>	IR 24	BB	Khush <i>et al.</i> , 1990
Back crossing	<i>O. glaberrima</i> (TOQ 5674, TOQ 5681)	ITA 212	RYMoV	Matsuo <i>et al.</i> , 1997
Back crossing	<i>O. minuta</i> (101141)	IR 31917-45-3-2	Blast, BB	Amante-Bordeos <i>et al.</i> , 1991
Somaclonal variation	<i>O. eichingeri</i> (RN 1041)	Swarnaprabha	BPH, WBPH	Sen <i>et al.</i> , 2005

resistance to BB from *O. longistaminata* (Khush *et al.*, 1990). More recently (Jena and Khush, 1989, 1990; Multani *et al.*, 1994) develop monosomic alien addition lines of *O. sativa* having alien chromosome of *O. officinalis*, *O. australinsis* and locate the genes for resistance to BPH, WBPH and BB from *O. officinalis* and *O. australinsis* to cultivated rice. (Amante *et al.*, 1991) also transferred genes for resistance to blast and BB from *O. minuta* to cultivated rice (Table 2).

**Disease and pest resistance:** The most common reason for wide hybridization is to transfer disease resistance when the resistance source in the cultivated gene pool becomes inadequate, the most valuable genes conditioning disease resistance are found in species distantly related to the cultigen with which interspecific hybrids are difficult to make. Further genes conditioning resistance that would justify interspecific transfer often behave as monogenic dominant genes for immunity or very high resistance (Clayton, 1954). Horizontal resistance is often desirable but transferring such gene complex to the cultigen requires very long time. Major diseases of rice are BB, blast, tungro (RTD) and Sh.B, which affect rice productivity. Breeding for resistance to many of these have been achieved using resistance source from cultivated germplasm. However, like Sh.B effective sources of resistance are not present in primary gene pool and in this regard wild species of *Oryza* might be extremely useful in providing alien genes for transfer into elite rice varieties. Similarly the insect species that cause severe damage to rice are stem borer, green leafhopper, BPH and gall midge. Though resistant varieties for these have been developed, the emergence of new biotypes often cause serious threat to rice crop and hence,

there is need to continue incorporation of genes from diverse sources (Khush, 1971; Brar and Khush, 1997).

**Conclusion:** In the foregoing review an attempt was made to put together the information available on various areas of wide hybridization, which is assuming special significance in present days. The main interest in wide hybridization is to select genotypes possessing a very limited alien chromatin material, hence precise methods are required in monitoring such introgression. In rice, chromosome and isozyme analyses are the commonly used methods for characterization of wide cross progenies. Recently, molecular markers such as RFLP and genome specific DNA probes have been available which offer potential to facilitate monitoring of alien gene introgression. The choice of a particular method like alien addition lines, anther culture, somaclonal variation and recombinant DNA technology for alien gene transfer through wide hybridization depends upon genomic relationship, extent of chromosome pairing and recombination between the genomes of the alien wild and cultivated species. If there is no restriction on chromosome pairing and recombination in wide hybrids, direct hybridization and backcrossing to the recurrent cultivated parent are followed. When the chromosomes of wide cross hybrids do not pair certain chromosome manipulation techniques like alien addition lines, alien substitution lines, induced homoeologous pairing and amphiploids are utilized.

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