

**Indian Farmer**

Volume 12, Issue 08, 2025, Pp. 472-474

Available online at: www.indianfarmer.net

ISSN: 2394-1227 (Online)

Original article**Role of Crop Wild Relatives in Rice Genetic Improvement****Hari Kesh and Khushi Ram Battan**

College of Horticulture and Forestry, CAU (Imphal), Pasighat – 791102

Department of Agriculture, Maharishi Markandeshwar University, Ambala – 133207

*Corresponding author: harikeshkaul55v2@gmail.com

Received: 22/08/2025

Published: 25/08/2025

INTRODUCTION

Asian cultivated rice, *Oryza sativa*, is one of the most important foodgrain crops to feed the world for thousands of years. The genus *Oryza* includes 25 wild species and 2 cultivated species namely, *O. sativa* L. and *O. glaberrima*. Among the cultivated species, high yielding *O. sativa* is grown worldwide and low yielding African Rice *O. glaberrima* is endemic to West Africa. *Oryza* species are broadly distributed across temperate, tropical, and subtropical regions worldwide, and can be categorised into six diploid types (AA, BB, CC, EE, FF, and GG) and five allotetraploid types (BBCC, CCDD, HHKK, HHJJ, and KKLL) (Fornasiero et al., 2024). Based on the degree of gene exchange, rice genera have been categorized into three classes: primary gene pool, secondary gene pool and tertiary gene pool (Harlan and De Wet, 1971). The primary gene pool includes *O. sativa*, *O. rufipogon* and *O. nivara*, secondary gene pool includes *O. glumipatula*, *O. longistaminata* and *O. meridionalis* and tertiary gene pool includes *O. punctata*, *O. minuta*, *O. officinalis*, *O. alata*, *O. coarctata*, *O. australiensis*, *O. brachyantha*, *O. ridleyi* and *O. meyeriana* (Zheng et al., 2024).

Wild rice germplasm represents rich genetic diversity associated with important agronomic, biotic and abiotic stress resistance traits that have largely been lost in cultivated rice during domestication. Incorporation of these essential traits/genes from wild relatives of rice into cultivated ones can significantly improve the adaptability and stress resistance, thereby improving yield and production (Yang et al., 2022). Therefore, the utilization of wild germplasm resources needs to be acknowledged as an important future source of genes for breeding high yielding, adaptable and stress tolerant genotypes.

1. Genes for grain yield and quality

Grain yield is a polygenic trait and is dependent on the number of tillers, number of panicles, number of grains per panicle, and the grain weight (Kesh and Khan, 2023). Moreover, kernel length and width are closely related with grain weight, contributing to overall grain yield. The identification and introgression of yield contributing genes from wild rice would dramatically enhance the heterosis in rice varieties and hybrids (Wu, 2009). Chromosomal segments from *O. rufipogon*, harbouring

gene Os11Gsk were transferred into KMR3 (indica rice line), resulting in a significant increase in the grain yield of rice hybrids (Thalapati et al., 2012). At Punjab Agricultural University, India, qsqSPP2.2 from *O. longistaminata* has been identified for increased number of spikelets per panicle and transferred into Basmati rice, which otherwise has few spikelets per panicle (Brar and Khush, 2018). As far as grain quality is concerned, *O. barthii* possesses high amylose content (Wang, et al., 2015). High amylose in rice has a lower glycemic index, therefore, it can be used in rice breeding programs for healthy rice production for the diabetic population (Gaikwad et al., 2020).

2. Genes for biotic stress resistance

Wild species of rice are reservoirs of many useful genes against biotic stresses like rice blast, bacterial blight and brown planthoppers. Many genes associated with bacterial blight resistance have been identified from wild relatives of rice such as Xa 21 from *O. longistaminata*, Xa 23 and Xa 30 from *O. rufipogon*, Xa29 and from *O. officinalis*, Xa 33 from *O. nivara* and; Xa 27 and Xa 35 from *O. minuta* (Kesh and Kaushik, 2020). Additionally, Pi9 from *O. minuta*, Pi54rh from *O. rhizomatis* and Pi57 from *O. longistaminata* exhibit broad-spectrum resistance against blast disease resistance and are extensively utilized in breeding. Likewise, alleles Bph14, Bph18 and bph29 have been cloned from *O. officinalis*, *O. australiensis* and *O. rufipogon*, respectively. Moreover, the grassy dwarf disease resistance gene Gsv, isolated from *Oryza nivara*, was introduced into IR24 and other rice varieties, rendering all IR series varieties resistant to grassy dwarf disease (Li et al., 2014). Green rice hoppers are a major insect pest of rice. Two dominant genes viz., Grh4, and Grh6 have been transferred from *O. nivara* into cultivated rice varieties (Zheng et al., 2024). These gene have been extensively used to develop biotic stress resistant rice varieties in India namely, Improved Pusa Basmati 1, Improved Samba Mahsuri 1, Dhanarasi, Matatag 9 and Yun Dao (Brar and Khush, 2018; Gaikwad et al., 2020).

3. Genes for abiotic stress resistance

As extreme climatic conditions significantly affect rice production, the identification and introgression of novel genes for abiotic stress tolerance (drought, salinity, high temperature and low temperature) in wild rice may lead to genetic improvements in rice. Many elite breeding lines selected from cross of rice variety Swarna and *O. nivara* showed introgression for tolerance to salinity, and a variety DRR Dhan 40 has been released in India. Similarly, another variety Chinsurah Nona 2 from the cross of KMR 3 with *O. rufipogon* has been released for cultivation in coastal saline area of West Bengal, India (Brar and Khush, 2018). Five novel genes conferring cold tolerance have been identified from *O. rufipogon*. This species is also a source of QTLs for drought tolerance, heat tolerance, and tolerance to acidic soils, iron toxicity and the phosphorus deficiency (Cao et al., 2020).

CONCLUSION

In this article, an attempt was made to put together the information available on importance and utilization of rice wild relatives for the genetic improvement of rice for grain yield, biotic stress, abiotic stress and quality parameters. The advanced techniques like tissue culture, molecular techniques, and omics approaches need to be adopted for utilizing the wild relatives in rice breeding programs. The development of improved genotypes with genetic resistance against the biotic and abiotic stresses could help to achieve the aim of climate resilient agriculture in future.

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