

**A Seminar Paper on**  
**Wild Relatives of Rice: A Valuable Source of Useful Genes for Rice Improvement**

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# **Wild Relatives of Rice: A Valuable Source of Useful Genes for Rice Improvement<sup>1</sup>**

**By**

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## **Abstract**

Rice is one of the most important crops worldwide, providing food for over half of the world's population. However, the genetic diversity of cultivated rice is limited, and this poses a challenge for breeders looking to improve yield, disease resistance, and other desirable traits. Wild relatives of rice, offer a valuable source of useful genes that can be used for rice improvement.

These wild relatives have evolved over millions of years and possess genetic traits that have allowed them to adapt to different environments and resist various biotic and abiotic stresses. By using traditional breeding techniques, breeders can transfer these beneficial genes from wild relatives into cultivated rice varieties. This can lead to the development of rice varieties that are more resilient and productive, with improved nutritional value and resistance to pests and diseases.

However, the conservation and utilization of wild rice relatives face many challenges, including habitat loss, climate change, and cultural and economic factors. Therefore, conservation efforts and sustainable use of wild rice relatives are essential to ensure the availability of genetic diversity for future rice improvement efforts. The International Rice Research Institute (IRRI) and Bangladesh Rice Research Institute (BRRI) already conserved a good amount of wild germplasm and this process is on-going.

The paper discusses the genetic diversity that exists within the wild relatives of rice and the potential of using this diversity to develop new rice cultivars with desirable traits. The information of the review paper might provide as a guideline for researchers as well as rice breeders.

**Key words:** crop wild relatives (CWRs), abiotic stresses, biotic stresses, Stress tolerance, conservation.

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# CHAPTER I

## INTRODUCTION

Rice is a staple food for over half of the world's population (FAO, 2004). Global rice demand is estimated to rise from 676 million tons in 2010 to 763 million tons in 2020 and to further increase to 852 million tons in 2035. Rice yield growth has fallen from 2.3% per year during 1970–1990 to 1.5% during 1990s and to < 1.0% during the first decade of present century. However, area planted to rice in major production countries has been decreasing because of conversion of land for housing, industries and highways. Therefore, improvement in the yield potential of rice is the major strategy to increase world rice production (Brar *et al.*, 2018).

Rice production faces numerous constraints, including biotic and abiotic stresses, limited availability of resources such as water and fertilizers, and climate change. These challenges require a comprehensive approach, integrating traditional and modern technologies, to achieve sustainable rice production (FAO, 2020).

To overcome these constraints particularly in the context of global climatic changes, there is urgent need to broaden the gene pool of rice; one of the options is to exploit wild species of *Oryza* which are reservoirs of useful genes/QTLs for rice improvement.

To date, a more comprehensive genomic sequencing and analysis of wild rice species has not been conducted, which hinders the full exploration of their genetic diversity and identification of useful genes for rice improvement. Additionally, there is a lack of knowledge about the mechanisms underlying the transfer of beneficial genes from wild relatives to cultivated rice, which could be further investigated (Saha *et al.*, 2022).

The present review provides information on the important wild rice species harbouring genes/QTLs for agriculturally important traits and their utilization in rice breeding programmes.

### **Obectives:**

1. To provide an overview of the genetic diversity of wild rice species and their potential use in rice breeding programs.
2. To discuss the challenges and opportunities associated with using wild rice species in rice breeding programs.

## **CHAPTER II**

### **MATERIALS AND METHODS**

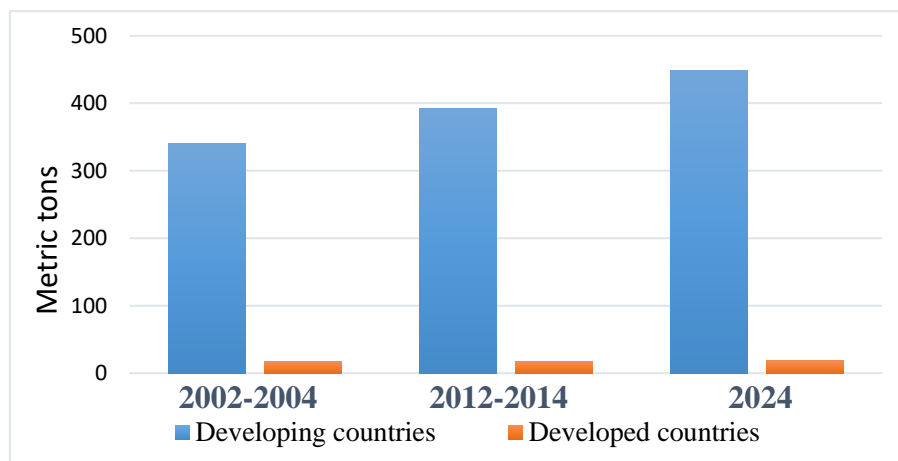
This seminar paper is a review paper that has been compiled by gathering information from various secondary sources. The secondary data were collected from different sources such as websites, national and international journals, reports, publications, and books available in the library of Bangabandhu Sheikh Mujibur Rahman Agricultural University. The review paper was prepared under the guidance and consultation of my major Professor.

## CHAPTER III

### REVIEW OF FINDINGS

#### 3.1 Rice consumption status

Rice (*Oryza sativa/ Oryza glaberrima*) is a grain crop under Poaceae family that has been cultivated for thousands of years. Rice is the primary food for over 3 billion people worldwide (FAO, 2021). It accounts for more than 20% of all calories consumed globally (FAO, 2021).



**Figure 1: Rice consumption in developing and developed countries.**

(Source: Rabara *et al.*,2018).

Rice is chiefly consumed in the developing countries (Figure 1) with about 340 metric tons (Mt) and 392 Mt. (15% increase) consumed in 2002–2004 and in 2012–2014, respectively, and projected to reach 449 Mt. in 2024, a 32% increase from 2004 consumption level. In contrast, developed countries consumed 17 Mt. of rice in 2002–2004 and about 3% more (17.5 Mt) in 2012–2014 and the consumption is expected to reach 18.2 Metric tons (Source: Rabara *et al.*,2018).

#### 3.2 Wild Relatives of Rice

Wild relatives of rice are wild plant species related to cultivated rice and used in breeding programs for their valuable traits. *Oryza* probably originated at least 130 million years ago and spread as a wild grass in Gondwanaland, the super continent that eventually broke up and drifted apart to become Asia, Africa, the Americas, Australia, and Antarctica.



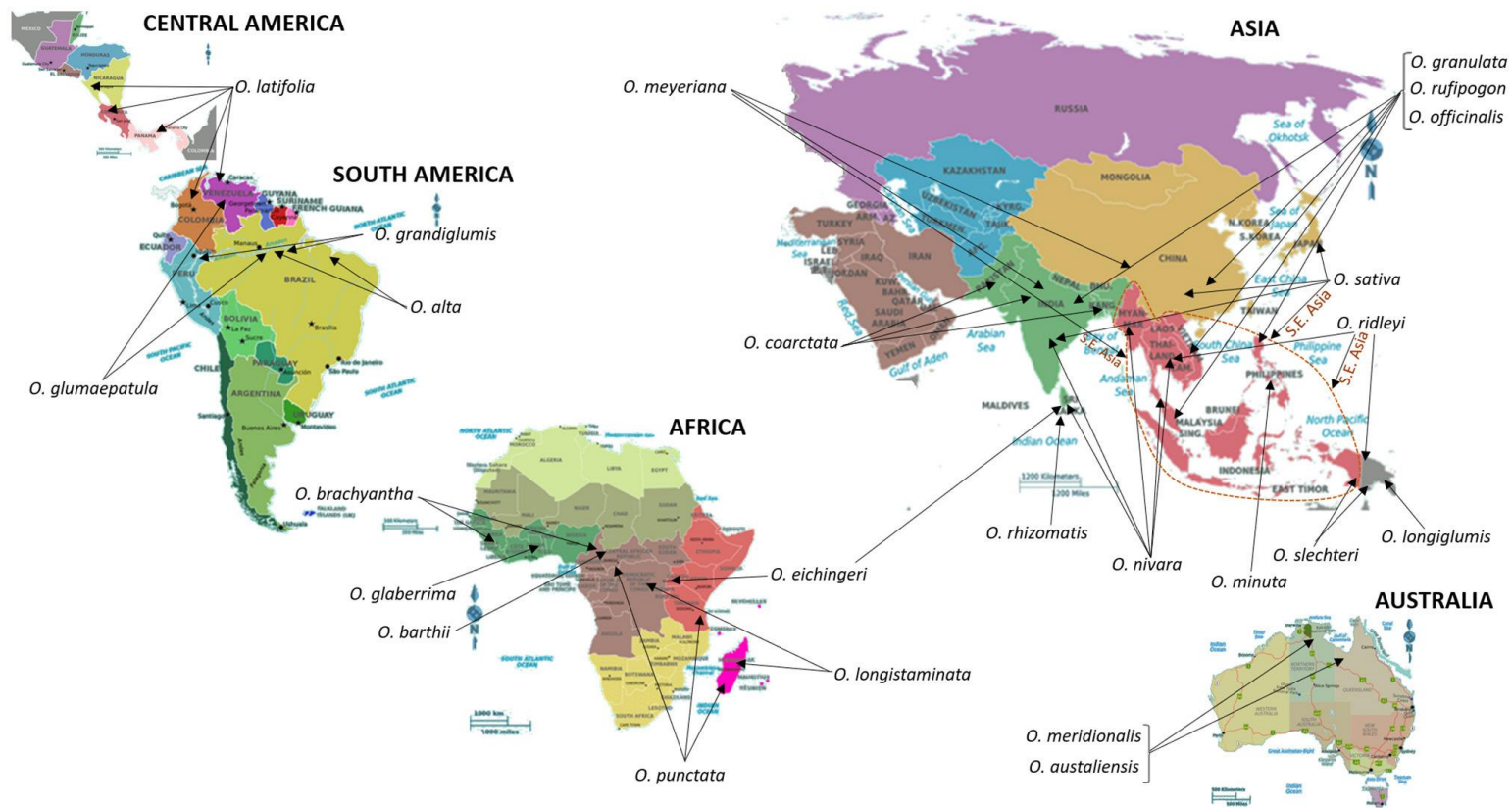


Figure 2: Centers of origin and/or primary sites of diversity and distribution of wild relatives of Rice.

(Source: Mammadov *et al.*, 2018)

The wild species are grass-like plants that are weedy and inferior in morphological traits, having poor plant type, poor grain characteristics, low grain yield and are shattering in nature. These wild species differ markedly in morphological characteristics (Figure 3).



**Figure 3: Plants of some wild species of *Oryza*.**

(Brar *et al.*, 2018).

In spite of their weedy nature, these wild species are important genetic resource for breeding and genomics research and are reservoir of useful genes/QTLs for tolerance to major biotic and abiotic stresses, yield-related traits, new source of cytoplasmic male sterility (CMS), and other traits related to rice improvement. The genus *Oryza* has two cultivated and 24 wild species ( $2n = 24$ , 48 chromosomes) representing genomes: AA, BB, CC, BBCC, CCDD, EE, FF, GG, HHJJ, KKLL (Ge *et al.* 1999). Of the two cultivated species, *O. sativa* ( $2n = 24$ , AA) commonly referred as ‘Asian rice’ is high yielding and cultivated worldwide, whereas *O. glaberrima* ( $2n = 24$ , AA) known as ‘African rice’ is low yielding and grown in a limited area in West Africa.

**Table 1: Wild Species of the genus *Oryza* and their potential traits**

Species	2n	Genome	Distribution	Life cycle	Special Useful traits
<i>O. nivara</i>	24	AA	Tropical and subtropical Asia	Annual-biennial	Resistance to grassy stunt virus, BB, blast, BPH, yield-enhancing QTLs.
<i>O. rufipogon</i>	24	AA	Asia, tropical Australia	Perennial	Resistance to BB, BPH, tungro virus; tolerance to aluminum and soil acidity; source of CMS, yield-enhancing loci (QTLs)
<i>O. breviligulata</i> ( <i>O. barthii</i> )	24	AgAg	Africa	Annual	Resistance to GLH, BB; drought avoidance
<i>O. longistaminata</i>	24	AIAI	Africa	Perennial	Resistance to BB, nematodes, stemborer, drought avoidance
<i>O. meridionalis</i>	24	AmAm	Tropical Australia	Annual-biennial	Elongation ability; drought avoidance
<i>O. glumaepatula</i>	24	AgpAgp	South and Central America		Resistance to blast, elongation ability; source of CMS
<i>O. punctata</i>	24	BB	Africa	Annual-biennial	Resistance to BPH, zigzag leafhopper
<i>O. minuta</i>	48	BBCC	Philippines and Papua	Perennial	Resistance to BB, blast, BPH, GLH
<i>O. officinalis</i>	24	CC	Tropical and Subtropical Asia, tropical Australia	Perennial	Resistance to thrips, BPH, GLH, WBPH, BB, stem rot
<i>O. rhizomatis</i>	24	CC	Sri Lanka	Perennial	Drought avoidance
<i>O. eichingeri</i>	24	CC	South Asia, EastAfrica	Perennial	Resistance to BPH, WBPH, GLH

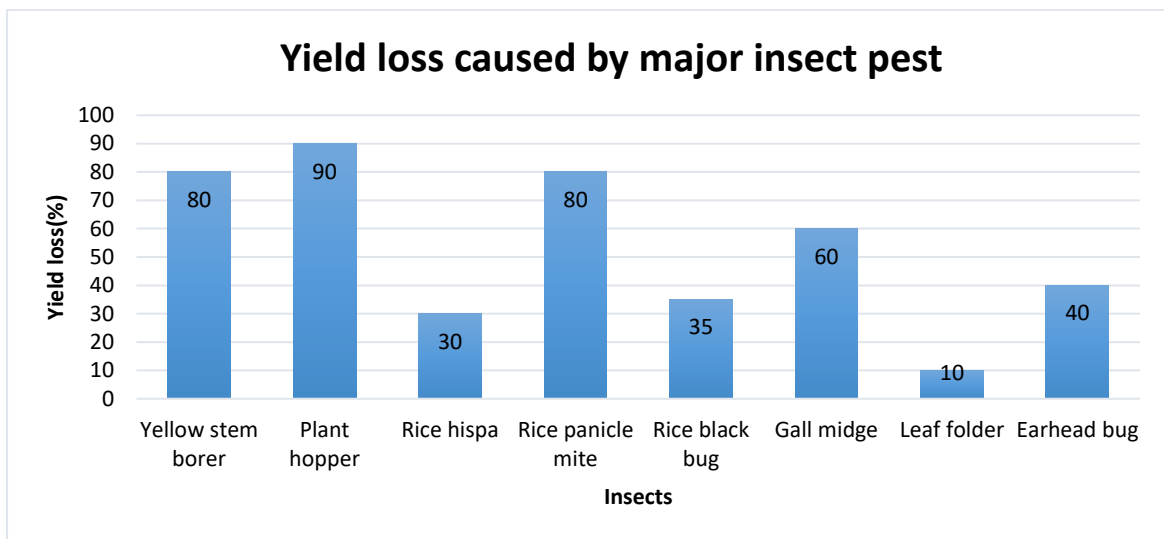
Species	2n	Genome	Distribution	Life cycle	Special useful traits
<i>O. latifolia</i>	48	CCDD	South and Central America	Perennial	Resistance to BPH, high biomass production
<i>O. alta</i>	48	CCDD	South and Central America	Perennial	Resistance to striped stemborer; high biomass production
<i>O. grandiglumis</i>	48	CCDD	America	Perennial	High biomass production
<i>O. australiensis</i>	24	EE	Tropical Australia	Biennial-perennial	Resistance to BPH, BB, blast; drought avoidance
<i>O. brachyantha</i>	24	FF	Africa	Biennial	yellow stemborer, leaf folder, whorl maggot; tolerance to laterite soil
<i>O. granulata</i>	24	GG	South and Southeast Asia	Perennial	Shade tolerance; adaptation to aerobic soil
<i>O. meyeriana</i>	24	GG	Southeast Asia	Perennial	Shade tolerance; adaptation to aerobic soil
<i>O. longiglumis</i>	48	HHJJ	Irian Jaya, Indonesia, and Papua	Perennial	Resistance to blast, BB
<i>O. schlechteri</i>	48	HHKK	Papua New Guinea	Perennial	-
<i>O. coarctata</i>			South Asia		Salt tolerance

(Source: Brar *et al.*, 2018)

### 3.3 Different useful traits of wild relatives of rice

#### 3.3.1 Tolerance to Biotic Stresses

**Insect Tolerance:** Rice is one of the world's most important foods, but its production suffers from insect pests, causing losses of billions of dollars, and extensive use of environmentally damaging pesticides for their control. Host-plant resistance has additional benefits including reducing production costs and the risk of possible environmental contamination when compared to chemical control. Exploration of resistance genes from wild relatives of rice and introgression in susceptible one is one of the way to overcome such problem.



**Figure 4: Yield loss caused by major insect of rice.**

(Source: Teng *et al.*, 1990)

The brown planthopper (BPH), *Nilaparvata lugens*, is a migratory insect that has become the most devastating pest of rice. BPH also transmits two disease causing viruses, rice grassy stunt virus and rice ragged stunt virus. Studies on the exploration of resistance species Seeds of 1003 wild rice accessions were received primarily. As many as 159 accessions were found to be resistant to BPH (Table 2) (Sarao *et al.*, 2016).

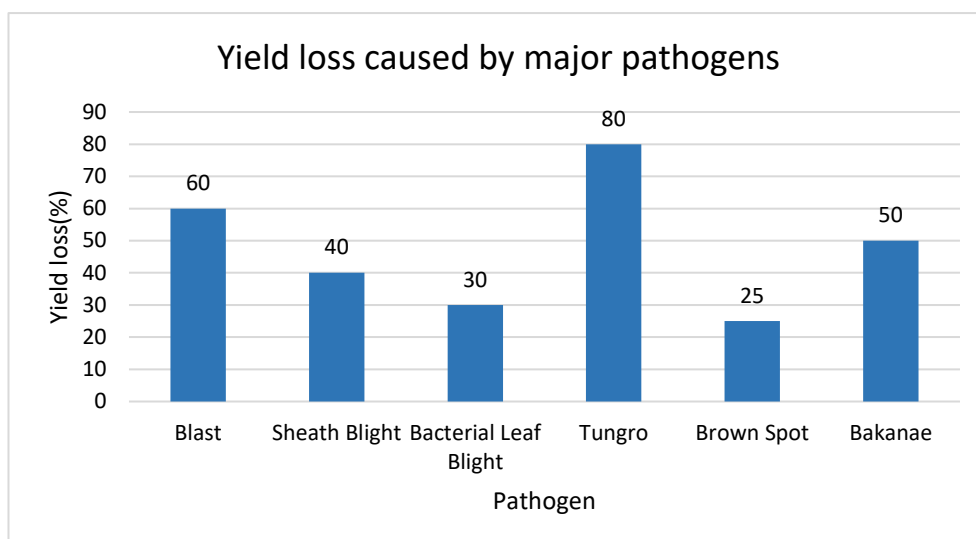
**Table 2: Number of accessions of *Oryza* species evaluated against brown planthopper**

Species	Genome	No. of accessions screened	No. of susceptible accessions	No. of resistant accessions
<i>O. glaberrima</i>	AA	44	44	0
<i>O. barthii</i>	AA	29	29	0
<i>O. nivara</i>	AA	451	391	60
<i>O. rufipogon</i>	AA	326	279	47
<i>O. longistaminata</i>	AA	51	38	13
<i>O. meridionalis</i>	AA	16	16	0
<i>O. glumaepatula</i>	AA	12	11	1
<i>O. officinalis</i>	CC	7	1	6
<i>O. australiensis</i>	EE	12	3	9
<i>O. punctata</i>	BB,BBCC	29	22	7
<i>O. minuta</i>	BBCC	2	0	2
<i>O. latifolia</i>	CCDD	24	10	14
Total		1003	844	159

(Source: Sarao *et al.*, 2016)

Several reports in the literature indicates that wild species *viz.*, *O. nivara*, *O. punctata*, *O. longistaminata*, *O. barthii*, *O. rufipogon*, *O. officinalis*, *O. australiensis*, *O. minuta*, *O. latifolia* and *O. glaberimma* are important source of planthopper resistance genes ( Fujita et al, 2013). But in table 2 *O. longistaminata*, *O. barthii* shows no resistant to BPH . This variation in resistance reaction may be due to difference in BPH biotype used for screening.

**Disease Tolerance:** Among the biggest problems in rice cultivation is the management and prevention of various devastating diseases caused by pathogens that reduce crop yields. Yield loss in rice due to pathogens has been estimated to be an average of 10%–15% which might cause absolute destruction in specific cases. Rice plant is the host for 58 fungal (43 of which are seed borne or seed-transmittable), 12 bacterial, 17 viral and mycoplasma-like pathogens (Nayak et al,2021), and more than 30 species of nematodes.



**Figure 5: Yield loss caused by major pathogens of rice.**

(Source: Nayak *et al.*, 2021)

The resistance of wild relatives and African cultivated race, *O. glaberrima* to tungro was evaluated (Kobayashi *et al.*, 1993 a). Representing the genetic diversity in the genus *Oryza*, 211 accessions were tested for resistance to RTBV and RTSV infection. Of these, 53 and 15 accessions were not infected with RTSV and RTBV respectively. The wild species identified as highly resistant to tungro are useful donors in developing tungro-resistant rice germplasm.

**Table 3: Number of accessions in wild relatives of rice resistant to tungro**

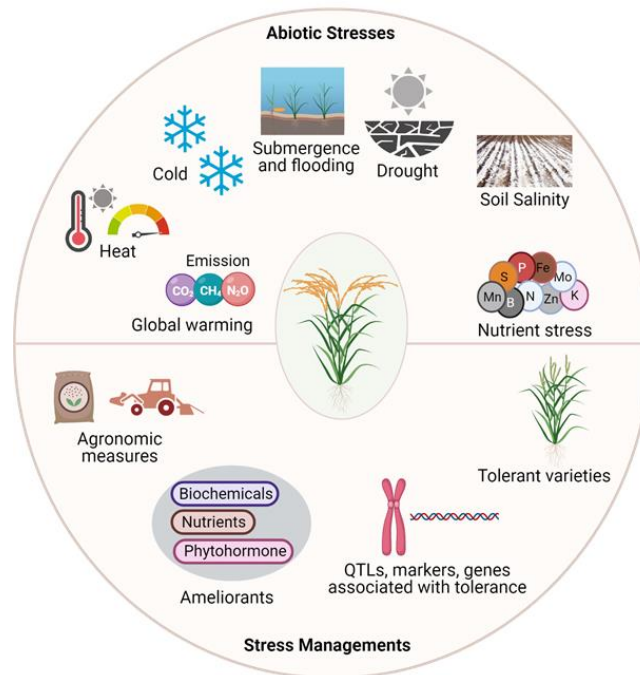
Species complex	No. of Accessions		
	Taxa	Non-infected with	
		Tested	RTBV
<i>O. brachyantha</i>	5	1	5
<i>O. saliva complex</i>	76	3	15
Natural hybrids	24	0	12
<i>O. ridleyi complex</i>	8	3	0
<i>O. officinalis complex</i>	63	8	21
<b>Total</b>	<b>211</b>	<b>15</b>	<b>53</b>
<b>(Avg. %)</b>		<b>7</b>	<b>25</b>

ELISA method was used to detect virus infection.

(Source: Ikeda *et al.*, 1994)

### 3.3.2 Tolerance to Abiotic Stresses

Abiotic (water, soil, atmospheric) stresses affect yield and quality of rice. Recent crop improvement strategy has partially managed to resolve the challenges presented by abiotic stresses such as high temperature, drought, salinity, alkalinity, waterlogging and mineral deficiency. Wild relatives have abiotic stress resistant QTLs to improve rice variety.



**Figure 6: Schematic showing different abiotic stresses rice plant encounters (upper panel) and their management strategies (lower panel).**

(Pathak *et al.*, 2021)

**Drought and Heat Tolerance:** Drought is one of the main environmental stresses that reduces agricultural productivity in rice. Exploratory studies have been performed to better understand the effects of drought using backcross inbred lines from a cross between an *O. sativa* line, WAB56-104, and an *O. glaberrima* line, CG14 (Ndjondjop *et al.*, 2010). Although several QTLs for drought tolerance have been identified in *O. sativa* and the underlying genes cloned, wild relatives are considered to harbor stronger/novel alternatives and, therefore, several promising species are being investigated (Menguer *et al.*, 2017). While the exploration of candidate wild relatives continues, some donors have already been used in crossing programs to develop varieties tolerant to heat (Sanchez *et al.*, 2013).



**Submergence Tolerance:** Rice is commonly grown in flooded soil containing a thin water layer. Although rice roots are well adapted to hypoxic conditions, most rice cultivars die rapidly if their shoots are submerged (Mackill *et al.*, 2012). SUB1 is the major QTL associated with submergence tolerance in rice cultivars that use the quiescent strategy (Fukao *et al.*, 2009). The SUB1 locus was mapped to chromosome 9, and is composed of a cluster of ethylene response factors (ERF) genes located *in tandem*, named *SUB1A*, *SUB1B* and *SUB1C*. Interestingly, tolerance to submergence is linked to a specific allele of the *SUB1A* gene, named *SUB1A-1* (Xu *et al.*, 2006). Accessions that lack *SUB1A* gene, or carry the *SUB1A-2* allele, are sensitive to submergence. Introgression of functional copies of *SUB1A-1* in sensitive genotypes is sufficient to generate tolerant plants (Xu *et al.*, 2006).

**Salinity Tolerance:** High soil salinity is a serious problem for rice. *Porteresia coarctata* (*Oryza coarctata*), an Asian halophyte and wild relative of rice, occurring in coastal environments shows high salinity and submergence tolerance (Zhang and Xie, 2014). Transcriptome sequence of *P. coarctata* suggested salinity and submergence tolerance in this species is due to substantial transcriptional reprogramming (Garg *et al.*, 2014). Such efforts pave the way for dissecting the mechanism(s) of tolerance and identifying key genes for salinity tolerance in rice. Ultimately, resistance could be transferred to *O. sativa* through bridge crossing or leveraging molecular techniques.

**Cold Tolerance:** The wild relative *O. rufipogon* was also found to harbor a QTL for cold tolerance and, therefore, an ideal donor for breeding programs (Koseki *et al.*, 2010).

**Table 4: Tolerance to abiotic stresses found in accessions of *Oryza* species and references**

Species	Tolerance compared to <i>O. sativa</i>	Reference
<i>Oryza coarctata</i>	Salt	Sengupta <i>et al.</i> , 2009
<i>Oryza eichingeri</i>	Submergence	Niroula <i>et al.</i> , 2012
<i>Oryza glaberrima</i>	Salt, Drought	Platten <i>et al.</i> , 2013
<i>Oryza glumaepatula</i>	Submergence	Hattori <i>et al.</i> , 2009
<i>Oryza grandiglumis</i>	Submergence	Okishio <i>et al.</i> , 2014, <sup>2015</sup>
<i>Oryza meridionalis</i>	Heat	Scafaro <i>et al.</i> , 2010
<i>Oryza nivara</i>	Drought	Singh <i>et al.</i> , 2015
<i>Oryza officinalis</i>	Heat (Early Morning Flowering)	Feng <i>et al.</i> , 2012
<i>Oryza rhizomatis</i>	Submergence	Niroula <i>et al.</i> , 2012
<i>Oryza rufipogon</i>	Salinity, Cold, Drought, Submergence	Hattori <i>et al.</i> , 2009, Tian <i>et al.</i> , 2011, Xiao <i>et al.</i> , 2014 (Menguere <i>et al.</i> , 2017)

### 3.4 Wild relatives of rice for improving rice quality

The wild relatives was also found to harbor of QTLs for good grain quality and high yield and, therefore, an ideal donor for breeding programs.

- ❑ Grain size and weight: *Oryza rufipogon* has been identified as a source of QTLs for grain size and weight, including the Grain Size 3 (GS3) and Grain Weight 5 (GW5) QTLs.
- ❑ Grain quality: *Oryza rufipogon* has also been found to possess QTLs for improved grain quality traits, such as amylose content, gel consistency, and aroma.
- ❑ Yield: *Oryza glaberrima* has been shown to possess QTLs for enhanced yield, including the Yield Enhancing QTL 1 (YE1) and Yield Enhancing QTL 2 (YE2) loci.

### 3.5 Rice wild relatives as a source of cytoplasmic male sterility (CMS)

These wild relatives of rice have been studied for their potential as sources of CMS traits that can be used to develop hybrid rice varieties.

**Table 5: List of some wild relatives those have CMS trait**

Wild Rice Relative	Reference
<i>Oryza rufipogon</i>	Li <i>et al.</i> , 2004
<i>Oryza nivara</i>	Wang <i>et al.</i> , 2006
<i>Oryza officinalis</i>	Liu <i>et al.</i> , 2013
<i>Oryza longistaminata</i>	Zhang <i>et al.</i> , 2017
<i>Oryza latifolia</i>	Marathi <i>et al.</i> , 2015
<i>Oryza punctata</i>	Liu <i>et al.</i> , 2015
<i>Oryza alta</i>	Tiwari <i>et al.</i> , 2020
<i>Oryza brachyantha</i>	Liang <i>et al.</i> , 2007
<i>Oryza glaberrima</i>	Fan <i>et al.</i> , 2015
<i>Oryza barthii</i>	Zhang <i>et al.</i> , 2022

### 3.6 Problems in using crop wild relatives of rice

- Cross incompatibility
- Poor adaptability
- Ploidy differences
- Chromosomal alteration
- Linkage drag

(Source: Kashyap *et al.*, 2022).

### 3.7 Emerging Technologies for The Identification, Characterization, And Transfer of Traits from Crop wild relatives of rice

**Backcross breeding:** Backcross breeding transfers traits from crop wild relatives to cultivated rice by crossing a hybrid with a parent species, selecting desired genes, and backcrossing with the cultivated species. This method transfers disease resistance, stress tolerance, and agronomic traits (Zhou *et al.*, 2011).

**Marker-Assisted Selection(MAS):** MAS identifies genes of interest from crop wild relatives using DNA markers and transfers them to cultivated species to improve disease resistance, yield, and abiotic stress tolerance (Choudhary *et al.*,2017).

**Hybridization:** Hybridization is a traditional method for transferring desired traits from crop wild relatives to cultivated rice through controlled breeding. This includes disease resistance, yield-related traits, and abiotic stress tolerance (Sangeetha *et al.*,2020)

**DNA sequencing:** DNA sequencing is a technique that determines the nucleotide sequence of a DNA molecule, enabling identification and characterization of genetic traits in rice wild relatives. It also identifies markers for trait transfer (Jaganathan *et al.*, 2020)

**Genome editing:** Genome editing is a precise technology to make targeted modifications to an organism's genome. It can be used to introduce beneficial traits from rice wild relatives to cultivated varieties (Tian *et al.*, 2021)

**High-throughput phenotyping:** measures an organism's physical traits and can identify desired traits in rice wild relatives for transfer to cultivated varieties (Xu *et al.*, 2014).

**Table 6: Technologies for The Identification, Characterization, And Transfer of Traits from Crop wild relatives of rice**

Technology	Advantages	Disadvantages
Backcross Breeding	Single step transfer of desired genes	Time-consuming process
Marker-Assisted Selection	Quick transfer of desired genes	Expensive and time-consuming process
Hybridization	Quick transfer of desired genes	Limited transfer of genes

(Source: Zhou *et al.*, 2011, Choudhary *et al.*, 2017 and Sangeetha *et al.*, 2020)

### 3.8 Rice varieties developed through inter-specific hybridization with wild relatives

Inter-specific hybridization between cultivated rice and wild relatives can introduce desirable traits like disease resistance, abiotic stress tolerance and improve grain quality. This increases rice's genetic diversity and adaptability.

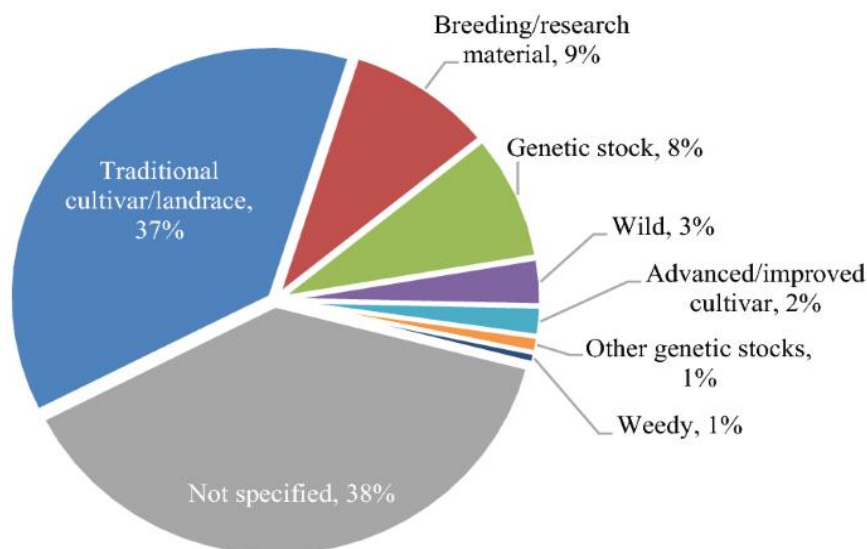
**Table 7: Rice varieties developed through interspecific hybridization**

<b>Key trait (s) introgressed</b>	<b>Wild species (donor)</b>	<b>Varieties released</b>	<b>Country</b>
Grassy stunt resistance	<i>O. nivara</i>	Many rice varieties	Several Asian countries.
BPH resistance	<i>O. officinalis</i>	MTL98, MT103	Vietnam
	<i>O. australiensis</i>	Suweon 523	South Korea
BPH and BB resistance	<i>O. rufipogon</i>	Dhanarasi	India
Tungro tolerance	<i>O. rufipogon</i>	Matatag 9	the Philippines
Acid sulfate tolerance	<i>O. rufipogon</i>	AS 996	Vietnam
Salinity tolerance	<i>O. rufipogon</i>	BRRRI Dhan 55(AS996)	Bangladesh
	<i>O. rufipogon</i>	Jaraya	India
Bacterial blight (BB) resistance	<i>O. logistaminata</i>	NSIc Rc 112	the Philippines India, China,
Blast resistance	<i>O. glaberrima</i>	Yun Dao	China
High yield, earliness, tolerance to abiotic stresses	<i>O. glaberrima</i>	Many NERICA lines/varieties	African countries
Yield-enhancing loci (QTL's): salinity tolerance	<i>O. nivara</i>	DRR Dhan 40	India
Salinity tolerance	<i>O. rufipogon</i>	Chinsurah Nona 2	India (Coastal saline area)

(Source: Brar *et al.*, 2011)

### 3.9 Conservation status of rice wild relatives

Many wild relatives of rice are endangered. A study found that 29% of wild rice species are threatened with extinction. Conservation efforts, such as seed banks and habitat restoration, are crucial for their survival (Khoury *et al.* 2015).



**Figure 07: Types of germplasm materials in the IRRI rice collection in % of total accessions. Total accessions in Genesys = 132,140.**

(Source: Jamora *et al.*, 2022)

This figure showed Types of rice germplasm materials in the IRRI collection. Total accessions in Genesys is 132,140. In which wild rice germplasm is 3%.

**Table 08: Rice genetic resources conserved in the BRRI genebank**

Variety/line	Collection	Registered in accession
<i>Indigenous indica</i>		
Local variety	4949	5132
Pure line	905	894
Exotic indica (IRRI, China, USA, Turkey etc.)	1722	790
<i>Exotic Japonica</i>		
Indica breeding lines	950	881
Wild Rice (4 species)	80	73
<b>Total</b>	<b>8745</b>	<b>7857</b>

(Source: Khalequzzaman *et al.*, 2012)

BRRRI conserved 80 accessions under 4 species in which 73 accession are registered.

**Table 09: Wild and weedy races of rice in Bangladesh**

Species	Sample no.
<i>Oryza rufipogon</i>	74
<i>Oryza officinalis</i>	4
<i>Oryza nivara</i>	1
<i>Oryza sativa f. spontanea</i>	1
Total	80

(Source: Khalequzzaman *et al.*, 2012)

In 80 accession collected by Bangladesh Rice Research Institute 74 are *Oryza rufipogon* , 4 are *Oryza officinalis* , 1 *Oryza nivara* , 1 *Oryza sativa f. spontanea* .

## **CHAPTER IV**

### **CONCLUSION**

Due to directional selection genetic bottlenecks occurring in rice gene pool. For that, cultivated rice variety become susceptible to different biotic and abiotic factors. Quality also deteriorated. Wild rice species exhibit substantial genetic diversity. They are more tolerance to pests, diseases and different climatic alterations. Because of their wider adaptability a single variety developed by using wild QTLs can cover a wide range of area for cultivation.

The use of wild rice species in rice breeding programs offers both challenges and opportunities. One of the main challenges is the genetic and phenotypic diversity of wild rice, which presents difficulties in effectively harnessing and incorporating desirable traits into cultivated rice varieties. Furthermore, the genetic incompatibility between wild and cultivated rice may limit the transfer of beneficial genes from wild rice.

Incorporating wild rice species can lead to the development of rice varieties that are more resistant to biotic and abiotic stresses, such as drought, salinity, and pests. Additionally, using wild rice can increase the genetic diversity of cultivated rice, leading to greater resilience against emerging threats and greater adaptability to changing environments.



## References

- Borromeo, T. H., Sanchez, P. L., Quintana, E. J., & Engle, L. M. (1994). Manual on rice genetic resources conservation and genebank management.
- Brar, D. S., & Khush, G. S. (2018). Wild relatives of rice: a valuable genetic resource for genomics and breeding research. *The wild Oryza genomes*, 1-25.
- Cairns, J. E., Crossa, J., Zaidi, P. H., Grudloyma, P., Sanchez, C., Araus, J. L., ... & Atlin, G. N. (2013). Identification of drought, heat, and combined drought and heat tolerant donors in maize. *Crop Science*, *53*(4), 1335-1346.
- Choudhary, M., Singh, V., Muthusamy, V., & Wani, S. H. (2017). Harnessing crop wild relatives for crop improvement.
- Fan, W., Lou, H. Q., Gong, Y. L., Liu, M. Y., Cao, M. J., Liu, Y., ... & Zheng, S. J. (2015). Characterization of an inducible C2H2-type zinc finger transcription factor Vu STOP 1 in rice bean (*Vigna umbellata*) reveals differential regulation between low pH and aluminum tolerance mechanisms. *New Phytologist*, *208*(2), 456-468.
- Fujita, D., Kohli, A., & Horgan, F. G. (2013). Rice resistance to planthoppers and leafhoppers. *Critical Reviews in Plant Sciences*, *32*(3), 162-191.
- Fukao, T., Harris, T., & Bailey-Serres, J. (2009). Evolutionary analysis of the Sub1 gene cluster that confers submergence tolerance to domesticated rice. *Annals of Botany*, *103*(2), 143-150.
- Garg, R., Verma, M., Agrawal, S., Shankar, R., Majee, M. & Jain, M. (2014). Deep transcriptome sequencing of wild halophyte rice, *Porteresia coarctata*, provides novel insights into the salinity and submergence tolerance factors. *DNA research*, *21*(1), 69-84.
- Gu, X. Y., Foley, M. E., Horvath, D. P., Anderson, J. V., Feng, J., Zhang, L., & Chen, Z. (2011). Association between seed dormancy and pericarp color is controlled by a pleiotropic gene that regulates abscisic acid and flavonoid synthesis in weedy red rice. *Genetics*, *189*(4), 1515-1524.

- Htet, A. H., Makabe, S., Takahashi, H., Samuel, P. A., Sato, Y. I., & Nakamura, I. (2022). A large deletion within intron 20 sequence of single-copy PolA1 gene as a useful marker for the speciation in *Oryza* AA-genome species. *Breeding Science*, 72(3), 267-273.
- Ikeda, R., Vaughan, D. A., & Kobayashi, N. (1994). Landraces and wild relatives of rice as sources of useful genes. In *JIRCAS International Symposium Series* (Vol. 2, pp. 104-111).
- Ismail, A. M. (2018). Submergence tolerance in rice: resolving a pervasive quandary. *New Phytologist*, 218(4), 1298-1300.
- Jackson, M. T. (1997). Conservation of rice genetic resources: the role of the International Rice Genebank at IRRI. *Plant molecular biology*, 35, 61-67.
- Jaganathan, D., Bohra, A., Thudi, M., & Varshney, R. K. (2020). Fine mapping and gene cloning in the post-NGS era: advances and prospects. *Theoretical and Applied Genetics*, 133(5), 1791-1810.
- Jamora, N., & Ramaiah, V. (2022). Global demand for rice genetic resources. *CABI Agriculture and Bioscience*, 3(1), 1-15.
- Kashyap, A., Garg, P., Tanwar, K., Sharma, J., Gupta, N. C., Ha, P. T. T., ... & Rao, M. (2022). Strategies for utilization of crop wild relatives in plant breeding programs. *Theoretical and Applied Genetics*, 135(12), 4151-4167.
- Khalequzzaman, M., Siddique, M. A., & Bashar, M. K. (2012, May). Rice genetic resources conservation and utilization in Bangladesh. In *National Workshop on Plant Genetic Resources for Nutritional Food Security held at BARC, Dhaka* (pp. 18-19).
- Khoury, C. K., Bjorkman, A. D., Dempewolf, H., Ramirez-Villegas, J., Guarino, L., Jarvis, A. & Struik, P. C. (2014). Increasing homogeneity in global food supplies and the implications for food security. *Proceedings of the national Academy of Sciences*, 111(11), 4001-4006.
- Koseki, M., Kitazawa, N., Yonebayashi, S., Maehara, Y., Wang, Z. X., & Minobe, Y. (2010). Identification and fine mapping of a major quantitative trait locus originating from wild rice, controlling cold tolerance at the seedling stage. *Molecular Genetics and Genomics*, 284(1), 45-54.

- Mackill, D. J., Ismail, A. M., Singh, U. S., Labios, R. V., & Paris, T. R. (2012). Development and rapid adoption of submergence-tolerant (Sub1) rice varieties. *Advances in agronomy*, *115*, 299-352.
- Mammadov, J., Buyyarapu, R., Guttikonda, S. K., Parliament, K., Abdurakhmonov, I. Y., & Kumpatla, S. P. (2018). Wild relatives of maize, rice, cotton, and soybean: treasure troves for tolerance to biotic and abiotic stresses. *Frontiers in plant science*, *9*, 886.
- Menguer, P. K., Sperotto, R. A., & Ricachenevsky, F. K. (2017). A walk on the wild side: *Oryza* species as source for rice abiotic stress tolerance. *Genetics and molecular biology*, *40*, 238-252.
- Nayak, S., Samanta, S., Sengupta, C., & Swain, S. S. (2021). Rice crop loss due to major pathogens and the potential of endophytic microbes for their control and management. *Journal of Applied Biology and Biotechnology*, *9*(5), 166-175.
- Ndjiondjop, M. N., Manneh, B., Cissoko, M., Drame, N. K., Kakai, R. G., Bocco, R., ... & Wopereis, M. (2010). Drought resistance in an interspecific backcross population of rice (*Oryza* spp.) derived from the cross WAB56-104 (*O. sativa*) $\times$  CG14 (*O. glaberrima*). *Plant Science*, *179*(4), 364-373.
- Nguyen, B. D., Brar, D. S., Bui, B. C., Nguyen, T. V., Pham, L. N., & Nguyen, H. T. (2003). Identification and mapping of the QTL for aluminum tolerance introgressed from the new source, *Oryza Rufipogon* Griff., into indica rice (*Oryza sativa* L.). *Theoretical & Applied Genetics*, *106*(4).
- Pathak, H., Kumar, M., Molla, K. A., & Chakraborty, K. (2021). Abiotic stresses in rice production: Impacts and management. *Oryza*, *58*(4), 103-125.
- Rome, I. (2020). Food and agriculture organization of the united nations. Durham, USA: Duke University.
- Saha, P., Singh, S., Bhatia, R., Dey, S. S., Das Saha, N., Ghoshal, C., & Kalia, P. (2022). Genomic designing for abiotic stress resistant brassica vegetable crops. In *Genomic designing for abiotic stress resistant vegetable crops* (pp. 153-185). Cham: Springer International Publishing.

- Sangeetha, J., Habeeb, J., Thangadurai, D., Alabhai, J. M., Hospet, R., Maxim, S. S., ... & Kushwaha, U. K. S. (2020). Potentiality of wild rice in quality improvement of cultivated rice varieties. *Rice Research for Quality Improvement: Genomics and Genetic Engineering: Volume 1: Breeding Techniques and Abiotic Stress Tolerance*, 61-85.
- Sarao, P. S., Sahi, G. K., Neelam, K., Mangat, G. S., Patra, B. C., & Singh, K. (2016). Donors for resistance to brown planthopper *Nilaparvata lugens* (Stål) from wild rice species. *Rice Science*, 23(4), 219-224.
- Teng, P. S., Torres, C. Q., Nuque, F. L., & Calvero, S. B. (1990). Current knowledge on crop losses in tropical rice. *Crop loss assessment in rice*, 39-53.
- Tian, Z., Wang, J. W., Li, J., & Han, B. (2021). Designing future crops: challenges and strategies for sustainable agriculture. *The Plant Journal*, 105(5), 1165-1178.
- Tseng, T. M., Burgos, N. R., Shivrain, V. K., Alcober, E. A., & Mauromoustakos, A. (2013). Inter-and intrapopulation variation in dormancy of *Oryza sativa* (weedy red rice) and allelic variation in dormancy-linked loci. *Weed Research*, 53(6), 440-451.
- Wang, C., Hu, S., Gardner, C., & Lübberstedt, T. (2017). Emerging avenues for utilization of exotic germplasm. *Trends in Plant Science*, 22(7), 624-637.
- Xu, K., Xu, X., Fukao, T., Canlas, P., Maghirang-Rodriguez, R., Heuer, S., ... & Mackill, D. J. (2006). Sub1A is an ethylene-response-factor-like gene that confers submergence tolerance to rice. *Nature*, 442(7103), 705-708.
- Xu, Y. (2016). Envirotyping for deciphering environmental impacts on crop plants. *Theoretical and Applied Genetics*, 129, 653-673.
- Zhou, Y. L., Uzokwe, V. N., Zhang, C. H., Cheng, L. R., Wang, L., Chen, K., ... & Li, Z. K. (2011). Improvement of bacterial blight resistance of hybrid rice in China using the Xa23 gene derived from wild rice (*Oryza rufipogon*). *Crop Protection*, 30(6), 637-644.
- Zhu, M., Chen, G., Zhang, J., Zhang, Y., Xie, Q., Zhao, Z., ... & Hu, Z. (2014). The abiotic stress-responsive NAC-type transcription factor SINAC4 regulates salt and drought

tolerance and stress-related genes in tomato (*Solanum lycopersicum*). *Plant Cell Reports*, 33, 1851-1863.

Zhu, Y., Ellstrand, N. C., & Lu, B. R. (2012). Sequence polymorphisms in wild, weedy, and cultivated rice suggest seed-shattering locus *sh4* played a minor role in Asian rice domestication. *Ecology and evolution*, 2(9), 2106-2113.