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## Use of crop wild relatives for biotic and abiotic stress tolerance in rice: A review

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### Abstract

World population is increasing day by day and it is expected to reach 9 billion by 2050. Global food demand is going to get doubled by 2050 due to increase in world's population. Rice (*oryza sativa*) is staple food for more than 3.6 billion people World Wide. Since rice is grown worldwide, its production is severely effected by biotic and abiotic stresses. Biotic stresses effecting the rice crop production include insects, bacteria, fungus and virus and abiotic stresses include drought, salinity, low temperature and aluminium toxicity. During domestication process from wild rice to cultivated rice selecting desirable traits for higher yield lead to reduction in the genetic diversity of cultivated rice gene pool. Narrow genetic base of cultivated rice is major constraint for rice breeding. Crop wild relatives are useful for broadening the gene pool of cultivated rice because crop wild relatives are the reservoirs of useful genes and QTLs for stress resistance. Molecular markers and QTL mapping techniques are useful to identify the QTLs for stress resistance and to transfer them from wild rice to cultivated rice. This article provides review on importance of crop wild relatives as a source of biotic and abiotic stress tolerance in rice.

**Keywords:** Rice, wild relatives, biotic stress tolerance, abiotic stress tolerance

### Introduction

Rice (*Oryza sativa*) is the second most important cereal crop in the world (Khush *et al.*, 2009). It can be grown under varied agro- climatic conditions World Wide (Anser *et al.* 2020) <sup>[4]</sup>. It provides staple food for nearly half of the total world's population (Zhou *et al.* 2020). With ever increasing population demand of rice is also increasing but rice productivity is highly effected by various environmental stresses (Ijaz *et al.*, 2019) <sup>[17]</sup>. Biotic stresses cause 30% yield losses which include insects, bacteria, virus and fungus. Abiotic factors are reason for 50% yield losses World Wide (Arif *et al.*, 2019) <sup>[11]</sup>. Major abiotic factors are drought, salinity, temperature and heavy metal toxicity (ref). Moreover, genetic variability for tolerance to biotic and abiotic stresses is very limited in cultivated gene pool of rice but abundantly present in wild gene pool of genus *Oryza*. There is a need to broaden the cultivated gene pool by transferring genes from wild species to cultivated species for improving tolerance to biotic and abiotic stresses (Sharma *et al.*, 2012) <sup>[41]</sup>. The use of crop wild relatives of rice for improving the genetic diversity of cultivated rice is a very promising approach (Jafar *et al.*, 2018) <sup>[18]</sup>. The genus *Oryza* consists of 24 species among which *O. sativa* and *O. glaberrima* are cultivated species and remaining are wild species (Jena, 2010) <sup>[19]</sup>. The wild species of genus *Oryza* has numerous genes that can be used as alternative sources of tolerance to biotic and abiotic stresses. Interspecific hybridization holds tremendous importance in combining higher productivity with biotic and abiotic stress tolerance (Paul *et al.*, 2013) <sup>[2]</sup>. It is easy to transfer valuable genes from AA genome of wild rice to cultivated rice by using conventional breeding methods (Jena, 2010) <sup>[19]</sup>. Although there are conventional breeding methods like backcrossing and recurrent selection which can be used to transfer desirable genes but it can be effected by a problem of linkage drag. So to avoid it molecular marker techniques like Marker assisted selection (MAS), marker assisted backcrossing can be used to ensure precise transfer of genome of interest and it also minimize the number of back crosses unlike conventional method (Das *et al.*, 2017) <sup>[8]</sup>. Gene pyramiding is another method of approach to combine desirable target genes from different sources into single cultivar. In this review article importance of wild species has been discussed.

### Insect tolerance

The most damaging pest of rice is Brown plant hopper (BPH) as it causes huge yield losses by sucking the cell sap from the leaves of rice (Ram *et al.*, 2010) <sup>[36]</sup>.

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This pest can infests all the stages of rice plant growth. BPH transmits the viral diseases by acting as a vector to the viruses like rice grassy stunt virus and rice ragged stunt virus (Hu *et al.*, 2016)<sup>[15, 16]</sup>. Host plant resistance is the most ideal method to control BPH as it increases the yield of rice crop without causing any harm to the environment (Jena 2010)<sup>[19]</sup>. Wild relatives are the important source for BPH resistant genes. Some of the donors for BPH resistant genes from wild and cultivated species are *Mudgo*, *ASD7*, *Rathu Heenati*, *Babawee*, *ARC10550*, *Swarnalata*, *T12*, *Chin Saba*, *Balamawee*, *O. officinalis*, *O. australiensis*, *O. minuta* and *O. rufipogon* (Jena 2010)<sup>[19]</sup>. *O. rufipogon* contain twelve brown plant hopper resistant genes i.e., bph18, bph19, bph20, Bph21, bph22, bph23, bph24, bph27, bph29, bph30, bph36 and bph38 and *O. officinalis* is the reservoir of bph10, bph11, bph13, bph14, bph15 genes (Khush *et al.*, 2009). IR 26 was the first resistant variety for bph with bph 1 gene and it was released in 1973 (Khush *et al.*, 2009). Total 573 cultivated varieties were identified at IRRI for bph resistance. Among them, 484 varieties are having resistance to biotype 1 (Jena, 2010)<sup>[19]</sup>. The cultivated variety *O. sativa* contain bph1 to 9, bph 19, bph 25, bph 26 genes and *O. officinalis* has seven genes i.e., bph 11, bph12, bph 14 to bph 17 (Jena, 2010)<sup>[19]</sup>. Some minor QTLs are also present in rice resistant cultivars along with the major genes. Both IR 26 and IR 64 has bph 1 gene but in addition to this IR 64 contain few minor QTLs providing IR 64 with more effective durable resistance (Jena, 2010)<sup>[19]</sup>. Green leaf hopper is the another most common pest of rice fields. The adults cause damage by sucking the plant cell sap and they act as vectors for rice tungro disease (Khush *et al.*, 2009). Donors for green leaf hopper resistance are *Pankhari 203*, *ASD7*, *Sigadis*, *Ptb8*, *DV85*, *Asmaita*, *ARC10313*, *ARC11554*, *O. rufipogon*. Gene *Grh5* showing resistance to green leaf hopper is located on chromosome 8 is closely linked to SSR markers RM3754 and RM3761. These markers are being used in marker assisted selection to develop green leaf hopper resistant rice (Fujita *et al.*, 2006)<sup>[12]</sup>.

*Sogatella furcifera*, commonly known as whited backed plant hopper (Wbph) is another serious pest of rice crop (Chen *et al.*, 2010). *O. officinalis* contain Wbph resistance genes i.e., Wbph7, Wbph8 and *O. rufipogon* contain three QTLs for white backed plant hopper resistance i.e., qWbph2, qWbph5 and qWbph9 (Gaikwad *et al.*, 2021)<sup>[14]</sup>. Marker assisted selection for insect resistance is done through markers like RFLP, RAPD, SSR and SNP markers. Gene *Grh5* showing resistance to green leaf hopper is located on chromosome 8 is closely linked to SSR markers RM3754 and RM3761. These markers are being used in marker assisted selection to develop green leaf hopper resistant rice (Fujita *et al.*, 2006)<sup>[12]</sup>.

### Disease tolerance

Rice blast is the most damaging disease of rice crop. It is caused by fungus *Magnaporthe oryzae* (Wang *et al.*, 2014). This fungus affects the rice crop at all the growth stages. It leads to total crop failure under suitable conditions for the fungal growth. Due to the narrow genetic base of cultivated varieties, they are favourable for pathogen survival. So there is a need to broaden the genepool of cultivated varieties for developing blast resistant cultivars. In India, this disease was first recorded in 1913. Kiyosawa identified the first blast resistant gene in 1967 in japonica variety (Sharma *et al.*, 2012)<sup>[41]</sup>. Nearly 100 blast resistant genes were identified

from wild and cultivated rice varieties. CWR are the major source of blast resistant genes (Gaikwad *et al.*, 2021)<sup>[14]</sup>. *O. minuta* possess blast resistant gene pi9. Gene *pirf2* is found in *O. rufipogon* and pi 40 is identified from *O. australiensis*. QTL mapping was first used to identify QTLs for blast resistance in japonica variety (Sharma *et al.*, 2012)<sup>[41]</sup>. Three blast resistant genes *Piz-5*, *pi1* and *Pita* are located on 6,11,12 chromosomes are pyramided using RFLP markers as they are showing high resistance in combination. These lines are being introgressed to other superior rice varieties by using marker assisted selection (Hittalmani *et al.*, 2000)<sup>[34]</sup>. RFLP, SSR and SNP markers are widely used to transfer blast resistant genes in crop breeding programs.

### Drought tolerance

Drought is one of the major constraints for rice crop production worldwide (panda *et al.*, 2021)<sup>[33]</sup>. In rice, reproduction growth stage is more critical to drought stress. Drought reduces the rice yields by reducing no. of tillers per plant and no. of leaves per plant (Shakiba and Eizenga, 2014)<sup>[40]</sup>. Worldwide, nearly one third of the total rice cultivated area is affected by drought stress. As the population increasing day by day, to meet the future global food security goals, there is a need to develop high yielding varieties having biotic and abiotic stress tolerance genes. But breeding for drought tolerance is very complex due to its quantitative nature (panda *et al.*, 2021)<sup>[33]</sup>. Knowing the drought stress responsive mechanism in plants is also a prerequisite for developing tolerant varieties for drought stress. Crop Wild Relatives are the excellent reservoirs for drought tolerance genes (Ndjiondjop *et al.*, 2010)<sup>[29]</sup>. *O. rufipogon* and *O. logistaminata* are the donors for the alleles with drought tolerance in rice (Liu *et al.*, 2004). *O. glaberrima* has the ability to grow in dry soil conditions thus it has numerous genes for drought tolerance (Karthika and Nakao, 2020). A QTL *qTWU3* confers drought tolerance to rice at vegetative stage. Marker assisted selection is very effective in developing the varieties for drought tolerance. In order combat with drought condition deep rooting is essential. Deep rooting mainly depends on root length and root angle. QTL *Drol* is deep rooting QTL mapped between markers RM24393 and RM7424 by using linkage analysis in order to detect deep rooting trait under less water conditions (Uga *et al.*, 2011). Commonly used markers for drought tolerance in rice are RFLP, RAPD, AFLP, SSR and SNP markers.

### Salinity tolerance

The concentration of salt present in the soil is called as salinity and the ability of plants to grow and complete their life cycle in the presence of high concentrations of soluble salts is called salt tolerance. Salinity is one of the major constraint for rice crop production (Solis *et al.*, 2020)<sup>[42]</sup>. Nearly one third of the irrigated rice lands around the world suffer from salinity (Mammadov *et al.*, 2018)<sup>[25]</sup>. Excess salinity causes osmotic stress and ion toxicity in crop plants which causes huge yield losses. So there is an important need to develop salt tolerant varieties to combat food supply (Garg *et al.*, 2014)<sup>[23]</sup>. Success in the development of salinity tolerant varieties is limited due to lack of donors for salinity tolerant genes (Solis *et al.*, 2020)<sup>[42]</sup>. Wild halophytes possess salt tolerant mechanisms to survive in high salt concentrations (Garg *et al.*, 2014)<sup>[23]</sup>. These are the reservoirs for salinity tolerant genes. Wild halophyte *Porteresia coarctata* is a wild

relative of rice having salinity and submergence tolerant genes. These genes are transferred to *Oryza sativa* by bridge crossing (Mammadov *et al.*, 2018) [25]. Cultivars like *Pokkali*, *getu*, *Bokra*, *Cheriveruppu* and *nona* possess salt tolerant genes. IR 29 and *pokkali* are crossed to develop FL479 which confers salt tolerance to rice at seedling stage. salinity tolerant QTLs of rice are qST1 and qST3 identified from inbred line developed by a cross between japonica varieties Milyang23 and Gihobyeo. QTL *Saltol* is identified at chromosome 1 loci of salinity tolerant cultivar pokkali. This QTL *saltol* confers tolerance to salinity mainly at vegetative stage. SSR markers RM8094 and RM10745 are used for Marker Assisted Selection of QTL *saltol* (Nejad *et al.*, 2008). Now a days SSR and SNP markers are being widely used for marker assisted selection of salinity tolerance in rice.

### Cold tolerance

One of the major constraint effecting rice crop production is the chilling injury. Worldwide, nearly 15 million hectares of rice fields are effected by chilling injury (Lou *et al.*, 2007) [24]. Average temperature required for rice crop growth is 20 °C to 27 °C. If temperature goes below 15 °C it leads to poor germination of seedlings. Major consequences of chilling injury are wilting, stunting and necrosis (Shakiba and Eizenga. 2014) [40]. So there is a need to develop cold resistant varieties to minimize rice yield losses. As Wild rice cultivars are the reservoirs for cold resistant genes, they are utilized to develop cold resistant varieties (Lou *et al.*, 2007) [24]. Over past few years, many QTLs for cold tolerance have been identified in *Indica* and *Japonica* cultivars. At reproductive stage, QTLs for cold tolerance are qCtb1, qCTB2a, qPSS2-3 and qLTB3 and at germination stage, QTL for cold tolerance is qCTP11 and QTLs qCtss11 and qCTS4a are for seedlings stage. *O. rufipogon* also contain QTLs for cold tolerance (Gaikwad *et al.*, 2021) [14]. These QTLs are tagged with molecular markers and transfer to develop elite genotypes in plant breeding programs (Gaikwad *et al.*, 2021) [14]. Cold tolerant variety of rice Norin-PL8 is developed by introgression of cold tolerance genes from Japonica variety *Silewah*. On 4th chromosome of Norin-PL8, two QTLs *Ctb1* and *Ctb2* were identified conferring resistance to cold tolerance (Saito *et al.*, 2001) [37]. These days SSR and SNP markers are being widely used for cold tolerance in rice.

### Tolerance to Aluminium toxicity

Aluminum toxicity is one of the major problems for rice growing in acidic soils (Ndjiondjop *et al.*, 2010) [29]. Al restricts the uptake of water and nutrients by plant by inhibiting the root growth leading to severe crop losses. Wild relatives of *Oryza* contain genes for aluminum tolerance. *O. rufipogon* is a donor for QTLs of aluminum tolerance (Gaikwad *et al.*, 2021) [14]. *Japonica* cultivar, *Asominori* contain genes for aluminum tolerance. It is crossed with *Indica* cultivar IR24 to develop recombinant inbred line possessing QTLs for aluminum tolerance in rice (Xue *et al.*, 2007) [47]. For gene pyramiding of al tolerance genes, marker assisted selection is widely used in crop improvement programs (Nguyen *et al.*, 2003) [30].

### Conclusion

In the process of domestication from wild rice to cultivated rice, valuable genes for resistance to biotic and abiotic stresses have been lost during selection. As the global food

demand is expected to increase to 852 million tonnes by 2035, there is an urgent need to develop cultivars possessing tolerance to biotic and abiotic stresses to minimize the yield losses. For this we need to broaden the cultivated gene pool of rice by transferring the tolerant genes from the crop wild relatives with the help of QTL mapping and marker assisted selection.

### References

1. Ali ML, Sanchez PL, Yu SB, Lorieux M, Eizenga GC. Chromosome segment substitution lines: a powerful tool for the introgression of valuable genes from *Oryza* wild species into cultivated rice (*O. sativa*). *Rice*. 2010;3:218-234. DOI: 10.1007/s12284-010-9058-3.
2. Ali N, Paul S, Gayen D, Sarkar SN, Datta K, Datta SK. Development of Low Phytate Rice by RNAi Mediated Seed-Specific Silencing of Inositol 1,3,4,5,6-Pentakisphosphate 2-Kinase Gene (IPK1). *PLoS one*. 2013;8(7):e68161.
3. Andaya VC, Tai TH. Fine mapping of the qCTS4 locus associated with seedling cold tolerance in rice (*Oryza sativa* L.). *Mol. Breed.* 2007;20:349–358. DOI:10.1007/s11032-007-9096-8
4. Anser MK, Hina T, Hameed S, Nasir MH, Ahmad I, Naseer MA. Modeling adaptation strategies against climate change impacts in integrated rice-wheat agricultural production system of Pakistan. *International Journal of Environmental Research and Public Health*. 2020;17(7):2522.
5. Ashkani S, Rafii MY, Shabanmofrad M, Miah G, Sahebi M, Azizi P. Molecular breeding strategy and challenges towards improvement of blast disease resistance in rice crop. *Front. Plant Sci.* 2015;6:886. DOI: 10.3389/fpls.2015.00886
6. Brar DS, Khush G. Alien introgression in rice. *Plant Mol. Biol.* 1997;35:35-47. DOI: 10.1023/A:1005825519998
7. Cao Y, Lou Y, Han Y, Shi J, Wang Y, Wang W, *et al.* Al toxicity leads to enhanced cell division and changed photosynthesis in *Oryza rufipogon* L. *Mol. Biol. Rep.* 2011;38:4839-4846. DOI: 10.1007/s11033-010-0618-9.
8. Das S, Jeong ST, Das S, Kim PJ. Composted cattle manure increases microbial activity and soil fertility more than composted swine manure in a submerged rice paddy. *Frontiers in microbiology*. 2017;8:1702.
9. Ellur RK, Khanna A, Bhowmick PK, Vinod K, Nagarajan M, Mondal KK, *et al.* Marker-aided incorporation of Xa38, a novel bacterial blight resistance gene, in PB1121 and comparison of its resistance spectrum with xa13+ Xa21. *Sci. Rep.* 2016;6:29188. DOI: 10.1038/srep29188
10. Engels MM, Thormann I. Main Challenges and Actions Needed to Improve Conservation and Sustainable Use of Our Crop Wild Relatives. *Plants*. 2020;9:968. DOI: 10.3390/plants9080968
11. Fahad S, Adnan M, Noor M, Arif M, Alam M, Khan IA, *et al.* Major constraints for global rice production. *Advances in rice research for abiotic stress tolerance*, 2019, 1-22.
12. Fujita D, Yoshimura A, Yasui H. Molecular mapping of a novel gene, Grh5, conferring resistance to green rice leafhopper (*Nephotettix cincticeps* Uhler) in rice, *Oryza sativa* L. *Theoretical and applied genetics*. 2006;113(4):567-573.



13. Fujita D, Kohli A, Horgan FG. Rice resistance to plant hoppers and leafhoppers. *Crit. Rev. Plant Sci.* 2013;32:162-191. DOI: 10.1080/07352689.2012.735986
14. Gaikwad KB, Singh N, Kaur P, Rani S, Babu HP, Singh K. Deployment of wild relatives for genetic improvement in rice (*Oryza sativa* L.). *Plant Breed.* 2021;140:23-52.
15. Hu J, Xiao C, He Y. Recent progress on the genetics and molecular breeding of brown plant hopper resistance in rice. *Rice.* 2016;9:1-12. DOI: 10.1186/s12284-016-0099-0.
16. Hu X, Wang C, Fu Y, Liu X, Jiao X, Wang K. Expanding the range of CRISPR/Cas9 genome editing in rice. *Molecular plant.* 2016;9(6):943-945.
17. Ijaz B, Formentin E, Ronci B, Locato V, Barizza E, Hyder MZ, *et al.* Salt tolerance in indica rice cell cultures depends on a fine tuning of ROS signalling and homeostasis. *PLoS One.* 2019;14(4):e0213986.
18. Jafar WNW, Mazlan N, Adam NA, Omar D. Evaluation on the effects of insecticides on biodiversity of arthropod in rice ecosystem. *Acta Biologica Malaysiana.* 2013;2(3):115-123.
19. Jena KK. The species of the genus *Oryza* and transfer of useful genes from wild species into cultivated rice, *O. sativa*. *Breed. Sci.* 2010;60:518-523. DOI: 10.1270/jsbbs.60.518
20. Khush G, Ling K, Aquino R, Aguiro V. Breeding for resistance to grassy stunt in rice. *Plant Breed. Papers Int. Congr. Soc. Adv. Breed. Res. Asia Ocean.* 1977;1:3-9.
21. Koseki M, Kitazawa N, Yonebayashi S, Maehara Y, Wang ZX, Minobe Y. Identification and fine mapping of a major quantitative trait locus originating from wild rice, controlling cold tolerance at the seedling stage. *Mol. Genet. Genomics.* 2010;284:45-54. DOI: 10.1007/s00438-0100548-1
22. Ling Y, Weilin Z. Genetic and biochemical mechanisms of rice resistance to plant hopper. *Plant Cell Rep.* 2016;35:1559-1572. DOI: 10.1007/s00299-016-1962-6.
23. Liu C, Mao B, Ou S, Wang W, Liu L, Wu Y, *et al.* OsbZIP71, a bZIP transcription factor, confers salinity and drought tolerance in rice. *Plant molecular biology.* 2014;84(1):19-36.
24. Lou Q, Chen L, Sun Z, Xing Y, Li J, Xu X, *et al.* A major QTL associated with cold tolerance at seedling stage in rice (*Oryza sativa* L.). *Euphytica.* 2007;158:87-94. DOI: 10.1007/s10681-00.
25. Mammadov J, Buyyarapu R, Guttikonda SK, Parliament K, Abdurakhmonov IY, Kumpatla SP. Wild relatives of maize, rice, cotton, and soybean: treasure troves for tolerance to biotic and abiotic stresses. *Frontiers in plant science.* 2018;9:886.
26. McCouch SR, Sweeney M, Li J, Jiang H, Thomson M, Septiningsih E. Through the genetic bottleneck: *O. rufipogon* as a source of trait-enhancing alleles for *O. sativa*. *Euphytica.* 2007;154:317-339. DOI: 10.1007/s10681-006-9210-8
27. Menguer PK, Sperotto RA, Ricachenevsky FK. A walk on the wild side: *Oryza* species as source for rice abiotic stress tolerance. *Genet. Mol. Biol.* 2017;40(1):238-252. DOI: 10.1590/1678-4685-gmb-2016-0093
28. Mussurova S, Al Bader N, Zuccolo A, Wing RA. Potential of Platinum Standard Reference Genomes to Exploit Natural Variation in the Wild Relatives of Rice. *Front. Plant Sci.* 2020;11:579980. DOI: 10.3389/fpls.2020.579980
29. Ndjioudjop MN, Manneh B, Cissoko M, Drame NK, Kakai RG, Bocco R, *et al.* Drought resistance in an interspecific backcross population of rice (*Oryza* spp.) derived from the cross WAB56-104 (*O. sativa*)× CG14 (*O. glaberrima*). *Plant Sci.* 2010;179:364-373. DOI: 10.1016/j.plantsci.2010.06.006
30. Nguyen BD, Brar DS, Bui BC, Nguyen TV, Pham LN, Nguyen HT. Identification and mapping of the QTL for aluminum tolerance introgressed from the new source, *Oryza rufipogon* Griff., into indica rice (*Oryza sativa* L.). *Theor. Appl. Genet.* 2003;106:583-593. DOI: 10.1007/s00122-002-1072-4
31. Normile D. Reinventing rice to feed the world. *Science.* 2008;321:330-333. DOI: 10.1126/science.321.5887.330
32. Ouyang S, Liu Y, Liu P, Lei G, He S, Ma B, *et al.* Receptor-like kinase OsSIK1 improves drought and salt stress tolerance in rice (*Oryza sativa*) plants. *The Plant Journal.* 2010;62(2):316-329.
33. Panda D, Mishra SS, Behera PK. Drought Tolerance in Rice: Focus on Recent Mechanisms and Approaches. *Rice Science,* 2021, 28-2. DOI: 10.1016/j.rsci.2021.01.002
34. Prasad SR, Bagali PG, Hittalmani S, Shashidhar HE. Molecular mapping of quantitative trait loci associated with seedling tolerance to salt stress in rice (*Oryza sativa* L.). *Current Science,* 2000, 162-16
35. Rahman ML, Jiang W, Chu SH, Qiao Y, Ham TH, Woo M, *et al.* High-resolution mapping of two rice brown plant hopper resistance genes, Bph20 (t) and Bph21 (t), originating from *Oryza minuta*. *Theoretical and Applied Genetics.* 2009;119(7):1237-1246.
36. Ram T, Deen R, Gautam S, Ramesh K, Rao Y, Brar D. Identification of new genes for brown plant hopper resistance in rice introgressed from *O. glaberrima* and *O. minuta*. *Rice Genet. Newsl.* 2010;25:67-69. DOI: 10.1186/s12284-017-0178-x.
37. Saito K, Miura K, Nagano K, Saito Y, Araki H, Kato A. Identification of two closely linked quantitative trait loci for cold tolerance on chromosome 4 of rice and their association with anther length. *Theoretical and Applied Genetics.* 2001;103(6):862-868.
38. Sanchez PL, Wing RA, Brar DS. The wild relative of rice: genomes and genomics, in *Genetics and Genomics of Rice*, Eds Q. Zhang and R. Wing (Berlin: Springer Science Business Media, LLC, 2013, 9-25.
39. Sarao PS, Sahi GK, Neelam K, Mangat GS, Patra BC, Singh K. Donors for resistance to brown plant hopper *Nilaparvata lugens* from wild rice species. *Rice Sci.* 2016;23:219-224. DOI: 10.1016/j.rsci.2016.06.005
40. Shakiba E, Eizenga GC. Unraveling the secrets of rice wild species, in *Rice Germ plasm, Genetics and Improvement*, Ed J Bao (London: Intec Open), 2014, 1-58.
41. Sharma T, Rai A, Gupta S, Vijayan J, Devanna B, Rays S. Rice blast management through host-plant resistance: retrospect and prospects. *Agric. Res.* 2012;1:37-52. DOI:10.1007/s40003011-0003-5
42. Solis CA, Yong MT, Vinarao R, Jena K, Holford P, Shabala L, *et al.* Back to the Wild: On a Quest for Donors Toward Salinity Tolerant Rice. *Front. Plant Sci.* 2020;11:323. DOI: 10.3389/fpls.2020.00323
43. Song WY, Wang GL, Chen LL, Kim HS. A receptor

- kinase like protein encoded by the rice disease resistance gene, Xa21. *Science*. 1995;270:1804. DOI: 10.1126/science.270.5243.1804.
44. Tanaka K, Endo S, Kazano H. Toxicity of insecticides to predators of rice plant hoppers: spiders, the mirid bug and the dryinid wasp. *Appl. Entomol. Zool.* 2000;35:177-187.
  45. Vasudevan K, Grisse W, Bhullar NK. Identification of novel alleles of the rice blast resistance gene Pi54. *Sci. Rep.* 2015;5:15678. DOI: 10.1038/srep15678.
  46. Uga Y, Sugimoto K, Ogawa S, Rane J, Ishitani M, Hara N, *et al.* Control of root system architecture by deeper rooting 1 increases rice yield under drought conditions. *Nature genetics*. 2013;45(9):1097-1102.
  47. Xue Y, Jiang L, Su N, Wang JK, Deng P, Ma JF, *et al.* The genetic basic and fine-mapping of a stable quantitative-trait loci for aluminium tolerance in rice. *Plants*. 2007;227(1):255-262.