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Marker-Assisted Selection for Disease Resistance in Rice: A Molecular Breeding Approach

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ABSTRACT

Background: Bacterial blight, blast and tungro remain major constraints on rice yield, and cloning of the underlying resistance genes has enabled DNA marker-based selection as an alternative to slow, environment-dependent phenotypic screening. Objective: To synthesise published evidence on marker development, gene pyramiding strategies and breeding outcomes for disease-resistant rice. Methods: Narrative review of marker-assisted selection (MAS) and molecular breeding studies for bacterial blight (Xa/xa), blast (Pi) and tungro resistance in rice, identified via PubMed, Google Scholar and Crossref, with each reference individually verified. Findings: Cloned genes including Xa21, xa5, xa13, Xa27, Pi9, Pi-ta, Pib and Pi5 have yielded gene-based and flanking markers that support foreground selection, while microsatellite-based background selection accelerates recovery of recurrent-parent genome during backcrossing; published pyramided lines recovered 91-96% of recurrent-parent genome and combined two to ten resistance genes/QTLs with improved field resistance and retained agronomic quality. Conclusions: MAS-based gene pyramiding has repeatedly converted elite but disease-susceptible rice varieties into broad-spectrum-resistant counterparts, and genomic selection now offers a route to breeding for resistances that are not governed by single major genes.

Keywords: *marker-assisted selection; rice; bacterial blight; blast resistance; gene pyramiding*

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Abstract

Background: Bacterial blight, blast and tungro remain major constraints on rice yield, and cloning of the underlying resistance genes has enabled DNA marker-based selection as an alternative to slow, environment-dependent phenotypic screening. **Objective:** To synthesise published evidence on marker development, gene pyramiding strategies and breeding outcomes for disease-resistant rice. **Methods:** Narrative review of marker-assisted selection (MAS) and molecular breeding studies for bacterial blight (Xa/xa), blast (Pi) and tungro resistance in rice, identified via PubMed, Google Scholar and Crossref, with each reference individually verified. **Findings:** Cloned genes including Xa21, xa5, xa13, Xa27, Pi9, Pi-ta, Pib and Pi5 have yielded gene-based and flanking markers that support foreground selection, while microsatellite-based background selection accelerates recovery of recurrent-parent genome during backcrossing; published pyramided lines recovered 91-96% of recurrent-parent genome and combined two to ten resistance genes/QTLs with improved field resistance and retained agronomic quality. **Conclusions:** MAS-based gene pyramiding has repeatedly converted elite but disease-susceptible rice varieties into broad-spectrum-resistant counterparts, and genomic selection now offers a route to breeding for resistances that are not governed by single major genes.

Keywords: marker-assisted selection; rice; bacterial blight; blast resistance; gene pyramiding

Introduction

Rice (Oryza sativa) production is repeatedly constrained by three major biotic stresses: bacterial blight caused by Xanthomonas oryzae pv. oryzae, blast caused by Magnaporthe oryzae, and rice tungro disease transmitted by the green leafhopper. Conventional breeding for resistance to these pathogens is slowed by pathogen race variation, environment-dependent phenotypic scoring, and the difficulty of combining several resistance genes with overlapping phenotypic effects in one genetic background. The cloning of major bacterial blight resistance genes such as Xa21 [1] and blast resistance genes such as Pi-ta [2] made it possible to design PCR-based markers tightly linked to, or diagnostic within, the causal gene itself, enabling marker-assisted selection (MAS)

to track individual resistance alleles in segregating populations independently of pathogen exposure. Because several Xa and Pi genes individually confer only race-specific or partial resistance, breeders have pursued gene pyramiding — combining multiple resistance genes in one cultivar via marker-assisted backcrossing (MABC) — to obtain broader-spectrum and more durable protection. Molecular markers also remove much of the guesswork associated with recessive resistance alleles (such as xa5 and xa13) and with genes whose phenotypic effects are masked or modified by genetic background, both of which are difficult to select for using pathogen inoculation alone. This review synthesises the published record on marker development for rice disease-resistance genes, pyramiding strategies, and the field performance of resulting varieties.

Methods

This is a narrative review of published studies on marker-assisted selection and molecular breeding for disease resistance in rice. Relevant articles were identified through structured searches of PubMed, Google Scholar and Crossref using combinations of the terms "marker-assisted selection", "gene pyramiding", "bacterial blight", "Xa gene", "blast resistance", "Pi gene", "tungro", "rice" and "backcross breeding", supplemented by citation chaining from key papers. Studies were included if they reported cloning or marker development for a rice disease-resistance gene, a marker-assisted backcrossing or pyramiding programme with quantitative background-recovery or disease-reaction data, or a review synthesising this literature; each reference was individually verified against its indexed publication record before inclusion. No new crosses, marker assays or field trials were conducted for this article; all genes, markers, breeding lines and outcomes reported below are drawn directly from the cited literature.

Major Disease-Resistance Genes and Molecular Markers in Rice

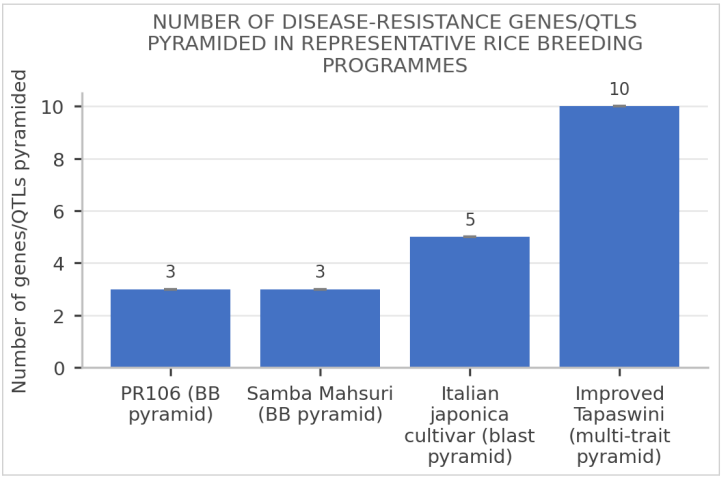
More than thirty bacterial blight resistance loci (Xa1-Xa41) and over twenty cloned blast resistance (Pi) genes have been reported in rice, but a smaller subset has been cloned and converted into gene-based markers routinely used in MAS. Xa21 encodes a receptor-like kinase with an extracellular leucine-rich-repeat domain and was the first bacterial blight resistance gene cloned by map-based methods [1]. The recessive gene xa5 encodes a variant transcription factor IIAγ subunit [3], xa13 (also known as Os8N3/OsSWEET11) is a sucrose-transporter susceptibility gene whose promoter mutation confers recessive resistance [4], and Xa27 is induced specifically by its cognate bacterial effector to trigger an executor-type resistance response [5]. Among blast resistance genes, Pi-ta encodes a cytoplasmic nucleotide-binding, leucine-rich-repeat (NBS-LRR) protein distinguished from the susceptible allele by a single amino acid [2], Pib [6] and Pi9 [7] are NBS-LRR genes from the same structural class, and Pi5 confers resistance through a pair of physically linked NBS-LRR genes acting together [8]. Sequence-tagged-site, simple-sequence-repeat (SSR) and gene-based (functional) markers derived from these cloned loci, together with genome-wide SSR marker sets developed for rice [9], now allow both foreground selection for the target allele and microsatellite-based background selection to accelerate recovery of the recurrent-parent genome during backcrossing [10,11].

Marker-Assisted Backcrossing and Gene Pyramiding Strategies

Table 1: Selected cloned bacterial blight and blast resistance genes in rice and the class of markers they support for marker-assisted selection.

Gene	Disease	Encoded product / marker basis	Reference
Xa21	Bacterial blight	Receptor-like kinase; gene-based PCR markers	[1]
xa5	Bacterial blight	Variant transcription factor IIAγ subunit; functional marker	[3]
xa13	Bacterial blight	Sucrose-transporter (SWEET11) promoter mutation	[4]
Xa27	Bacterial blight	Effector-induced executor R gene	[5]
Pi-ta	Blast	Cytoplasmic NBS-LRR protein; single amino-acid marker	[2]
Pib	Blast	NBS-LRR protein	[6]
Pi9	Blast	NBS-LRR protein, multigene family member	[7]
Pi5	Blast	Paired NBS-LRR proteins	[8]

Figure 1: Number of disease-resistance genes/QTLs combined by marker-assisted backcrossing in four representative rice breeding programmes: a three-gene bacterial blight (BB) pyramid in PR106 [14], a three-gene BB pyramid in Samba Mahsuri [15], a five-gene blast-resistance pyramid in an elite Italian japonica cultivar [20], and a ten-gene/QTL multi-trait pyramid (four BB genes plus blast, submergence, salinity and gall-midge resistance) in Improved Tapaswini [21].



The principle of pyramiding — combining two or more resistance genes with independent, tightly linked markers in a single genetic background — was first demonstrated for bacterial blight resistance using RFLP and PCR markers to track Xa4, xa5, xa13 and Xa21 [12], and subsequently refined with sequence-tagged-site markers for combinations of these same genes [13]. Marker-assisted backcrossing (MABC) programmes have since introgressed three-gene bacterial blight pyramids (xa5 + xa13 + Xa21) into indica cultivars such as PR106 [14] and the fine-grain variety Samba Mahsuri, where three-gene pyramid lines showed a significant yield advantage over the recurrent parent under blight pressure while retaining its grain and cooking quality [15]. Analogous MABC pipelines have pyramided major blast resistance genes: Pi1, Piz-5 and Pita were fine-mapped and combined using flanking markers in early proof-of-concept work [16], Pi9 and Pi-ta were pyramided into the Basmati variety Pusa Basmati 1 [17], and bacterial blight resistance was combined with Basmati grain-quality traits by joint phenotypic and

marker-assisted selection [18]. Foreground selection with gene-based markers is typically paired with background selection using genome-wide SSR panels, and reported programmes have recovered 91-96% of recurrent-parent genome within two to three backcross generations [19,20], illustrating that pyramiding need not come at the cost of the elite agronomic background into which resistance genes are introgressed.

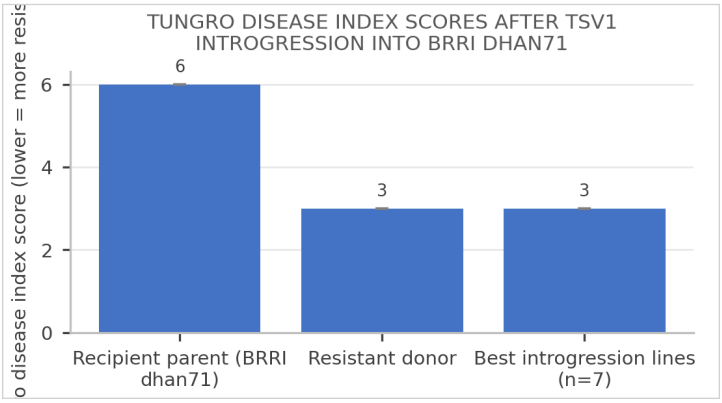
Field Performance of MAS-Derived Resistant Varieties

Several MAS-derived pyramided lines have been advanced to multi-location field evaluation. Introgression of Xa21 and Pi54 into the maintainer line DRR17B via MABC recovered approximately 94% of the recurrent-parent genome in the selected BC3F1 plant and produced progeny with a high level of combined resistance to bacterial blight and blast [19]. In japonica rice, pyramiding of the blast resistance genes Piz, Pib, Pi-ta and Pik (with an additional Pita2/Ptr allele identified during the programme) into an elite Italian cultivar achieved 95.65% recurrent-parent genome recovery and yielded lines with broad-spectrum resistance across multiple Magnaporthe oryzae strains [20]. A more extensive pyramid was assembled in Improved Tapaswini, which combines four bacterial blight genes (Xa4, xa5, xa13, Xa21) with blast resistance genes Pi2 and Pi9, submergence tolerance (Sub1), salinity tolerance (Saltol) and gall-midge resistance genes (Gm1, Gm4) — ten genes/QTLs in total — in one genetic background [21]. For tungro, marker-assisted introgression of the resistance locus tsv1 into the popular Bangladeshi variety BRRI dhan71 produced introgression lines with disease index scores of 3-5 against a susceptible recipient score of 6, with seven lines matching the resistant donor's score of 3 and about half yielding at least as well as the recurrent parent [22]. Collectively these programmes, and related pyramiding efforts reviewed elsewhere [23], show that MAS reliably converts susceptible elite backgrounds into multiply resistant lines without major yield or quality penalties.

Genomic Selection and Future Breeding Directions

Gene pyramiding via MABC is most effective when resistance is governed by a small number of major genes with validated diagnostic markers; many quantitative and partial resistance traits, and durability against evolving pathogen populations, are less amenable to this approach. Genomic selection, which uses genome-wide marker data to predict breeding values without requiring prior knowledge of causal loci, has been evaluated in elite tropical rice breeding populations and shown to give useful prediction accuracy for complex traits, with accuracy sensitive to trait genetic architecture, training-population composition, marker density and statistical model [24]. Ongoing cloning of additional Xa and Pi genes, and continued documentation of durability and race-specificity in the field, are expanding the pool of validated markers available for both MABC and marker-assisted recurrent selection [25,26]. Broader adoption will depend on cost-effective high-throughput genotyping, better characterisation of gene-gene interactions among pyramided resistance loci, and integration of MAS/MABC with genomic selection so that major-gene and background polygenic resistance can be improved within the same breeding pipeline, as emphasised in general treatments of MAS practice [27]. Practical constraints such as genotyping cost per sample, the size of populations that must be screened at each backcross generation, and the availability of trait-specific pathogen isolates for phenotypic confirmation continue to shape how quickly newly cloned resistance genes move from gene discovery into routine breeding pipelines.

Figure 2: Tungro disease index scores (lower values indicate greater resistance) for the recipient variety BRRI dhan71, the resistant tsv1 donor, and the seven best marker-assisted introgression lines matching the donor's resistance level [22].



Conclusion

Published literature on marker-assisted selection for disease resistance in rice demonstrates a mature and repeatedly validated pipeline: cloning of major bacterial blight (Xa21, xa5, xa13, Xa27) and blast (Pi-ta, Pib, Pi9, Pi5) resistance genes has generated diagnostic and flanking markers that, combined with genome-wide background selection, allow breeders to pyramid two to ten resistance genes/QTLs into elite backgrounds while recovering over 90% of the recurrent-parent genome and preserving grain quality and yield. Field-tested products spanning Samba Mahsuri, DRR17B, Improved Tapaswini, an Italian japonica cultivar and tungro-resistant BRRI dhan71 lines confirm that this approach delivers durable, field-relevant gains. Extending these gains to quantitatively inherited and durability-related resistance will increasingly depend on combining established MAS/MABC pipelines with genomic selection.

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Conflict of Interest

The authors declare no conflict of interest.

Author Contributions

Girard T conceived the review, conducted the literature search, and drafted the manuscript. Todorova E contributed to the literature screening and technical framing and critically revised the manuscript for important intellectual content. Golob A contributed additional context and approved the final version for submission.

Ethics Statement

Not applicable. This is a narrative review of previously published

literature and did not involve new experimental data, human participants, or animal subjects.

Table 2: Recurrent-parent genome (RPG) recovery and resistance outcomes reported for representative marker-assisted breeding programmes.

Variety / line	Genes introgressed	RPG recovery	Reported outcome	Reference
DRR17B	Xa21, Pi54	~94%	High combined resistance to bacterial blight and blast	[19]
Italian japonica cultivar	Piz, Pib, Pi-ta, Pik (+Pita2/Ptr)	95.65%	Broad-spectrum resistance across multiple blast strains	[20]
Improved Tapaswini	Xa4, xa5, xa13, Xa21, Pi2, Pi9, Sub1, Saltol, Gm1, Gm4	Not applicable (10-gene pyramid)	Combined biotic and abiotic stress resistance/tolerance	[21]
BRRI dhan71 (tsv1 lines)	tsv1 (tungro resistance)	91-95%	Disease index reduced from 6 (recipient) to 3 in best lines	[22]

Data Availability

No new data were generated or analyzed for this review. All sources synthesized are cited in the reference list and are available through their original publishers.

References

1. Song WY, Wang GL, Chen LL, Kim HS, Pi LY, Holsten T, Gardner J, Wang B, Zhai WX, Zhu LH, Fauquet C, Ronald P. A receptor kinase-like protein encoded by the rice disease resistance gene, Xa21. Science. 1995;270(5243):1804-1806. doi:10.1126/science.270.5243.1804

2. Bryan GT, Wu KS, Farrall L, Jia Y, Hershey HP, McAdams SA, Faulk KN, Donaldson GK, Tarchini R, Valent B. A single amino acid difference distinguishes resistant and susceptible alleles of the rice blast resistance gene Pi-ta. Plant Cell. 2000;12(11):2033-2046. doi:10.1105/tpc.12.11.2033

3. Iyer AS, McCouch SR. The rice bacterial blight resistance gene xa5 encodes a novel form of disease resistance. Mol Plant Microbe Interact. 2004;17(12):1348-1354. doi:10.1094/MPMI.2004.17.12.1348

4. Chu Z, Fu B, Yang H, Xu C, Li Z, Sanchez A, Park YJ, Bennetzen JL, Zhang Q, Wang S. Targeting xa13, a recessive gene for bacterial blight resistance in rice. Theor Appl Genet. 2006;112(3):455-461. doi:10.1007/s00122-005-0145-6

5. Gu K, Yang B, Tian D, Wu L, Wang D, Sreekala C, Yang F, Chu Z, Wang GL, White FF, Yin Z. R gene expression induced by a type-III effector triggers disease resistance in rice. Nature. 2005;435(7045):1122-1125. doi:10.1038/nature03630

6. Wang ZX, Yano M, Yamanouchi U, Iwamoto M, Monna L, Hayasaka H, Katayose Y, Sasaki T. The Pib gene for rice blast resistance belongs to the nucleotide binding and leucine-rich repeat class of plant disease resistance genes. Plant J. 1999;19(1):55-64. doi:10.1046/j.1365-313x.1999.00498.x

7. Qu S, Liu G, Zhou B, Bellizzi M, Zeng L, Dai L, Han B, Wang GL. The broad-spectrum blast resistance gene Pi9 encodes a nucleotide-binding site-leucine-rich repeat protein and is a member of a multigene family in rice. Genetics. 2006;172(3):1901-1914. doi:10.1534/genetics.105.044891

8. Lee SK, Song MY, Seo YS, Kim HK, Ko S, Cao PJ, Suh JP, Yi G, Roh JH, Lee S, An G, Hahn TR, Wang GL, Ronald P, Jeon JS. Rice Pi5-mediated resistance to Magnaporthe oryzae requires the presence of two coiled-coil-nucleotide-binding-leucine-rich repeat genes. Genetics. 2009;181(4):1627-1638. doi:10.1534/genetics.108.099226

9. Panaud O, Chen X, McCouch SR. Development of microsatellite markers and characterization of simple sequence length polymorphism (SSLP) in rice (Oryza sativa L.). Mol Gen Genet. 1996;252(5):597-607. doi:10.1007/BF02172406

10. Collard BCY, Mackill DJ. Marker-assisted selection: an approach for precision plant breeding in the twenty-first century. Philos Trans R Soc Lond B Biol Sci. 2008;363(1491):557-572. doi:10.1098/rstb.2007.2170

11. Xu Y, Crouch JH. Marker-assisted selection in plant breeding: from publications to practice. Crop Sci. 2008;48(2):391-407. doi:10.2135/cropsci2007.04.0191

12. Huang N, Angeles ER, Domingo J, Magpantay G, Singh S, Zhang G, Kumaravadivel N, Bennett J, Khush GS. Pyramiding of bacterial blight resistance genes in rice: marker-assisted selection using RFLP and PCR. Theor Appl Genet. 1997;95(3):313-320. doi:10.1007/s001220050565

13. Sanchez AC, Brar DS, Huang N, Li Z, Khush GS. Sequence tagged site marker-assisted selection for three bacterial blight resistance genes in rice. Crop Sci. 2000;40(3):792-797. doi:10.2135/cropsci2000.403792x

14. Singh S, Sidhu JS, Huang N, Vikal Y, Li Z, Brar DS, Dhaliwal HS, Khush GS. Pyramiding three bacterial blight resistance genes (xa5, xa13 and Xa21) using marker-assisted selection into indica rice cultivar PR106. Theor Appl Genet. 2001;102(6-7):1011-1015. doi:10.1007/s001220000495

15. Sundaram RM, Vishnupriya MR, Biradar SK, Laha GS, Reddy GA, Rani NS, Sarma NP, Sonti RV. Marker assisted introgression of bacterial blight resistance in Samba Mahsuri, an elite indica rice variety. Euphytica. 2008;160(3):411-422. doi:10.1007/s10681-007-9564-6

16. Hittalmani S, Parco A, Mew TV, Zeigler RS, Huang N. Fine mapping and DNA marker-assisted pyramiding of the three major genes for blast resistance in rice. Theor Appl Genet. 2000;100(7):1121-1128. doi:10.1007/s001220051395

17. Khanna A, Sharma V, Ellur RK, Shikari AB, Gopala Krishnan S, Singh UD, Prakash G, Sharma TR, Rathour R, Variar M, Prashanthi SK, Nagarajan M, Vinod KK, Bhowmick PK, Singh NK, Prabhu KV, Singh AK. Marker assisted pyramiding of major blast resistance genes Pi9 and Pita in the genetic background of an elite Basmati rice variety, Pusa Basmati 1. Indian J Genet Plant Breed. 2015;75(4):401-408.

18. Joseph M, Gopalakrishnan S, Sharma RK, Singh VP, Singh AK, Singh NK, Mohapatra T. Combining bacterial blight resistance and Basmati quality characteristics by phenotypic and molecular marker-assisted selection in rice. Mol Breed. 2004;13(4):377-387. doi:10.1023/B:MOLB.0000034093.63593.4c

19. Balachiranjeevi CH, Bhaskar Naik S, Abhilash V, Akanksha S, Viraktamath BC, Madhav MS, Hariprasad AS, Laha GS, Prasad

MS, Balachandran SM, Neeraja CN, Satendra Kumar M, Senguttuvel P, Kemparaju KB, Bhadana VP, Ram T, Harika G, Mahadeva Swamy HK, Hajira SK, Yugander A, Pranathi K, Anila M, Rekha G, Kousik MBVN, Dilip Kumar T, Swapnil RK, Giri A, Sundaram RM. Marker-assisted introgression of bacterial blight and blast resistance into DRR17B, an elite, fine-grain type maintainer line of rice. Mol Breed. 2015;35(7):151. doi:10.1007/s11032-015-0348-8

20. Zampieri E, Volante A, Marè C, Orasen G, Desiderio F, Biselli C, Canella M, Carmagnola L, Milazzo J, Adreit H, Tharreau D, Poncelet N, Vaccino P, Valè G. Marker-assisted pyramiding of blast-resistance genes in a japonica elite rice cultivar through forward and background selection. Plants (Basel). 2023;12(4):757. doi:10.3390/plants12040757

21. Das G, Rao GJN, Varier M, Prakash A, Prasad D. Improved Tapaswini having four BB resistance genes pyramided with six genes/QTLs, resistance/tolerance to biotic and abiotic stresses in rice. Sci Rep. 2018;8:2413. doi:10.1038/s41598-018-20495-x

22. Hore TK, Inabangan-Asilo MA, Wulandari R, Latif MA, Nihad SAI, Hernandez JE, Gregorio GB, Dalisay TU, Diaz MGQ, Balachiranjeevi Ch, Swamy BPM. Introgression of tsv1 improves tungro disease resistance of a rice variety BRRI dhan71. Sci Rep. 2022;12:18820. doi:10.1038/s41598-022-23413-4

23. Ramalingam J, Raveendra C, Savitha P, Vidya V, Chaithra TL, Velprabakaran S, Saraswathi R, Ramanathan A, Arumugam Pillai MP, Arumugachamy S, Vanniarajan C. Gene pyramiding for achieving enhanced resistance to bacterial blight, blast, and sheath blight diseases in rice. Front Plant Sci. 2020;11:591457. doi:10.3389/fpls.2020.591457

24. Spindel J, Begum H, Akdemir D, Virk P, Collard B, Redoña E, Atlin G, Jannink JL, McCouch SR. Genomic selection and association mapping in rice (Oryza sativa): effect of trait genetic architecture, training population composition, marker number and statistical model on accuracy of rice genomic selection in elite, tropical rice breeding lines. PLoS Genet. 2015;11(2):e1004982. doi:10.1371/journal.pgen.1004982

25. Sharma TR, Rai AK, Gupta SK, Vijayan J, Devanna BN, Ray S. Blast resistance in rice: a review of conventional breeding to molecular approaches. Mol Biol Rep. 2012;39(4):3833-3850. doi:10.1007/s11033-012-2318-0

26. Huang X, Yao W, Chen Q, Lin J, Huang J, Zou Y, Guo C, He B, Yuan X, Xu C, Liu X, Xiao Y, Wu J, Liu J. A century of advances in molecular genetics and breeding for sustainable resistance to rice blast disease. Theor Appl Genet. 2025;138(7):174. doi:10.1007/s00122-025-04962-4

27. Hospital F. Challenges for effective marker-assisted selection in plants. Genetica. 2009;136(2):303-310. doi:10.1007/s10709-008-9307-1