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Marker assisted introgression: To generate precisely engineered crops against rice blast disease

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Abstract
Blast disease is the most damaging disease to rice which severely reduces its productivity. Traditional control systems are uneconomical at the business level. Utilizing resistant cultivars is the most efficient and sustainable strategy which is beneficial. Advancements in rice genomics have opened innumerable number of doors for the researchers to enhance the rice-productivity. As a viable procedure, Marker Assisted Backcross Breeding (MABB) is becoming more and more liked among researchers. Its key benefit is that it uses cultivars that farmers are already fond of, ensuring that the improved variety will possess the needed traits and also there is no any issue occurring in the method like transgenics. The potential to utilize this strategy with novel features in rice is made possible by the presence of widely cultivated popular varieties. Furthermore, the MABB method not only helps in early improvement of varieties but also essential for basic research applications in rice since it allows for far more precise production of novel varieties than traditional backcrossing. The revised data will be beneficial for the long-term, resistant rice breeding programme against the improved trait(s). Previous research on the current approach and challenges in disease improvement, such as the pyramiding resistance gene for creating new rice varieties with durable resistance, will undoubtedly aid in the fight against rice disease.

Keywords: Blast, backcrossing, MABB-marker assisted backcross breeding, pyramiding

Introduction
More than half of the world's population rely on rice as a staple meal, which is farmed in 100 different nations with Asia accounting for 90% of worldwide output. It is one of the main food crops and is important to the diets of more than three billion people worldwide (Khush, 2005) [29]. According to the third Advance Estimates for 2020-21, the country's overall foodgrain production is anticipated to reach a record 305.44 million tonnes, with rice production alone accounting for an estimated 40% of that total i.e., 121.46 million tonnes.

It has become more crucial in recent years to protect food security and get ready for the effects of climate change and many efforts are being made to transform agriculture and adopt climate-smart practices which will help in achieving the SDGs. This became a fundamental part of the 2030 Agenda for Sustainable Development (https://sdgs.un.org/goals) after being endorsed by all UN Member States. It will be crucial to promote sustainability of rice production systems internationally as the globe faces environmental concerns, shifting demographics, and consumer demands (Fukagawa and Jiska 2019) [14]. The crop is vulnerable to a variety of biotic and abiotic stresses (Onyango 2014) [35]. Pest insects, fungi, bacteria and viruses are a few examples of biotic stressors while drought, cold and salinity are three major abiotic conditions that rice is facing extensively.

As one among the major constraints in the rice production, the blast disease has given the maximum attention. *Magnaporthe oryzae* grow rapidly and causes disease outbreak under favourable environment. It causes a 30-50% yield loss of rice worldwide each year, which is equivalent to the feed value of 60 million people worldwide. Neck blast disease can result in 100% yield loss in rice, depending on the variety, crop stage, inoculum potential, and conducive environment for pathogen growth and development (Skamnioti and Gurr, 2009; Nalley *et al*. 2016) [49, 31]. Many resistance genes have been mapped against this disease and their functional characterization has been done so far which could be utilised for the development of improved varieties of rice. Also due to the continual evolving relationship between the host and the pathogen, a single gene resistance is practically impossible and hence gene pyramiding is a boon to this problem. The gene stacking with various genes against different races not only slows down the evolution of the pathogen but provides the crop with the durable resistance.

Several group of scientists had worked and still working on the issue in a sustainable way to develop the improved varieties without harming the nature.

Availability of complete rice genome sequencing and bioinformatics has opened up many doors for the scientists to counteract these challenges and safeguard rice crops, several genes have been discovered, cloned, and described (Perez- de-Castro *et al*. 2012) [39] and transgenic plants are successfully created introducing the identified genes into rice plants (Ansari *et al*. 2015) [4].

Backcross breeding is traditional breeding method developed by Harland and Pope which is used to correct a specific defect in a well-adapted agronomically superior cultivar (Harland and Pope 1922) [16]. The rapid growth of the world's population, the decline in rice cultivable area, the depletion of freshwater supplies, the emergence of new diseases and pests, and the effects of climate change are all pressing concerns that need to be addressed by researchers in order to advance their field. Crop varieties that are resilient to both biotic and abiotic stresses are to be developed through scientific ways. In this regard, MABC can aid in the development of resistant or high-yielding or stress resistant cultivars effectively and precisely. In conventional backcross breeding method, the homozygosity increases by 50 % in each backcross generation and heterozygosity decreases by 50 %. It generally takes 6-7 backcrosses to reach approximately 99% of the homozygosity. Marker Assisted Backcross Breeding (MABB), however, comes into play as researchers nowadays strive to focus on cultivar development that takes less time. This approach is one among the various approaches which helps in targeted introgression of the desirable genes in the genetic constitution of any genotype without disrupting the later. MABB could help researchers to create the improved version of the well adapted variety in a very less time where the molecular markers (DNA Markers) are used for the assistance in selection of introgressed donor segment (Foreground selection), minimum linkage drag (Recombinant selection) along with maximum Recurrent Parent Genome (RPG) recovery (Background selection) in an earlier stage of backcross generation. A single locus controlling a specific trait can be introgressed precisely and successfully using MABB while maintaining the fundamental traits of the Recurrent Parent (RP) in a less time as compared to conventional backcross programme. As a result, molecular markers can be utilized to identify the presence of desirable trait to which it is closely/tightly linked. The most important point is that there are no contradictions or ethical issues, as have been raised with this approach, because cultivars are developed using MABC and molecular marker-based research does not involve genetic modification.

Many group of scientists have been utilizing MABB for the improvement of various biotic stresses *viz*; bacterial blight, blast, gall midge, Brown plant hopper and even virus resistant varieties were developed (Pan *et al*. 2003; Chen *et al*. 2008; Xu *et al*. 2012; Bentur *et al*. 1987; Hindu *et al*. 2010; Vijayalakshmi *et al*. 2010; Suh *et al*. 2011; Roy *et al*. 2012; Ahmadi *et al*. 2001) [38, 7, 59, 6, 18, 56, 51, 45, 3]. The advancements in rice genomics has progressed tremendously over the decade which provided a complete spectrum of tightly linked/gene derived markers to the genes involved in various abiotic and biotic stresses. These information could be successfully exploited in MABB (Nongpiur *et al*. 2016; Kalia and Rathour 2019) [34, 25]. This review focuses on the potential application of MABB in the past for the development of blast resistant cultivar which could be a useful source for the further improvement in the rice breeding programme.

Blast Disease in Rice

Soong Ying-shin first reported the disease as "rice fever" in China in 1637, and Imochi-byo later reported it from Japan in 1704 and soon it was now found in approximately 85 countries around the world, including India (Srijan *et al*. 2015) [1]. In India, The first devastating epidemic was reported in 1919 in the Tanjore delta of former Madras state (Padmanabhan *et al*. 1965) [37]. Later, the disease was reported to have spread to various parts of India (Padmanabhan *et al*. 1970; Rathour *et al*. 2004) [36, 43].

The fungus *Magnaporthe oryzae* (anamorph: *Pyricularia oryzae*), is the causal agent of blast disease (Couch and Kohn, 2002) [10]. The fungus colonises the leaves (leaf blast), panicles (panicle blast), node (node blast), neck (neck blast) and other above ground parts of the plants causing severe crop loss. The management of the disease includes cultural method which tends to reduce the blast epidemics by creating less favourable environment (Upadhyay and Bhatta 2020) [54], Chemical control specifically Triacyclazole was used extensively to combat the disease but was baneful to the crop and severely affected the export of the crop (Joshi *et al*. 2019) [24]. Hubert *et al*. 2015 suggested the effectiveness of certain antibiotics in controlling rice blast. On the other way, biological control also helps in preventing disease by reduction in inoculum of the pathogen (decreased production and release of viable spores, decreased survival and decreased spread, reduction of infection of the host by the pathogen and reduction of severity of attack by a pathogen). The method was eco-friendly but preservation, storage and transport of biocontrol agent in a viable stage was one of the challenges faced here. Since *M. oryzae* has a changeable character, ongoing study is required to manage the disease. Several disease prevention methods and approaches have been used to combat rice blast disease, however they have had mixed results (TeBeest *et al*. 2012) [53]. Therefore, it is essential for the successful management of rice blast to choose an appropriate strategy and use best management practises. Additionally, research must be focused on creating high yielding and broadly-resistant cultivars by pyramiding the R genes to improve the sustainability of resistance to rice blast.

Marker assisted backcross breeding (MABB) for blast resistance in rice

Backcross breeding is a traditional method which helps in targeted introgression of the desirable genes in the genetic constitution of any genotype without disrupting the later (Rathour *et al*. 2022) [44]. The first backcross generation is created by mating the Recurrent Parent (RP) with the donor parent to create an F_1 hybrid, which is then crossed with the RP (BC_1F_1). The backcross plants are regularly crossed with the RP to create subsequent back-cross populations. The homozygosity increases by 50% in each generation and hence it takes around 6-7 backcrosses to recover approximately 99% of recurrent parent genome (RPG). The method takes a significant amount of time in developing an improved version of variety. At this point of time MABB assist the breeders in early selection of the desired plants with the help markers mainly molecular markers. Molecular markers are the DNA markers which is either closely or tightly linked with the gene

of interest and co-herit together. So it would be possible to select the gene positive plants along with the maximum RPG recovery in the earlier generation itself rather than waiting for the specific stage of the plant or its final maturity. It not only cut the labour costs but also helps in precise improvement of the crop in a very less time as compared with the traiditional backcross breeding. This strategy helps us in selecing gene positive plants i.e., foreground selection with the help of the markers linked with the donor's gene of interest, background selection which accelerate the RP genome recovery using markers that are not linked to the target locus with minimum linkage drag (recombinant selection) (Hospital *et al*. 2001) [20]. Linkage drag is the introgression of the unwanted donor's segment along with the gene of interest and this also can be minimized with the help of molecular markers. Recombinant selection involves selecting Backcross progeny with the target gene and recombination events between the target locus and linked flanking markers (Collard and Mackill 2007) [9]. Single to few genes can be targeted into a single cultivar (Gene pyramiding) or Near Isogenic Lines (NILs) also could be developed through marker assisted backcrossing method for a durable resistance in the crop.

But due to the continual evolving relationship between the host and the pathogen, a single gene resistance is practically impossible and hence gene pyramiding is a boon to this problem. The gene stacking with various genes against different races not only slows down the evolution of the pathogen, but provides the crop with the durable resistance. Several group of scientists had worked and still working on the issue in a sustainable way to develop the improved varieties without harming the nature, not only in the rice, but in the various other important crops. As one among the major constraints in the rice production, the blast disease has given the maximum attention. In rice breeding, developing long-lasting blast resistance has been a top priority. New pathogen races restrain the effects of resistance genes which hinders the attempts to achieve persistent resistance. Therefore, the single gene-specific resistance is futile in maintaining the durable resistance and hence breeder generally practise to pyramid many race-specific resistance genes with the help of markers to increase the endurance (Kalia and Rathour 2019) [25]. Many resistance genes have been mapped against this disease and their functional characterization has been done so far which could be utilized for the development of improved varieties of rice. Table 1 summarises many studies conducted by various scientists using MABB to combat rice blast in a sustainable manner.

Table 1: Blast disease improvement through MABB

Gene/QTLs	Markers used to select target genes	Application	References
Pi1, Piz-5 and Pita	Npb181, RZ536 (Pi1) RZ64,RZ612, RZ456, RJ64-SAP (Piz-5), RJ869, RJ397, RG241 (Pita)	They used three Near isogenic lines (NILs) C101LAC, C101A51 and C101PKT, each carrying the major genes Pi1, Piz-5 and Pita, respectively to pyramid these genes into CO-39	Hittalmani *et al*. 2000 [19]
qBl11 and qBl1	RM224 and RM144 (qBl11) RM212 and RM319 (qBl1)	Introgressed two QTLs from rice cultivar Jao Hom Nim (JHN) conferring resistance against blast disease into Thai glutinous jasmine rice cultivar RD6	Wongsaprom *et al*. (2010) [57]
Pi-z-5 and Pi-54	AP5930, RM206 and RM6100 respectively for genes Pi-z-5, Pi-54 and Rf1	Used C101A51 containing Pi-z-5 and Tetep containing Pi-54 gene for blast resistant, as donor parent in two independent backcross programme to transfer these genes into PRR78 (containing restorer gene Rf1).	Singh *et al*. (2012) [48]
Pi-1 and Piz-5	RM5926 (Pi-1) and AP5696-3 and AP5696-5 (Piz-5)	Enhanced resistance of PRR-78 by introgressing Pi-1 and Piz-5 blast resistance genes from ARBN 141	Gouda *et al*. (2013) [15]
pi1, pi2 and pi33	RM224, RM 1223, RM5926, RM1233, PR10,RM527, RM136, RM549, RM6836, AP5659-3, RM72, RM331, RM404, RM483, RM3374, RM284 and RM25	Improved a popular rice variety ADT43 for blast resistance using a resistant Near Isogenic Lines CT13432-3R harbouring different alleles viz; pi1, pi2 and pi33 and finally selected three gene pyramided lines based on the phenotyping and genotypic screening for blast resistance.	Divya *et al*. (2014) [12]
Pi2,Pi9, Gm1, Gm4 Sub1 and Saltol	RG64 (Pi2), P-28 (Pi9), RM444 (Gm1), RM547 (Gm4), SUB1BC2 (Sub1), RM10745 (Saltol)	Pyramid blast (Pi2, Pi9), gall midge (Gm1, Gm4), submergence (Sub1) and salinity (Saltol) resistance genes into 'Improved Lalat' variety already contained with BB resistance genes xa5, xa13, Xa21 and Xa4.	Das and Rao (2015) [11]
Xa23 and Pi9	C189 (Xa23), Pb8 (Pi9)	Incorporated Pi9 and Xa23 gene in GZ635 and Liangyou6326	Ni *et al*. (2015) [62]
Pi2 and Xa23	RM 527 (Pi2), M-Xa23 (Xa23)	Improved a thermo-sensitive genetic male sterile (TGMS) line Guangzhan63-4s (GZ63-4S) through introgression of blast resistance gene pi2 and bacterial blight (BB) resistance gene Xa23. Donor parents used for Blast and BB resistance were VE6219 and HBQ810, respectively	Jiang *et al*. (2015) [23]
Pi9 and Pita	AP5659-5/NBS2Pi9 and YL155/YL87 linked with Pi9 and Pita, respectively.	Combined two blast resistance genes Pi9 and Pita into the genetic background of Pusa Basmati-1 (PB-1) through inter-crossing between two PB-1 NILs viz; Pusa 1637-18-7-6-20 (Pi9) and Pusa 1633-3-8-8-16-1 (Pita).	Khanna *et al*. (2015a) [27]
Xa21 and Pi2	pTA248(Xa21) and AP5659-5 (Pi2)	Targeted introgression of Xa21 and Pi2 into RPHR-1005 by crossing with donor parent RPBio Patho-1	Kumar *et al*. 2017 [2]
Pi-b and Pi-kh,	RM 208 and RM 206 aided in the foreground selection of the gene Pi-b and Pi-kh, respectively	Improved a Malaysian variety MR219 by transferring two broad spectrum dominant blast resistant genes Pi-b	Tanweer *et al*. (2015) [52]

		and Pi-kh from donor parent Pongsu seribu 2.	
Pi2, Pi54, xa13 and xa21	AP5659-5 (Pi2), RM206 (Pi54), xa13prom (xa13), Pta248 (xa21)	Improved Pusa basmati 1121 and Pusa basmati-6 (PB6). The Near isogenic lines of basmati line restorer PRR78, Pusa 1602 and Pusa 1603 had blast resistance genes Pi2 and Pi54, Pusa 1460 and SPS97 contained xa13 + xa21, were used as donor parents and developed PB-1121 and PB6 NILs for blast and bacterial resistance	Ellur *et al.* (2016) [13]
Pi54, Pi1, Pita, Pi2, Pib, Pi5 and Pi9	YL155/YL187 (Pita), NBS2Pi9 (Pi9), Pibdom (Pib), RM224 (Pi1), RM206 (Pi54), C1454 (Pi5), RM208 (Pib),AP5659-5 (Pi9), AP4007 (Pi2)	Incorporated seven blast resistant genes from different donor namely DHMASQ164-2a (Pi54, Pi1, Pita), IRBLz5-CA (Pi2), IRBLb-B (Pib), IRBL5-M (Pi5) and IRBL9-W (Pi9) into Pusa basmati-1 (PB-1) and developed 14 monogenic, 16 two gene and 6 three-gene pyramid NILs	Khanna *et al.* (2015b) [28]
Pi46 and Pita	RM224 (Pi46), YL155/YL87 and YL183/YL87 (Pita)	Incorporated Pi46 and Pita into from an indica rice H4 into an elite restorer line Hang-Hui-179 (HH-179) and developed three improved lines R1791 (Pi46), R1792 (Pita) and R1793 (Pi46+Pita)	Xiao *et al.* (2016) [58]
xa13, xa21 and Pi54	xa13-prom(xa13), pTA248 (xa21), Pi54-MAS (Pi54)	Intorgressed two bacterial blight resistant gene xa13, xa21 from Improved Samba Mahsuri (ISM), and a blast resistant gene Pi54 from NLR145 into MTU1010,	Arunakumari *et al.* (2016) [5]
Pi2, Pi1 and Pi33	RM 527 and RM140 (Pi2), RM 144 and RM 224 (Pi1), RM 72 and RM 310 (Pi33)	improve 2 elite varieties Buyarin and Kuboyar by using C101-A-51 (Pi2) and C101-LAC (Pi1 and Pi33) as donor parents	Usatov *et al.* (2016) [55]
Pi2 and Pi5	AP-5903(Pi2), 40N23R Pi5	Introgressed two blast resistance genes viz., Pi2 from C101A51 and Pi5 from IRBL-5M, into BPT-5204 (Samba Mahsuri)	Krishnamurthy *et al.* (2017) [30]
Pi-54, Pi-1 and Pi-ta	Pi54-MAS (Pi-54), RM224 (Pi-1) and YL155/87 and YL155/83 (Pi-ta)	introgressed three major blast resistance genes Pi-54, Pi-1 and Pi-ta into a susceptible aromatic landrace Mushk Budji	Khan *et al.* (2018) [26]
Pi1	RM224 (Pi1)	Introgressed Pi1 gene into Swarna from C101LAC	Rambabu *et al.* (2019) [42]
qBl1, qBl2, qBl11 and qBl12	RM319/RM212 (qBl1), RM48/RM207 (qBl2), RM144/RM224 (qBl11) and RM27933 (qBl12)	Improved Sakon Nakhon rice cultivar of Thailand. RD6 was used as a donor parent which contained four blast resistant quantitative trait loci (QTLs) located on chromosomes 1(qBl1), 2 (qBl2), 11(qBl11) and 12 (qBl12)	Srichant *et al.* (2019) [50]
Xa4, Xa21, xa5, xa13, Piz, Pi2 and Pi9	MP (Xa4), Xa21FR, pTA248 (Xa21), RM13, RM21 (xa5), Xa13prom (xa13), RM6836 (Piz, Pi2, Pi9), RM8225 Xoo (Piz)	Introgressed two dominant (Xa4 and Xa21) and two recessive (xa5 and xa13) BLB resistance genes from the donor parent IRBB60 into a high yielding Malaysian elite rice variety Putra-1 with genetic background of three blast resistance (Piz, Pi2 and Pi9) genes.	Chukwu *et al.* (2020) [8]
Pi54, Pi1, xa13 and xa21	pTA248 (Xa21), xa13prom (xa13), Pi54MAS (Pi54) and RM224 (Pi1).	They pyramided two blast resistant gene Pi54 and Pi1 (NLR-145) and two bacterial blight resistant gene xa13 and xa21 from improved Samba Mahsuri to improve a cold tolerant variety Tellahamsa	Jamaloddin *et al.* 2020 [22]
xa13, xa21, Pi2 and Pi54	Xa13prom (xa13), pTA248 (xa21), AP5930 (Pi2) and RM206 (Pi54)	Reported introgression of four resistant genes namely xa13, xa21, Pi2 and Pi54, from Pusa 1709 into PB 1509 against bacterial blight and blast disease respectively.	Sagar *et al.* (2020) [46]
Pi9, Xa21, Gm8, qDTY1.1, qDTY2.2 and qDTY4.1	Pi9STS2 (Pi9), pTA248 (Xa21), GM8 PRP (Gm8), RM3825, RM431 and RM12091(qDTY1.1), RM154, RM279, RM555 (qDTY2.2) and M551, RM518 and 16367 (qDTY4.1)	Introgressed Pi9 for blast from IRBL9, Xa21 for bacterial blight (BB) from IRBB60, and Gm8 for gall midge resistance from Aganni and qDTY1.1, qDTY2.2 and qDTY4.1 for drought resistance from IR 96321-1447-561-B-1and IR 87707-445-B into Naveen.	Ramayya *et al.* (2021) [41]
Pi9, Xa21 and Sub1	NBS2-1 (Pi9), RM238827 (Sub1A), pTA248 (Xa21), S2-24 (tms5)	Introduction of blast resistance (R) gene Pi9, bacterial blight R gene Xa21 and submergence tolerance gene Sub1A into 1892S genetic background already carrying tms5 gene.	Yanchang *et al.* 2021 [60]
qDTY1.1, qDTY3.1, qDTY12.1, Xa4, xa5, xa13, Xa21 and Pi9	snpOS00400,snpOS00402, and snpOS0040 (qDTY1.1), npOS00085,snpOS00086 and snpOS00089 (qDTY3.1) and snpOS00483 andsnpOS00484 (qDTY12.1), snpOS00481 (Xa4), xa5, snpOS00493and snpOS494 (xa13), snpOS0061 (Xa21), snpOS00451 (Pi9)	Combined three drought tolerant quantitative trait loci (QTL) viz; qDTY1.1, qDTY3.1 from IR96321-1447-561-B-1 and qDTY12.1 from IR74371-46-1-1, four BLB genes—Xa4, xa5, xa13, and Xa21 from IRBB60 and one blast-resistance gene Pi9 from in the elite rice cultivar Lalat. A japonica cultivar IRBL9 was used as a donor parent for blast resistant gene.	Singh *et al.* (2022) [47]
Pi9	Pi9-Pro (Pi9)	Introgressed a broad-spectrum resistance locus Pi9 from a Basmati donor PB1637 into a cold tolerant variety Himalayan 741	Rathour *et al.* 2022 [44]
Pb1, pi21, Piz and qPbj-6.1	RM206 (Pb1), RM1359 (pi21), RM8225 (Piz), RM276 (qPbj-6.1)	Improved a blast susceptible variety MR263 and incorporated genes ond QTL for blast resistance from	Nihad *et al.* 2022 [33]

		Pongsu seribu-2	
	Nbs2Pi-9, Pi9-Pro (Pi9), Pi54STS1(Pi54), SD1 (sd1)	Incorporated sd1 gene for semi-dwarfism and Pi9 and Pi54 gene for blast resistance into a traditional basmati rice variety i.e., Ranbir basmati	Pote *et al*. 2022 [40]
Xa23, Pi9, Pi1, and Pi2	Closely linked SNP markers, which are located upstream and downstream of the target genes (Xa23, Pi1, Pi2/Pi9), were used to track the target genes for foreground selection	Used resistance gene donors (HZ02455 containing Xa23 + Pi9 and HZ02411 containing Pi1 + Pi2) to cross with the hybrid rice restorer line R900. As a result, they were able to develop a series of improved lines, including iR900-1 (Xa23 + Pi9), iR900-2 (X To create the iS1000 hybrids iS1000-1 (Xa23 + Pi9), iS1000-2 (Xa23 + Pi1 + Pi2), and iS1000-3 (Xa23 + Pi1 + Pi9) which were disease-resistant.	Zhizhou *et al*. 2022 [63]
Piz, Pib, Pita, Pik	Pik2-2AE(Pik), Pib5 (Pib), Pita-10 (Pita), Z56592 (Piz)	Piz, Pib, Pita, Pik were introgressed into japonica Italian rice variety	He *et al*. 2022 [17]

Conclusion

Magnaporthe oryzae, the casual agent of rice blast is one of the most severe rice diseases in the world, and crop losses as a result of blast are very substantial. Farmers in various rice-growing nations have embraced a number of blast-resistant rice cultivars that have been developed through traditional plant breeding. The blast fungus's variable pathogenicity in relation to environment, however, rendered the disease a significant concern for farmers and a continuing threat to the rice sector. Farmers typically choose well-adapted varieties over new varieties, and with time, due to the ongoing development of diverse diseases, resistance breaks down. Therefore, the breeder is constantly looking for ways to improve the well-adapted variety, and MABB is a simple way to start. Because they do not require disease-favoring environmental conditions and can select resistant genotypes even without pathogen inoculation, marker-based selection methods are more accurate, reliable, and time-saving. As a result, many plant breeders have used blast-resistant varieties developed using these methods in general. The availability of the genome and the development of numerous biotechnology methods have resulted in the identification of various genes associated with biotic and abiotic challenges, which has in turn opened a plethora of opportunities for crop improvement. To further improve the MABB, many technologies can be combined, including high throughput genotyping, sequencing and genetic engineering.

Conflict of interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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