Current Applicable DNA Markers for Marker Assisted Breeding in Abiotic and Biotic Stress Tolerance in Rice (*Oryza sativa* L.)

Franz Marielle Nogoy¹, Jae-Young Song¹, Sothea Ouk¹, Shadi Rahimi¹, Soon Wook Kwon², Kwon-Kyoo Kang³, Yong-Gu Cho¹*

¹Department of Crop Science, Chungbuk National University, Cheongju 28644, Korea
²Department of Plant Bioscience, Busan National University, Busan 50463, Korea
³Department of Horticultural Life Science, Hankyong National University, Anseong 17579, Korea

**ABSTRACT** Abiotic and biotic stresses adversely affect rice (*Oryza sativa* L.) growth and yield. Conventional breeding is a very effective method to develop tolerant rice variety; however, it takes a decade long to establish a new rice variety. DNA-based markers have a huge potential to improve the efficiency and precision of conventional plant breeding via marker-assisted selection (MAS). The large number of quantitative trait loci (QTLs) mapping studies for rice has provided an abundance of DNA marker-trait associations. The limitations of conventional breeding such as linkage drag and lengthy time consumption can be overcome by utilizing DNA markers in plant breeding. The major applications of DNA markers such as MAS, QTL mapping and gene pyramiding have been surveyed. In this review, we presented the latest markers available for some of the most important abiotic and biotic stresses in rice breeding programs. Achieving a significant impact on crop improvement by marker assisted breeding (MAB) represents the great challenge for agricultural scientists in the next few decades.

**Keywords** Marker-assisted selection, Marker assisted breeding, Abiotic stress, Biotic stress, Rice, Resistant, Climate change

**INTRODUCTION**

Climate change is causing huge effects in all living creatures on earth. Few decades ago, scientists have proven that rising greenhouse gas emissions caused by the use of fossil fuels and industries lead to higher temperatures (Harvey 2015). Last year, the United Nations (U.N.) Climate Change Conference in Paris was able to come up with an agreement for a global climate effort. One of the key outcomes of the conference is to reaffirm the goal of limiting global temperature increase well below 2°C, while urging efforts to limit the increase to 1.5°C (Outcomes of the U.N. Climate Change Conference in Paris 2015). Climate change, increasing world population and food security all together requires rice scientists to address these issues in their respective researches.

Rice (*Oryza sativa* L.) is one of the most important food crops in the world and maintaining stable rice production is extremely important to feed the constantly growing human population in changing climate (Sasaki and Burr 2000; Maclean *et al.* 2002). Rice has been exposed to many environmental stresses. There are two broad areas of environmental stresses, abiotic (salinity, heat, drought, cold, submergence, radiation, and heavy metals) and biotic (pathogens and herbivore) factors (Gomez 2013). Environmental stresses such as heat, cold, drought, and salinity factors have extremely affected on average yield losses in world agriculture (Wang *et al.* 2003). Among these stresses, the single most common limiting abiotic stress is low water supply simply described as drought (Tester and Bacic 2005). Heat stress is one of the environmental stresses that limits biomass productivity and grain production of crops (Boyer 1982). Other significant abiotic stresses limiting growth of both forage grasses and cereals are salinity and acidity, next to these is low temperature (Tester and Bacic 2005). Furthermore, there...
was a huge impact on plants by biotic stresses such as pests and pathogens. Among biotic stresses, three diseases have been considered to be the most devastating worldwide in rice, bacterial blight caused by *Xanthomonas oryzae* pv. *oryzae*, blast by *Pyricularia grisea*, and sheath blight by *Rhizoctonia solani*. Similarly, three groups of insects, stemborers (yellow stemborer *Tryporyza incertulas* and striped stemborer *Chilo suppressalis*), leafhoppers (*Marasmia patnalis* and *Cnaphalocrocis medinalis*), and planthoppers (mostly brown planthopper [BPH], *Nilaparvata lugens*), have been the most damaging pests (Jiang *et al.* 2012). In addition, infestation of white-backed planthopper (WBPH), *Sogatella furcifera* (Horvath) which is a phloem sucking insect of rice has affected rice growth and productivity.

Development of the disease-resistant or stress-tolerant plant is an important objective in rice breeding programs, because the production of rice can be constantly interfered by several major abiotic and biotic stresses. Rice and other crops have their own mechanisms to tolerate stress and there are many uncovered defense mechanisms at molecular level. The knowledge of physiology and molecular biology of stress tolerance in rice are helpful for the biotechnological improvement of rice productivity (Gomez 2013). One useful biotechnological tool that was developed throughout the years is DNA-based markers. From conventional breeding that takes place around 10 years to select a stable and desirable phenotype to marker-assisted selection (MAS), genetic functional markers were able to shorten rice varietal development. Another use of DNA-based markers is overcoming the barrier of “linkage drag” which refers to the presence of undesirable genes in the chromosomal region of the target gene thereby making it difficult to avoid such traits when using conventional breeding (Kottearachchi 2013). Also, economic analysis has shown the potential impacts of utilizing marker assisted breeding (MAB) by overcoming drawbacks of conventional breeding in rice that ultimately reduce the cost of production and promote economic growth (Kottearachchi 2013).

For this review, we present the recent DNA-based markers for some of the most significant abiotic and biotic stress tolerant genes and for MAS application in rice breeding programs like screening resistant plants from a germplasm and genotyping breeding populations. These markers are proven to work from different studies published recently from germplasm screening, results of fine mapping and gene pyramiding methods.

**DNA-BASED MOLECULAR MARKERS**

DNA markers are defined as a fragment of DNA revealing changes in sequences, which can be used to detect polymorphism between different genotypes or alleles of a gene for a particular sequence of DNA in a population or gene pool (Andersen 2013). DNA marker is a small region of DNA sequence showing polymorphism (base deletion, insertion, and substitution) between different individuals (Andersen 2013). It is a part of the gene itself to be representative of the phenotypic traits and/or a fragment of flanking regions, which is located very close to the candidate gene, and are also considered useful tools that can be indirectly displaying the variable phenotypic traits. There are two basic methods to detect the polymorphism: southern blotting and polymerase chain reaction (PCR). Mohler and Singrün (2004) gave three key issues for an effective molecular marker in MAS: i) markers should co-segregate or map as close as possible to the target gene (within 2 cM), in order to have low recombination frequency between the target gene and the marker, ii) for unlimited use in MAS, markers should display polymorphism between genotypes with and without the target gene, iii) cost-effective, simple PCR markers are needed to confirm genotyping efficiency for the rapid screening of large populations. Lateef (2015) simplified the different marker systems based on generation development. The first and low-throughput marker system is restriction fragment length polymorphisms (RFLPs), medium-throughput marker systems include random amplified polymorphic DNAs (RAPDs), simple sequence repeats (SSRs), and amplified fragment length polymorphisms (AFLPs) while the latest generation is the high-throughput marker system comprised of single nucleotide polymorphisms (SNPs), KBioscience Competitive Allele-Specific PCR (KASpar), and genotyping by sequencing (GBS). Based on various MAS breeding approaches, RFLPs are the best marker type...
for many purposes, but are low throughput technology and have high cost of genotyping. Therefore, PCR-based markers like RAPDs and AFLPs are faster and cheaper, and can also be applied in genetic diversity and gene mapping, however, their limiting factors are lack of reproducibility and specificity (Lateef 2015). With the availability of rice whole genome sequence and re-sequencing data, SNPs are exhorted in construction of high resolution genetic maps, investigation of population evolutionary history and discovery of marker–trait associations. The use of SNPs is further exemplified in KASPar assay, which is the patented SNP genotyping system from KBioscience based on fluorescent resonance energy transfer (FRET) (Robinson and Holme 2011). It allows detection of SNPs without a separation step coupled with the use of competitive allele specific PCR, thus, the KASP system offers a superior system for determination of SNP or insertion/deletion genotypes (Robinson and Holme 2011). As different kinds of markers were described above, each kind can be more advantageous to one breeding design and less valuable to another breeding method.

Conventional plant breeding has depended on phenotypic factors for the selection/confirmation of agronomic traits. MAB approaches to conventional breeding substantially has reduced the plant breeding cycles and increased the precision and efficiency of new cultivar development in plant breeding programs (Ribaut and Hoisington 1998; Morris et al. 2003).

**ABIOTIC STRESSES**

**Drought**

Water is the carrier of nutrients and minerals from soil through roots to all parts of the plant for distribution, aside from the transport of biomolecules. Drought is one of the most common stresses that impact growth and development of plants under water-limiting environments. The drought tolerance of plants can be divided into following various types including drought avoidance, escape, recovery, and dehydration tolerance (Kramer and Boyer 1995). Drought avoidance includes root depth, which can absorb available water in deep soil and dehydration tolerance consists of plant’s capability such as drought recovery and growing again (Salekdeh et al. 2002). As drought mainly occurs in upland, selection for a well-developed root system with long and thick roots should improve the drought tolerance of upland rice because the plant will be able to absorb stored water in the deep soil layers. Phenotypic selection for root morphological traits in conventional breeding programs is impractical. The use of molecular markers could provide a useful tool to support phenotypic selection. Several mapped populations were developed to detect quantitative trait locus (QTLs) influencing root morphology and other drought-related traits that could be used in MAS to improve upland varieties. Uga et al. (2011) detected a new major QTL controlling ratio of deep rooting (RDR) on chromosome 9 by using 117 recombinant inbred lines (RILs) between lowland cultivar IR64 and upland cultivar Kinandang Patong (KP). The RDR QTL Dro1 (deeper rooting 1) was mapped within 1 cM between RM24393 and RM7424. They suggested Dro1 QTL, which is associated with root growth angles, would be useful for detecting an increased deep rooting trait under limited water conditions. In a report by Lang and Buu (2008), they worked on the mapping and MAS of major genes for drought stress in rice, they found out drought tolerance in the region that indicated the occurrence of recombination between segments derived from 329 plants of BC:F2 from OM1490/WAB880-1-38-18-20-P1-HB. Twenty markers were used to genotype the 329 BC:F2 plants. SSR markers located at the drought recovery score (DRS) genes between RM201 (0.4 cM) and RM328 (13.8 cM) on chromosome 9 (Lang and Buu 2008). The target segment on chromosome 9 (RM201) significantly related to increase root length and drought tolerance under drought stress treatment (Lang and Buu 2008). Another SSR marker that can be used for MAS is RM8085, it is the only marker that showed complete co-segregation among individual RILs. RM8085 was mapped on chromosome 1 at 139.9 cM and is linked to leaf rolling and leaf drying under drought stress (Salunkhe et al. 2011). Shamsudin et al. (2016) used three drought yield QTLs, qDTY 2.2, qDTY 3.1, and qDTY 12.2, with consistent effect on grain yield under reproductive stage drought stress in gene pyramiding work for an elite Malaysian rice
cultivar. These three QTLs have effectively worked in foreground selection in each of their breeding generation. The markers mentioned above can be applied in QTLs related to DRS, leaf rolling, leaf drying and drought yield.

**Salinity**

Soil salinity is an increasing limiting factor in rice growing areas. The precise effect of salinity on the rice harvest is determined by a complex interaction of various factors including the severity, timing, and duration of the stress (Thitisaksakul *et al.* 2015). Salinity tolerance at seedling, vegetative, flowering and ripening stages of rice seems to be managed by independent genes (Linh *et al.* 2012). *Saltol* is a major QTL and was identified in the salt-tolerant cultivar Pokkali. Its location was found on chromosome 1. This QTL confers salinity tolerance at the vegetative stage and explains from 64% to 80% of the phenotypic variance (Linh *et al.* 2012). The SSR marker, RM8094 found in *Saltol* is considered to be superior for analysis of genetic diversity (Nejad *et al.* 2008). Rice genotypes with the Pokkali band type for locus RM8094 marker were either highly tolerant or tolerant to salinity stress at the seedling stage (Nejad *et al.* 2008). Aside from RM8094, some of salt-tolerant genotypes had the Pokkali marker allele for RM10745 as well. Nejad *et al.* (2008) have proven in their results that RM8094 and RM10745 are useful for MAS of *Saltol* QTL. In a more recent study, three sequence tagged site (STS) markers were presented for MAS, from the genome sequences of *SKC1*, *SalT*, and *DST*. STS markers were developed based on Insertion/Deletions (InDels) between Nipponbare and 9,311 genome sequences of the previously mentioned gene names. STS markers, Wn11463 and Wn11466, were designed based on 4 bp and 17 bp InDels downstream of SKC1 (LOC_Os01g20160); Wn13900 was based on a 4 bp InDel upstream of *SalT* (LOC_Os01g24710); Wn13902 and Wn13903 were based on 7 bp and 8 bp InDels in the *SalT* coding region; Th32637 was based on a 3 bp InDel upstream in *DST* (LOC_Os03g57240); and Th32638 and Th32369 were based on 12 bp and 18 bp InDels in the coding region of *DST* (Emon *et al.* 2015). There were some efforts towards breeding salinity tolerance in plant via MAS (Ashraf *et al.* 2012) for the development of salt tolerant cultivars. It is expected that the utility of MAS for breeding of salinity tolerance traits will be increased.

**Chilling stress**

Rice is commonly grown in tropical areas, thus it is more sensitive to low temperature. The optimum temperature for seed germination and early seedling growth is from 25°C to 35°C (de los Reyes *et al.* 2003). Chilling stress affects rice growth throughout its development from germination until harvest. Hence, development of chilling stress tolerant cultivar is a common breeding goal. And of course, to aid fast and effective selection of lines with chilling stress tolerance, MAS is a useful and precise strategy. In a review done by Zhang *et al.* (2014), they summarized various QTLs related to chilling tolerance at different growth stages. Here, we’ll simply present the markers that can be directly used for MAB. In one research work, a RIL population derived from a japonica/indica cross was assessed for chilling tolerance at early seedling stage at 10°C. Main-effect QTL for the trait was mapped via composite interval mapping using a linkage map with 198 marker loci. The group was able to identify four putative QTLs for the trait, which were mapped on chromosomes 1, 3, 7, and 11. Among these QTL, *qSCT-11* showed a large additive effect on the trait, explaining 26% to 30% of the phenotypic variation in the treatment of 13 days at 10°C with a LOD of 16-19. This QTL was closely linked to SSR marker RM202 and its positive allele came from the parent Lemont (Chen and Li 2005). This allele would be useful for the improvement of rice chilling tolerance through MAS. There are also molecular markers associated with chilling response related phenotypes, like, membrane integrity, photoinhibition and visual assessment of damage (Bonnecarrère *et al.* 2014). SSR marker RM22034 is associated with membrane integrity, RM6547 and RM14978 with photoinhibition, and RM144 with visual assessment of damage (Bonnecarrère *et al.* 2014). All the markers are currently available for marker assisted selection in rice breeding programs located in temperate regions (Bonnecarrère *et al.* 2014). Three more QTLs, *qPSST-3*, *qPSST-7*, and *qPSST-9* were verified from ten chilling-tolerant lines with spikelet fertility (SF) of 51% to
81% compared to 7% (chilling-sensitive parent) and 73% (chilling-tolerant donor) (Jena et al. 2012). 

**Heat**

The year 2016 is the hottest year to date. The temperature recorded in the month of June across global land and ocean surfaces was 1.62°F (0.90°C) higher than the 20th century average of 59.9°F (15.5°C). This was the highest for June in the 1880-2016 record (Climate Central 2016). Heat stress is one of the growing major factors that affect crop productivity negatively. High temperature is detrimental to both the vegetative and reproductive stages of rice (Pareek et al. 1995). In rice, once the temperature goes 5°C higher than the threshold level at flowering stage, it can induce floret sterility thereby affecting yield losses with maximum yield loss up to 80% (Ahmad et al. 2014). Through molecular breeding strategy, studies have been carried out to create molecular map of heat tolerance QTLs at booting, flowering, grain filling, and ripening stages in rice. In different rice population used by Ye et al. (2015), they identified QTL qHTSF4.1 consistently present across different genetic backgrounds (IR64/Giza178 and IR64/N22 populations; three-way-cross population IR64//Milyang23/Giza178; BC5F2 population with clean background of IR64) and solely mentioned that it could be an important source for enhancing heat tolerance in rice at flowering stage. The SF under high temperature was able to increase at 15% by qHTSF4.1 (Ye et al. 2015). In a more recent study, 48 stable lines (17 KMR3/Oryza rufipogon introgression lines [KMR3 ILs], 15 Swarna/Oryza nivara ILs [Swarna ILs] along with their parents, Nagina 22 [N22], and its 4 ethyl methanesulfonate induced mutants and 7 varieties) were examined for heat tolerance during dry and wet season (Prasanth et al. 2016). They found out that 18 of 49 SSR markers linked to SF were valid for five traits related to heat tolerance. RM430 and RM210 in dry season and RM229 in wet season were significantly associated with both SF and its heat susceptibility index (HSI) under heat stress. RM430 was also significantly related in both yield per plant (YP) and its HSI in dry season (Prasanth et al. 2016). For an actual application of SSR markers in breeding programs for heat tolerance in rice, a group from Vietnam used RM3735 as one of their six markers to select heat tolerant lines in backcross population at flowering stage (Buu et al. 2013a; Buu et al. 2013b; Lang et al. 2015). Rice breeders can employ these QTLs in pyramiding genes to increase heat tolerance in rice.

**BIOTIC STRESSES**

**Bacterial blight**

Bacterial leaf blight (BLB) is the most destructive disease, which affects greatly the rice yield loss. Enhancing genetic resistance of rice has proven to be the most effective method of controlling BLB disease (Khan et al. 2014a). To date, at least 38 BLB resistance genes (R genes) (both dominant and recessive) have been identified (Bhasin et al. 2012; Kumar et al. 2012) and designated in a series from Xa1 to Xa38 (given the prefix Xa for Xanthomonas) (Khan et al. 2014a). There are various DNA markers that have been already developed for many Xa genes. Hajira et al. (2016) have developed simple PCR-based functional markers for xad13 and xad5. For xad13, they designed a functional, PCR-based marker, xad13-prom targeting the Indel polymorphism in the promoter of candidate gene, Os8N3 located on Chr. 8 of rice. For xad5 a multiplex-PCR based functional marker system, named xad5FM, consisting of two sets primer pairs targeting the 2-bp functional nucleotide polymorphism in the exon II of the gene, TFIIAγ 5 (candidate for xad5), has been developed (Hajira et al. 2016). Both xad13-prom and xad5FM can differentiate the resistant and susceptible alleles for xad13 and xad5, respectively in a co-dominant fashion. Using these two functional markers along with the already reported functional, PCR-based marker for Xa21 (pTA248), Hajira et al. (2016) designed a single-tube multiplex PCR based assay for simultaneous detection of all the three major resistance genes and demonstrated the utility of the multiplex marker system in a segregating population.

In the study of Hur et al. (2013), they cloned and sequenced the Xa3/xa3 gene in the Korean cultivars Hwayeong, Ilmi, and Goun, conferring resistance or susceptibility to bacterial blight. Xa3 is involved in the receptor-like kinases, which contain an extracellular leucine-rich repeat (LRR) and an intracellular serine-
Blast

Rice blast is another devastating disease causing major yield losses globally. Singh et al. (2015) reported that there are more than 100 major blast resistance genes from japonica (45%), indica (51%), and other (4%) genotypes that have been identified and documented, and many blast resistant varieties have been developed; however, stronger virulent isolates of rice blast fungus have emerged. So up to now, rice cultivar with broad-spectrum of resistance to highly adaptive virulent isolates/races remains a challenge. In a MAS breeding for blast resistance, F3 population derived from the cross of Pongsu seribu 2 (resistant) and Mahsuri (susceptible) allowed the association of four SSR markers RM413, RM1233, RM8225, and RM5961 to blast resistant genes (Ashkani et al. 2012). Because these markers had high selection accuracy for resistant plant sources, they were suggested to be used in MAS for the resistant gene. Lei et al. (2013) identified and mapped two blast resistance genes, Pi60(t) and Pi61(t), in Chinese rice cultivar 93-11 using F2 and F3 populations derived from a cross between the susceptible cv. Lijiangxintuanheigu and resistant cv. 93-11. Pi60(t) and Pi61(t) are both embedded in recombination-suppressed regions with several clustered NBS-LRR genes. In addition to these SSR markers, Khan et al. (2014b) suggested gene-based molecular markers for MAS in identifying blast resistance gene in fragrant rice. In their study they found out that the reaction pattern of single-spore isolate of Magnaporthe oryzae to differential varieties showed that Pish, Pi9, Pita-2, and Pita are the effective blast-resistant genes against the tested blast isolates in Bangladesh. After using the four gene-based molecular markers, among the 16 germplasms selected, they found BRRI dhan50, Chinigura, and Bawaibhog that contain more than one target gene and the remaining germplasm contained only one target gene, either Pish or Pita. Recently, Singh et al. (2015) applied 10 SSR markers linked to blast resistance genes (Pi-9, Pi-1, Pi5-t(t), Pi5-z, Pi-b, Pi-ta, Pi33, Pi-27(t), Pi5p(t), and Pi5) in 192 rice accessions to identify which accession contain the most number of resistance genes. They have identified as much as eight blast resistant genes in more than one accession. They also concluded that the linked markers used in their study are well established and effective, thus making them a marker of choice for molecular screening of rice blast resistance genes. We have enlisted blast marker resistant genes for MAS in Table 1 (Jia et al. 2002; Fjellstrom et al. 2004; Hayashi et al. 2006; Qu et al. 2006; Takahashi et al. 2010; Ashkani et al. 2012)
### Table 1. Markers used in MAS for abiotic and biotic stresses.

<table>
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<tr>
<th>Marker</th>
<th>QTL/gene</th>
<th>Forward (5'–3')</th>
<th>Reverse (5'–3')</th>
<th>Reference</th>
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<td><strong>Drought</strong></td>
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<td>RM201</td>
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<td>CTCGTTTATACCTACGATCC</td>
<td>CTACCTCCTTCGCTAGA</td>
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3a)Resistant. 3b)Susceptible.

Sheath blight

In a comprehensive review done by Yellareddygari et al. (2014) on disease and pathogen management approaches in rice sheath blight (ShB), ShB is caused by R. solani Kuhn (Teleomorph: Thanatephorus cucumeris [Frank] Donk), and is a destructive disease worldwide that causes significant yield loss and quality degradation. Aside from rice, it can also infect other crops like lettuce, tomato and maize. This fungus is a universal soil saprotrophic and facultative plant parasite. The sclerotia of R. solani can survive even in unfavorable conditions. Once the field is set up with plants, the sclerotia will attached to the soaked organ of rice and starts the disease development. To combat almost all kinds of rice diseases, integrated disease management in the field is still highly recommended.

There are about 50 ShB resistance QTLs that have been mapped to all the 12 rice chromosomes and pyramiding of diverse ShB resistance QTLs could help achieve higher levels of resistance to ShB (Yadav et al. 2015). One study showed pyramiding of ShB resistance, qSB-9TQ and tiller angle TAC1TQ resulted to NILs carrying both QTLs showing more resistance than the NILs containing only one of them (Zuo et al. 2014). Pyramiding major SB resistance QTLs like qShB9-2 (Liu et al. 2013) can give rise to an efficient and effective host resistance. The markers RM215 and RM245 were closely linked to qShB9-2 and can be used as reliable markers for improving ShB resistance in brown plant hopper resistance in rice (Hu et al. 2016) was written and it presents the positional information of BPH-resistance genes and several markers available for MAB (Table 1). In addition, there are reported SSR markers that are specific for BPH biotypes. Shabanimofrad et al. (2015) have concluded that their chi-square analysis showed a good fit to a ratio of 3:1 for the segregation of resistance and susceptibility for biotypes 2 and 3 of BPH. SSR markers RM545, RM401, RM22, RM5953, RM210, RM242, RM217, RM224 and RM1103 were significantly associated with BPH resistance to biotypes 2 and 3 of BPH in rice (P≤0.01). These markers showed high selection accuracy for resistant plant sources with confirmation of resistance effect of about 17% to 20% for phenotypic variation and can be used in MAS for the resistant gene (Shabanimofrad et al. 2015).

Relative to BPH, WBPH is less concerned in research, resistance genes Wbph7 and Wbph8 happens to work as well in resistance to BPH (Tan et al. 2004). In addition to these two genes, an ovicidal gene (Ovc) shows a general response to WBPH and BPH (Fujita et al. 2013). According to Fujita et al. (2013), all other WBPH genes have been identified by segregation analysis but have undergone no further genetic analyses and have no iden-
tified DNA markers. But there is a recent study that applied SSR markers in MAS for WBPH, that study showed 64.9% of coincidence rate of bioassay and MAB efficiency after using SSR marker RM11669 for WBPH resistance when used in double haploid lines derived from the cross of JSNDH13 with CNDH32 (Yi et al. 2014).

Stem borer

There are two common stem borers in Asia, yellow stem borer (Scirpophaga incertulas) and white stem borer (S. innotata). In general, stem borers are polyvoltine, meaning they produce several broods in a year, but the number of generations in a year depends on environmental factors, primarily temperature, rainfall, and crop availability (Pathak and Khan 1994). In places having distinct generations, the first generation usually appears when the plants are in seedling stage; the population increases in subsequent broods and the later generations are often the ones that cause serious damage. This is why the borers are more destructive to the late-planted crops, or the second crop where double cropping is observed (Pathak and Khan 1994). The damage of stem borer becomes evident only as deadheart and whitehead, significant losses are also inflicted by larvae that feed within the stem without severing the growing plant parts at the base. Such damage results in reduced plant vigor, fewer tillers, and many unfilled spikelets (Pathak and Khan 1994). Selvi et al. (2002) reported the identification of RAPD markers associated with yellow stem borer resistance and susceptibility, the markers C1320 and K6695 were linked with resistance and AH5660 and C41300 with susceptibility. The markers K6695 and AH5660 were linked to the genes at distances of 12.8 cM and 14.9 cM, respectively, their sufficiently closer linkage to the genes regulating the trait and their unambiguous scorability in the resistant and susceptible cultivars were tested. Also, they investigated and described the possibility of screening for yellow stem borer resistance using micro satellite markers. This marker, RM241, located on chromosome 4, was also found to be associated with the trait and is closed to the genes for yellow stem borer resistance (Selvi et al. 2003).

CONCLUSION

In this review, we have summarized some of the recently used DNA-based markers for MAS in abiotic and biotic stress tolerance in rice as shown in Fig. 1. The efficiency of MAS largely depends on the distance between molecular markers and genes/QTLs associated with target traits. The development of useful markers tightly linked to abiotic and biotic stress resistance traits is accomplished by QTL mapping experiments. Generally, the markers are validated in fine mapping studies. MAB greatly increase the efficiency and effectiveness of breeding. By determining and developing DNA markers for target genomic regions, desired individuals possessing particular genes or QTLs can be identified in germplasm collections based on genotyping rather than phenotyping only. Based on the readings made, in any abiotic and biotic stress tolerance, stronger resistance can be attained by pyramiding validated tolerance genes and QTLs. MAS refers to selection by DNA markers linked to QTLs associated target genes. DNA-based genetic markers are recently expected to play an important role in the future of MAB and molecular genetics analysis for development of stress-tolerance and
disease-resistance in plants through molecular linkage maps. The information of markers for abiotic and biotic tolerant traits gathered here will provide a one-stop read for practical rice breeders and the like to aid in their MAB.

ACKNOWLEDGEMENTS

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