Enhancement of Panicle Blast Resistance in Korean Rice Cultivar 'Saeilmi' by Marker Assisted Backcross Breeding

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ABSTRACT Panicle blast is a serious disease in rice production in Korea. To develop rice cultivar resistant to panicle blast, the *Pb1* gene, originating in the *indica* cultivar 'Modan', was incorporated into an elite *japonica* cultivar 'Ilmi', which is highly susceptible to panicle blast, by marker assisted backcross breeding. 'Hwayeong' was selected as the donor parent for the *Pb1* gene based on 10 years of panicle blast data. The inheritance of panicle blast resistance in 'Hwayeong' is controlled by a single dominant gene. This panicle blast resistance gene, *Pb1*, from 'Hwayeong' was incorporated into the susceptible variety, 'Ilmi', by marker assisted backcross approach using DNA marker RM206. As a result, 'Saeilmi' containing the *Pb1* gene showed resistance to panicle blast. The agronomical and grain quality traits of 'Saeilmi' were similar to those of the recurrent parent 'Ilmi'. Molecular background analysis revealed that 'Saeilmi' had the least donor segment introgression in the locus of the *Pb1* gene on chromosome 11.

Keywords Rice, Panicle blast, Marker assisted selection, Saeilmi

INTRODUCTION

Disease and insect pests seriously constrain rice yields. Among these, rice blast, which is caused by the fungus *Magnaporthe grisea*, is the most widespread disease in most commercial rice-growing areas of the world. Annual losses caused by the rice blast fungus vary from 10% to 30% of the harvest, with even 10% loss being enough to feed 60 million people for one year (Skamnioti *et al.* 2009). To minimize the loss from rice blast, the use of resistant varieties is one of the most effective ways to control the disease. However, the useful life span of resistant varieties was only about three years due to the breakdown of resistance induced by the pathogenic variability of *M. grisea* rice (Khush and Brar 1991). In the 1970s, Tongil-type cultivars accounted for more than 75% of the total rice production in Korea. However, the proliferation of diverse cultivars triggered genetic mutations of rice blast leading to differentiation of the blast fungus, *M. grisea*. This development

eventually led to the breakdown and loss of blast resistance in Tongil-type rice cultivars (Lee and Park 1979; Ryu *et al.* 1987). The same virulent *M. grisea* isolates also caused great damage to leaf and panicle blast in *japonica* rice. This is attributed to the narrow genetic diversity of *japonica* cultivars to panicle blast resistance and the rapid expansion of cultivation area (Han *et al.* 2001; Kwon *et al.* 2002). Thus, the development of a blast-resistant cultivar has still been considered to be the most effective and economical breeding strategy to control the spread of the disease (Bonman 1992). Up to date, approximate 50 resistance genes to blast disease have been identified. Some major genes, such as *Pi-z*, *Pi-zt*, *Piz-5* (*Pi2*), *Pi5*, *Pi9*, and *Pi40*, were reported to have resistance to a broad spectrum of *M. grisea* isolates (Hayashi *et al.* 2004; Jeon *et al.* 2003; Liu *et al.* 2002; Suh *et al.* 2009). However, those blast resistance genes were identified for a leaf blast disease not to panicle blast. The genetic and QTLs of the resistance to leaf blast and panicle blast might be independently controlled by

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different genes (Sirithunya *et al.* 2002). The damage of panicle blast is more destructive than that of leaf blast in practical rice cultivation. Therefore, development of high resistance to panicle blast variety is considered in breeding programs.

A broad-spectrum panicle blast resistance gene *Pb1*, a single dominant locus, was found in the *japonica* rice cultivar ‘Tsukinohikari’ derived from the *indica* cultivar ‘Modan’ (Fujii *et al.* 1999; Fujii *et al.* 2000). The *Pb1* gene was identified on chromosome 11 encoding coiled-coil (CC)-NBS-LRR and contains two putative CC domains in the N terminus (Hayashi *et al.* 2010). The *Pb1* gene has been classified as a field resistance gene (or adult resistance) because of its durability and quantitative nature of resistance (Hayashi *et al.* 2010). Rice cultivars containing *Pb1* gene were rather weakly resistant to leaf blast, but remarkable resistant to panicle blast (Fujii *et al.* 2000; Hayashi *et al.* 2010).

The use of molecular markers increases the speed of the selection process in breeding programs. The marker-assisted backcrossing strategy is to transfer a specific allele at the target locus from a donor line to a recipient line while selecting against donor introgressions across the rest of the genome (Jairin *et al.* 2009; Suh *et al.* 2011; Wongsaproma *et al.* 2010). The PCR based marker RM206 for panicle blast resistant gene was identified by Hayashi *et al.* (2004). However, there has been no scientific report in the development of a rice cultivar resistant to the panicle blast. Here, we report a new variety ‘Saeilmi’ carrying *Pb1* gene using the marker-assisted backcrossing approach.

MATERIALS AND METHODS

Plant materials and development of near isogenic lines (NILs)

The rice cultivars ‘Ilmi’ and ‘Hwayeong’ were used as the parents in the marker assisted backcross program. ‘Ilmi’ was used as the recipient variety and ‘Hwayeong’, one of the ‘Modan’-derived panicle blast resistant cultivars, was used as the donor of *Pb1* gene. Near isogenic lines (NILs) were developed through the marker assisted backcross strategy. In each backcross generation (BC_nF_1),

individual BC_nF_1 were selected based on the heterozygous allele of SSR marker RM206 linked to the *Pb1* gene based on a report of Hayashi *et al.* (2004). A total of 687 individuals of BC_3F_2 were obtained and used to identify the *Pb1* gene. One hundred and ten NILs were developed by anther culture method in the BC_4F_1 generation and used to evaluate the agronomic traits, their grain quality, and association of SSR marker RM206 analysis.

Field test of panicle blast

We carried out field tests of panicle blast using the standard evaluation method (RDA 2003). One hundred and ten NILs and 687 individuals of BC_3F_2 were grown in an experimental plot at the Department of the Functional Crop, Miryang, Korea. Seeds were sown on 30 June and transplanted on 20 July in 2007 and in 2008. The planting density was 22.22 m^{-2} ($15\text{ cm} \times 30\text{ cm}$) and N- P_2O_5 - K_2O fertilizers were applied at the level of 90 - 45 - 57 kg/ha. The incidence of panicle blast was evaluated based on the percentage of infected panicles per plant at 40-50 days after heading. The number of panicles showing symptoms of panicle blast disease was expressed as percent infection.

Evaluation of agronomic and grain quality traits

The parents and eight NILs derived from marker assisted backcross were planted in a eight-row plot with 200 plants per row by $30 \times 15\text{ cm}$ spacing in a randomized complete block design with three replications. The were evaluated for agronomic traits in the rice experimental plot of the Department of the Functional Crop, Miryang, Korea, using the standard evaluation method of rice (RDA 2003). For each line, ten plants in the middle rows were used to determine heading date, culm length, panicle length, panicle number, number of grains per panicle, grain filling ratio, and grain yield. Grain yield per plot was evaluated based on a grain harvest of 100 plants in the central row of each plot.

Grain quality was estimated for chalkiness (0: non-chalkiness, 3: high chalkiness) of brown rice, amylose content and protein content of milled rice. Amylose content was determined by the relative absorbency of starch-iodine color by Juliano’s (1971) modified method. Protein content was calculated by multiplying grain nitrogen content by 5.95, the nitrogen-protein conversion factor. Grain nitrogen

content was measured by the Micro-Kjeldahl method (2300 Kjeltex Analyzer, Foss). Palatability characteristics of the rice samples were measured using a TOYO meter (MB-90A and MA-90B, Toyo Co.) to determine the glossiness of the cooked rice. The head rice ratio of milled rice was measured by a single grain rice inspector (RN600, Kett Co.)

DNA marker analysis for *Pb1* gene validation

The SSR marker RM206, which is the most tightly linked to panicle blast resistance gene *Pb1*, was used to confirm the presence of *Pb1* gene in marker assisted backcross lines. Polymerase chain reaction (PCR) was performed in an ABI 9700 Thermocycler (Germany) with a total volume of 20 µl containing 20 ng of template DNA, 5 pmoles of each primer, 1.5 mM of MgCl₂, 0.2 mM of dNTP and 0.5 U of *Taq* polymerase. The PCR amplification condition was one cycle of denaturation at 95°C for 5 min, followed by 40 cycles at 95°C for 30 s, 55°C for 30 s, and 72°C for 1 min, with a final extension at 72°C for 10 min. After determining the amplification success, the PCR product was detected using 3% agarose gel electrophoresis with ethidium bromide staining.

Molecular analysis of genetic background

A total of 192 SSR markers distributed evenly on the 12 chromosomes with an average interval of 1.0-2.0 Mb were used in a genome-wide survey to identify the chromosome

segment substitution locations in ‘Saeilmi’. The polymorphism analysis was conducted following the procedure of McCouch *et al.* (2002). The PCR products were detected using 4% denaturing polyacrylamide gel electrophoresis.

Statistical analysis

The least significant difference (LSD) was used for multiple mean comparisons using the SAS statistical software package (version 8.2; SAS Institute, Cary, NC).

RESULTS

Donor parent selection and genetic background of panicle blast resistance gene *Pb1*

In order to select the donor parent of *Pb1* gene among Korean *japonica* rice, varietal reactions data to panicle blast was surveyed from 2001 to 2010 in Jecheon province, a known area prone to panicle blast in Korea. During these 10 years, the incidence of panicle blast in ‘Hwayeong’ and ‘Dongjin’ ranged from 0.0 to 1.0% and 0.0 to 0.4%, respectively. However, the incidence of panicle blast in ‘Ilpum’, ‘Hwaseong’, and ‘Juan’ ranged from 0.0 to 45.0%, 0.0 to 37.5%, and 0.0 to 50.0%, respectively (Fig. 1). The incidence of panicle blast of ‘Hwayeong’ was significantly lower than that of susceptible cultivars ‘Ilpum’, ‘Hwaseong’, and ‘Juan’. As a result, we selected the ‘Hwayeong’ as the donor parent for *Pb1* gene based on

Fig. 1. Fluctuation of the percentage of blast-diseased panicle in Jecheon located in the northern part of south Korea for 10 years (2001 to 2010). HY: Hwayeong, DJ: Dongjin, IP: Ilpum, HS: Hwaseong, JA: Juan.

the 10 years of field tests. In pedigree analysis, the panicle blast resistance gene, *Pb1*, derived from ‘Hwayeong’ was introduced from *indica* cultivar ‘Modan’ at an early stage of the *japonica* rice breeding program in Korea.

Development of NILs

F₁ progenies were produced from a cross between the panicle blast susceptible cultivar ‘Ilmi’ and the *Pb1* donor ‘Hwayeong’. The BC₁ progenies were obtained by backcrossing the F₁ plants with ‘Ilmi’ as recurrent parent.

In the BC_nF₁ generation, individual plants showing heterozygous at the *Pb1* gene locus were identified and used for further backcrossing with the recurrent parent using a marker-assisted backcrossing scheme (Fig. 2). The advanced backcross progenies of BC₂, BC₃, and BC₄ were obtained from the crosses of selected resistant BC₁F₁ (7 plants from 20 plants), BC₂F₁ (17 plants from 42 plants), BC₃F₁ (16 plants from 34 plants), and BC₄F₁ (10 plants from 20 plants) plant based from marker allele of RM206.

Fig. 2. Flow diagram showing steps involved in marker-assisted backcross breeding program.

Fig. 3. Frequency distribution of the percentage of panicle blast in 110 backcrossed double haploid lines (BC₄DH) derived from a donor parent Hwayeong and a recurrent parent Ilmi.

Genetic analysis of *Pb1* gene

The panicle blast reaction was carried out using the modified method (Roh *et al.* 2007). ‘Hwayeong’ showed significantly lower infection ratio to panicle blast than ‘Ilmi’ at 40-50 days after heading. The average percentage of panicle blast infection was 3.0% for ‘Hwayeong’ and 67.3% for ‘Ilmi’, respectively (Fig. 3). The frequency distribution of panicle blast in the BC₄DH population (N=110) was bimodal distribution, resistance (0 to 40%) and susceptible (60 to 100%), suggesting that the inheritance of panicle blast resistance in ‘Hwayeong’ is controlled by a single gene (Table 1).

The mode of panicle blast inheritance in donor parent, ‘Hwayeong’, was investigated in the BC₃F₂ population developed by the serial backcross with the panicle blast susceptible recurrent parent ‘Ilmi’. A total of 679 individuals

of BC₃F₂ were classified as either resistant or susceptible, based on the infected percentage of panicle blast with 40% as the boundary. Segregation ratio of 519 resistant, and 160 susceptible plants was fit to a 3:1 ratio and ($\chi^2 = 0.747$, df = 1, $p = 0.388$) (Table 1). This result confirmed that the inheritance of panicle blast resistance in ‘Hwayeong’ was controlled by a single dominant gene.

Agronomic traits and grain quality performance of elite NILs

The field performances of the selected NILs were evaluated in 2007. The days to heading of elite NILs were almost the same as those of ‘Ilmi’. The culm length of NILs varied from 73.6 to 78.5 cm with an average of 76.2 cm. In major traits of yield components, the average number of grains per panicle in NILs was 125.5, which was much

Table 1. Genetic analysis of resistance to panicle blast disease BC₄ DH and BC₃F₂ population derived from a backcross Ilmi (recurrent) and Hwayeong (donor).

Designation	Generation	No. of tested plants	Reaction to PB ²⁾		Expected ratio	χ^2	P-value
			Resistance	Susceptible			
YR26754	BC ₄ -DH	110	59	51	1:1	0.582	0.446
YR26175	BC ₃ F ₂	679	519	160	3:1	0.747	0.388

²⁾PB: panicle blast.

Table 2. Agronomic traits of eight BC₄ DH lines showing resistance to panicle blast.

Designation	²⁾ DH ¹⁾ (days)	CL ²⁾ (cm)	PL ³⁾ (cm)	NP ⁴⁾	NGP ⁵⁾	GFR ⁶⁾ (%)	HR ⁷⁾ (%)	GY ⁸⁾ (MT/ha)
Ilmi	85 ^{y)}	75.0	21.1	16.1	111.4	89.5	82	6.82
Hwayeong	78	75.4	22.4	15.8	110.8	90.6	83	6.19
YR26754Acp13	83	76.9	20.9	15.7	124.5	89.9	82	7.27
YR26754Acp15	83	78.5	20.6	15.1	141.0	90.3	82	7.30
YR26754Acp29	84	77.1	20.8	15.4	124.1	91.9	82	7.10
YR26754Acp40	85	73.6	19.2	15.5	119.7	90.7	80	6.43
YR26754Acp58	84	76.9	20.5	14.8	133.3	89.0	82	7.18
YR26754Acp61	83	74.8	21.3	15.6	121.9	84.5	82	7.16
YR26754Acp79	84	75.9	20.7	15.8	120.5	89.3	82	6.96
YR26754Acp91	84	75.8	20.0	14.6	118.7	86.7	82	7.12
Mean	84	76.2	20.5	15.3	125.5	89.0	82	7.06

²⁾1: DH (days to headings), 2: CL (culm length), 3: PL (panicle length), 4: NP (number of panicles per hill), 5: NGP (number of grain per panicle), 6: GFR (grain filling ratio), 7: HR (husking recovery- percentage of brown rice per rough rice), 8: GY (grain yield per ha).

^{y)}No significance was observed between ‘Ilmi’ and BC₄ DH lines for statistical computing.

higher compared to that of 'Ilmi'. The grain filling ratio and brown rice per rough rice ratio were also almost the same. Compared to that of 'Ilmi', NILs showed a little bit higher rice yield, with an average of 7.06 MT/ha. Consequently, except the number of grains per panicle, the main agronomic traits of the NILs were similar to those of 'Ilmi' because of the backcross progenies possessing undesirable agronomic

traits were eliminated in early generations. As a results, one of the elite NIL of YR26754Acp13 possessing the *Pbl* gene with similar grain quality was selected and designated as 'Saeilmi' through a local adaptability test over 3 year (2009 to 2011). And most of the grain features in NILs, such as amylose and protein contents, were the same as those of 'Ilmi' (Table 3).

Table 3. Grain qualities of eight BC₄ DH lines resistant to panicle blast.

Designation	²⁾ AC ¹⁾ (%)	PC ²⁾ (%)	HRR ³⁾ (%)	WC/WB ⁴⁾ (0-9)	PA ⁵⁾
Ilmi	19.1 ^{y)}	6.2	93.1	0/0	68.9
Hwayeong	18.6	6.5	92.1	0/0	67.4
YR26754Acp13	19.0	6.3	94.7	0/0	67.6
YR26754Acp15	18.9	6.2	94.6	0/0	67.8
YR26754Acp29	19.2	6.3	96.0	0/0	67.8
YR26754Acp40	19.3	6.2	95.0	0/0	67.9
YR26754Acp58	18.5	6.3	95.3	0/0	67.0
YR26754Acp61	19.6	6.2	93.4	0/0	68.0
YR26754Acp79	19.4	6.3	93.6	0/0	68.6
YR26754Acp91	19.1	6.4	92.9	0/0	69.0
Mean	19.1	6.2	94.4	0/0	68.0

¹⁾1: AC (amylase content), 2: PC (protein content), 3: HRR (head rice ratio of milled rice), 4: WC/WB (chalkiness degree of brown rice in white core and white back), 5: PA (Palatability-Toyo meter).

^{y)}No significance was observed between 'Ilmi' and BC₄ DH lines for statistical computing.

Table 4. Simple sequence repeat markers with polymorphism between recurrent parent and donor parent and substituted chromosome segments from donor parent in Saeilmi.

Chromosome No.	No. of tested SSR markers	Chromosome length (Mb)	Marker interval (Mb)	Polymorphism (%)	substituted chromosome segments (%)
1	16	43.2	2.7	12.5	0
2	16	35.9	2.2	6.3	0
3	16	36.2	2.3	6.3	0
4	16	35.5	2.4	33.3	0
5	16	29.6	2.0	6.7	0
6	16	30.7	1.9	6.3	0
7	16	29.6	1.9	20.0	0
8	15	28.4	1.9	40.0	0
9	15	22.6	1.5	26.7	0
10	16	22.7	1.4	25.0	0
11	16	28.4	1.8	43.8	31.3
12	16	27.6	1.7	68.8	0
Total	188	30.9	2.0	24.6	2.6

Genetic background analysis of ‘Saeilmi’.

‘Saeilmi’, developed from the backcross of recurrent parent ‘Ilmi’ and panicle blast resistant donor ‘Hwayeong’, was investigated for background degree of the whole genome using SSR markers. A total of 188 SSR markers were used to identify introgression of chromosome segments of donor parent. The marker polymorphism between ‘Hwayeong’ and ‘Ilmi’ was 24.6%. In ‘Saeilmi’, the introgression chromosome segments of ‘Hwayeong’ were distributed around the region of the *Pb1* gene located on chromosome 11 only. The percentage of donor parent chromosome substitution on chromosome 11 was 31.3%

(Table 4).

Validation of *Pb1* gene in ‘Saeilmi’ and NILs

Field response of *Pb1* gene was conducted for panicle blast disease prone area such as Icheon, Jaechon, Yaesan, and Iksan during the 3 years from 2009 to 2011. The average infected panicle blast percentage of the ‘Saeilmi’ ranged between 0.6% and 3.3%. The panicle blast resistance varieties ‘Dongjin’ and ‘Hwayeong’ also showed 0.6% and 1.3% of infected panicle blast, respectively. However, the average percentage of infected panicle blast of the susceptible varieties, ‘Hwaseong’ and ‘Ilpum’ ranged

Fig. 4. Association between reaction to panicle blast disease and marker allele of RM206 tightly linked to *Pb1* gene in NILs. HY: Hwayeong (Donor parent), IM: Ilmi (recurrent parent), R: resistance, S: susceptible.

Fig. 5. Symptoms of rice panicle blast in cultivar Ilmi (*Pb1*-) and Saeilmi (*Pb1*+).

Table 5. Field test of panicle blast in disease prone experimental plots for 3 years from 2009 to 2011.

Varieties	Icheon	Jaechon	Yaesan	Iksan	Average	Range ²⁾
Hwaseong	3.9	4.5	3.8	6.6	4.7	0.0 – 18.7
Ilpum	7.2	9.2	0.8	5.5	5.7	0.0 – 25.0
Dongjin	0.9	0.0	1.4	0.0	0.6	0.0 – 4.3
Hwayeong	1.3	0.1	3.6	0.1	1.3	0.0 – 10.8
Saeilmi	1.9	0.5	0.0	0.1	0.6	0.0 – 3.3

²⁾Range is a minimum and maximum of panicle blast obtained from 2009 to 2011.

between 4.7% and 18.7% and between 5.7% and 25.0%, respectively (Table 5).

To confirm the presence of the *Pb1* gene, RM206, which is tightly linked to panicle blast gene *Pb1*, was screened in BC₄DH lines. Consequently, the RM206 DNA marker was well associated with the field resistance of panicle blast in each individual line (Fig. 4). And as shown in Fig. 5, ‘Saeilmi’ showed clear resistance, while ‘Ilmi’ was susceptible to panicle blast.

DISCUSSIONS

The main objective of this study was to combine panicle blast resistance gene *Pb1* into an elite cultivar using marker assisted backcross. Conventional breeding programs for disease resistance are laborious, time consuming, and highly dependent on environmental conditions compared to marker assisted selection, which is simple, efficient, and precise (Babujee and Gnanamanickam 2000). Application of a marker assisted selection program has been successfully utilized in developing new varieties for resistance to blast diseases (Jairin *et al.* 2009; Suh *et al.* 2011).

At present, most of the Korean *japonica* cultivars to carry the blast resistance genes *Pia*, *Pib*, *Pii*, *Pik*, *Pita*, and *Piz* based on pedigree analysis, molecular marker analysis, and reaction to leaf blast disease (Cho *et al.* 2007; Kwon *et al.* 2008). However, because of difficulty in infection of panicle blast under fluctuating environmental conditions in which each plant’s tendency to escape infection during the heading and maturing stage, which is the genetic and molecular basis of panicle blast resistance, has been poorly understood in Korea. Fujii *et al.* (1999) reported that the *Pb1* gene is located on the long arm of chromosome 11 and linked to the RSV resistance gene originating from *indica* cultivar ‘Modan’. The *Pb1* gene has been classified as a field resistance gene because of its durability and quantitative reaction. Interestingly, the *Pb1* gene was blast susceptible during young vegetative stages, however the resistance level increased as the plant grew, and persisted even after heading (Fujii and Hayano-Saito 2007).

The best way to understand the durability of the panicle blast resistance mechanism is probably to examine a

cultivar or genotype that has remained resistant to a highly variable pathogen for a long period of cultivation. ‘Hwayeong’ was selected as the donor parent of the *Pb1* gene for marker-assisted backcross in this study because ‘Hwayeong’ has shown the durable resistance to panicle blast from 2001 to 2010 in Jecheon. In analysis of breeding pedigree, ‘Hwayeong’ revealed that the *Pb1* gene originated from Japanese cultivar ST.No.1, which is derived from the *indica* cultivar ‘Modan’ (Fujii *et al.* 1999).

In rice genetic improvement such as disease resistance and abiotic stress tolerance, the amount of linkage drag would increase as more major resistance genes combine into a variety (Jairin *et al.* 2009; Lee *et al.* 2005). So it is important to consider how to optimize the combination of a broader spectrum resistance. When the target gene is linked with an unfavorable allele, background selection using molecular marker can be performed to break down the linkage drag (Jena and MacKill 2008). Although marker-assisted selection technology is well known as a powerful tool for dissecting linkage drag, the most efficient way in a breeding program is the utilization of donor parent with no undesirable alleles in the target gene locus.

The agronomic characteristics and grain quality traits of NILs developed from marker assisted backcross were almost the same as ‘Ilmi’, indicating that any linkage drags with unfavorable alleles of ‘Hwayeong’ did not occur. In addition, NILs developed from marker assisted backcross showed resistance to K₃ race of bacterial blight disease. In this respect, it is clear that the bacterial blight resistance gene *Xa3* of ‘Hwayeong’ located on the end of the long arm of chromosome 11 (Kang *et al.* 2003) is closely linked to *Pb1* gene.

Agronomic traits related to yield stability and sustainability are major concerns of rice breeding efforts. No significant difference was statistically observed in agronomic characteristics and grain quality between ‘Ilmi’ and NILs developed from marker assisted backcross. However, the grain yield of the NILs was slightly increased than greater of ‘Ilmi’, apparently because of increased number of grains per plant. Finally, as a result, we selected the best line among of the NILs and developed a new variety, ‘Saeilmi’. The results obtained from the NILs clearly showed that ‘Saeilmi’ had similar agronomic characteristics to the

recurrent parent 'Ilmi'.

The effectiveness of marker-assisted backcrossing in enhancing the introgression of major resistance QTL alleles has been well documented (Jairin *et al.* 2009; Suh *et al.* 2011). The present study demonstrated that marker assisted backcross was sufficient to recover the majority of the important characteristics of the original plant without any linkage drag of unfavorable background. In many cases, molecular markers linked to disease and insect resistance are available to facilitate direct selection in the breeding program. And those techniques apparently enhance stable resistance to elite varieties that are renowned for their wide adaptation and production stability across environments.

The majority of resistance breeding has depended on field screening methods in Korea. It was difficult to develop a durable resistance to panicle blast using conventional breeding methods due to the failures to infect satisfactorily individual plants by fluctuating environmental conditions. In this report, we demonstrated that marker assisted backcross effectively enhanced the introgression of panicle resistance gene *Pb1*. We have successfully developed a near isogenic variety 'Saeilmi' which is carrying the *Pb1* gene and is identical to *japonica* elite cultivar 'Ilmi' by using marker-assisted backcrossing. Thus, marker assisted backcross was shown to be a great tool in breeding programs.

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