# Note

# *Rice tungro spherical virus* resistance into photoperiod-insensitive japonica rice by marker-assisted selection

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Rice tungro disease (RTD) is one of the destructive and prevalent diseases in the tropical region. RTD is caused by *Rice tungro spherical virus* (RTSV) and *Rice tungro bacilliform virus*. Cultivation of japonica rice (*Oryza sativa* L. ssp *japonica*) in tropical Asia has often been restricted because most japonica cultivars are sensitive to short photoperiod, which is characteristic of tropical conditions. Japonica1, a rice variety bred for tropical conditions, is photoperiod-insensitive, has a high yield potential, but is susceptible to RTD and has poor grain quality. To transfer RTD resistance into Japonica1, we made two backcrosses (BC) and 8 three-way crosses (3-WC) among Japonica1 and RTSV-resistant cultivars. Among 8,876 BC<sub>1</sub>F<sub>2</sub> and 3-WCF<sub>2</sub> plants, 342 were selected for photoperiod-insensitivity and good grain quality. Photoperiod-insensitive progenies were evaluated for RTSV resistance by a bioassay and marker-assisted selection (MAS), and 22 BC<sub>1</sub>F<sub>7</sub> and 3-WCF<sub>7</sub> lines were selected based on the results of an observational yield trial. The results demonstrated that conventional selection for photoperiod-insensitivity and MAS for RTSV resistance can greatly facilitate the development of japonica rice that is suitable for cultivation in tropical Asia.

Key Words: Rice tungro spherical virus, rice tungro disease, marker-assisted selection, photoperiodinsensitivity, japonica rice (Oryza sativa L. ssp japonica).

# Introduction

Rice tungro disease (RTD) is one of the most destructive diseases of rice in tropical Asia (Hibino *et al.* 1991). Rice (*Oryza sativa* L.) plants affected by RTD show stunted growth, yellow to orange leaf discoloration, and few reproductive tillers (Thomas *et al.* 1980). RTD is caused by *Rice tungro bacilliform virus* (RTBV) and *Rice tungro spherical virus* (RTSV). Both RTSV and RTBV are transmitted by green leafhoppers (GLH) in a semi-persistent manner (Hibino *et al.* 1991). RTSV is independently transmitted by GLH, whereas RTBV can be transmitted by GLH only in the presence of RTSV (Hibino *et al.* 1990).

An evaluation of more than 40,000 rice germplasm accessions for RTSV and RTBV showed that dozens of traditional cultivars are resistant to RTSV, whereas only two cultivars are resistant to RTBV (Hibino *et al.* 1990, Shahjahan *et al.* 1990, Zenna *et al.* 2006). A genetic analysis of RTD-

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resistant rice cultivar Utri Merah showed that RTSV and RTBV resistance are independently inherited, and the interaction between both resistance traits is necessary to suppress RTD effectively (Encabo *et al.* 2009). RTSV resistance is a recessive trait controlled by the translation initiation factor 4 gamma (eIF4G) gene located between 22.05 and 22.25 Mb in chromosome 7 (Lee *et al.* 2010). The molecular marker, RM336 was successfully used for mapping the RTSV resistance gene (Lee *et al.* 2010). Sequence analysis of the eIF4G gene in cultivars resistant to RTSV identified single nucleotide polymorphisms (SNPs) in five combinatorial patterns that are associated with RTSV resistance (Lee *et al.* 2010).

The need for japonica rice (*O. sativa* L. ssp *japonica*) in Asia is increasing due to the increasing japonica rice consumers and trading (Magno and Yanagida 2000). Typical temperate japonica rice cultivars require a long-day photoperiod and are not adaptable to the short-day length conditions of the tropical regions. Photoperiod-sensitive japonica rice cultivars usually yield less than 1.2 ton/ha whereas photoperiod-insensitive japonica cultivars can yield up to 5.5 ton/ha in tropical regions (Philippine Rice Research

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Table 1. Selection for photoperiod-insensitivity and good grain quality at BC<sub>1</sub>F<sub>2</sub> and 3-WCF<sub>2</sub>

Cross combinations	No. of plants No. of selected photoperiod- examined insensitive plants		No. of selected plants with good grain quality	Selection intensity (%)	
IR97705 (Hwaseong/MS11)/Japonica1	225	17	9	4.0	
IR97707 (Hwaseong/Japonica1)/MS11	101	12	7	6.9	
IR97708 (Hwaseong/Japonica1)/Japonica1	1,025	124	64	6.2	
IR97709 (Hwaseong/Japonica1)/Jinmi	1,000	119	71	7.1	
IR97711 (Dongjin/MS11)/Japonica1	750	37	25	3.3	
IR97715 (Dongjin/Japonica1)/Jinmi	1,775	97	53	3.0	
IR97717 (Sangju/MS11)/Japonica1	1,000	19	18	1.8	
IR97719 (Sangju/Japonica1)/MS11	1,300	56	26	2.0	
IR97720 (Sangju/Japonica1)/Japonica1	700	21	14	2.0	
IR97721 (Sangju/Japonica1)/Jinmi	1,000	91	55	5.5	
Total	8,876	593	342	3.9	

Institute 2014). The rice variety Japonica1, which has been bred for tropical regions, has a high yield but is highly susceptible to RTD and has poor grain quality. Breeding of rice varieties for resistance to tungro viruses had relied exclusively on phenotypic selection. Here we report the application of marker-assisted selection (MAS) to transfer RTSVresistance into photoperiod-insensitive japonica rice breeding lines to assure their stable yield in tropical environment. Numerous rice molecular markers linked to specific traits have been developed (Jena and Mackill 2008), but only a limited number of these molecular markers are actually being used for conventional rice breeding. This is the first case of molecular MAS for tungro virus disease resistance in the course of developing a japonica variety that is adaptable to tropical conditions.

# **Materials and Methods**

#### **Plant materials**

Photoperiod-insensitive japonica varieties (Jinmi, Maligaya Special 11 (MS11) and Japonica1), photoperiod-sensitive varieties (Dongjin and Hwaseong) and an intermediately photoperiod-sensitive japonica variety (Sangju) were used in 10 cross combinations of backcrosses and three-way crosses (3-WC) (**Table 1**). Japonica1 has a high yield but has a poor grain quality and is susceptible to RTSV. Dongjin (Lee *et al.* 2010), Hwaseong, Sangju, Jinmi, and MS11 are resistant to RTSV. MS11 and Jinmi were included in the 3-WC as a source of good grain quality and photoperiod insensitivity. Jinmi, Dongjin, Hwaseong, Sangju, MS11, and Japonica1 have short and bold grains with an average of 1.8 length to width ratio and an average of 17–19% amylose content. Grains of these 6 varieties are clear and translucent with no significant chalkiness.

#### MAS for RTSV resistance

MAS for RTSV resistance was carried out for  $F_1$ ,  $F_3$ ,  $F_4$ , and  $F_5$  generations (**Fig. 1**). The  $F_2$  generations were excluded from MAS for RTSV resistance because of the selection of the  $F_2$  generations for photoperiod insensitivity. Genomic DNA samples were prepared from the young leaves of plants using the modified TPS method (Miura et al. 2009). The tips of rice leaves (5 cm) were excised and ground in TPS buffer (100 mM Tris-HCl [pH 8.0], 1 M KCl, 10 mM EDTA) using a GenoGrinder (OPS Diagnostics). After centrifugation, the supernatant was recovered and an equal volume of isopropyl alcohol was added. The isopropyl alcohol-insoluble material was recovered by centrifugation, and the pellet was rinsed with 75% ethanol. The pellet was then dried and dissolved in TE (10 mM Tris-HCl [pH 8.0], 1 mM EDTA, RNase A [10 mg/ml]). The DNA samples were then used for genotyping using the simple sequence repeat marker, rice microsatellite 336 (RM336, McCouch et al. 2002, forward primer: CTTACAGAGAA ACGGCATCG, reverse: GCTGGTTTGTTTCAGGTTCG, 21.87 Mb of chromosome 7, according to IRGSP 1.0 of the rice annotation project database at http://rapdb.dna.affrc. go.jp/) that is tightly linked to the RTSV resistance gene



**Fig. 1.** Breeding scheme for the development of *Rice tungro spherical virus* (RTSV)-resistant photoperiod-insensitive rice via selection for RTSV resistance and grain quality. RTSV-resistant varieties, Dongjin, Hwaseong, and Sangju were crossed with Japonical to produce  $F_1$ . MS11 and Jinmi were used as the donor for photoperiod insensitivity. DS) dry season, WS) wet season, OYT) observatory yield trial, PYT) preliminary yield trial, RYT) replication yield trial.

(Lee *et al.* 2010). The PCR profile was as follows: predenaturation for 5 min at 95°C, 35 cycles of denaturation for 1 min at 95°C—annealing for 30 sec at 55°C—extension for 30 sec at 72°C, and final extension for 7 min at 72°C. The PCR products were resolved on TAE (Tris-Acetate-EDTA) agarose gel (3%) for 1 h at 250 volts.

# Background selection for photoperiod insensitivity and grain quality

The photoperiod-sensitive japonica rice varieties typically exhibit early flowering and poor vegetative growth when grown under tropical conditions (12-14 hour day length; 25–33°C average day temperature). In the tropical condition of Philippines, the average height of highly photoperiodsensitive japonica varieties is about 55 cm; they flower earlier than 45 days after seeding (Fig. 2A); and their panicles are shorter than 15 cm (Fig. 2B). Stricter criteria were applied for background selection of the BC<sub>1</sub>F<sub>2</sub> and 3-WCF<sub>2</sub> generations for photoperiod insensitivity. Plants that were taller than 75 cm; had panicles longer than 22 cm; and that flowered at or after 60 days after seeding were considered photoperiod-insensitive. The selection criteria for good grain quality include grain chalkiness, opacity, color, boldness and appearance (Webb et al. 1985). The grains were dehulled and examined by visual test. Plants with grains that are not chalky, clear translucent, bold (length/width ratio less than 1.9), and short (shorter than 5.5 mm in length) were selected (Fig. 2C).

#### **Evaluation for reaction to RTSV**

RTSV strain A (Cabauatan *et al.* 1995) was used as the source of inoculum. The GLH-mediated inoculation of plants with RTSV was carried out using the modified water tray method as described by Azzam *et al.* (1999). BC<sub>1</sub>F<sub>2</sub> and 3-WCF<sub>2</sub> plants from the respective cross combinations that had been selected for good grain quality and photoperiod insensitivity were advanced to BC<sub>1</sub>F<sub>3</sub> and 3-WCF<sub>3</sub>. Twenty

BC<sub>1</sub>F<sub>3</sub> and 3-WCF<sub>3</sub> plants per line were grown in seed boxes. At 10 days after germination, the seedlings were placed inside a water tray and covered with a screen cage. RTSV-viruliferous GLH that had been allowed to feed on RTSV-infected plants for 4 days were released into the cage at an average of seven GLH per seedling for 3 hours to effect RTSV transmission. After inoculation, the trays were filled with water until the test seedlings were submerged to remove the GLH. One month after inoculation, leaves were collected from each plant and RTSV infection in the seedlings was examined by a double-antibody sandwichenzyme-linked immunosorbent assay (Bajet et al. 1985). The presence of RTSV in the leaf extracts was determined by measuring the absorbance of the leaf extracts at 405 nm (Cabunagan et al. 1993). Plants whose 10-fold-diluted leaf extracts exhibited an absorbance value greater than 0.1 were considered to be infected with RTSV. F3 lines with an infection rate of <20% were classified as resistant, those with 21 to 79% infection as segregating, and those with >80% infection as susceptible (Lee et al. 2010).

#### Results

# *Hybridization between photoperiod-insensitive and RTSVresistant varieties*

 $F_1$  plants were obtained by crossing the photoperiodinsensitive varieties Japonica1 or MS11 with three RTSVresistant varieties Hwaseong, Sangju, or Dongjin (**Fig. 1**). The  $F_1$  plants from two crosses (Hwaseong/Japonica1 and Sangju/Japonica1) were backcrossed to Japonica1, and the  $F_1$  plants from the other six crosses (Hwaseong/Japonica1, Hwaseong/MS11, Dongjin/Japonica1, Dongjin/MS11, Sangju/Japonica1, and Sangju/MS11) were used for 3-WC with Japonica1, Jinmi, or MS11 to produce 10 different cross combinations (**Fig. 1**, **Table 1**). Among the 236 BC<sub>1</sub> $F_1$  and 3-WCF<sub>1</sub> plants, 110 were identified to have a homozygous RTSV resistance allele, 22 have a homozygous susceptible



**Fig. 2.** Phenotypic selection criteria for photoperiod insensitivity and grain quality. (a) Difference in height among photoperiod-sensitive varieties (Sangju, Dongjin and Hwaseong) and photoperiod-insensitive varieties (MS11, Jinmi and Japonica1). (b) Typical segregation of panicle length and grain number in  $BC_1F_2$  plants. Panicles from  $BC_1F_2$  plants of IR97705. Scale bar equals 10 cm. (c) Typical segregation in grain chalkiness and opacity in  $BC_1F_2$  plants. Grains from  $BC_1F_2$  plants of IR97705.

Table 2.	Phenotypic selection	n for RTSV resistance	at BC1F3 and 3-WCF
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Cross combinations	No. of lines examined	No. of resistant lines	No. of segregating lines	No. of susceptible lines	No. of lines selected <sup>a</sup>
IR97705 (Hwaseong/MS11)/Japonica1	9	2	5	2	5
IR97707 (Hwaseong/Japonica1)/MS11	7	3	2	2	5
IR97708 Hwaseong/Japonica1)/Japonica1	64	22	23	19	39
IR97709 (Hwaseong/Japonica1)/Jinmi	71	71	0	0	27
IR97711 (Dongjin/MS11)/Japonica1	25	16	9	0	13
IR97715 (Dongjin/Japonica1)/Jinmi	53	33	1	19	26
IR97717 (Sangju/MS11)/Japonica1 <sup>b</sup>	18	_	-	_	7
IR97719 (Sangju/Japonica1)/MS11	26	7	2	17	9
IR97720 (Sangju/Japonica1)/Japonica1	14	5	0	9	5
IR97721 (Sangju/Japonica1)/Jinmi	55	50	2	3	18
Total	342	209	44	71	154

<sup>a</sup> Three panicles were harvested from each line selected.

<sup>b</sup> Penotyping for RTSV infection was not conducted for IR97717, and the selection was made on the basis of field performance.

allele, and 104 have heterozygous RTSV resistance/susceptible alleles by MAS using RM336. All the 110 BC<sub>1</sub>F<sub>1</sub> and 3-WCF<sub>1</sub> plants with homozygous resistance alleles were advanced to the next generation. Also, 25 of the 104 heterozygous BC<sub>1</sub>F<sub>1</sub> and 3-WCF<sub>1</sub> plants that are over 70 cm tall, with panicles that are 20 cm long and that had wide, deep green and erect leaves were advanced to the next generation.

# Selection of $BC_1F_2$ and 3-WCF<sub>2</sub> for photoperiod insensitivity and grain quality

The F<sub>2</sub> progenies derived from the 10 cross combinations segregated for plant height, panicle length, vegetative growth period, and flowering date. Among the  $8,876 \text{ BC}_{1}\text{F}_{2}$ and 3-WCF<sub>2</sub> plants generated from the 10 cross combinations, 593 plants were selected as photoperiod-insensitive (Table 1).  $F_2$  plants that were shorter than 75 cm in height were considered as photoperiod-sensitive and were discarded (Fig. 2A). The average panicle length of plants selected as photoperiod-insensitive was 22 cm. F<sub>2</sub> plant panicles that were shorter than 22 cm, and flowered earlier than 60 days after seeding were considered photoperiod-sensitive and were discarded in the field (Fig. 2B). A total of 593 photoperiod-insensitive F<sub>2</sub> plants were harvested and dehulled for grain quality test. Grains that were chalky, opaque, or irregularly-shaped were discarded (Fig. 2C). A total of 342 BC<sub>1</sub>F<sub>2</sub> and 3-WCF<sub>2</sub> plants were selected for photoperiod insensitivity and good grain quality and were advanced to  $BC_1F_3$  and 3-WCF<sub>3</sub> (Table 1). Only 3.9% of the  $F_2$  plants were selected and advanced to the next generation indicating that photoperiod sensitivity resulting in short plant height, early flowering and short panicle length, as well as poor grain quality, is highly heritable in tropical regions.

### Evaluation of $BC_1F_3$ and 3-WCF<sub>3</sub> by RTSV bioassay

Among the 342  $BC_1F_3$  and 3-WCF<sub>3</sub> lines, 324 were examined for their reaction to RTSV (18 lines of IR97717 were excluded from phenotyping for RTSV infection). Among the 324 lines examined, 209 were classified as resistant to RTSV, 44 as segregating for RTSV resistance, and

71 as susceptible to RTSV. From the 209 resistant lines and 44 segregating lines, a total of 154 plants were selected. Three panicles were harvested from each of the 154 plants, and a total of 462 plants were advanced to the next generations (Table 2).

# MAS of $BC_1F_4$ and 3-WCF<sub>4</sub> for RTSV resistance

A total of 462  $BC_1F_4$  and 3-WCF<sub>4</sub> lines were planted in the field. Among the 462 lines, 78 lines were selected for MAS based on field performance. Three plants from each of the 78 lines were subjected to genotyping for RTSV resistance using RM336 (**Fig. 3**, **Table 3**). Among the 78 lines, all plants of 50 lines were found to have homozygous RTSV resistance alleles, whereas 11 lines segregated into resistant,



**Fig. 3.** Representative genotypes of 3-WCF<sub>4</sub> plants using the SSR marker RM336 which is tightly linked to RTSV resistance. Japonical is susceptible whereas Hwaseong, Dongjin, Sangju, MS11, and Jinmi are resistant to RTSV. Three plants per line were examined for genotypes with RM336. Genotypes from different lines were separated by dashed lines. Underlined italic genotypes indicate segregation of genotypes in a line. M) marker, Hw) Hwaseong, Ja) Japonica1, Ji) Jinmi, Do) Dongjin, Ms) MS11, Sa) Sangju, R) resistant, S) susceptible, H) heterozygous.

#### RTSV resistance in photoperiod-insensitive rice

#### **Table 3.** Marker-assisted selection for RTSV resistance at $BC_1F_4$ and 3-WCF<sub>4</sub> using RM336

	No of lines	No. of lines		No of lines		
Cross combination	planted <sup>a</sup>	selected for genotyping	Resistant	Heterozygous	Susceptible	selected
IR97705 (Hwaseong/MS11)/Japonica 1	15	2	2	0	0	2
IR97707 (Hwaseong/Japonica1)/MS11	15	5	3	0	2	3
IR97708 (Hwaseong/Japonica1)/Japonica1	117	17	4	4	9	8
IR97709 (Hwaseong/Japonica1)/Jinmi	81	14	13	1	0	14
IR97711 (Dongjin/MS11)/Japonica1	39	7	4	1	2	5
IR97715 (Dongjin/Japonica1)/Jinmi	78	6	5	1	0	6
IR97717 (Sangju/MS11)/Japonica1	21	3	2	1	0	3
IR97719 (Sangju/Japonica1)/MS11	27	7	3	1	3	3
IR97720 (Sangju/Japonica1)/Japonica1	15	5	4	0	1	4
IR97721 (Sangju/Japonica1)/Jinmi	54	12	10	2	0	12
Total	462	78	50	11	17	60

<sup>*a*</sup> Three panicles were harvested from each of the previous 154 BC<sub>1</sub>F<sub>3</sub> and 3-WCF<sub>3</sub> lines; therefore 462 BC<sub>1</sub>F<sub>4</sub> and 3-WCF<sub>4</sub> lines were planted. Of the 462 lines, 78 were selected for MAS for RTSV.

 Table 4.
 Marker-assisted selection for RTSV resistance at BC1F5 and 3-WCF5 using RM336

Correct combined in a	No. of lines		No. of lines		
Cross combination	planted <sup>a</sup>	Resistant	Heterozygous	Susceptible	selected
IR97705 (Hwaseong/MS11)/Japonica1	6	6	0	0	3
IR97707 (Hwaseong/Japonica1)/MS11	9	9	0	0	6
IR97708 (Hwaseong/Japonica1)/Japonica1	24	3	0	21	1
IR97709 (Hwaseong/Japonica1)/Jinmi	42	42	0	0	11
IR97711 (Dongjin/MS11)/Japonica1	15	12	2	1	10
IR97715 (Dongjin/Japonica1)/Jinmi	18	16	2	0	7
IR97717 (Sangju/MS11)/Japonica1	9	9	0	0	$0^b$
IR97719 (Sangju/Japonica1)/MS11	9	9	0	0	2
IR97720 (Sangju/Japonica1)/Japonica1	12	12	0	0	7
IR97721 (Sangju/Japonica1)/Jinmi	36	28	3	5	15
Total	180	146	7	27	42

<sup>a</sup> Three panicles were harvested from each of the previous 60 BC<sub>1</sub>F<sub>4</sub> and 3-WCF<sub>4</sub> lines; therefore 180 BC<sub>1</sub>F<sub>5</sub> and 3-WCF<sub>5</sub> lines were planted.

<sup>b</sup> No IR97717 lines were selected due to bacterial blight infection.

susceptible, or heterozygous genotypes (underlined italic genotypes in Fig. 3, Table 3). It appeared that the locus linked to RM336 is heterozygous in Japonica1, and that only either of the two alleles in Japnoical was passed on to some progenies (genotypes indicated as 'S' in Fig. 3). In case of IR97709, no segregating or susceptible lines were found among the previous 71 lines of 3-WCF<sub>3</sub> examined for phenotypes for RTSV infection (Table 2); however, the genotype data showed segregation in the 3-WCF<sub>4</sub> generation of IR97709 (underlined italic genotypes in Fig. 3), suggesting that the contradictory results may be due to missed inoculation of RTSV via GLH on some 3-WCF<sub>3</sub> plants of IR97709 that might have occurred during the phenotyping of the 3-WCF<sub>3</sub> lines. Three panicles were harvested from each of the 60 BC1F4 and 3-WCF4 lines that have homozygous or heterozygous RTSV resistance alleles (Table 3), and a total of 180 lines were advanced to the next generation (Table 4). Another MAS for RTSV resistance for 180 BC<sub>1</sub>F<sub>5</sub> and 3-WCF<sub>5</sub> lines identified 62 lines to be homozygous for RTSV resistance alleles. The grains of 62 lines were dehulled and evaluated by visual examination. Forty-two lines were selected for good grain quality (**Table 4**). Three panicles were taken from each of the 42 lines and consequently a total of 126 lines were advanced to the next generation for observatory yield trial (OYT). Based on yield performance and agronomic traits in the OYT, we finally selected 22 lines (**Table 5**). The 22 lines selected showed a yield higher compared to MS11 and Japonica1 (**Table 5**).

#### Discussion

RTSV and RTBV resistance traits in rice are independently inherited (Encabo *et al.* 2009). Both RTBV resistance and RTSV resistance may be necessary for the effective management of RTD in fields. However, MAS for RTSV resistance alone might have a significant impact on the management of RTD because RTBV cannot be transmitted by GLH without the helper virus RTSV. Moreover, RTSV enhances the damages caused by RTBV (Hibino *et al.* 1990). The DNA marker RM336 is tightly linked to the RTSV resistance gene (Lee *et al.* 2010). Therefore, transfer of RTSV resistance by MAS into varieties to be cultivated in RTDprone areas is a practical approach toward RTD resistance

Table 5.	Yield and	agronomic cha	racteristics of	of the $22$ a	advanced b	reeding 1	lines selected b	v observator	v vield trial
								/	/ /

Designation	Heading date (Days after seeding) <sup>a</sup>	Culm length (cm) <sup>b</sup>	Panicle length (cm) <sup>b</sup>	Tiller number <sup>b</sup>	Reproductive panicle number <sup>b</sup>	Total plant mass (kg) <sup>a</sup>	Total grain weight (kg) <sup>a</sup>	Yield (kg) <sup>a</sup>	Yield (ton/ha)
IR 97705-8-1-1-1-2	83	75	19	12	10	3.61	0.93	0.77	4.73
IR 97705-8-1-2-2-1	75	77	20	15	13	3.84	0.93	0.75	4.55
IR 97708-15-1-3-3-1	77	71	18	12	11	3.53	1.01	0.79	4.89
IR 97708-15-1-3-3-2	80	72	24	13	12	3.40	0.97	0.79	4.80
IR 97708-23-1-1-1-3	75	64	20	11	10	3.53	0.96	0.78	4.79
IR 97708-23-1-1-2-2	74	66	23	15	14	3.55	0.98	0.75	4.66
IR 97709-30-1-3-3-1	77	69	19	16	16	4.11	0.77	0.83	5.07
IR 97709-30-1-3-3-2	75	74	24	13	13	3.56	1.10	0.83	5.25
IR 97709-30-1-3-3-3	77	71	22	11	11	3.26	0.95	0.76	4.73
IR 97711-25-1-1-3-3	75	62	19	12	11	3.26	0.96	0.73	4.52
IR 97711-25-1-3-1-2	70	60	21	11	9	3.25	0.94	0.73	4.50
IR 97719-22-1-3-3-3	74	77	24	16	16	3.62	0.94	0.73	4.51
IR 97721-29-1-3-3-2	72	72	21	16	16	4.19	1.19	0.74	4.59
IR 97721-29-1-3-3-3	75	76	22	15	14	4.36	1.01	0.77	4.77
IR 97721-38-3-2-1-1	74	77	24	17	17	4.40	1.01	0.75	4.63
IR 97721-38-3-2-1-2	74	72	18	16	14	3.98	1.04	0.76	4.73
IR 97721-38-3-2-1-3	65	66	17	16	15	3.98	1.01	0.75	4.67
IR 97721-43-2-1-3-1	70	67	15	14	15	4.03	1.27	0.78	4.82
IR 97721-43-2-1-3-2	70	65	20	16	14	4.16	0.99	0.77	4.74
IR 97721-43-2-2-3-1	72	61	14	16	15	4.29	1.13	0.75	4.67
IR 97721-43-2-2-3-3	77	70	21	22	21	4.73	1.36	0.93	5.78
IR 97721-45-2-1-3-3	83	73	21	19	18	4.07	1.29	0.84	5.17
Japonica1	79	71	20	12	11	3.28	0.77	0.57	3.50
MS11	76	68	19	15	14	3.18	0.83	0.58	3.55

<sup>a</sup> Average value among 30 plants.

<sup>b</sup> Average value among 3 plants.

breeding. Several virus species have been recognized to cause serious damages to rice production (Hibino 1996). Locations of resistance genes for rice viruses such as RTSV (Lee *et al.* 2010), *Rice yellow mottle virus* (Albar *et al.* 2003, Thiémélé *et al.* 2010), and *Rice strip virus* (RSV) (Hayano-Saito *et al.* 2000) have already been determined. MAS for resistance to RSV has been successfully implemented to breed RSV-resistant rice varieties (Chen *et al.* 2010).

Photoperiod sensitivity is a trait closely associated with flowering time. Rice is a facultative, short-day plant that requires certain periods of dark to flower (Ichitani et al. 1998, Yano et al. 2000). Photoperiod-sensitive japonica rice varieties in temperate regions are usually planted during periods of long day-length to ensure that plants achieve their full vegetative growth. Once subjected to short day-length (more than 14 hours of darkness), the plants start flowering (Vergara and Chang 1985). Cultivation of photoperiodsensitive japonica rice varieties under the consistently shortday condition in tropical regions usually results in short vegetative growth, early flowering, short plant height, and short panicles that eventually lead to very low yield. Japonica rice cultivars such as Dongjin, Sangju and Hwaseong are photoperiod-sensitive and yield an average of 1.2 ton/ha at 40% grain filling ratio in tropical regions. The average number of filled grains/reproductive tiller of these varieties is about 25 grains (data not shown). On the other hand, photoperiod-insensitive cultivar Japonical yields an average of 5.5 ton/ha at 80% grain filling ratio, and at 150 grains/tiller. Therefore, selection of japonica cultivars for photoperiod insensitivity is important to improve the vegetative growth of the plants and to increase crop yield.

Photoperiod insensitivity is a complex and quantitative trait (Yano et al. 2000), thus multiple molecular markers might be required for MAS for the trait. Heading date 1 (*Hd1*) confers long vegetative growth (Yano *et al.* 2000) whereas Hd3a is closely associated with photoperiodic flowering time in rice (Zhang et al. 2012). The expression of Hd3a promotes flowering under short-day length conditions, and suppresses it under long-day length conditions (Tamaki et al. 2007). At least seven other genes (Hd1, Hd2, Hd4, Hd5, Hd6, Hd7, and Hd9) are also reported to be associated with vegetative growth and flowering time (Lin et al. 1998, 2002, Yamamoto et al. 1998, 2000, Yano and Sasaki 1997), suggesting that photoperiod sensitivity is a trait too complicated for MAS application. Despite of the genetic complexity associated with photoperiod insensitivity, the phenotypes resulting from photoperiod insensitivity distinctively segregated among the japonica rice populations examined in this study (Fig. 2A, 2B). Therefore, the evaluation for measurable phenotypes such as flowering date, plant height, and panicle length appears to be a more practical option than the use of genetic markers for selection for photoperiod insensitivity. The results of this study demonstrated that MAS for RTSV resistance can be adopted to facilitate breeding of RTSV-resistant, photoperiod-insensitive rice RTSV resistance in photoperiod-insensitive rice

varieties for the stable production of rice in RTD-prone areas.

# **Literature Cited**

- Albar, L., M.-N. Ndjiondjop, Z. Esshak, A. Berger, A. Pinel, M. Jones, D. Fargette and A. Ghesquière (2003) Fine genetic mapping of a gene required for *Rice yellow mottle virus* cell-to-cell movement. Theor. Appl. Genet. 107: 371–378.
- Azzam, O., R.C. Cabunagan and T.C.B. Chancellor (1999) Methods for the evaluation of resistance to rice tungro disease. IRRI Discussion Paper 38: 1–40.
- Bajet, N.B., R.D. Daquioag and H. Hibino (1985) Enzyme-linked immunosorbent assay to diagnose rice tungro. J. Plant Prot. Trop. 2: 1124–1129.
- Cabauatan, P.Q., R.C. Cabunagan and H. Koganezawa (1995) Biological variants of rice tungro viruses in the Philippines. Phytopathology 85: 77–81.
- Cabunagan, R.C., Z.M. Flores, E.C. Coloquio and H. Koganezawa (1993) Virus detection in varieties resistant/tolerant to tungro. Int. Rice Res. Notes 18: 22–23.
- Chen, F., S.Y.Zhang, W.Y.Zhu, S.Y.Zeng, Y.C.Yang, S.J.Yuan and L.Q.Yang (2010) Improving resistance of japonica varieties Shengdao13 and Shengdao14 to rice stripe virus disease by molecular marker-assisted. Sci. Agric. Sinica 43: 3271–3279.
- Encabo, J.R., P.Q. Cabauatan, R.C. Cabunagan, K. Satoh, J.-H. Lee, D.-Y. Kwak, T.B. De Leon, R.J.A. Macalalad, H. Kondoh, S. Kikuchi *et al.* (2009) Suppression of two tungro viruses in rice by separable traits originating from cultivar Utri Merah. Mol. Plant Microbe Interact. 22: 1268–1281.
- Hayano-Saito, Y., K. Saito, S. Nakamura, S. Kawasaki and M. Iwasaki (2000) Fine physical mapping of the rice stripe resistance gene locus, *Stvb-i*. Theor. Appl. Genet. 101: 56–63.
- Hibino, H., R.D. Daquioag, E.M. Mesina and V.M. Aguiero (1990) Resistances in rice to tungro-associated viruses. Plant Dis. 74: 923–926.
- Hibino, H., K. Ishikawa, T. Omura, P.Q. Cabauatan and H. Koganezawa (1991) Characterization of rice tungro bacilliform and rice tungro spherical viruses. Phytopathology 81: 1130–1132.
- Hibino, H. (1996) Biology and epidemiology of rice viruses Annu. Rev. Phytopathol. 34: 249–274.
- Ichitani, K., Y. Okumoto and T. Tanisaka (1998) Genetic analyses of low photoperiod sensitivity of rice cultivars from the northernmost regions of Japan. Plant Breed. 117: 543–547.
- Jena, K.K. and D.J. Mackill (2008) Molecular markers and their use in marker-assisted selection in rice. Crop Sci. 48: 1266–1276.
- Lee, J.-H., M. Muhsin, G.A. Atienza, D.-Y. Kwak, S.-M. Kim, T.B. De Leon, E.R. Angeles, E. Coloquio, H. Kondoh, K. Satoh *et al.* (2010) Single nucleotide polymorphisms in a gene for translation initiation factor (eIF4G) of rice (*Oryza sativa*) associated with resistance to *Rice tungro spherical virus*. Mol. Plant Microbe Interact. 23: 29–38.
- Lin, H., M.Ashikari, U.Yamanouchi, T.Sasaki and M.Yano (2002) Identification and characterization of a quantitative trait locus, *Hd9*, controlling heading date in rice. Breed. Sci. 52: 35–41.
- Lin, S.Y., T. Sasaki and M. Yano (1998) Mapping quantitative trait loci controlling seed dormancy and heading date in rice, *Oryza sativa* L., using backcross inbred lines. Theor. Appl. Genet. 96: 997–1003.

McCouch, S.R., L. Teytelman, Y. Xu, K.B. Lobos, K. Clare, M. Walton,

B. Fu, R. Maghirang, Z. Li, Y. Xing *et al.* (2002) Development and mapping of 2240 new SSR markers for rice (*Oryza sativa* L.). DNA Res. 9: 1999–1207.

- Miura, K., M.Agetsuma, H. Kitano, A. Yoshimura, M. Matsuoka, S.E. Jacobsen and M.Ashikari (2009) A metastable *DWARF1* epigenetic mutant affecting plant stature in rice. Proc. Natl. Acad. Sci. USA 106: 11218–11223.
- Magno, R.C. and J.F. Yanagida (2000) Effect of trade liberalization in the short-grain japonica rice market: A spatial-temporal equilibrium analysis. J. Philipp. Dev. 27: 71–99.
- Philippine Rice Research Institute (2014) 60<sup>th</sup> Annual Meeting of the National Rice Cooperative Testing Project: 2013 Wet season trials, June 2–3. Philippine Rice Research Institute, Department of Agriculture, Philippines, pp. 282–290.
- Shahjahan, M., B.S. Jalani, A.H. Zakri, T. Imbe and O. Othman (1990) Inheritance of tolerance to rice tungro bacilliform virus (RTBV) in rice (*Oryza sativa* L.). Theor. Appl. Genet. 80: 513–517.
- Tamaki, S., S. Matsuo, H.L. Wong, S. Yokoi and K. Shimamoto (2007) Hd3a protein is a mobile flowering signal in rice. Science 316: 1033–1036.
- Thiémélé, D., A. Boisnard, M.-N. Ndjiondjop, S. Chéron, Y. Séré, S. Aké, A. Ghesquière and L. Albar (2010) Identification of a second major resistance gene to *Rice yellow mottle virus*, *RYMV2*, in the African cultivated rice species, *O. glaberrima*. Theor. Appl. Genet. 121: 169–179.
- Thomas, J., P.Officer and V.T.John (1980) Suppression of symptoms of rice tungro virus disease by carbendazim. Plant Dis. 64: 402–403.
- Vergara, B.S. and T.T. Chang (1985) The flowering response of the rice plant to photoperiod, In 4<sup>th</sup> Ed, International Rice Research Institute, Manila, Philippines, pp. 1–25.
- Webb, B.D., C.N. Bollich, H.L. Carnahan, K.A. Kuenzel and K.S. McKenzie (1985) Utilization characteristics and qualities of United States rice. *In*: Rice grain quality and marketing, June 1–5, International Rice Research Institute, Manila, Philippines, pp. 25–35.
- Yamamoto, T., Y. Kuboki, S.Y. Lin, T. Sasaki and M. Yano (1998) Fine mapping of quantitative trait loci *Hd-1*, *Hd-2* and *Hd-3*, controlling heading date of rice, as single Mendelian factors. Theor. Appl. Genet. 97: 37–44.
- Yamamoto, T., H. Lin, T. Sasaki and M. Yano (2000) Identification of heading date quantitative trait locus *Hd6* and characterization of its epistatic interactions with *Hd2* in rice using advanced backcross progeny. Genetics 154: 885–891.
- Yano, M. and T. Sasaki (1997) Genetic and molecular dissection of quantitative traits in rice. Plant Mol. Biol. 35: 145–153.
- Yano, M., Y. Katayose, M. Ashikari, U. Yamanouchi, L. Monna, T. Fuse, T. Baba, K. Yamamoto, Y. Umehara, Y. Nagamura *et al.* (2000) *Hd1*, a major photoperiod sensitivity quantitative trait locus in rice, is closely related to the Arabidopsis flowering time gene CONSTANS. Plant Cell 12: 2473–2484.
- Zenna, N.S., F.C. Sta Cruz, E.L. Javier, I.A. Duka, A.A. Barrion and O.Azzam (2006) Genetic analysis of tolerance to rice tungro bacilliform virus in rice (*Oryza sativa* L.) through agroinoculation. J. Phytopathol. 154: 197–203.
- Zhang, Z.-H., K. Wang, L. Guo, Y.-J. Zhu, Y.-Y. Fan, S.-H. Cheng and J.-Y. Zhuang (2012) Pleiotropism of the photoperiod-insensitive allele of *Hd1* on heading date, plant height and yield traits in rice. PLoS ONE 7: e52538.