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ERRATUM

K. K. Jena · J. U. Jeung · J. H. Lee · H. C. Choi
D. S. Brar

High-resolution mapping of a new brown planthopper (BPH) resistance gene, *Bph 18* (t), and marker-assisted selection for BPH resistance in rice (*Oryza sativa* L.)

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Figure 2 and Table 5 were rendered incorrectly. The correct version are given here.

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K. K. Jena · J. U. Jeung · D. S. Brar
Plant Breeding, Genetics, and Biotechnology Division,
International Rice Research Institute, DAPO Box 7777,
Metro Manila, Philippines

J. H. Lee · H. C. Choi · K. K. Jena (✉) · J. U. Jeung
Genetics and Breeding Division,
National Institute of Crop Science, RDA,
Suwon 441-857, South Korea
E-mail: kjena@rda.go.kr
Tel.: +82-31-2906871
Fax: +82-31-2948185

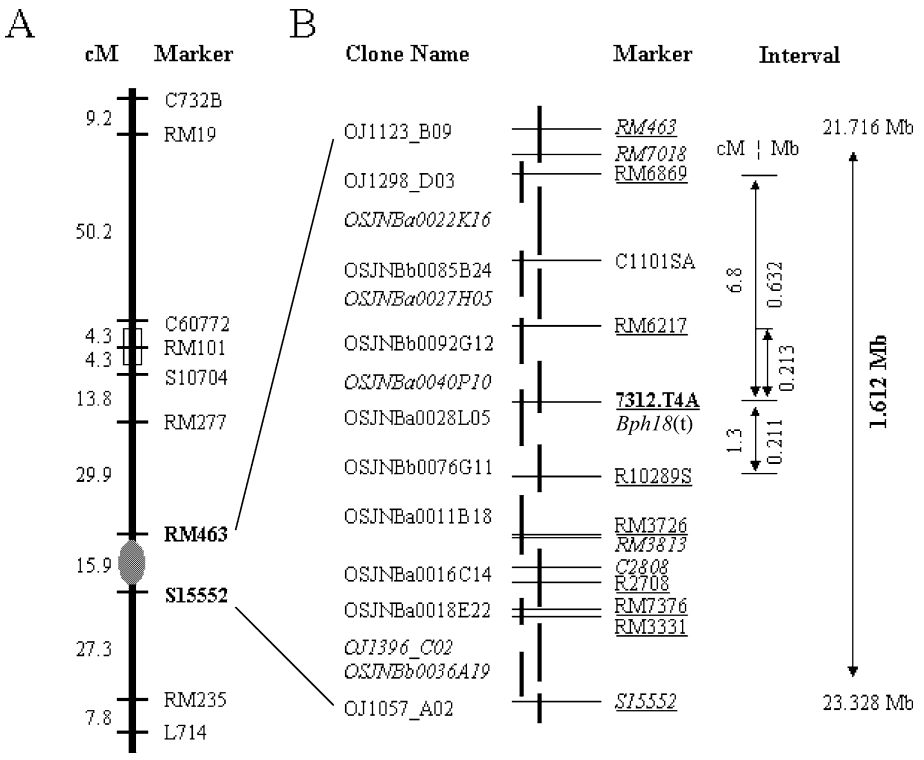

Fig. 2 **a** Linkage map skeleton of rice chromosome 12 showing ten polymorphic anchor markers and the putative R-gene location obtained by association analysis between marker genotypes of F2 progenies. Quantitative phenotyping of F_3 lines (single-locus ANOVA) is indicated by two R- or S-associated markers (in *boldface*; RM463 and S15552). The *open rectangle* indicates the centromere region. **b** High-resolution map of *Bph18*(t) locus showing 15 Nipponbare BAC clones corresponding to the 15.9 cM interval delimited by RM463 and S15552. The BAC clones, which were not tested with any DNA marker, are indicated in *italics*. The negative markers for the integration events of *O. australiensis* segmented into IR31917-45-3-2 (*progenitor line*) are indicated in *italics*. The R- or S-associated DNA markers, polymorphic between Jinbubyeo and IR65482-7-216-1-2, are *underlined*. The PCR primer set for the 7312.T4A (in *boldface*) marker tagging the *Bph18*(t) gene originated from Nipponbare BAC clone OSJNBa0028L05. The intervals between tested loci were estimated by using 94 F_2 mapping populations and corresponding physical distances (cM and Mb) were calculated based on the genome sequence information of Nipponbare chromosome 12

Table 5 *e*-Landing procedure to determine the most putative chromosomal region of the *Bph18*(t) locus through bioassay of F_2 progenies and genotyping susceptible progenies with DNA markers representing each BAC clone region

Collections [b]			No	Tested chromosomal regions [a]																			
				Centromere region						OJ1298_D03 → OSJNBa0028L05 ← OSJNBb0076G11									OSJNBa0016C14				
				RM101			S10704/ *Hinf*I			RM6869			7312.T4A/ *Hinf*I			R10289S/ *Rsa*I			R2708/ *Hae*III		
				A	H	B	A	H	B	A	H	B	A	H	B	A	H	B	A	H	B
After infestation (days)	Early	3rd	6	3	2	1	3	1	2	6	0	0	6	0	0	5	1	0	5	1	0
		5th	8	6	1	1	5	2	1	6	2	0	7	1	0	7	1	0	6	2	0
		7th	22	13	9	0	14	8	0	20	2	0	21	1	0	20	2	0	19	3	0
		9th	13	5	6	1	7	5	1	7	6	0	7	6	0	8	5	0	7	5	1
		Subtotal	**49**	**27**	**18**	**3**	**29**	**16**	**4**	**39**	**10**	**0**	**41**	**8**	**0**	**40**	**9**	**0**	**37**	**11**	**1**
	Late	12th	26	6	17	4	5	17	4	3	15	8	5	13	8	3	15	8	3	15	8
		15th	11	3	6	2	3	6	2	2	7	2	6	3	2	3	6	2	3	6	2
		Subtotal	37	9	23	6	8	23	6	5	22	10	11	16	10	6	21	10	6	21	10
		Total	86	36	41	9	37	39	10	44	32	10	52	24	10	46	30	10	43	32	11
Genotypic expression [c]				2 (B → A) 2 (H → A)						7 (H → A)			6 (A → H) 1 (H → A)			4 (A → H) 2 (H → B)					

[a] Three chromosomal regions were selected for testing: 1) the presence of *Bph10* near the centromere region, 2) the 1.056 Mb interval delimited by two polymorphic DNA markers (RM6869 and R10289S) between the parental lines, Jinbubyeo and IR65482-7-216-1-2, and 3) another subterminal region tagged by R2708. The tested chromosomal regions are also illustrated in Fig. 2.

[b] To optimize the screening duration for fine mapping of *Bph18*(t), time-based collection of susceptible seedlings was conducted. Out of 245 F_2 seedlings tested, 86 susceptible seedlings were collected (6 time-point collections during 15 days after infestation). The genotyping data sets of 49 seedlings (until fourth-time collections) were used to judge the most putative location of *Bph18*(t). A and B are homozygous F_2 individuals for Jinbubyeo and IR65482-7-216-1-2, respectively, and H is heterozygous individuals.

[c] All 86 collected seedlings were individually checked for the changed genotypes at each switching position of tested DNA markers.