26. Identification of new genes for Brown Planthopper resistance in rice introgressed from *O. glaberrima* and *O. minuta*

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Brown planthopper (*Nilaparvata lugens* Stål.) is one of the most destructive pests of rice through out Asia. It causes severe yield reduction by directly sucking the plant sap and acting as a vector of virus diseases such as rice grassy stunt and ragged stunt (Khush and Brar, 1991). Host plant resistance has been recognized as important strategy to control BPH damage in contrast to the chemical control. The genetics of BPH resistance is well studied and as many as 21 major genes have been identified in cultivated and wild species (Qifa Zhang, 2007 and Fujita et al., 2008). Among the BPH biotypes prevailing in South East Asia, biotype 4 is the most destructive and distributed over the Indian sub continent (Heinrichs, 1986). The biotype variations results in overcome of resistance to several major genes, therefore, the identification of additional BPH resistance genes is required to address the issue of durable resistance.

The repeated screening over the years of different donors with known gene, against local BPH biotype available at the Directorate of Rice Research, Hyderabad, India, recorded consistent resistance in Rathu Henati (*Bph3* & *Bph17*), Swarnalatha (*Bph 6*) and ADR 52 (*bph20*(t) & *Bph21*(t)). While rest of other donors Mudgo (*Bph1*), IR 56 (*Bph3*), Pokkali (*Bph9*), IR 65482-4-136-2-2 (*Bph10*), IR 65482-7-216-1-2 (*Bph18*) showed either susceptible or moderate resistance (Table 1).

We screened two introgression lines (IR 75870-5-8-5-B-1-B) and IR 75870-5-8-5-B-2-B) derived from the cross IR64 x *O. glaberrima* (TOG 5674) and two introgression lines (IR 71033-62-15 and IR 71033-121-15) derived from the cross IR 31917-45-3-2 x *O. minuta* (Acc. 101141) generated at IRRI, Philippines, along with the parents and the resistant (PTB33 and Sinnasivappu) and the susceptible (TN1) checks against local biotype at seedling stage using standard seed box technique. Twenty days old seedlings were infested with second and third instar nymphs at the rate of approximately 4-5 nymphs/seedling. Damage on 0-9 scale was scored for individual plants after 3 weeks of infestation when TN1 was completely wilted (Heinrichs et al., 1985).

The two introgression lines derived from *O. glaberrima* and the parent *O. glaberrima* (TOG 5674) showed resistance reaction over the years in replicated screening, while the recurrent parent IR 64 possessing *Bph1* gene along with minor genes recorded moderate level of resistance indicating that the genes for higher level of BPH resistance in the introgression lines have introgressed from *O. glaberrima* (Table 1).

The other two introgression lines (IR 71033-62-15 and IR 71033-121-15) derived from *O. minuta* also showed resistance reaction in repeated screening, while its recurrent parent IR 31917-45-3-2 showed susceptible reaction, suggesting that the gene for BPH resistance in both the lines introgressed from *O. minuta*. The crosses were made between the susceptible variety BPT 5204 x IR 64, BPT 5204 x IR 75870-5-8-5-B-1-B, BPT 5204 x IR 75870-5-8-5-B-2-B, with recurrent parent IR 64 x IR 75870-5-8-5-B-1-B, IR64 x IR 75870-5-8-5-B-2-B and between both introgression lines IR 75870-5-8-5-B-1-B x IR 75870-5-8-5-B-2-B, to study the inheritance of resistance. The introgression line IR 71033-121-15 derived from *O. minuta* was also crossed with susceptible variety BPT 5204 and its recurrent parent IR 31917-45-3-2. All the F_2 populations along with the recurrent parent, donor (*O. glaberrima*), susceptible variety BPT 5204, susceptible check TN-1 and resistant check PTB 33 were screened using standard seed box technique. The results showed that the F_2 populations of BPT 5204 x IR 75870-5-8-5-B-1-B and BPT 5204 x IR 75870-5-8-5-B-2-B segregated in 3:1 ratio (resistant: susceptible) indicating the inheritance of monogenic dominant gene for BPH resistance in both the lines. While the F_2 plants of BPT 5204 x IR64 segregated in 1:3 ratio (resistant: susceptible) indicating the involvement of recessive gene in IR 64 for BPH resistance. The segregation pattern in F_2 population of IR 64 x IR 75870-5-8-5-B-1-B and IR 64 x IR 75870-5-8-5-B-2-B was observed in 13:3 ratio (resistant : susceptible) indicating the inheritance of one dominant and one recessive gene for BPH resistance. While the cross of IR 75870-5-8-5-B-1-B x IR 75870-5-8-5-B-2-B did not segregate for susceptible plant indicating that both the introgression lines have same gene introgressed from *O. glaberrima* (Table 2). Though the *O. glaberrima* belongs to AA genome as cultivated species

(*O. sativa* var *indica*) but the several incompatibility barriers restrict the natural gene flow from *O. glaberrima* into *indica* suggested that the dominant gene for BPH resistance in IR 75870-5-8-5-B-1-B and IR 75870-5-8-5-B-2-B introgressed from *O. glaberrima* is new and tentatively designated as *Bph 22*(t). We are in the process of mapping this gene with molecular markers.

Table 1 Reaction to gene donors, introgression lines, recurrent parent and checks against local BPH biotype-4

Donors/ introgression lines	Parentage/Acc no.	Genes present	BPH damage score in 0-9 scale					Reaction
			2007	2006	2005	2003	Mean	
Mudgo	Acc. 6663	*Bph1*	7.0	6.3	6.0	5.0	6.1	S
IR 56		*Bph3*	8.5	7.0	7.9	8.2	7.9	S
Rathu Henati	Acc. 11730	*Bph3 & Bph17*	3.0	3.2	3.4	2.8	3.1	R
Swarnar nalata	Acc. 33964	*Bph6*	3.0	3.5	NA	5.0	3.8	R
Pokkali		*Bph9*	9.0	8.0	7.0	7.6	7.9	S
IR 65482-4-136-2-2	IR 31917-45-3-2-2 / *O.australiensis*//2* IR31917-45-3-2-2	*Bph10*	9.0	8.2	8.0	NA	8.4	S
IR 65482-7-216-2	IR 1529-680-3-2 / *O.officinalis* //2*IR1529-680-3-2	*Bph18*	5.3	3.3	3.4	NA	4.0	MR
ADR 52		*Bph21*(t) & *bph20*(t)	1.3	3.1	2.3	NA	2.2	R
TOG 5675	*O.glaberrima*	--	1.8	1.4	2.1	NA	1.8	R
IR 75870-5-8-5-B-1-B	IR 64/TOG 5675//IR 64	--	2.2	2.1	3.1	NA	2.5	R
IR 75870-5-8-5-B-2-B	IR 64/TOG 5675//IR 64	--	2.3	2.4	2.9	NA	2.5	R
IR 64 (RC)		--	4.4	4.2	5.4	3.6	4.4	MR
IR 71033-62-15	IR 31917-45-3-2-2/ *O.minuta* //2*IR 31917-45-3-2-2	--	2.3	3.1	1.9	NA	2.4	R
IR 71033-121-15	IR 31917-45-3-2-2 / *O.minuta* //2*IR 31917-45-3-2-2	--	2.1	2.7	2.4	NA	2.4	R
IR 31917-45-3-2 (RC)		--	9.0	8.6	7.9	NA	8.5	S
PTB 33 (resistant)		--	1.2	2.1	1.3	1.2	1.5	R
Sinnasivappu (resistant)	Acc15444		1.6	1.2	1.4	1.6	1.5	R
TN-1 (susceptible)		--	9.0	NA	9.0	9.0	9.0	S
BPT 5204 (susceptible)		--	9.0	NA	8.8	9.0	8.9	S

RC: recurrent parent, R: resistant, MR: moderately resistant, S: susceptible, NA: not screened.