28. A new gene for gall midge resistance in rice variety MR1523

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The Asian rice gall midge *Orseolia oryzae* (Wood-Manson) is a serious pest of rice in certain regions of south, central and east India causing significant yield loss mainly during *kharif* season. Breeding rice varieties with pest resistance has been a viable, ecologically acceptable approach for the management of the gall midge. However, rapid development of virulent biotypes capable of overcoming the host plant resistance has been posing problem in recent years. Systematic germplasm evaluation has led to the identification of important sources of resistance like Eswarakora, Ptb18, Ptb21, Siam29, Leuang152 etc. (see, Bentur et al., 2003) which have been extensively used in breeding resistant varieties. Genetic studies have identified, so far, 10 major genes conferring resistance (Kumar et al., 2005). Most of the 60 plus gall midge resistant rice varieties developed to date contain one of the three major genes *viz*., *Gm1*, *Gm2* and an unidentified gene(s) in Ptb21 conferring immune level of resistance. Seven distinct gall midge biotypes have been characterized so far (Vijaya Lakshmi et al., 2006), some of them being selected as direct consequence of extensive cultivation of these varieties. In most of the studies, resistance to gall midge has been found to be conferred by a single dominant or (as in case of *gm3*) a recessive gene (Kumar et al., 2005). Exceptionally, sources deriving resistance from Ptb18 and Ptb21 have displayed complex pattern of inheritance of resistance (Kalode and Bentur, 1989). The rice variety MR1523 derives its gall midge resistance from Ptb18 & Ptb21 which have contributed resistance in 25% of the released varieties. But genetics of resistance in this breeding line has not been studied. This paper attempts to note inheritance of gall midge resistance in MR1523 and we note that possibly a new gene present in this variety confers resistance against gall midge biotype 4.

The rice variety CR57-MR1523 (Ptb18/Ptb21//IR8), developed at Central Rice Research Institute, Cuttack, India was crossed with the susceptible check TN1 as well as with the rice varieties with known resistance genes *viz*., W1263 (with *Gm1*), Phalguna (*Gm2*), RP2068 (*gm3*), Abhaya (*Gm4*), ARC5984 (*Gm5*) and with other resistance sources with unknown gene(s) like Bhumansan, NHTA8, Banglei, Aganni and ARC6605. F_3 families consisting of progeny from individual F_2 plants were evaluated in field at Ragolu and Warangal and in greenhouse at DRR against gall midge biotypes 1, 3 and 4. Individual families were scored for resistance.

Results revealed a complex segregating pattern of resistance depending upon the biotype used for evaluation (Table 1). Families derived from the cross MR1523/TN1 showed segregation ratio of 13 resistant: 3 susceptible families when evaluated against gall midge biotype (GMB)1, 15:1 ratio against GMB3 and 3:1 ratio against GMB4 in the greenhouse test at DRR, Hyderabad. While all the families were found susceptible in the field test at Warangal, these segregated in 3:1 ratio in the field test at Ragolu. Crosses between MR1523 and rice varieties with known and unknown gall midge resistance genes did not show any distinct segregation pattern (data not shown). This suggested higher order of interaction.

Table 1 Reaction of F_3 families derived from the cross between MR1523 and TN1 against rice gall midge biotypes 1, 3 and 4 in greenhouse at DRR, Hyderabad

Cross	Biotype	Number of F_3 families			Ratio (R:S)	χ^2 (cal) value
		Tested	Resistant	Susceptible		
MR1523/ TN1	1	197	158	39	13:3	0.1417
MR1523/ TN1	3	194	188	6	15:1	3.3
MR1523/ TN1	4	187	139	48	3:1	0.0445
χ^2 (tab) value: 3.84(0.05), 6.63(0.01)						

R: resistant including heterozygous; S: susceptible

It is obvious from these results that genes controlling gall midge resistance in MR1523 interacted differently against different biotypes tested. While two genes contributed resistance against biotype 1 and 3, only one gene was effective against biotype 4. These two genes interacted differently against biotypes 1 and 3. For biotype 1 the interaction appeared as one dominant and one recessive gene while for biotype 3 two dominant gene interaction was evident. For biotype 4, a single dominant gene segregation ratio was observed. We set to identify this gene.

The rice varieties with known resistance genes including the susceptible variety (TN1) were screened in the greenhouse against gall midge biotypes 1, 4 and 4M (Vijaya Lakshmi et al., 2006). Against gall midge biotype 1, all the ten genes were found to confer resistance. Against biotype 4 only three genes *viz*., *gm3* (RP2068), *Gm4* (Abhaya) and *Gm8* (Jhitpiti) provided resistance. We retested these varieties along with MR1523 against these three biotypes. MR1523 recorded resistance against biotypes 1 and 4 but was susceptible against biotype 4M. This suggested that the single dominant gene in MR1523 conferring resistance to biotype 4 is not alleleic to *Gm4* or *Gm8*. Obviously, this gene would not be allelic to the recessive gene *gm3* also.

Since allelic tests through crosses involving MR1523 with the other known gene sources did not reveal identity of the gene in MR1523, we used SSR markers reported to be closely linked with different gall midge resistance genes (Bentur et al., 2003) to tag this gene. A RIL population derived from MR1523/ TN1 cross in the tenth generation was used. In all, 530 lines from these RILs were phenotyped against gall midge biotype 4 and resistant and susceptible lines were identified. DNA from leaf samples from 12 highly resistant (with nil damage) and 12 highly susceptible (with 100% plant damage) were separately pooled. A set of SSR markers were used to amplify genomic DNA from the resistant and susceptible parents and the resistant and susceptible lines.

Earlier reported results showed lack of gene specific amplification with MR1523 in respect of RM444 and RM219 markers linked to *Gm1* gene and RM241, RM317 linked to *Gm2* gene (Himabindu et al., 2007). Further testing with RM547 and RM22687 linked to *Gm4* gene also did not show desired amplification specific to the gene (data not shown). However, two SSR markers RM235 and RM28706 mapped on chromosome 12 displayed polymorphism between MR1523 and TN1 (Fig. 1). This polymorphism was also seen between resistance and susceptible selected lines. Thus, it is likely that the gall midge resistance gene in MR1523 is on chromosome 12 and hence is not likely to be allelic to *Gm4* and *Gm8*, both located on chromosome 8 (Mohan et al., 1997 Jain et al., 2004). We propose to designate this new gene as Gm11(t). We are analyzing the rest of the mapping population for computing linkage precision.

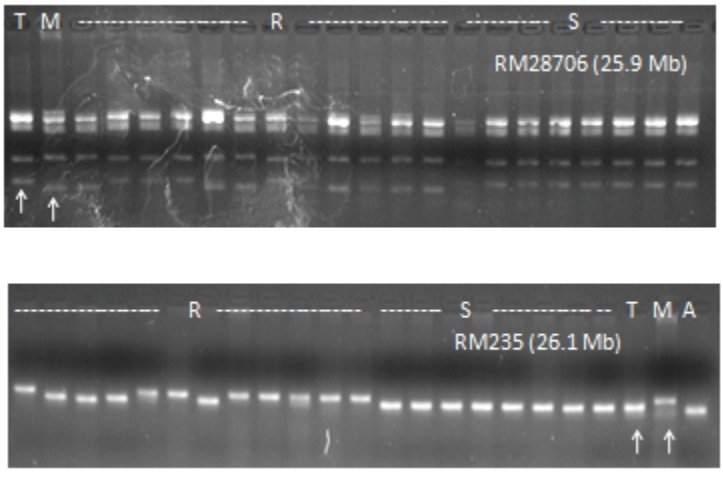

Fig. 1 Amplification pattern noted for SSR markers RM28706 and RM235 with genomic DNA from rice varieties TN1 (T), MR1523 (M), Abhaya (A) and 12 resistant (R) and 8 susceptible (S) lines from RILs generated from the cross TN1/MR1523. Polymorphic bands are indicated by arrows.

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