Indian J. Genet., **65**(4): 313-314 (2005)

Short Communication

Reaction of gene differential rice varieties against gall midge *Orseolia oryzae* (Wood-Mason) biotypes in the greenhouse

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(Received: November 2004; Revised: August 2005; Accepted: November 2005)

The Asian rice gall midge, *Orseolia oryzae* (Wood-Mason) is a serious pest of rice in India. This pest has been contained during the last three decades through cultivation of over 50 high yielding resistant rice varieties suited to different pest endemic areas within the country [1]. However, extensive cultivation of a single variety with one major gene for resistance over a large area resulted in rapid development of virulent biotypes capable of overcoming host-plant resistance. A reoriented breeding strategy to counter the situation involves development of gene pyramids with two or more resistance genes in a single cultivar through marker aided selection approach. So far, ten gall midge resistance genes have been identified and designated [1-3]. However, the reaction of different gall midge biotypes against these specific genes is not completely known. This information is essential to make an informed choice of genes for pyramiding in a single cultivar to confer durable gall midge resistance. Hence, the differential rice varieties with known genes against gall midge biotypes 1, 3 and 4 were screened under greenhouse conditions at the Directorate of Rice Research (DRR), Hyderabad and the findings are presented in this paper.

Gall midge culture is being maintained in the greenhouse at DRR since 1975. This population, initially collected from the rice fields around DRR, is found to be least virulent and based on the reaction of the standard set of differentials is designated as biotype 1. During the course of culturing, the population is periodically replaced with adults collected afresh from field. This biotype is maintained on the rice TN1 which has no gall midge resistance gene. Biotype 4 population was established from the field population collected from Srikakulam of Andhra Pradesh during 1986 and replaced from fresh collection during 1998. This population is virulent on rice varieties containing gall midge resistance genes *Gm1* and *Gm2* and is designated as biotype 4. This population is maintained on rice variety Kavya (with *Gm1* gene). Population of gall midge collected from Jagtiyal in Karimnagar district of Andhra Pradesh during 1993 and replaced with fresh collections during 1998 represented biotype 3. It has virulence against rice varieties with *Gm2* gene and is maintained on Phalguna variety with *Gm2* gene. The three biotype cultures are maintained in the air-cooled greenhouse under physical isolation. Since only the adult flies are mobile, adult collection and subsequent release on new set of plants is done in confined rooms using cages. Further, to monitor the purity of the population, suitable check lines are maintained in trays with rice seedlings for rearing of cultures and for evaluation of rice varieties.

A set of differential rice varieties used in genetic characterization of resistance at the Indira Gandhi Krishi Visva Vidyalaya, Raipur is used in the present study. Greenhouse evaluation protocols were the same as described earlier [4]. Three replications were maintained. Plant damage was recorded 25 days after adult release when all the susceptible plants had galls. Total plants and damaged plants were recorded. A test was considered valid only when at least 75% of the susceptible check TN1 plants recorded damage. Test lines recording nil or less than 10% plant damage were rated as resistant while higher level of damage was rated as susceptible. In view of marginal level (12-15%) of damage noted against some of the differentials, tests were repeated against biotype 1 and 4 during 2005. Test against biotype 3 could not be done during 2005. The plants were also dissected after noting plant damage to see the nature of resistance on basis of presence or absence of hypersensitive reaction (HR). Plants with tissue necrosis at the apical meristem region were counted as HR+ plants while those which did not show HR but were with dead maggots were rated as HR plants [5]. This rating was on qualitative basis since few of the plants escaped damage or in some cases the dead maggots could not be observed.

Pooled data from greenhouse test during 2004 and 2005 (Table 1) clearly indicated that *gm3*, *Gm4* and *Gm8* genes conferred resistance against all the three biotypes used in the test. While *Gm1* conferred resistance against biotypes 1 and 3, *Gm2* did so only against biotype 1. Interestingly, *Gm5*, *Gm7* and *Gm10* genes showed reaction pattern similar to that displayed by *Gm2* gene, whereas *Gm6* and *Gm9* had reaction pattern similar to *Gm1*. Thus the following three basic

Table 1. Reaction of gene differentials from Raipur against gall midge biotypes 1,3 and 4 in greenhouse at DRR, Hyderabad tested during 2004 and 2005

Differential	Gene	2004						2005			
		Biotype 1		Biotype 3		Biotype 4		Biotype 1		Biotype 4	
		DP[$]	TP	DP	TP	DP	TP	DP	TP	DP	TP
Samridhi	*Gm1*	0	30	0	39	17	24	0	26	16	22
Phalguna	*Gm2*	0	25	29	42	23	25	0	29	18	21
RP 2068-18-3-5	*gm3*	0	34	3	39	0	34	0	20	0	14
Abhaya	*Gm4*	0	39	0	47	0	37	0	25	0	16
ARC 5984	*Gm5*	0	43	26	37	14	20	0	17	20	23
Dukong 1	*Gm6*	0	42	3	40	21	28	1	27	19	20
RP2333-156-8	*Gm7*	0	41	25	36	18	25	0	22	19	19
Jhitpiti	*Gm8*	0	42	0	45	4	33	1	27	0	29
Madhuri 9	*Gm9*	0	49	1	49	26	28	0	30	13	20
BG 380-2	*Gm10*	1	44	16	22	28	31	2	31	25	25
INDRC-1351	?	6	40	6	43	29	32	3	26	11	26
TN1	None	44	56	39	41	34	37	23	26	20	23

DP[$]-Damaged plants from pooled data; TP-Total plants tested

reaction patterns were evident through this evaluation of differentials represented by *Gm1*, *Gm2* and *Gm4* gene reactions: Group 1: *Gm1, Gm6 and Gm9*; Group 2: *Gm2, Gm5, Gm7 and Gm10*; Group 3: *Gm4, gm3 and Gm8*.

The plants were also dissected to see the nature of resistance. The differentials possessing *Gm2, gm3, Gm4, Gm5, Gm6, Gm7, Gm8* and *Gm10* showed HR+ mechanism of reaction and those which have *Gm1* and *Gm9* showed HR reaction. Thus, reaction pattern-wise and on basis of nature of resistance *Gm1* and *Gm9* genes appeared identical. However, it may be noted that Madhuri 9 carrying *Gm9* gene is a sister line of susceptible cultivar Madhuri [2] and may be considered a spontaneous mutant. Mutations leading to induction of gall midge resistance have been noted in cases of land race Orumundakan and American rice Calrose. Among the biotypes, Biotype 4 had greater degree of virulence while biotype 1 had the least virulence. All the three biotypes were virulent on TN1 containing no resistance gene.

The best known feature of gall midge-grass interactions is the genetic variability associated with both the plant's defense response to gall midge and the gall midge's response to plant's resistance [6]. As in many insect-plant interactions, genetic variability arises from R genes in the plant and *avr* (avirulence) genes in the gall midge. In most cases, grass R genes and gall midge *avr* genes fit the gene-for-gene concept of co-evolutionary interactions between plants and their enemies. It is known that virulence in gall midge biotypes 3 and 4 against Phalguna with *Gm2* gene is conferred by a single recessive gene [7] which is sex linked [8]. Thus it may be of interest to study if this gene, designated as *avrGm2*, will also provide virulence against *Gm5, Gm7* and *Gm10* genes in the same group. Alternatively, separate *avr* genes may be involved. INDRC 1351 was included in this set since the studies at Raipur are suggestive of involvement of yet another new gene in the differential. However, the results showed low but > 10% damage in this differential against biotypes 1 and 3 during 2004 and against biotype 1 during 2005 also. Dukong 1 containing *Gm6* gene was found to be resistant to biotypes 1 and 3 in the present evaluation contrary to the earlier observation that this gene was not effective against Indian biotypes of the gall midge [2, 9]. This disparity may be attributed to the seed source, seed purity and the gall midge populations. Reaction of the gene differentials against remaining three of the six biotypes prevailing in the country is being investigated through All India Coordinated Rice Improvement program of DRR.

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