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GENETICS OF RESISTANCE TO RICE GALL MIDGE (*ORSEOLIA ORYZAE*)

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ABSTRACT

A representative set of donor parents of rice with consistently high level of resistance to different biotypes of rice gall midge, *Orseolia oryzae* (Wood Mason) (Diptera : Cecidomyiidae), was crossed to T(N)1, the susceptible check and the F_1's F_2's and F_3's along with parents were screened under glasshouse as well as field conditions against the biotypes 1, 2 and 4 to understand the mode of inheritance of biotype-specific resistance. Crosses were also made among the parents resistant to different biotypes and the F_1, F_2 and F_3 plants were screened to study the allelic relationships of the biotype-specific resistance genes. The inheritance studies revealed a simple mode of inheritance with resistance being dominant over susceptibility. Reciprocal combinations in selected crosses revealed no maternal influence in the manifestation of resistance in respect of all the biotypes studied. Allelic relationship studies revealed that the dominant gene governing resistance against biotype 1 in Eswarakora, W 1263 and NHTA 8, designated as *Gm1*, was nonallelic and independent of the gene *Gm3* conferring resistance in Bhumansan, Banglei and T 1432. Against biotype 2, the gene *Gm4* conferring resistance in Bhumansan is nonallelic to the resistance gene *Gm5*, which is allelic in NHTA 8, Banglei and T 1432. The dominant resistance gene *Gm6* against biotype 4 in NHTA 8 is nonallelic to the resistance gene *Gm7* in Banglei, T 1432 and T 1477, which is allelic in them.

Key words : Gall midge, rice, biotype, resistance.

Rice gall midge, *Orseolia oryzae* (Wood-Mason) (Diptera : *Cecidomyiidae*) is one of the major pests of rice. In India, crop losses from 10 to 100% have been reported [1] valued at US $ 550 million. Genetic resistance has been exploited since the discovery of resistance sources like Eswarakora, W 1263 etc. [2]. All earlier attempts to understand the genetics of resistance had been confined to the pest *per se* in endemic regions, not taking into consideration, the existence of distinct biotypes[3].

The present study aims to obtain basic information on the genetics of biotype-specific resistance and allelic relationships among the resistance genes using two different indices of pest reaction, under field and glasshouse conditions.

MATERIAL AND METHODS

The experimental material comprised F_1, F_2 and F_3 populations of (a) crosses involving seven donors resistant to one or more biotypes of the pest with Taichung(Native)1, which is susceptible to all the known biotypes of rice gall midge, and (b) crosses among the resistance donors (Table 1). Although manifestation of

Table 1. Pest reaction of the parent varieties used in the study of genetics of resistance to gall midge biotypes in rice

Parent variety	Source	Resistance to gall midge biotypes*
Taichung(Native)1	Taiwan	Susceptible to all biotypes
Eswarakora	Andhra Pradesh, India	Resistant to biotype 1
W 1263	Andhra pradesh, India	Resistant to biotype 1
Bhumansan	India	Resistant to biotypes 1 & 2
NHTA 8	Tripura, India	Resistant to biotypes 1, 2 & 4
Banglei	India	Resistant to biotypes 1, 2 & 4
T 1432	Tamil Nadu, India	Resistant to biotypes 1, 2 & 4
T 1477	Tamil Nadu, India	Resistant to biotypes 1, 2 & 4

*Biotype 1 : Endemic to Warangal district, Andhra Pradesh and Madhya Pradesh

Biotype 2 : Endemic to Orissa

Biotype 3 : Endemic to Bihar and Manipur

Biotype 4 : Endemic to Srikakulam, Vizianagaram and Visakhapatnam districts of Andhra Pradesh

resistance in the donors was of two kinds, viz., hypersensitive negative as in Eswarakora, W 1263 and NHTA 8, and hypersensitive positive as in Bhumansan, Banglei, T 1432 and T 1477, the mode of inheritance was studied on the basis of overall expression of resistance i.e., even if the plants showed a single silver shoot, they were rated as susceptible. The experimental populations (F_1, F_2 and F_3 along with parents) were exposed to biotypes 1 and 4 at the Directorate of Rice Research (DRR), Hyderabad, under glasshouse conditions and to biotypes 2 and 4 under field conditions at Central Rice Research Institute (CRRI), Cuttack, and Agricultural Research Station, Ragolu (Andhra Pradesh), respectively. The test material comprised 10-15

plants for F_1, 200-500 plants for F_2 and 85-100 lines for F_3. Mass screening techniques developed for greenhouse[4] and field conditions [5] were followed to distinguish resistant plants from susceptible. T(N)1 was used as the susceptible check against all the biotypes, while Phalguna as the differential for biotype 4. Observations on the test material were recorded when the susceptible check showed 100% infestation. The F_1's and F_2's were screened for resistance/susceptibility reaction on single plant basis and the F_3 populations on line basis as resistant, segregating or susceptible.

The phenotypic observations on resistance and susceptible plants in F_2 and F_3 were subjected to χ^2 test of significance.

RESULTS AND DISCUSSION

INHERITANCE OF BIOTYPE-SPECIFIC RESISTANCE

The resistance-susceptibility reaction of F1's and segregating populations of the crosses involving different donors of resistance and susceptible T(N)1 against different biotypes was as under:

Biotype 1 : the F_1s of T(N)1 with Eswarakora, W 1263, Bhumansan, NHTA 8, Banglei and T 1432 were resistant. The F_2 populations segregated in the ratio of 3R : 1S (Table 2). F_3 families were in the ratio of 1R (homozygous dominant) : 2 segregating: 1S (homozygous recessive), confirming the F_2 results.

Table 2. Reaction of F_1, F_2 and F_3 populations derived from the crosses of T(N)1 with six gall midge resistant varieties to biotype 1 under glasshouse conditions at DRR, Hyderabad

Cross	F_1 reaction	F_2 segregation		χ^2 (3 : 1)	Pattern of F_3 segregation			χ^2 (1:2:1)
		R	S		R	Segr.	S	
T(N) 1 × Eswarakora	R	336	104	0.436	22	45	19	0.395
T(N)1 × W 1263	R	338	107	0.216	22	51	26	0.290
T(N)1 × Bhumansan	R	282	92	0.032	22	53	24	0.575
T(N)1 × NHTA 8	R	308	96	0.330	19	44	22	0.320
T(N)1 × Banglei	R	306	96	0.268	24	51	21	0.562
T(N)1 × T 1432	R	268	92	0.059	27	52	21	0.640

Biotype 2 : The F_1's of T(N)1 with Eswarakora and W 1263 were susceptible, while those with Bhumansan, NHTA 8, Banglei and T 1432 were resistant. The F_2 populations

of the latter crosses segregated in the ratio of 3R : 1S. The F_3 families segregated as 1 true breeding R : 2 segregating : 1 true breeding S (Table 3).

Table 3. Reaction of F_1, F_2 and F_3 populations derived from the crosses of T(N)1 with six gall midge resistant varieties to biotype 2 under field conditions at Cuttack

Cross	F_1 reaction	F_2 segregation		χ^2 (3 : 1)	Pattern of F_3 segregation			χ^2 (1:2:1)
		R	S		R	Segr	S	
T(N)1 × Eswarakora	S	0	58	-	0	0	85	-
T(N)1 × W 1236	S	0	66	-	0	0	99	-
T(N)1 × Bhumansan	R	142	45	0.087	25	46	28	0.680
T(N)1 × NHTA 8	R	118	41	0.052	21	44	20	1.160
T(N)1 × Banglei	R	144	46	0.063	21	49	26	0.560
T(N)1 × T 1432	R	184	56	0.355	24	54	22	0.720

Biotype 4 : The F_1's of the crosses among Eswarakora, W 1263 and Bhumansan with T(N)1 were susceptible. F_2 populations and F_3 families of these crosses also remained susceptible to the biotype in glasshouse at DRR as well as under field conditions at ARS, Ragolu (Tables 4, 5). The F_1s of crosses of NHTA 8, Banglei, T 1432 and T 1477 with the susceptible parent were resistant. Their F_2 populations segregated in the ratio of 3R : 1S, while the ratio of true breeding resistant, segregating and true breeding susceptible F_3 families was 1 : 2 : 1, confirming the F_2 results.

Table 4. Reaction of F_1, F_2 and F_3 populations derived from the crosses of T(N)1 with gall midge resistant varieties to biotype 4 under glasshouse conditions at DRR, Hyderabad

Cross	F_1 reaction	F_2 segregation		χ^2 (3 : 1)	Pattern of F_3 segregation			χ^2 (1 : 2 : 1)
		R	S		R	Segr	S	
T(N)1 × Eswarakora	S	0	167	-	0	0	85	-
T(N)1 × W 1263	S	0	172	-	0	0	99	-
T(N)1 × Bhumansan	S	0	151	-	0	0	99	-
T(N)1 × NHTA 8	R	244	81	0.902	19	46	20	0.600
T(N)1 × Banglei	R	260	84	0.062	26	47	23	0.230
T(N)1 × T 1432	R	288	88	0.510	28	47	25	0.440
T(N)1 × T 1477	R	259	80	0.355	14	34	16	0.790

Table 5. Reaction of F_1, F_2 and F_3 populations derived from the crosses of T(N)1 with gall midge resistant varieties to biotype 4 under field conditions at Ragolu, Andhra Pradesh

Cross	F_1 reaction	F_2 segregation		χ^2	Pattern of F_3 segregation			χ^2
		R	S	(3 : 1)	R	Segr	S	(1:2:1)
T(N)1 × Eswarakora	S	0	387	-	0	0	85	-
T(N)1 × W 1263	S	0	187	-	0	0	99	-
T(N)1 × Bhumansan	S	0	270	-	0	0	99	-
T(N)1 × NHTA 8	R	321	98	0.579	23	42	20	0.220
T(N)1 × Banglei	R	294	106	0.480	24	52	20	1.000
T(N)1 × T 1432	R	372	116	0.393	25	55	20	1.500
T(N)1 × T 1477	R	317	97	0.544	21	43	20	0.120

The F_1, F_2 and F_3 populations of reciprocal crosses of T(N)1 with Eswarakora, Banglei and NHTA 8 were exposed to all the three biotypes to find out maternal influence, if any, on the expression of resistance (Table 6). The F_1, F_2 and F_3 populations of T(N)1 with Eswarakora and its reciprocals were susceptible to biotypes 2 and 4. The reciprocal F_1's of T(N)1 with Banglei and NHTA 8 were resistant to biotypes 1, 2 and 4. Their F_2 populations segregated in the ratio of 3R : 1S, and the F_3 pattern confirmed F_2 results, thereby confirming absence of any role of cytoplasm for the expression of resistance reaction.

Table 6. Reaction of F_1, F_2 and F_3 populations derived from the three reciprocal crosses against three different biotypes

Cross	F_1 reaction	Observed F_2 segregation		χ^2 (3:1)	Observed F_3 frequency segregation			χ^2 (1:2:1/ 7:8:1)
		R	S		R	Segr	S	
Biotype 1								
Eswarakora × T(N)1	R	328	94	0.671	24	48	22	0.126
Banglei × T(N)1	R	344	126	0.820	18	48	26	1.560
NHTA 8 × T(N)1	R	227	82	0.389	30	40	28	3.385
Biotype 2								
Eswarakora × T(N)1	S	0	214	-	0	0	95	-
Banglei × T(N)1	R	168	52	0.218	20	53	25	1.164
NHTA 8 × T(N)1	R	208	63	0.444	26	47	19	1.108
Biotype 4								
Eswarakora × T(N)1	S	0	294	-	0	0	100	-
Banglei × T(N)1	R	285	88	0.394	20	50	29	1.553
NHTA 8 × T(N)1	R	380	121	0.192	29	42	27	2.082

ALLELIC TESTS

Biotype 1 : The F_1 hybrids of all possible crosses among Eswarakora, W 1263 and NHTA 8 were resistant and there was no segregation in F_2 and F_3 generations (Table 7). Similarly, the F_1, F_2 and F_3 populations of Bhumansan with Banglei and T 1432, and Banglei with T 1432 were resistant. However, the crosses of Eswarakora, W 1263 or NHTA 8 with Bhumansan, Banglei and T 1432 although resistant in F_1, segregated in the ratio of 15R : 1S in F_2. Further, they showed a segregation ratio of 7R : 8 segregating : 1S families in F_3, confirming the F_2 ratios.

Table 7. Reaction of F_1, F_2 and F_3 populations derived from the crosses among resistant parents to biotype 1 under glasshouse conditions at DRR, Hyderabad

Cross	F_1 reaction	Observed F_2 segregation		χ^2 (15:1)	Observed F_3 segregation			χ^2 (7:8:1)
		R	S		R	Segr	S	
Eswarakora × W 1263	R	186	0		100	0	0	
Eswarakora× Bhumansan	R	178	10	0.277	44	49	5	0.060
Eswarakora × NHTA 8	R	196	0		100	0	0	
Eswarakora × Banglei	R	191	12	0.082	41	55	5	0.923
Eswaraora × T 1432	R	181	13	0.067	41	46	9	1.607
W 1263 × Bhumansan	R	232	15	0.013	38	53	8	1.186
W 1263 × NHTA 8	R	180	0		98	0	0	
W 1263 × Banglei	R	188	13	0.021	36	52	8	1.857
W 1263 × T 1432	R	244	15	0.092	40	50	9	1.530
Bhumansan × NHTA 8	R	196	12	0.082	46	50	4	1.464
Bhumansan × Banglei	R	198	0		100	0	0	
NHTA 8 × Banglei	R	174	12	0.009	40	47	9	1.116
NHTA 8 × T 1432	R	164	12	0.096	41	53	6	0.362
Banglei × T 1432	R	184	0		100	0	0	

Biotype 2 : The F_1 hybrids of Eswarakora with W 1263 were susceptible and F_2 populations and F_3 families did not segregate even though the parents themselves were susceptible to this biotype. The F_1 hybrids of Eswarakora with Bhumansan, NHTA 8, Banglei and T 1432 were resistant and gave 3R : 1S segregation in F_2 and 1 : 2 : 1 ratio in F_3 (Table 8). The F_1s of Bhumansan with NHTA 8, Banglei and T

1432 were resistant and their F_2 populations segregated in the ratio of 15 R : 1s. The F_3 ratio of 7R : 8 segregating : 1S families confirmed the F_2 observations. The F_1, F_2 and F_3 populations of the crosses NHTA 8 with Banglei and T 1432 and Banglei with T 1432 were resistant.

Table 8. Reaction F_1, F_2 and F_3 populations derived from the crosses among the resistant parents to biotype 2 under field conditions at Cuttack, Orissa

Cross	F_1 reaction	Observed F_2 segregation		χ^2 (3:1/15:1)	Observed F_3 segregation			χ^2 (1:2:1/7:8:1)
		R	S		R	Segr	S	
Eswarakora × W 1263	S	0	298		0	0	94	
Eswarakora × Bhumansan	R	244	73	0657	20	52	28	1.440
Eswarakora × NHTA 8	R	286	88	0.431	300	46	24	1.429
Eswarakora × Banglei	R	199	62	0.216	30	50	20	2.000
Eswarakora × T 1432	R	204	78	1.064	26	44	30	1.593
Eswarakora × NHTA 8	R	197	12	0.092	40	50	9	1.580
Bhumansan × Banglei	R	168	12	0.053	40	42	8	1.211
Bhumansan × T 1432	R	2136	10	0.093	38	53	9	2.146
NHTA 8 × Banglei	R	188	0		100	0	0	
NHTA 8 × T 1432	R	184	0		100	0	0	
Banglei × T 1432	R	188	0		100	0	0	

Biotype 4 : The parents Eswarakora, W 1263 and Bhumansan were susceptible to this biotype. The F_1, F_2 and F_3s of the cross Eswarakora X W 1263 were susceptible (Tables 9, 10). The F_1 hybrids of Eswarakora with NHTA 8, Banglei, T 1432 and T 1477, and Bhumansan with NHTA 8, Banglei, T 1432 and T 1477 were resistant. The F_2s of these crosses segregated in the ratio of 3R : 1S in F_2 and 1R : 2 segregating: 1S in F_3. However, the resistant F_1s of NHTA 8 with Banglei, T 1432 and T 1477 segregated in the ratio of 15R : 1S in F_2 and 7R : 8 segregating : 1S in F_3. The F_1, F_2 and F_3 plants of the cross Banglei with T 1432 and T 1477 as well as T 1432 with T 1477 were resistant (Tables 9, 10).

The results of field screening at Ragolu corraborated the above results from glasshouse. One exception to this was the cross Eswarakora X W 1263, where two plants showed no gall midge incidence, which can be considered as escapes.

Table 9. Reaction of F_1, F_2 and F_3 populations derived from the crosses among resistant parents to biotype 4 under glasshouse conditions at DRR, Hyderabad

Cross	F_1 reaction	Observed F_2 segregation		χ^2 (3:1/15:1)	Observed F_3 segregation			χ^2 (1:2:1/7:8:1)
		R	S		R	Segr	S	
Eswarakora × W 1263	S	0	162		0	0	98	
Eswarakora × NHTA 8	R	297	90	0.628	20	50	29	1.640
Eswarakora × Banglei	R	341	103	0.769	280	50	22	0.720
Eswarakora × T 1432	R	219	68	0.261	29	43	28	1.980
Eswarakora × T 1477	R	188	58	0.265	29	41	30	2.900
Bhumansan × NHTA 8	R	314	106	0.013	22	57	21	1.980
Bhumansan × Banglei	R	189	67	0.187	24	46	20	0.400
Bhumansan × T 1432	R	242	74	0.422	30	46	23	1.360
Bhumansan × T 1477	R	232	84	0.422	280	51	21	1.020
NHTA 8 × Banglei	R	189	14	0.145	450	49	6	0.066
NHTA 8 × T 1432	R	169	12	0.044	400	55	5	1.071
NHTA 8 × T 1477	R	188	12	0.021	45	51	4	0.866
Banglei × T 1432	R	194	0		88	0	0	
Banglei × T 1477	R	179	0		100	0	0	
T 1432 × T 1477	R	195	0		94	0	0	

Inheritance of gall midge resistance has been studied earlier since the early 1970s with no knowledge of biotypic variation. Early studies carried out in different gall midge endemic areas of India, such as Warangal and DRR in Andhra Pradesh, Cuttack in Orissa and Raipur in Madhya Pradesh, revealed either a single dominant gene [6-9] or a multigenic system [2, 10-12] to govern resistance.

The diverse reports on the genetics of resistance could be due to total dependence on field infestation for screening, which could vary from year to year. Following the reports of possible existence of biotypic variations of the insect in India [2], the problem was studied systematically and as many as four distinct biotypes were identified [3]. Very little is known about the identity of the resistance genes and the extent of exploitable variability available for resistance to the region-specific biotypes. In the course of the present investigation, seven potential donors vis-a-vis the recognised biotypes have been characterized. The results of the present genetic studies indicate that the resistance was controlled by a single dominant gene, which is specific to each of the three biotypes.

Table 10. Reaction of F_1, F_2 and F_3 populations derived from the crosses among resistant parents to biotype 4 under field conditions at Ragolu, Andhra pradesh

Cross	F_1 reaction	Observed F_2 segregation		χ^2 (3:1/15:1)	Observed F_3 segregation			χ^2 (1:2:1/7:8:1)
		R	S		R	Segr	S	
Eswarakora × W 1263	S	2	204		0	0	100	
Eswarakora × NHTA 8	R	270	84	0.305	20	44	28	1.371
Eswarakora × Banglei	R	312	96	0.470	28	52	20	1.440
Eswarakora × T 1432	R	406	126	0.491	22	46	32	2.640
Eswarakora ×T 1477	R	288	81	1.829	19	45	30	2.940
Bhumansan × NHTA 8	R	327	101	0.448	30	47	23	1.340
Bhumansan × Banglei	R	212	65	0.348	28	44	28	1.440
Bhumansan × T 1432	R	286	82	1.450	27	54	19	1.920
Bhumansan × T 1477	R	304	96	0.413	230	46	31	1.920
NHTA 8 × Banglei	R	284	21	0.210	400	56	4	1.851
NHTA 8 × T 1432	R	441	34	0.668	370	57	6	2.031
NHTA 8 × T 1477	R	360	31	1.904	40	54	6	0.651
Banglei × T 1432	R	334	0		92	0	0	
Banglei × T 1477	R	412	0		98	0	0	
T 1432 × T 1477	R	324	0		100	0	0	

Differences in the degree of gall midge resistance were reported [8] in reciprocal crosses involving the donor parent W 1263. In the present study, the reciprocal crosses made in respect of all the three biotypes, however, revealed no perceptiable differences in the level of resistance, thus ruling out maternal influence.

GENE SYMBOLIZATION AND DEDUCTION OF GENETIC CONSTITUTION OF THE DONORS

Based on the study of inheritance and allelic relationship, the genetic constitution of the donors may be given biotype-wise as follows :

Bictype 1 : Crosses of T(N)1 with Eswarakora, W 1263 and NHTA 8 when tested against biotype 1, reveal resistance to be monogenic dominant. No segregation in

the crosses Eswarakora X W 1263, Eswarakora X NHTA 8 and W 1263 X NHTA 8 suggest the dominant gene carried by them to be allelic and are thus designated as *Gm1*. Chaudhary *et al.* (1985) working with biotype 1 designated the dominant resistance gene in W 1263 as *Gm1* and a different dominant resistance gene in Siam 29 as *Gm2*. The mode of inheritance observed in the crosses of T(N)1 with Bhumansan, Banglei and T 1432, suggest these donors also to carry a dominant resistance gene. The F_1, F_2 and F_3s of the crosses Bhumansan X Banglei, Bhumansan X T 1432 and Bangei X T 1432 showed complete resistance reaction, indicating the dominant gene to be allelic in these donors. The test of allelism in the crosses of Eswarakora, W 1263 or NHTA 8 with Bhumansan, Banglei and T 1432, which segregated in the ratio of 15R : 1S, however, revealed the dominant gene in the latter (Bhumansan, Banglei and T 1432) to be non-allelic to that of the former (Eswarakora, W 1263 and NHTA 8). Thus, the dominant gene conferring resistance to biotype 1 in Bhumansan, Banglei and T 1432 has been designated as *Gm3* having *Gm2* been already assigned to Siam 29 by Chaudhary *et al.* (1985). In the absence of crosses involving Siam 29, no definite inference could be drawn as to whether the gene *Gm2* assigned earlier to Siam 29 is allelic to *Gm3* of Bhumansan, Banglei or T 1432.

Biotype 2 : The test populations of crosses of TN(1) with Eswarakora and W 1263 are susceptible against biotype 2 indicating that they have no resistance gene in them. The crosses of Eswarakora or W 1263 with Bhumansan, however, segregate simply indicating the latter to carry a dominant gene for resistance to biotype 2. This gene Bhumansan is designated as *Gm4*. Study of crosses of Bhumansan with NHTA 8, Banglei and T 1432, which segregated in a digenic ratio indicates the resistance gene in them to be non-allelic to that of Bhumansan (*Gm4*), hence designated as *Gm5*.

Biotype 4 : The crosses of T(N)1 with Eswarakora, W 1263 and Bhumansan were susceptible to this biotype. The test populations of the cross T(N)1 X NHTA 8 segregated in the ratio of 3R : 1S. This dominant resistance gene in NHTA 8 is designated as *Gm6*. The crosses of NHTA 8 with Banglei, T 1432 and T 1477 segregated in a digenic ratio, showing that the resistance gene in NHTA 8 (*Gm6*) to be non-allelic to the one in Banglei, T 1432 and T 1477 thus, it is designated as *Gm7*. Crosses among Banglei, T 1432 and T 1477 did not segregate confirming that the resistance gene in them (*Gm7*) is allelic.

The genetic constitution of the parents in relation to their reaction to the three biotypes of the rice gall midge and the gene symbols tentatively assigned to the resistance genes are as follows :

	Biotype 1	Biotype 2	Biotype 4
Eswarakora and W 1263	Gm_1Gm_1 gm_3gm_3	gm_4gm_4 gm_5gm_5	gm_6gm_6 gm_7gm_7
Bhumansan	gm_1gm_1 Gm_3Gm_3	Gm_4Gm_4 gm_5gm_5	gm_6gm_6 gm_7gm_7
NHTA 8	Gm_1Gm_1 gm_3gm_3	gm_4gm_4 Gm_5Gm_5	Gm_6Gm_6 gm_7gm_7
Banglei and T 1432	gm_1gm_1 Gm_3Gm_3	gm_4gm_4 Gm_5Gm_5	gm_6gm_6 Gm_7Gm_7
T 1477	Not studied	Not studied	gm_6gm_6 Gm_7Gm_7

EVOLUTION OF GALL MIDGE RESISTANCE

It is evident from past records that gall midge existed as only one form in various endemic pockets in the states of Orissa, Andhra Pradesh and Madhya Pradesh, where Eswarakora or its derivatives with resistance gene were resistant (13). In the early 1970s, the pest in Orissa showed intrinsic variation with Eswarakora becoming susceptible and Siam 29 having the gene (9) confirmed to be resistant (2). By 1990, a new biotype with high virulence emerged in the northern coastal Andhra Pradesh, where Siam 29 as well as Eswarakora became susceptible. Concomitant to the development of progressively virulent biotypes of the insect, resistance genes in the host plant may also have evolved. The genotypes like NHTA 8 and Banglei, for instance, confer resistance to biotypes 1, 2 and 4. Similarly, Bhumansan confers resistance to biotype 1 as well as biotype 2. Occurrence of such genotypes with the genes conferring resistance not only to progressively more virulent biotype(s) but also to less virulent biotypes is suggestive of coevolution of resistance and virulence genes.

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