Original Research Article

IDENTIFICATION OF NEW SOURCES OF RESISTANCE TO RICE GALL MIDGE BIOTYPE 3 (GMB 3) PREVAILING IN JAGTIAL, TELANGANA, INDIA

ABSTRACT

Aim: To screen different rice entries against rice gall midge, (*Orseolia oryzae)* biotype 3 under field conditions.
Place and Duration of Study: A total of 84 rice germplasm lines along with resistant and susceptible checks were evaluated against rice the gall midge, (*Orseolia oryzae)* biotype 3. These studies were conducted during *Kharif season (*2021) under field conditions at the Regional Agricultural Research Station (RARS), Jagtial.
Methodology: Data on the total number of plants and plants with silver shoots including the number of silver shoots per plant were also recorded on 30 and 50 days after transplantation. Gall midge incidence as silver shoot scored according to the standard evaluation system, International Rice Research Institute (IRRI) for gall midge (IRRI, 2013).
Results: Six entries viz., KAKAI, SINNA SIVAPPU, PTB-12, WGL-1145, WGL-1147 and WGL-1127 had shown high resistant (score 0) to gall midge. Four entries viz., IR72476-B-P-9-3-1-1, RP-5332-54-11-8-2-13, WGL-1143 and SUDD HONDARAWALA were found resistant (score 1) against gall midge.
Conclusion: The entries KAKAI, SINNA SIVAPPU, PTB-12, WGL-1145, WGL-1147 and WGL-1127 exhibited the high resistance against gall midge. Hence, they can be developed as varieties or can be used in breeding programme as a source of gall midge resistance.

Keywords: Gall midge, Screening, Rice entries, GMB3

1. INTRODUCTION

Rice *(Oryza sativa L.)* is the leading food crop and a staple food for 40% of the world population. Worldwide, rice is cultivated in 164 million hectares with an annual production of 756.7 million tonnes (*FAOSTAT*. 2020). More than 90% of rice is produced and consumed in Asia. India stands first in area with 45 million hectares and second in production with 178.3 million tonnes, constituting up to 23.5% of global rice production (*FAOSTAT*. 2020). It thrives in a variety of geographical and hydrologic conditions, from rain-fed highland to rain-fed lowland, as well as deep water. However, as high yielding varieties became susceptible to a wide range of pests and diseases, stability in rice production could not be sustained. Approximately 52% of global rice production is lost annually owing to the damage caused by biotic stress factors, of which 25% is attributed to the attack by insect pests (Yarasi, *et al.,* 2008). Major insect pests of rice that cause huge economic losses in South Asia are stem borer, brown plant hopper and gall midge. Of these, gall midge alone is responsible for a worldwide damage of more than US$ 700 million annually (Herdt, 1991). Two species of the rice gall midge have been identified so far, the Asian rice gall midge, (*Orseolia oryzae*) and the African rice gall midge*, (O. oryzivora)*.

Asian rice gall midge is prevalent in almost all the rice growing states in India except the Western Uttar Pradesh, Uttaranchal, Punjab, Haryana and Hill states of Himachal Pradesh and Jammu and Kashmir (Bentur *et al.,* 1992). In India, it is rated as third most important pest of rice in terms of spread and severity of damage and yield loss, next to stem borers and plant hoppers. It is essentially a monsoon pest and prefers high humidity and moderate temperature

UNDER PEER

with peak activity extending between last week of August and first week of October. The external symptom of damage caused by gall midge is the production of a silvery-white, tubular leaf sheath gall called a “silver shoot” or “onion shoot”. This is due to the feeding and salivary secretion by the larvae which turn the growing shoot meristem into a gall (Bentur *et al.,* 1992). This renders the tiller sterile and do not bear panicle (Seni *et al.,* 2017). Since gall midge is an internal feeder so chemical control is inefficient, host plant resistance is the best alternative approach available for its management. However, Gall midge resistance genes must first be identified and utilized in rice breeding programs. So far 12 gall midge resistance genes *(Gm1* through *Gm12)* and seven biotypes (*GMB1* through *GMB6* and *GMB4M*) of gall midge have been identified (Leelagud *et al.,*2020 and Himabindu *et al.,* 2010) based on a set of host plant gene differentials**.** Interestingly, none of the identified genes confers resistance to all the gall midge biotypes, while none of the gall midge biotypes is virulent against all the resistance (R) genes (Anusha *et al.,* 2022). However, cultivation of varieties containing a single resistance gene has resulted in frequent breakdown of resistance due to emergence of virulent biotypes of the insect across many regions in India. It is thus imperative to identify new resistance sources and find novel genes and deploy them effectively. so, screening for host-plant resistance against Gall midge is necessary at hot-spot locations. Jagtial in Telangana State is considered as one of the endemic pockets for gall midge in Indi so, the present work was undertaken for identification of new donors for resistance to gall midge biotype 3 (*GMB3*) prevailing in Jagtial, Telangana.

2. Materials and Methods

2.1. Experimental site

Based on the reaction of field population to a standard set of host plant differentials, the gall midge population at Jagtial has been characterized as *GMB 3* (Srinivas, 1999). Since gall midge prevails under high humid conditions, field evaluation of all the test material was done against *GMB3* at the experimental farm of Regional Agricultural Research Station (RARS), Jagtial of Professor Jayashankar Telangana State Agricultural University, Hyderabad during Wet seasons *(Kharif)* of 2021. The Station is situated at 18 49’ 40” N latitude and 78 56’ 45” E longitude in Jagtial district at an altitude of 258 m above MSL. The climate of the area is warm/sub humid.

2.2. Field experiment

Total 84 entries of rice along with *TN-1* (susceptible check) and *Aganni* (Resistant check) were screened for resistant to *GMB 3*. The seeds were sown in lines on raised nursery beds and the time of sowing was adjusted to coincide with pest infestation. and transplanting was done after 25 days of sowing. A spacing of 20 cm between rows and 12 cm between plants within the row was followed in the transplanted field. All the agronomic practices were followed during crop growth period. No insecticidal spray was given. Each entry was transplanted in single row of 20 hills per entry. Every 10^{th} row was transplanted with check. For building sufficient gall midge population, susceptible check *(TN-1)* was also transplanted as border covering the field experiment.

2.3. Data collection and analysis

UNDER PEER REVIEW

The test entries were scored for plant damage at 30 days after transplanting (DAT) and 50 DAT. Data collected included the total number of plants, the total number of tillers per plant, damaged plants (with silver shoots), number of silver shoots/damaged plants. Percent damaged plants (DP%) and percent silver shoots (SS%) were calculated.

percentage of silver shoot (SS) was worked out by using the formula;

$$SS\ (\%) = \frac{\text{Number of silver shoot}}{\text{Total number of tillers observed in 10 hills}} \times 100$$

Then, the pest intensity was scored as per standard evaluation system (Table 1), International Rice Research Institute (IRRI) for gall midge (IRRI, 2013).

Table 1: Standard evaluation system for rice gall midge

Scale	Damage *(%)*	Reaction
0	No damage	HR
1	<1%	R
3	1-5%	MR
5	6-10%	MS
7	11-25%	S
9	>25%	HS

3. Results and Discussion

Rice gall midge is one of the major pests of rice in Jagtial, Telangana. The test entries were screened and assessed their resistance against gall midge by using standard evaluation system of IRRI for gall midge as per damage score found during second observation i.e., 50 DAT (Table 2). In the test entries, incident of gall midge was ranged from 0-84.18 per cent silver shoots. Among 84 entries screened against rice gall midge, “Nil” gall midge incidence was noticed in six

Table 2: Reaction of different rice entries against rice gall midge

Sl. No.	Name of Entry	Silver Shoot (SS) %		Reaction
		30 DAT	50 DAT	
1	IR-71604-4-1-4-4-4-2-2-2R	7.74	64.84	HS
2	IR72476-B-P-9-3-1-1	2.14	0.65	R
3	IR-74101-3R-1-1	1.26	9.29	MS
4	IR-74102-3R-9-3	4.58	66.77	HS
5	IR-74015-3R-2-2	13.19	49.26	HS
6	IR-74016-3R-8-2-1	8.23	69.74	HS
7	IR-712402-B-P-253-1	12.43	73.62	HS
8	IR-74106-3R-9-1-1	3.51	62.87	HS
9	IR-71991-3R-2-1	6.67	52.31	HS

UNDER PEER REVIEW

10	IR-72593-B-3-2-2-2	8.08	69.06	HS
11	IR-72593-B-3-2-3-5	4.29	63.64	HS
12	IR-72048-B-R-16-2-3-3	2	67.7	HS
13	IR-72049-B-R-22-3-1-1	6.18	67.43	HS
14	IR-72046-B-R-7-2-2-1	4.55	67.58	HS
15	IR-54751-2-41-10-5-1-B	7.1	72.03	HS
16	IR-54751-1-2-44-15-2-3-B	7.55	74.83	HS
17	IR-65482-4-136-2-2-B	11.24	74.38	HS
18	IR-65482-17-50-5-7-B	3.16	72.36	HS
19	IR-65482-1-219-1-B	7.74	73.6	HS
20	IR-71033-62-15-B	9.92	69.8	HS
21	WGL-1127	0	0	HR
22	WGL-1143	0	0.58	R
23	WGL-1145	0	0	HR
24	WGL-1147	0	0	HR
25	WGL 1289	14.8	61.48	HS
26	WGL 1413	12.81	66.06	HS
27	Calotoc	9.09	58.51	HS
28	Dular	4.35	24.66	S
29	KNM-630	4.72	69.92	HS
30	KNM-604	9.41	72.4	HS
31	NDLR-7	8.39	73.36	HS
32	Sampada	11.25	65.08	HS
33	Dukong-1	9.79	64.43	HS
34	FFC	4.26	67.65	HS
35	RP-5332-54-11-8-2-13	1.44	0.52	R
36	RP-1641-907-1-397	5.03	60.91	HS
37	HH-25-SAL-10-D2-DT-1	5.26	24.88	S
38	MUT NS 1	5.63	55.21	HS
39	IR-10A-199	4.48	50.18	HS
40	IR-04A-216	2.73	45.23	HS
41	NSN 1/120-2016	12.42	68.44	HS
42	NSN 1/296-2016	4.67	39.75	HS
43	NSN 1/95-2016	8.67	57.18	HS

UNDER PEER REVIEW

44	Betangamblin	10.91	66.98	HS
45	PTB-12	0	0	HR
46	Chittimutyalu	1.53	67.63	HS
47	CT 376	13.04	73.91	HS
48	GONDRABIDHAN	9.49	73.86	HS
49	HPR-2177	9.49	72.76	HS
50	IR-62048-47-3-3-2R	3.82	58.67	HS
51	IR-678-25-5	9.29	63.79	HS
52	IR-79218-93-1-4-3	15.61	67.18	HS
53	IR-79597-56-1-2-1	12.29	70.66	HS
54	SINNA SIVAPPU	0	0	HR
55	IRBL-1-LA(CO)	8.29	42.23	HS
56	IRBL-9-WIRL	11.38	70.15	HS
57	IRBL-T-K59	12.18	84.18	HS
58	IRBL-Z5-CA (10)	14.85	69.84	HS
59	IRBLZ-FU/RL	13.7	76.92	HS
60	IRTON 270	16.29	70.9	HS
61	SUDD HONDARAWALA	0	0.6	R
62	Kapurala vadlu	5.71	70.41	HS
63	Mahamaya	9.63	74.15	HS
64	CGZR 1	10	43.12	HS
65	CGZR 2	6.25	42.59	HS
66	JGL 34594	11.76	69.6	HS
67	RDR 1210	7.32	62.11	HS
68	Tahat	8.57	68.34	HS
69	Kamer samba	3	50.78	HS
70	Kudel	6.71	66.04	HS
71	Sammela Bogulu	3.82	59.84	HS
72	Njavara	2.67	36.8	HS
73	Laicha	6.57	24.51	S
74	Kalabunt	12.96	64.86	HS
75	Kakirekaalu	2.65	52.67	HS
76	Bahurupi	12.66	63.52	HS
77	Manipuri black	5.98	57.94	HS

UNDER PEER REVIEW

78	Burma Black	9.94	40.83	HS
79	KAKAI	0	0	HR
80	Didianga	5.24	53.5	HS
81	Chattisgarh local	9.36	62.5	HS
82	Rani kandi	9.71	59.71	HS
83	Geetanjali	13.57	70.65	HS
84	Umleng-1	4.93	56.11	HS

HR-Highly resistant, R-Resistant, MR- Moderately resistant, MS- Moderately susceptible, S- Susceptible, HS- Highly susceptible

entries viz., KAKAI, SINNA SIVAPPU, PTB-12, WGL-1145, WGL-1147 and WGL-1127 and they had shown high resistant (score 0) to gall midge in field condition. Four entries viz., IR72476-B-P-9-3-1-1, RP-5332-54-11-8-2-13, WGL-1143 and SUDD HONDARAWALA were found resistant (score 1) against gall midge. The entries viz., GP-279 and IR-74101-3R-1-1 were found to be moderately resistant (score 3) and moderately susceptible (score 5) respectively. All the remaining entries were found to be susceptible to highly susceptible against gall midge.

After extensive research of host-plant differentials it is found that biotype 3 is present in Jagtial district of Telangana State (Srinivas, 1999). Beside this biotype 3 is also present in Ranchi (Jharkhand) and Wangbal (Manipur) (Seni *et al.,* 2017). Although gall midge biotype 3 is present at Jagtial but from last few years it infested RP 2068 variety containing *Gm3* gene and Abhaya variety containing *Gm4* gene so, there is possibility of another biotype present here.

Sources of resistance that have been identified can be further investigated for known genes. It is crucial to characterise these donors that have consistently shown resistant reactions for their mechanisms in order to identify the genes giving resistance using the gene-specific markers that have already been established. This would allow the proper donors for the resistance breeding programme to be selected. These resistant lines have a better potential to be used as donors in the rice breeding programme for the development of gall midge resistant varieties as well as for monitoring virulence in gall midge populations. In different rice cultivars, the use of molecular markers for the improvement of gene pyramids in the desired combination is now being investigated, and DNA markers for the selection of resistant plants for gene pyramiding has been accepted as an established tool. (Sundaram *et al*, 2008; Suvendhu *et al*, 2014).

CONCLUSION

The entries KAKAI, SINNA SIVAPPU, PTB-12, WGL-1145, WGL-1147 and WGL-1127 exhibited high resistance against gall midge so, they can be developed as varieties or can be used in breeding programme as a source of gall midge resistance.

References

1. Anusha C, Maheswari TU, Raju CD, Malathi S, Padmakumari SO. Identification of new sources of resistance to rice gall midge biotypes prevailing in telangana, india. *J. Exp. Zool. India. 2022; 25:793-803*
2. Bentur JS, Pasalu IC, Kalode MB. Inheritance of virulence in rice-gall midge (*Orseolia oryzae*). Indian Journal of Agricultural Sciences. 1992; 62:492-493.

UNDER PEER REVIEW

3. *FAOSTAT*. 2022. [online]Available at: <https://www.fao.org/faostat/en/#data/QCL/ visualize [Accessed 9 June 2022].
4. Herdt RW. Research priorities for rice biotechnology. *Rice biotechnology*. 1991; *6:19*-54.
5. Himabindu K, Suneetha K, Sama VS, Bentur JS. A new rice gall midge resistance gene in the breeding line CR57-MR1523, mapping with flanking markers and development of NILs. Euphytica. 2010 Jul;174(2):179-87.
6. IRRI. Standard Evaluation System for Rice. 5th Edition. IRRI, Los Banos, Philippines, 2013; 55.
7. Leelagud P, Kongsila S, Vejchasarn P, Darwell K, Phansenee Y, Suthanthangjai A *et al.* Genetic diversity of Asian rice gall midge based on mtCOI gene sequences and identification of a novel resistance locus *Gm12* in rice cultivar MN62M. *Molecular Biology Reports*. 2020;47: 4273-4283.
8. Seni A, Naik BS. Efficacy of some insecticides against major insect pests of rice, *Oryza sativa* L. Journal of Entomology and Zoology Studies. 2017; 5(4):1381-1385.
9. Seni A, Naik BS. Screening of different Rice entries against Rice Gall Midge, *Orseolia oryzae* (Wood-Mason). International Journal of Environment, Agriculture and Biotechnology. 2017; 5(2):2427-2432.
10. Srinivas C. Characterization and distribution of biotypes of rice gall midge, *Orseolia oryzae* (Wood-Mason) in Andhra Pradesh. *Ph. D. Thesis*, ANGRAU, Hyderabad, India.1999.
11. Sundaram R M, Manne R, Vishnupriya, Biradar S K, Laha G S, Ashok Reddy G *et al*. Marker-assisted introgression of bacterial blight resistance in Samba Mahsuri, an elite indica rice variety. *Euphytica. 2008;*160, 411- 422.
12. Suvendhu D S, Divya D, Durga Rani Ch V, Dayakar Reddy T, Visalakshmi V, Cheralu C *et al.* Characterization of gall midge resistant rice genotypes using resistance gene-specific markers*. J. Exp. Biol. Agric. Sci*. 2014; 2(4), 439-446.
13. Yarasi B, Sadumpati V, Immanni C P, Vudem D R and Khareedu VR. Transgenic rice expressing *Allium sativum* leaf agglutinin (ASAL) exhibits high-level resistance against major sap-sucking pests. *BMC Plant Biology*. 2008; *8*(1):1-13.

UNDER PEER REVIEW