Studies on gall midge(biotype 3)resistance and genetic analysis in rice (*Oryza sativa* L) genotypes

ABSTRACT

22 rice genotypes were evaluated for gall midge resistance and genetic analysis of yield traits during *kharif,* 2022.Field screening for gall midge resistance revealed highly susceptible (1 entry), susceptible (11entries), moderate susceptible (6 entries) and moderate resistance (4 entries) reaction among all tested entries.JGL 44143 (2%), JGL 44146 (4%), JGL 44147 (5%) and JGL 44088 (5%) recorded least percent of silver shoots and exhibited moderate resistance. Days to 50% flowering, plant height, effective bearing tillers/m^2 and panicle length recorded low values of PCV and GCV, whereas, 1000 grain weight recorded moderate values and percent of galls recorded high. Grain yield exhibited moderate values of PCV and high values for GCV. Grain yield, 1000 grain weight and percent galls exhibited high values of both heritability and genetic advance which can be improved with simple selection based on phenotypic performance in desirable direction. Higher inter cluster distance was noticed between clusters of III and IV (2094.45) followed by I and IV (927.52), II and IV (745.94) and II and III (525.61). Based on cluster mean values, genotypes of cluster I found to be promising gall midge resistance and MTU 1001 (cluster II) for high yield. Crossing between genotypes of clusters I and IV could generate gall midge resistant segregants. The trait, days to 50% flowering (38.10%) contributed highest towards total divergence followed by 1000 grain weight (20.78%) and grain yield (19.91%).

Key words: Rice, variability, genetic divergence, gall midge resistance, yield

1. INTRODUCTION

Rice is the basic energy source food for most of Asian country's people being cultivated in 165.25 m.hawith an annual production of 515.05 m.t per annum. In India, rice cultivation spreads over the area of 47 m.ha with a production of 135.75 lakh tones (INDIASTAT, 2022-23). Telangana, the state named as seed hub of India has largest area (4.66 m.ha) under rice cultivation producing 15.87 m.t with a productivity of 3406 kg ha^{-1}(INDIASTAT, 2022-23).The major abiotic stresses that cause yield reduction are cold injury at seedling and reproductive stage, extreme heat during flowering to maturity stage and hail storms during harvest. Apart from, abiotic injuries, rice also experiences a number of biotic stresses which cause a major reduction in yield. BPH, stem borer, gall midge, blast and bacterial leaf blight are the major biotic stresses contribute a major share of all yield reduction factors. Of these, The Asian rice gall midge (ARGM), *Orseolia oryzae* (Wood-Mason), is a significant pest found in nearly all rice-growing states in India. It attacks rice from the seedling to the end of the tillering stage. Grub feeding and secreting saliva transform the shoot meristem into a gall, making the tiller sterile and preventing panicle formation. In India, it is rated as the third most important pest of rice in terms of spread and severity of damage and yield loss (Bentur*et al*., 2016). In India, rice gall midge has been reported from almost all the states with crop losses rangingfrom 10-100% (Siddiq, 1991). Across India, incidence of different biotypes of gall midge causing significant yield reduction. Biotype 3 and 4M are specific to Telangana state and biotype 3 is confined specifically to Northern Telangana Zone. Development of tolerant varieties with good yield potential to these endemic areas is one of the key objectives of present day breeding programs. Even though a good number of resistant varieties have been released so far, continuous cultivation of same resistant varieties for long period in same locations resulted in breakdown of resistance and evolution of new biotypeswhich favored by changing climatic conditions.Variability for the examining traits in experimental material is utmost important for improvement of any characters and plays a key role in selection of parents and development of high yielding varieties and hybrids.Creation of broad range of variability in any crop could be possible using more divergent parents in breeding programs. Present work focused on identification of divergent rice lines with gall midge tolerance and high yield potential.

2. MATERIALS AND METHODS

The experiment was conducted with 22 rice genotypes (Table 1)during *kharif*, 2022 at Regional Agricultural Research Station (RARS), Polasa, Jagtial located at 18^0 50’ 20.24” N latitude, $78^0$56’54.20” E longitude and 249 m above mean sea level. Each genotype was transplanted in a plot size of 7.56 m^2(12 no. of rows and 28 no. of hill/row), replicated twice in randomized block design. The spacing adapted was 15 cm between and within the rows. Data on eight parameters were recorded, of which days to 50% flowering and grain yield were obtained on whole plot basis. Five random plants at maturity were used to record data on plant height whereas effective bearing tillers were counted in 1 m^2 area in each genotype from each replication. Panicle length was recorded from 5 random panicles from each entry and threshed seed from these 5 panicles was used to count the number of grains per panicle, whereas random sample from each entry was used to record 1000 grain weight. RARS, Jagtial is being a hot spot for gall midge biotype 3 incidence, the experimental material was examined against gall midge to identify the tolerant lines in addition to variability and divergence studies. 10 random plants from each entry and each replication were used to record gall midge data at 50 days after transplanting. For scoring the incidence, total tillers and infected tillers (silver shoots) were counted from each plant and percent infestation was calculated as per below given formula.

$$\text{Per cent silver shoots (\%SS)} = \frac{\text{No of silver shoots}}{\text{Total number of tillers}} \times 100$$

The reaction to the entries in terms of susceptibility or resistance is given as per the 0-9 scale following the Standard Evaluation System, (IRRI, SES, 2013).

List 1-Standard Evaluation System (SES) for rice gall midge (IRRI, 2013)

Score	Percent silver shoot damage	Category
0	No damage	Highly Resistant
1	<1	Resistant
3	1-5	Moderately Resistant
5	6-10	Moderately Susceptible
7	11-25	Susceptible
9	>25	Highly Susceptible

Genetic distance among the genotypes for the studied traits was estimated using Mahalonobis D2 analysis (1936). The estimates of PCV and GCV were classified as low (<10%), medium (10–20%), and high (>20%) (Sivasubramanian and Madhavamenon, 1973). Broad-sense heritability (h2) was calculated using the formula according to Allard (1960) and they were categorized using the criteria of Robinson *et al.* (1949): 0–30%=low; 31–60%=moderate; >60%=high. Genetic advance was estimated as per Burton (1952).

3. RESULTS AND DISCUSSION

Analysis of Variance (Table 2) showed significant variation among the genotypes for all the characters studied except effective bearing tillers per plant revealed much scope for these traits for further improvement.

Gall midge screening:

Gall midge screening data (Table 3) revealed that, out of 22 genotypes evaluated for gall midge resistance, none of the entry showed complete resistance to this pest. One entry (RNR 15048) exhibited highly susceptible reaction with 32 % silver shoots, whereas, 11 entries *viz.*, JGL 44085, JGL 44150, JGL 44158, JGL 44163, JGL 44165, JGL 44167, JGL 44167, JGL 44173, JGL 44174, JGL 18047 and MTU 1001 showed susceptible reaction with percent silver shoot damage ranged from 11 to 22. Six genotypes namely, JGL 44148 (6%), JGL 44086 (7%), JGL 44144 (8%), JGL 44089 (9%), JGL 11470 (9%) andJGL 44152 (10%) recorded moderate susceptibility reaction. Similar studies were conducted by Shravan Kumar *et al.* (2020) in 173 rice genotypes and found 3 highly resistant and 6 with resistant reaction. Only four entries exhibited moderate resistance of which JGL 44143 (2%) recorded least percent of silver shoots followed by JGL 44146 (4%), JGL 44147 (5%) and JGL 44088 (5%). Anil Kumar *et al.* (2022) evaluated 84 rice germplasm lines among which six entries *viz.*, Kakai, Sinna Sivappu, PTB-12, WGL-1145, WGL-1147 and WGL-1127 had shown high resistance (score 0) and four entries *viz.*, IR72476-B-P-9-3-1-1, RP-5332-54-11-8-2-13, WGL-1143 and SuddHondarawalashown resistance (score 1) against gall midge biotype 3.The test entries were developed through pedigree method of breeding from seven crosses.Most of the entries derived from the cross (NSN 1/296-2016 X JGL 24423) X JGL 11727 exhibited less incidence of silver shoots among all test entries, where 3 of them exhibited moderate resistance. The reason behind obtaining good segregants for gall midge tolerance could be one of the parent i.e JGL 11727 of this crossis highly resistant genotype for gall midge biotype 3 developed at Regional Agricultural Research Station, Jagtial, PJTAU. The derivatives of other cross NSN 1/95-2016 X RNR 15048 also performed well for gall midge tolerance and one entry from this cross exhibited moderate resistance. The reaction of the parent NSN 1/95-2016 towards gall midge incidence needs to be revealed in further studies. Similarly, Anusha *et al.* (2017) screened 38 pre breeding rice lines derived from 6 crosses under green house conditions at IIRR, Hyderabad for GMB 1 and underfield conditions at RARS, Jagtial for biotype 3 and RARS, Warangal for 4M and found that12 lines showed nil damage from four crosses against biotype 1 and 6 lines against biotype 3. Of these RNR17927-1 of cross Tellahamsa X JGL11690) andRNR19872, RNR19875, RNR19880, RNR19881 and RNR19883derived from MTU1010 X JGL3855 were found resistant against both biotype 1 and 3 but susceptible to biotype 4M.

Variability studies:

Table 4 illustrated minimum, maximum, PCV, GCV, heritability and genetic advance values for all 8 traits under study.The traits exhibited low, medium and high range of PCV and GCV. Days to 50% flowering, plant height, effective bearing tillers/m^2 and panicle length recorded low values indicating the less variability in the genotypes studies for these traits and hence less scope for improvement. Creation of more variability through hybridization is the prime step to improve these traits. 1000 grain weight recorded moderate values whereas percent of galls had high values for PCV and GCV. The trait number of grains per panicle and grain yield exhibited moderate values of PCV and high values for GCV. Hence, simple selection can be practiced for further improvement of these characters. Minimal differences between PCV and GCV for all the characters show the less influence of environment on expression of these traits. PCV values observed for all the traits were higher than GCV indicating the higher level interaction of test entries with environment. Rahul Kumar Maurya *et al.* (2022), Anusha *et al.* (2024) andHima Bindu *et al.* (2024) quoted similar findings for yield and yield attributing traits from their research, whereas, Sreedhar Siddi and Anil Deva (2020) and Gonya Nayak *et al.* (2023) noticed high values of PCV and GCV for percent gall midge incidence in their studies. Heritability denotes the level of transmission of a character from parent to its progeny. Effective bearing tillers/m^2 (5.10) and number of grains per panicle (48.50) exhibited low heritability and remaining traits showed high level of transmission to next progeny. Hence, the selection in desirable direction for days to 50% flowering, plant height, panicle length, 1000 grain weight, percent of galls and grain yield on phenotype basis would certainly results in improvement of these traits as influence of environment on expression of these characters is negligible. Genetic advance is the measure of genetic gain under selection. The characters with high heritability and genetic advance are said to be fixed governed by additive gene action. Grain yield and 1000 grain weight with high values for both heritability and genetic advance can be improved with simple selection based on phenotypic performance. High heritability with moderate genetic advance was observed for days to 50% flowering, plant height, panicle length, whereas, number of grains per panicle exhibited moderate heritability and high genetic advance values indicating role of both additive and non additive genes in governing these traits. Hence, hybrid program coupled with selections and other breeding approaches like recurrent selections needs to be practised to improve these traits. Heterosis breeding could be the best choice for trait effective bearing tillers/M^2 to improve as it recorded low values for both. High heritability coupled with high genetic advance in case of percent of galls clearly shows thehigh transmission rate of the trait *i.e,* either susceptibility or tolerance nature to next generation. Hence, phenotypic selection for gall midge resistance along with desirable yield traits in each generation will end up with high yielding rice varieties with gall midge resistance. Similar findings of heritability and genetic advance for yield traits and percent gall midge incidence were reported byChhodavadiya*et al.* (2023), Sourav Paramanik *et al.* (2023), Mounika *et al.* (2024)and Tripti Singh *et al.* (2024),.

Divergence studies:

D^2 analysis revealed that the genotypes under study were grouped into 4 clusters (Table 5) of which cluster I accommodated with highest number of genotypes (18) followed by cluster IV (2) and clusters II and III each with one genotype. Formation of 4 clusters with 22 genotypes indicated presence of ample diversity among the genotypes. The magnitude of distance between two clusters indicates the amount of diversity between the genotypes belongs to those clusters.Higher the distance between the clusters, higher is divergence among the genotypes of clusters. Highest divergence (Table 6) was noted between the genotypes of clusters III and IV (2094.45) followed by clusters I and IV (927.52), clusters II and IV (745.94) and clusters II and III (525.61), whereas, least distance was exhibited between cluster IV and V (264.89) and cluster I and II (285.92). From the inter cluster distance data, it was noted that genotypes of cluster IV have considerable diversitywith genotypes from other clusters.Least intra cluster distance recorded in cluster I denote the presence of less divergence among the genotypes of this cluster. Based on cluster mean values (Table 7) of traits studiedand the distancebetween the clusters,selection of parents could be done for hybridization to develop the varieties with trait of interest.Consumers prefers mostly fine grain rice in their daily diet, hence genotypes from cluster IV can be used in breeding program for developing high yielding fine grain rice varieties. Similarly, JGL 18047 (Cluster III) could be good source for development of short duration cultures and MTU 1001 (Cluster II) for developing high yielding varieties with good test weight and optimum plant height. Cluster I exhibited good mean values forgall midge tolerance than other clusters as all the genotypes showing moderate resistance reaction included in this cluster. Thus, making crosses between genotypes from clusters I and IV having greater inter cluster distance could generate fine grain varieties with gall midge tolerance. Possibility of deriving short duration varieties with fine or coarse grain nature is high from the crosses involving parents from clusters III and IV. Highest contribution towards total divergence was made by days to 50%

flowering (38.10%) followed by 1000 grain weight (20.78%) and grain yield (19.91%). Hence present experimental material is good source for developing varieties with different duration groups like short and medium and grain types like fine, super fine and coarse nature. The findings pertaining to cluster means, inter and intra clusters distances, percent contribution towards total divergence are in accordance to the results of Prasanna *et al.* (2022),Likitha *et al.* (2023), Bhargavi *et al.* (2023) andBandela Chandana *et al.* (2024)

4. CONCLUSIONS

Out of 22 entries tested, four entries namely JGL 44143, JGL 44146, JGL 44147 and JGL 44088 showed moderate resistance which can be used as parents in future breeding program. Grain yield, number of grains per panicle, 1000 grain yield and gall midge resistance can be improved through simple selections. These traits also exhibited high value of both heritability and genetic advance which are governed by additive genes and said to be fixed.High inter cluster distances were noticed between clusters III and IV and I and IV, hence hybridization between genotypes belongs to these clusters would generate desirable segregants.Days to 50% flowering, 1000 grain weight and yield contributed maximum towards total divergence, hence, present experimental material could be good source for developing high yielding varieties of different duration groups and grain segments.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

REFERENCES

Allard, R.W. (1960). Principles of plant breeding. Publishers by John Wiley and Sons Inc. New York USA. 485.

Anil Kumar, Suresh, J., Srinivas, B., Narendra Reddy, C., & Omprakash, S. (2022). Identification of New Sources of Resistance to Rice Gall Midge Biotype 3 (GMB 3) Prevailing in Jagtial, Telangana, India. *International Journal of Plant and Soil Science,34*(20), 764-769.

Anusha, Ch., Padma Kumari, A. P., Uma Maheshwari, Malathi, S., Omprakash, S., & Damodar Raju, Ch. (2017). Evaluation of rice pre-breeding lines for gall midge resistance. *Agriculture Update,12*(5), 1300-1307.

Anusha, K., Srinivas, B., Hari, Y., Gouri Shankar, V., Omparakash, S., & Shravan Kumar, R. (2024). Genetic Variability Studies for Yield and Yield Attributing Traits in Rice (*Oryza sativa* L.) Genotypes. *Journal of Experimental Agriculture,46*(8), 700-709.

Bandela Chandana, Adheena Ram, A., Seeja, G., Surendran, M., &Susha, S. (2024). Genetic Diversity Analysis of Rice (*Oryza sativa* L.) Genotypes for Yield and Sheath Blight Screening. *Journal of Advances in Biology & Biotechnology,27*(11), 413-420.

Bentur, J. S., Rawat, N., Divya, D., Sinha, D. K., Agarwal, R., &Atray, I. (2016). Rice-gall midge interactions: Battle for survival. *Insect Physiology,84,* 40-49.

Bhargavi, B., Suneetha, Y., Aravind Kumar, J., & Srinivas, T. (2023). Genetic divergence studies for yield and quality traits in high protein landraces of rice (*Oryza sativa* L.). *Plant Science Today,10*(2), 195-204.

Burton, G. W. (1952). Quantitative inheritance in grasses. *Proceedings of sixth International Congress*, 277–283.

Chhodavadiya, R. J., Patel, P. B., Patel Harsh., Naveena, Y. K.V., Bharda, S. P., & Sampurna Bhattacharya. (2023). Genetic Divergence and Variability Assessment of Rice (*Oryza sativa* L.) Genotypes for Yield and its Contributing Traits. *International Journal of Environment and Climate Change,13*(12), 1008-1016.

Gonya Nayak, P.,Madhukar, P., Laxmi Prasanna B., & Srinivas, B. (2023). Genetic Analysis of Quantitative Traits, Gall Midge and Brown Spot Tolerance in Rice (*Oryza sativa* L.) Genotypes under Irrigated Ecosystem. *International Journal of Environment and Climate Change,13*(11), 1467-1478.

Hima Bindu, P., Sundaram, R. M., Shiva Prasad, G., Damodar Raju, Ch., & Sumalini, K. (2024). Studies on Genetic Variability and Heritability in Rice Genotypes (*Oryza sativa*. L.) under Salinity. *Journal of Advances in Biology & Biotechnology,27*(10), 1007-1016.

IRRI. (2013). Standard Evaluation System for Rice, International Rice Research Institute, Los Banos, Philippines.

Likhita, U., Madhu Kumar, K ., Harita, T., & Udaya Babu, P. (2023). Genetic Divergence for Yield and its Components in Gall midge Resistant Rice Genotypes (*Oryza sativa* L.). *The Andhra Agricultural Journal,70* (2), 165-171.

Mahalanobis, P. C. (1936). On the generalized distance in statistics. *Proceedings of the National Institute of Sciences of India, 2*(1), 49–55.

Mounika, J., Krishna Veni, B., Rani Chapara., & Bhuvaneswari, V. (2024). Genetic variability and association studies in rice (*Oryza sativa* L.). *The Andhra Agricultural Journal,71*(1), 23-28.

Prasanna, G., Eswari, K. B., Senguttuvel, P., Narendar Reddy, S., Sundaram, R. M., Beaulah, P., & Veerendra, J. (2022). Studies on genetic divergence and screening of parental lines for *Rf3* and *Rf4* genes through molecular markers in hybrid rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding,13*(4), 1170-1179.

Rahul Kumar Maurya, Dwivedi, D. W., Khan, N. A., Giri, S. P., & Saurabh Dixit. (2022). Genetic variability studies for qualitative and quantitative traits in rice (*Oryza sativa* L.). *The Pharma Innovation Journal,11*(5), 1140-1143.

Robinson, H. F., Comstock, R. E., & Harvey, P. H. (1949). Estimation of heritability and the degree of dominance in corn. *Agronomy Journal, 41*(8), 353–359.

Shravan Kumar, R., Malathi, S., & Jagan Mohan Rao, P. (2020). Screening of certain rice entries against Asian rice gall midge, Orseolia oryzae (Wood-Mason) in Warangal, Telangana. *Journal of Entomology and Zoology Studies,8*(5), 1888-1893.

Siddiq, E. A. (1991). Genes and rice improvement. *Oryza*, *28,* 1-7.

Sivasubramanian., &Madhavamenon. (1973). Genotypic and Phenotypic variability in rice. *Madras Agricultural Journal*, *60*(9–12), 1093–1096.

Sourav Paramanik, M., Subba Rao., Rashmi, K., Koustava Kumar Panda., & Aninda Chakraborty. (2023). Studies on genetic variability, heritability and genetic advance for quantitative traits and nutritional traits in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding,14*(4), 1537-1537.

Sreedhar Siddi., & Anil Deva. (2020). Genetic variability studies for gall midge incidence, yield and its components in rice (*Oryza sativa* L.) genotypes in Northern Telangana. *Journal of Entomology and Zoology Studies,8*(4), 821-825.

Tripti Singh, P. K., Singh, R. K., Yadav, Prateek Saxena., & Saloni Singh. (2024). Assessment of Genetic Variability, Character Association of Yield Related Traits and Genetic Divergence Study in Rice (*Oryza sativa* L.). *International Journal of Plant & Soil Science,36*(9), 545-555.

Table 1: List of 22 rice genotypes under study with source and pedigree

S.No	Entry	Pedigree	Source
1	JGL 44085	NSN 1/95-2016 X RNR 15048	RARS, Jagtial, PJTAU
2	JGL 44086	NSN 1/95-2016 X RNR 15048	RARS, Jagtial, PJTAU
3	JGL 44088	NSN 1/95-2016 X RNR 15048	RARS, Jagtial, PJTAU
4	JGL 44089	NSN 1/95-2016 X RNR 15048	RARS, Jagtial, PJTAU
5	JGL 44143	(NSN 1/296-2016 X JGL 24423) X JGL 11727	RARS, Jagtial, PJTAU

6	JGL 44144	(NSN 1/296-2016 X JGL 24423) X JGL 11727	RARS, Jagtial, PJTAU
7	JGL 44146	(NSN 1/296-2016 X JGL 24423) X JGL 11727	RARS, Jagtial, PJTAU
8	JGL 44147	(NSN 1/296-2016 X JGL 24423) X JGL 11727	RARS, Jagtial, PJTAU
9	JGL 44148	(NSN 1/296-2016 X JGL 24423) X JGL 11727	RARS, Jagtial, PJTAU
10	JGL 44150	(NSN 1/296-2016 X JGL 24423) X JGL 11727	RARS, Jagtial, PJTAU
11	JGL 44152	(NSN 1/296-2016 X JGL 24423) X JGL 11727	RARS, Jagtial, PJTAU
12	JGL 44158	(NSN 1/296-2016 X JGL 24423) X JGL 11727	RARS, Jagtial, PJTAU
13	JGL 44163	(JGL 30292 X MUT NS1)X JGL 13595	RARS, Jagtial, PJTAU
14	JGL 44165	(JGL 30292 X MUT NS1)X JGL 13595	RARS, Jagtial, PJTAU
15	JGL 44167	(JGL 30292 X MUT NS1)X JGL 13595	RARS, Jagtial, PJTAU
16	JGL 44168	(JGL 30292 X MUT NS1)X JGL 13595	RARS, Jagtial, PJTAU
17	JGL 44173	(JGL 30292 X MUT NS1)X JGL 13595	RARS, Jagtial, PJTAU
18	JGL 44174	(JGL 30292 X MUT NS1)X JGL 13595	RARS, Jagtial, PJTAU
19	JGL 18047	MTU 1010 X JGL 13595	RARS, Jagtial, PJTAU
20	RNR 15048	MTU 1010 X JGL 3855	IRR, Hyderabad, PJTAU
21	JGL 11470	JGL 418 X Gedongibeton	RARS, Jagtial, PJTAU
22	MTU 1001	MTU 5249 X MTU 7014	RARS, Maruteru, ANGRAU

Table 2: ANOVA for 22 rice genotypes of 8 characters

Source of variation	**Degrees of freedom**	**Days to 50 % flowering**	**Effective bearing tillers/M2**	**Plant height**	**Panicle length**	**1000 grain weight**	**Number of grains/panicle**	**Percent of galls (%)**	**Grain yield (kg/ha)**
Replications	1	4.45**	1420.45	223.65**	3.96	3.90	1872.02	76.61*	302286.60
Treatments	21	46.74**	1072.98	132.67**	8.97**	19.15**	3132.61**	101.90**	3855312.74**
Error	21	0.17	969.45	5.86	1.11	1.08	1086.17	11.13	682675.66

Table 3: Reaction of 22 rice genotypes screened against gall midge (biotype 3)

S.No	**Entry**	**% silver shoots**	**Score**	**Gall midge reaction**
1	JGL 44085	11	7	S
2	JGL 44086	7	5	MS
3	JGL 44088	5	3	MR

4	JGL 44089	9	5	MS
5	JGL 44143	2	3	MR
6	JGL 44144	8	5	MS
7	JGL 44146	4	3	MR
8	JGL 44147	5	3	MR
9	JGL 44148	6	5	MS
10	JGL 44150	11	7	S
11	JGL 44152	10	5	MS
12	JGL 44158	11	7	S
13	JGL 44163	22	7	S
14	JGL 44165	16	7	S
15	JGL 44167	21	7	S
16	JGL 44168	11	7	S
17	JGL 44173	14	7	S
18	JGL 44174	13	7	S
19	JGL 18047	22	7	S
20	RNR 15048	32	9	HS
21	JGL 11470	9	5	MS
22	MTU 1001	15	7	S

HS: Highly susceptible, S: Susceptible, MS: Moderate susceptible, MR: Moderate resistance

Table 4: Genetic variability parameters for yield, yield components and percent of galls

Character	**Range**		**GCV**	**PCV**	**h^2 (Broad Sense)**	**GA in % over mean**
	Min	**max**				
Days to 50% flowering	93	117	4.76	4.78	99.3	12.53
Effective bearing tillers/M2	348	436	1.9	8.43	5.1	1.13

Plant height	114	145	6.05	6.33	91.5	15.29
Panicle length	24	33	7.26	8.22	78	16.94
1000 grain weight	12	26	16.24	17.19	89.3	40.51
Number of grains/panicle	95	269	15.73	22.58	48.5	28.92
Percent of galls (%)	2	32	55.88	62.34	80.3	132.19
Grain yield (kg/ha)	4024	9393	17.81	21.3	69.9	39.3

Table 5: Grouping of genotypes into different clusters

Cluster	**No. of genotypes**	**Name of the genotype**
I	18	JGL 44085, JGL 44086, JGL 44088, JGL 44089, JGL 44143, JGL 44144, JGL 44146, JGL 44147, JGL 44148, JGL 44150, JGL 44152, JGL 44158, JGL 44163, JGL 44165, JGL 44167,JGL 44168, JGL 44173, JGL 44174
II	1	MTU 1001
III	1	JGL 18047
IV	2	RNR 15048, JGL 11470

Table 6: Intra (Diagonal) and inter cluster distances (Tocher method) of the 22 rice genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	61.32	285.92	367.89	927.52
Cluster II		0	525.61	745.94
Cluster III			0	2094.45
Cluster IV				264.89

Table 7: Cluster means and percent contribution of 8 traits towards total divergence

Cluster	**Days to 50% flowering**	**Effective bearing tillers/M2**	**Plant height (cm)**	**Panicle length (cm)**	**1000 grain weight (g)**	**No. of grains/panicle**	**Percent galls (%)**	**Yield (kg/ha)**
Cluster I	100	378	133.2	27.6	18.27	211	10.40	7134

Cluster II	103	372	114.2	25.1	25.75	157	15.41	8023
Cluster III	93	434	115.6	24.3	26.15	95	22.21	7130
Cluster IV	115	357	133.2	26.9	13.2	214	20.24	6031
Times ranked first	88	0	16	9	48	1	23	46
Percent contribution	38.10	0.00	6.93	3.90	20.78	0.43	9.96	19.91