

Genetic Divergence for Yield and its Components in Gall midge Resistant Rice Genotypes (*Oryza sativa* L.)

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ABSTRACT

Fifty rice gall midge resistant genotypes were evaluated during *Kharif*, 2022 for genetic diversity by Mahalonobis D^2 analysis for nine yield and its component characters under late sown conditions. In the present study based on D^2 analysis, 50 genotypes were grouped into 7 clusters. Considerable extent of genetic divergence between genotypes in the present study was observed by magnitude of D^2 values. The maximum inter-cluster distance was found between cluster IV and cluster VII. Greater inter cluster distance indicating the presence of greater diversity between genotypes of these groups. Days to fifty percent flowering, test weight and total grains per panicle contributed maximum towards divergence.

Keywords: *Gall midge resistant, Genetic divergence and Rice.*

Rice is a cereal crop belonging to genus *Oryza* of family Poaceae and it is the major staple food crop for majority of global population. Next to China, India is the second largest producer and consumer of rice. The rice gall midge *Orseolia oryzae* has been one of the major insect pests in many Asian countries. In India gall midge damage causes an average annual yield loss of about 477 thousand tons of grain or 0.8% of the total production amounting to US\$ 80 million (Bentur *et al.*, 2003). Gall midge being an endophytic pest, breeding rice varieties has been a viable and ecologically acceptable approach to manage this pest. Prasad Rao *et al* (2004) reported that inheritance of gall midge resistance is governed by major genes. The systematic breeding for gall midge resistance in India was boosted with the introduction of high-yielding varieties in 1965. Five cultivary with built-in resistance to gall midge were released as varieties for commercial cultivation in the country during the 1970s, 28 during the 1980s, and more than 15 since then. The majority of these varieties carried a single gene from three known resistance sources. These varieties made a big impact on yield advantage and lowering of pest incidence during the first decade of cultivation. Deploying a single gene in any variety

and its wide cultivation would only lead to a new cycle of boom and bust as evidenced in the past.

The development of virulent biotypes accompanied by a breakdown in resistance is being reported in many pest endemic regions in the country. The initial response of breeders to this situation has been to look for alternate sources of resistance against new biotypes and incorporate the resistance. Knowledge of genetic variability present in a given crop species for the character under improvement is of paramount importance for the success of any plant breeding program. Keeping in view of the importance, the objectives of the study were to estimate the genetic diversity among the gall midge resistant genotypes to provide a basis for crop improvement through selection of parents for hybridization.

Materials and Methods

The experimental material used in the study comprised of 50 genotypes with 47 gall midge resistant genotypes and 3 susceptible genotypes. All genotypes were evaluated for grain yield and their attributing characters following Alpha Lattice Design with three replications during *Kharif* season, 2022 at Agricultural Research Station, Ragolu, Srikakulam, India. Transplanting was done 30 days after sowing

of seeds in nursery bed in a 6 m² plot. Plant to plant distance was 10 cm, row to row distance was 30 cm and the crop was raised as per recommended package of practices to ensure normal crop. Data on plant height (cm), total number of tillers/ m², EBT/ m², panicle length (cm), number of filled grains per panicle, total grains per panicle, gall midge incidence (% tillers) were recorded on 10 plants per genotype in each replication and were used for statistical analysis. However data on days to fifty percent flowering, test weight (g), grain yield (kg) were recorded on plot basis per genotype per replication. Data was subjected to Mahalanobis D² analysis to study the genetic divergence between genotypes. Based on the D² values the 50 genotypes studied were grouped into clusters of genetically closer groups following the Tocher's method as described by Rao (1952).

Results and Discussion

The performances of 47 genotypes along with three checks were evaluated for various morphological and yield characters. The 50 genotypes subjected to D² analysis revealed the presence of considerable amount of genetic diversity among them. Based on D² values, 50 genotypes were grouped into 7 clusters. The distribution of genotypes into different clusters is presented in Table 1. Each cluster consisted of a different number of genotypes ranging from 15 to 1. Cluster II contained the highest number of genotypes *i.e.*, 15 genotypes followed by 13 genotypes in cluster I, 9 genotypes each in clusters III and VI and 2 genotypes in cluster IV. V and VII clusters consisted of single genotype in each cluster. The clustering pattern revealed that the genotypes from different sources clustered together was an indication of no association between eco-geographical distribution of genotypes and genetic divergence. Similar reports were reported by Thippeswamy *et al.* (2016).

The data on cluster means is presented in Table 2. The cluster means for plant height (123.77 cm), days to fifty per cent flowering (126), panicle length (27.10 cm), total grains per panicle (240.33), filled grains per panicle (188.67) and grain yield (6780.09 kg/ha) were high where as test weight (19.05 g) was least in Cluster VII. cluster IV recorded high cluster mean for test weight (21.94 g) and least cluster means for the plant height (107.01 cm), days to fifty per cent

flowering (76.67 days), panicle length (21.74 cm), total grains per panicle (149.01), filled grains per panicle (133.00) and grain yield (3997.28 kg/ha). Cluster I had second high cluster mean values for total grains per panicle (209.86), filled test weight (21.88 g) and grain yield (6210.59 kg/ha). Cluster II had high mean values for total tillers per square meter (347.49) where as least number of tillers (323.26) was observed in cluster III.

Maximum inter-cluster distance suggested wider diversity between the groups; while minimum inter cluster distance indicated closer relationship. The inter cluster distances in most of the cases higher than the intra cluster distances suggesting genetic diversity among the genotypes of different clusters. These results are in agreement with reports from Mohan *et al.*, (2015). The values of intra and inter cluster distances for the 50 genotypes was determined and presented in Table 3. From the inter cluster distance values, it was clear that the maximum inter cluster distance was between cluster IV and cluster VII (2785.39) followed by cluster III and cluster VII (2378.24), cluster I and cluster IV (2221.48), cluster V and cluster VII (2087.95) indicating the presence of greater diversity between genotypes of these groups which could be exploited in crop improvement by considering these genotypes in selection of parents for hybridization. The lowest inter cluster distance was observed between cluster III and V (328.22) indicating that the genotypes of these clusters had genetic resemblance.

Considerable variation occurred in intra cluster distances ranged from 0 to 257.77, indicating wider diversity prevailing among the germplasm lines within clusters. The maximum intra cluster distance was in cluster VI (257.77) followed by cluster I (253.26), cluster III (233.67), cluster II (233.41), cluster IV (74.11) while it was zero for the remaining clusters (clusters V and VII), germplasm under the cluster VI was most heterogeneous and germplasm under clusters I, III, II and IV were comparatively homogeneous or less divergent. Genotypes falling in the cluster VI which were having high degree of divergence would produce more desirable novel recombinants and having more scope to select superior genotype for the trait of interest. Minimum inter-cluster distance was observed between cluster III and cluster V indicating their relatively closer relationship and similarity with regards to the

characters studied for most of the genotypes in the two clusters. Similar results were obtained by Ranjit *et al.* (2018), Sreedhar (2018), Siddi (2020) and Chandra *et al.* (2022).

Contribution of different characters towards genetic divergence revealed that maximum contribution was by days to fifty percent flowering (27.18) followed by test weight (23.26), total grain per panicle (20.40) and the results revealed that these three characters are contributing towards divergence and for discriminating genotypes. Similar results were reported by Eswaran *et al.* (2012) for days to fifty percent flowering and number of grains per panicle and Nirmaladevi *et al.* (2015) for test weight.

On the basis of the present finding, it can be concluded that genotypes under study were genetically

divergent. The genotypes RGL 2537 and MTU 2077 were divergent from other genotypes and had high mean values for yield and its component traits and shown moderately resistant reaction to gall midge. The genotypes PTB 10, JGL 384, JGL 11727, Erramallelu and luit were more divergent from RGL 2537 and crosses made between these genotypes leads to wide variability and transgressive segregants with high heterotic effects. Similar results were presented by Prasad Rao *et al.*, (2004) and Srinivas *et al.*, (2016). Adapted varieties and advanced breeding lines highly resistant to gall midge *i.e.*, RGL 11414, MTU 1341, MCM 100 and RGL 7005 can be used as parents in rice improvement programmes to develop high yielding gall midge resistant varieties.

Table. 1. Rice genotypes and their reaction to Gall midge Biotype-4

| S. No. | Genotype | Parentage/ Source | Reaction to Gall midge Biotype-4* |
|--------|----------------|---|-----------------------------------|
| V1 | Anjali | RR 19-2/RR 149-1129 | MR |
| V2 | IR 36 | IR 1561-228/ 1 IR 244/ <i>O.nivara</i> / CR 94-13 | MR |
| V3 | Suraksha | Sasyasree / MR 1523 | HR |
| V4 | Abhaya | CR157-392/OR57-21 | HR |
| V5 | Erramallelu | BC 5-55/W 12708 | MR |
| V6 | Phalguna | IR 8/Siam 29 | MR |
| V7 | Varalu | WGL 20471/ CR 544-1-2 | MR |
| V8 | RGL 1 | MTU-5/ MTU-10 | MR |
| V9 | RGL 52 | RGL-1/ IR-8 | MR |
| V10 | RGL 2624 | IR-8/ Tellahamsa | MR |
| V11 | RGL 2332 | BPT 5204/IR 64 | MR |
| V12 | RGL 2537 | T-145 X CR1014 | MR |
| V13 | RGL 2538 | Phalguna x IET 6858 | MR |
| V14 | Kharvela | Daya/IR 13240-108-2-2-3 | MR |
| V15 | Lalat | OBS 677/IR 2071//Vikram/W 1263 | R |
| V16 | Pratap | Kumar/CR 57-49 | MR |
| V17 | Luit | Heera/Annada | MR |
| V18 | Vasumathi | PR 109/Pak.Basmati | MR |
| V19 | RP-2068-18-3-5 | Swarnadhan x Velluthacheera | HR |
| V20 | Aganni | Local land race from Kerala | HR |
| V21 | JGL 11727 | JGL 420/ Vijetha | R |
| V22 | JGL 384 | Samba Mahsuri/Kavya | MR |
| V23 | RGL 11414 | RGL 4166/MTU 7029 | HR |
| V24 | RGL 1746 | BAM-3/ TN-1 | HR |
| V25 | RGL 1880 | RGL-1231/ Phalguna// RGL-1231/ IR-36 | MR |

| | | | |
|-----|----------------|--|----|
| V26 | MTU 1190 | MTU 1081/Swarnasub 1 | HR |
| V27 | MTU 1341 | MTU 1010/ KMP 149 | HR |
| V28 | MTU 1010 | Krishnaveni/ IR 64 | MR |
| V29 | MTU 2077 | Sowbhagya / ARC 5984 | MR |
| V30 | BPT 2270 | BPT 5204/CR 15MR 1523 | MR |
| V31 | BPT 2846 | MTU 1061/ IR 78585-64-2-4-3-1 | MR |
| V32 | RGL 7001 | RGL-4107 / Swarna | HR |
| V33 | RGL 7002 | RGL 232/RGL 3250 | HR |
| V34 | RGL 7005 | RGL – 3250/ Swarna | HR |
| V35 | RGL 7004 | Lalat/CR-308-408 | MR |
| V36 | RGL 7006 | Parijatham/RGL 10098 | HR |
| V37 | RGL 7013 | RGL-1880/JGL 1798 | MR |
| V38 | RGL 7014 | RGL-2538/NLR-34449 | MR |
| V39 | RGL 7015 | RGL-2538 X NLR-34449 | MR |
| V40 | MCM 100 | MTU 1042/MTU 1061 | HR |
| V41 | PTB33 | Pure line selection from Arikarai | HR |
| V42 | PTB 10 | Breeding line from Patambi | HR |
| V43 | SuduHondrawala | Local germplasm accession | MR |
| V44 | SinnaSivappa | Local germplasm accession | MR |
| V45 | Kalajira | Local selection from Kohlapur (MS) | MR |
| V46 | Parijatha | TKM-6 x TN1 | MR |
| V47 | Jhitpiti | Local germplasm accession from Chattisgarh | MR |
| V48 | MTU 7029 | Vasista/ Mahsuri | S |
| V49 | TN 1 | Dee Geo Woo Gen x Tsai-yuan-chung | HS |
| V50 | BPT 5204 | GEB 24 X TN1// MAHSURI | S |

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

Table 2. Distribution of 50 Genotypes into Clusters

| Cluster number | No. of genotypes | Genotypes in cluster | Name of the genotypes in the cluster |
|----------------|------------------|---|---|
| I | 13 | 35, 38, 32, 25, 33, 2, 6, 39, 24, 23, 20, 34, 10 | IR 36, Phalguna, RGL 2624, Aganni, RGL 11414, RGL 1746, RGL 1880, RGL 7002, RGL 7001, RGL 7005, RGL 7004, RGL 7014, RGL 7015 |
| II | 15 | 4, 40, 50, 3, 49, 9, 27, 41, 26, 45, 48, 13, 11, 36, 37 | Suraksha, Abhaya , RGL 52, RGL 2332, RGL 2538, MTU 1341, MTU 1190, RGL 7006, RGL 7013, MCM 100, PTB33, MTU 7029, TN 1, BPT 5204, Kalajira |
| III | 9 | 8, 21, 42, 22, 7, 1, 47, 15, 14 | Anjali, Varalu, RGL 1, Kharvela, Lalat, JGL 384, JGL 11727, PTB 10, Jhitpiti |
| IV | 2 | 5, 17 | Erramallelu, Luit |
| V | 1 | 29 | MTU 2077 |
| VI | 9 | 18, 43, 16, 28, 46, 30, 44, 31, 19 | Pratap, Vasumathi, Sudu Hondrawala, MTU 1010, Parijatha, BPT 2270, BPT 2846, RP-2068-18-3-5, Sinna Sivappa |
| VII | 1 | 12 | RGL 2537 |

Table 4. Average intra (diagonal) and inter cluster distances (Tocher’s method) for 50 rice genotypes

| | cluster 1 | cluster 2 | cluster 3 | Cluster 4 | Cluster 5 | Cluster 6 | Cluster 7 |
|-----------|---------------|---------------|---------------|--------------|-----------|---------------|-----------|
| Cluster 1 | 253.26 | 555.16 | 1817.71 | 2221.48 | 1527.33 | 1111.49 | 596.99 |
| Cluster 2 | | 233.41 | 1318.77 | 1719.53 | 1027.2 | 627.91 | 1085.53 |
| Cluster 3 | | | 233.67 | 443.92 | 328.22 | 758.37 | 2378.24 |
| Cluster 4 | | | | 74.11 | 699.33 | 1145.85 | 2785.39 |
| Cluster 5 | | | | | 0 | 469.51 | 2087.96 |
| Cluster 6 | | | | | | 257.77 | 1663.66 |
| Cluster 7 | | | | | | | 0 |

Clustering by Tocher’s Method

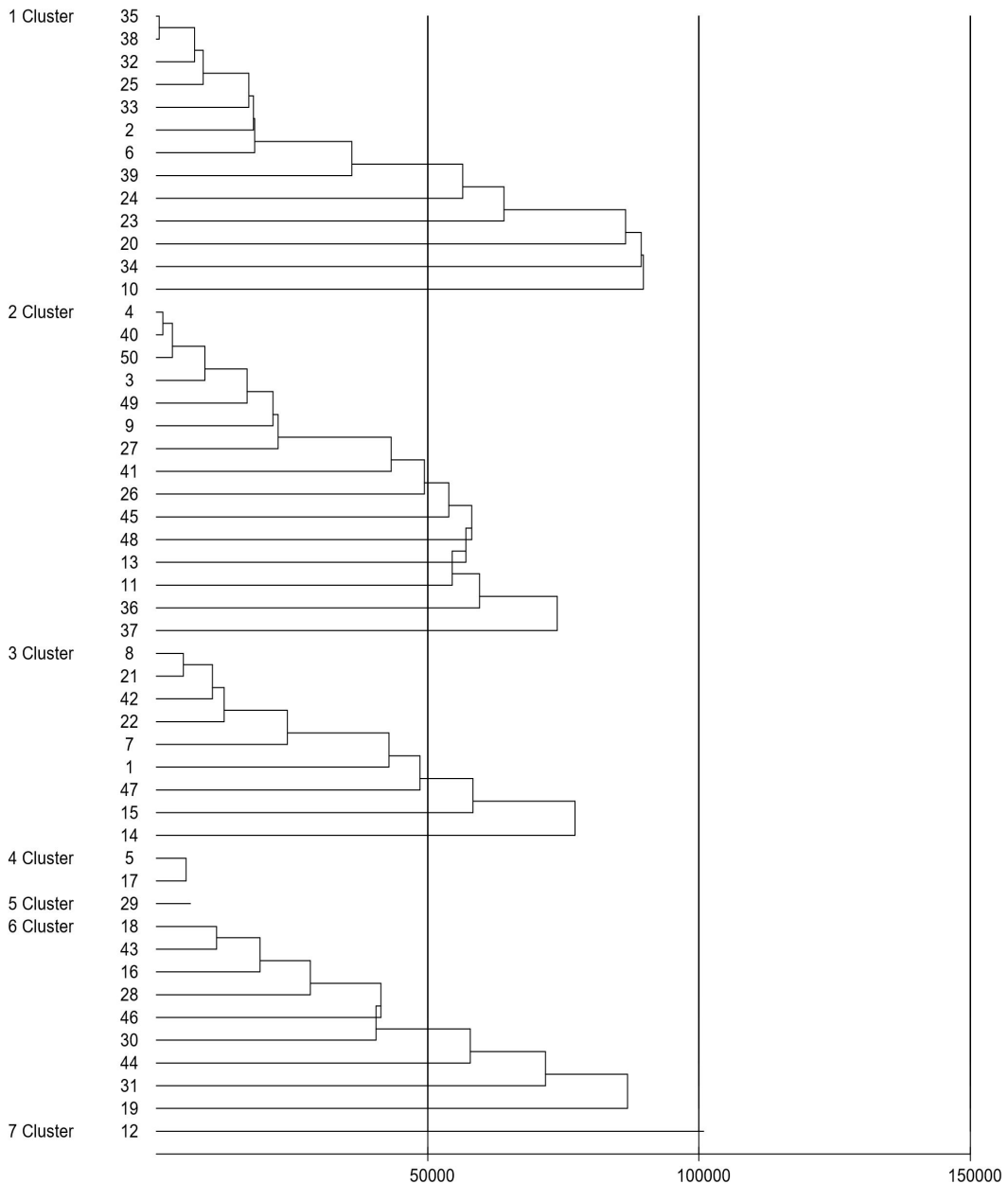


Table 3. Cluster Means Values for different characters

| Cluster group | Plant height | DFF | Total tillers/ sq.m | EBT/ sq.m | Panicle length | Total grains/ panicle | Filled grains/ panicle | Ill Filled grains/ panicle | Test weight | Grain yield |
|-----------------------|--------------|--------|---------------------|-----------|----------------|-----------------------|------------------------|----------------------------|-------------|-------------|
| Cluster I | 118.39 | 99.62 | 352.15 | 312.87 | 22.90 | 209.86 | 185.36 | 24.50 | 21.88 | 6210.59 |
| Cluster II | 115.27 | 105.98 | 347.49 | 301.37 | 23.57 | 202.80 | 178.71 | 24.08 | 20.37 | 5707.73 |
| Cluster III | 115.36 | 100.00 | 323.26 | 280.82 | 22.44 | 169.17 | 150.74 | 18.43 | 20.73 | 4409.08 |
| Cluster IV | 107.01 | 76.67 | 343.68 | 302.63 | 21.74 | 149.01 | 133.00 | 16.01 | 21.94 | 3997.76 |
| Cluster V | 110.20 | 119.00 | 358.10 | 303.23 | 23.93 | 165.60 | 149.00 | 16.60 | 20.91 | 4694.28 |
| Cluster VI | 121.92 | 103.59 | 367.72 | 326.80 | 24.27 | 208.27 | 186.85 | 21.41 | 19.69 | 5126.25 |
| Cluster VII | 123.77 | 126.00 | 346.33 | 315.48 | 27.10 | 240.33 | 188.67 | 51.67 | 19.05 | 6780.09 |
| Contribution % | 7.71 | 27.18 | 1.28 | 6.21 | 4.36 | 20.40 | 4.52 | 3.14 | 23.26 | 1.94 |

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