

## Studies on Genetic Variability in Gall midge Resistant Genotypes for Yield and its Components in Rice (*Oryza sativa* L.)

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### ABSTRACT

Fifty gall midge resistant genotypes in rice were evaluated during *Kharif*, 2022 for genetic diversity for yield and its component characters under late sown conditions. The analysis of variance has revealed significant differences among the genotypes for all the nine characters studied. The moderate per cent of GCV and PCV was recorded for days to 50% flowering, total tillers/ m<sup>2</sup>, EBT/ m<sup>2</sup>, filled grains per panicle, total grains per panicle, test weight and grain yield indicating the existence of moderate amount of variability for effective selection towards improvement of these traits. The heritability and genetic advance as per cent of mean is high for days to fifty per cent flowering, total tillers/ m<sup>2</sup>, EBT/ m<sup>2</sup>, filled grains per panicle, test weight, total grains per panicle and grain yield reflecting the existence of additive gene action in the expression of these traits. Therefore, simple direct selection may be effective for the improvement of these traits based on the phenotypic values.

**Key words:** *Rice, Variability, Gall midge and Resistant genotypes*

Rice is a cereal crop belonging to genus *Oryza* of family Poaceae. India is the second largest producer and consumer of rice after China. The rice gall midge *Orseolia oryzae* has been one of the major insect pests in many Asian countries. Gall midge being an endophytic, breeding rice varieties has been a viable and ecologically acceptable approach to manage this pest. The yield component does not act independently and in general, they are interrelated with each other that ultimately bring about the grain yield in rice. 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. Heritability and genetic advance are important selection parameters while selection is made based on yield contributing traits. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. Keeping in view of the importance, the objectives of the study were to estimate the genetic variability among the gall midge resistant genotypes for yield and its traits.

### MATERIAL AND METHODS

The experimental material used in the study comprised of 50 genotypes includes 47 gall midge resistant genotypes and 3 susceptible genotypes. All genotypes were evaluated for grain yield and its 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 m<sup>2</sup> 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/ m<sup>2</sup>, EBT / m<sup>2</sup>, panicle length (cm), number of filled grains per panicle, total grains per panicle were recorded on 10 plants per genotype in each replication and were used for statistical analysis. However data on days to 50% flowering, test weight (g), grain yield (kg) were recorded on plot basis per genotype per replication.

The analysis of variance for different characters was carried out in order to assess the

genetic variability among genotypes. Both phenotypic and genotypic coefficient of variability for all characters as estimated using the formula of Burton and De Vane (1953). The broad sense heritability ( $h^2$ ) was estimated for all characters as the ratio of genotypic variance to the total or phenotypic variance as suggested by Lush (1949) and Hanson *et al.* (1956). Genetic advance for each character was estimated by using the formula of Johnson *et al.* (1955). Genetic advance as per cent mean was categorized as suggested by Johnson *et al.* (1955).

## RESULTS AND DISCUSSION

The Analysis of variance has revealed significant differences among the genotypes for all the nine characters studied. The ANOVA and the estimates of GCV, PCV, heritability, genetic advance and genetic advance as percent of mean are presented in Table.1 and Table. 2 respectively. A wide range of variation was observed among fifty rice genotypes for nine yield contributing traits and yield as well. This suggested that there were inherent genetic differences among the genotypes. Phenotypic variance was higher than the genotypic variances for all the traits thus indicated the influences of environmental factor on these traits. Coefficient of variation studied indicated that estimates of phenotypic coefficient of variation (PCV) were higher than the corresponding genotypic coefficient of variation (GCV) for all the traits indicating that they all interacted with the environment to some extent. Bhadru *et al.* (2012) also reported similar results in rice. The overall range of PCV found between 9.07 (panicle length) and 19.72 (number of filled grains per panicle) while the overall range of GCV was from 8.03 (panicle length) to 18.91 (number of filled grains per panicle). The moderate percent of GCV and PCV was recorded for days to 50% Flowering, total tillers / m<sup>2</sup>, EBT / m<sup>2</sup>, filled grains per panicle, total grains per panicle, test weight, grain yield indicating the existence of moderate amount of variability for effective selection towards improvement of these traits. The low GCV and moderate PCV values was recorded for plant height. The low GCV and PCV values was recorded for panicle length indicating little scope for improvement of these traits through selection.

The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore, high heritability helps in effective selection for a particular trait. Heritability was classified

as low (below 30%), medium (30-60%) and high (above 60%) as suggested by Johnson *et al.* (1955). The traits studied in the present investigation expressed high heritability estimates ranging from 69 to 99 percent. Among the traits, high heritability was observed for days to 50% flowering followed by test weight, total grains per panicle, filled grains per panicle, plant height, panicle length, total tillers/ m<sup>2</sup>, EBT / m<sup>2</sup>, grain yield. Similar results were earlier reported by Ravi Kumar *et al.* (2015) for days to 50% flowering, Allam *et al.* (2015) for plant height and Dhurai *et al.* (2014) for number of grains per panicle and panicle length. High heritability values indicate that the traits under study are less influenced by environment in their expression.

The Genetic advance as percent of mean is high >20% for total grains/panicle followed by filled grains /panicle, DFF, test weight, EBT / m<sup>2</sup>, Total tillers/ m<sup>2</sup> and grain yield. Moderate genetic advance (10-20%) was observed in panicle length and plant height. These results are in agreement with Bisne *et al.* (2009) for the characters days to 50% flowering, EBT / m<sup>2</sup> test weight and grain yield and Thippeswamy *et al.* (2016) for plant height, filled grains per panicle, total grains per panicle, DFF, total tillers/ m<sup>2</sup>, EBT / m<sup>2</sup> and test weight.

Heritability should be considered along with genetic advance as per cent of mean, however it is not necessary that character showing high heritability will also exhibit high genetic advance (Johnson *et al.*, 1955). The heritability and genetic advance as per cent of mean is high for days to fifty per cent flowering, total tillers / m<sup>2</sup>, EBT / m<sup>2</sup>, filled grains per panicle, test weight, total grains per panicle and grain yield reflecting the existence of additive gene action in the expression of these traits. Therefore, simple direct selection may be effective for the improvement of these traits based on the phenotypic values. These results are in conformity with the earlier findings of Dhurai *et al.* (2014) for total grains per panicle, Srujana *et al.* (2017) for grain yield, tillers per plant and test weight and Bisne *et al.* (2009) for grain yield. High heritability coupled with moderate genetic advance as per cent of mean was observed for characters panicle length and plant height suggesting both additive and non-additive gene action. These results are in accordance with the earlier findings of Ravi Kumar *et al.* (2015) for plant height and panicle length and Thippeswamy *et al.* (2016) for plant height.

**Table 1. Analysis of variance for yield and yield components among 50 genotypes of rice (*Oryza sativa* L.)**

Source of Variation	Treatment	Residuals
Degree of Freedom	49	96
Mean Sum of Squares		
Plant Height (cm)	399.35	25.6
DF	668.76	1.87
Total tillers/ m <sup>2</sup>	6976.7	727.8
Ear bearing Tillers/ m <sup>2</sup>	6165.2	745.1
Panicle Length (cm)	11.483	0.963
Total Grains/Panicle	4018.1	95.2
Filled Grains/Panicle	3346.4	94.6
Ill filled grains/panicle	152.416	36.526
Test Weight (g)	23.7527	0.1954
Grain yield (kg)	1708214	222836

\*Significance codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

**Table 2. Mean variability, heritability and genetic advance as per cent of mean for yield and yield component traits in rice (*Oryza sativa* L.)**

S. No.	Character	Mean	Range		Coefficient of variation		Heritability (broad sense) (%)	Genetic advance as per cent of mean
			Maximum	Minimum	GCV (%)	PCV (%)		
1	Days to 50% flowering	102.31	133.33	68.67	14.57	14.6	99.15	29.89
2	Plant height (cm)	117.03	145.98	95.77	9.52	10.5	81.71	17.73
3	Total tillers/ m <sup>2</sup>	348.02	457.03	239.23	13.18	15.3	74.02	23.36
4	Ear bearing Tillers/ m <sup>2</sup>	305.61	413.22	198.59	14.03	16.7	70.52	24.28
5	Panicle length (cm)	23.32	28.16	19.97	8.03	9.07	78.37	14.64
6	Filled Grains/Panicle	174.65	268	125	18.91	19.7	91.99	37.37
7	Total Grains/Panicle	197.42	297.75	144.6	18.52	19.2	93.21	72.73
8	Test Weight (g)	20.77	25.81	13.78	13.51	13.7	97.55	27.48
9	Grain Yield (kg)	5415.1	6780.09	3972	13.12	15.8	69.02	22.45

GCV= Genotypic coefficient of variation

PCV= Phenotypic coefficient of variation

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