



DIVERSITY ANALYSIS FOR YIELD AND GALL MIDGE RESISTANCE IN RICE (*Oryza sativa* L.) IN NORTHERN TELANGANA ZONE, INDIA

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SUMMARY

Rice (*Oryza sativa* L.) is one of the most important food crops and a primary source of food for more than half the world's population. Gall midge is an important pest especially during rainy season with delayed sowings resulting in huge losses to the farm produce. Host plant resistance is proven method for enabling protection from gall midge incidence. Use of diverse parents and knowing inheritance of traits helps breeders to develop new varieties. Forty-three genotypes derived through pedigree method of breeding involving 11 divergent parents were evaluated for variability and genetic divergence. The GCV and PCV were high for gall midge incidence, number of grains per panicle and test weight whereas low for panicle length, plant height, effective bearing tillers per hill, days to flowering. High to moderate values of heritability and genetic advance were observed for test weight, number of grains per panicle revealed the predominance of additive gene effects. Grain yield recorded significantly positive correlation with plant height, test weight and days to flowering. Test weight had significant positive correlations with gall midge incidence indicating fine grain varieties were relatively tolerant and bold grain varieties were susceptible. Path analysis revealed that maximum direct effect on grain yield was exhibited by test weight followed by plant height, number of grains per panicle. D² studies revealed that highest inter cluster distance (8.69) was observed between cluster II & V followed by cluster II & III (7.87) suggesting wide diversity between traits. Among the traits studied, test weight and days to flowering contributed highest. The genotypes grouped in cluster II could be crossed with JGL 21002 and JGL 21005 of cluster III to derive transgressive segregants for improvement of grain yield, number of grains per panicle and test weight.

Key words: Rice, *Oryza sativa* L., variability, correlations, genetic divergence, gall midge incidence

Key findings: Host plant resistance is feasible and economical way for the control of gall midge pest. It would be of immense need to study the extent of diversity and association among various traits including gallmidge incidence. The study enabled the selection of parents for breeding the gall midge resistance apart from identifying the divergent groups for attempting crosses for further improvement.

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INTRODUCTION

Rice is the staple cereal food grain for more than half the world's population. Rice provides 21% of the global human per capita energy and 15% of per capita protein. Asia alone accounts for over 90% of the world's production of rice with China, India and Indonesia producing the most (Tyagi *et al.*, 2004).

Rice is grown in more than 23% of gross cropped area in India (about 40.0 M Ha.) being largest in the world with annual production of about 111 million tones. Even though quite good number of varieties were developed and released, the productivity levels were stagnated and far below than expected. More often majority of the high yielding varieties are not being accepted by the farmers due to lack of desired traits. It is very imperative to further refine the varieties with more yield, quality and pest resistance for wide acceptability and more production.

Gall midge, insect pest caused by *Orseolia oryzae* is endemic in Northern Telangana region of South India. More recently the incidence of gall midge was increased and yield losses were quite common. Significant advance had been made in developing rice varieties resistant to gall midge, but noted that it had proved difficult to provide farmers with varieties of acceptable grain quality and multiple resistance to gall midge (Henrichs and Pathak, 1981).

Estimation of genetic variability, heritability and genetic advance is prerequisite for attempting any breeding program as it provides basis for selection and scope of improvement. Heritability is the heritable portion of a character from parents to their offspring (Falconer, 1989). The estimate of heritability helps the plant breeders in selection of elite genotypes from diverse genetic populations. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection (Singh and Narayanan, 2006). However, the association analysis among the yield contributing trait along with their direct and indirect effects enables the breeders in selecting plants with high yield through characters of simple expression.

Study of genetic divergence is of great interest for plant breeder to formulate successful breeding program. It was proved in many cases that wider the divergence between the parents more choice for obtaining wide segregants to enable scope for selection of superior plants with desirable trait combinations. Multivariate analysis is an important tool for the assessment of genetic divergence. Sabesan and Saravanan (2008) indicated that there was no association between geographical distribution of genotypes and genetic distance. The possible reason for grouping of genotypes pertaining to different regions in one cluster could be the practice of unidirectional selection by breeder in tailoring the promising cultivars. Similarly the genotypes of one geographic region were distributed in different clusters (Senapati and Sarkar, 2005; Sabesan *et al.*, 2009; Banumathy *et al.*, 2010) which might be due to differential adaptation to varied agro-ecosystems.

Keeping in view of the importance, this study was formulated to: (1) assess the variability, heritability and genetic advance, (2) find out the extent of association among the various traits with yield and gall midge incidence (3) estimate the genetic diversity among the genotypes to enable for selection of genotypes for further improvement.

MATERIALS AND METHODS

The material for study comprised of 43 elite cultures developed through pedigree method of breeding involving 11 diverse parental lines (Table 1). It was confirmed with the previous study that there was enough diversity among the cultures even within sister cultures which might be due to various selection pressures. The investigation was carried out at Rice Research Scheme, Regional Agricultural Research Station, Polasa, Jagtial, Karimnagar District, Telangana, India during rainy seasons of 2011 and 2012. The experiment was laid out in randomized block design with two replications. The seed was raised on nursery beds and 25 days old seedlings were transplanted in main field under irrigated system. Kulkarni *et al.* (1989) indicated that incidence of gall midge was more in late sown crop. Hence, the date of sowing was

Table 1. List of genotypes studied along with pedigree and grain type.

Genotype	Pedigree	Grain type
JGL 20616	IET 20473 x JGL 11118	LS
JGL 20621	IET 20473 x JGL 11118	LS
JGL 20624	MTU 1010 X JGL 11118	LS
JGL 20634	MTU 1010 X JGL 11118	LS
JGL 20644	MTU 1010 X JGL 11118	LS
JGL 20668	JGL 11727 x JGL 11470	MS
JGL 20670	JGL 11727 x JGL 11470	LS
JGL 20753	MTU 1001 x JGL 11470	LS
JGL 20756	MTU 1001 x JGL 11470	LS
JGL 20769	MTU 1001 x JGL 13595	MS
JGL 20773	MTU 1001 x JGL 13595	MS
JGL 20776	MTU 1010 x JGL 13595	MS
JGL 20777	MTU 1010 x JGL 13595	MS
JGL 20778	MTU 1010 x JGL 13595	MS
JGL 20779	MTU 1010 x JGL 13595	MS
JGL 21002	MTU 1010 x JGL 11727	LS
JGL 21005	MTU 1010 x JGL 11727	LS
JGL 21031	MTU 1010 x JGL 11727	LS
JGL 21034	MTU 1010 x JGL 11727	LS
JGL 21037	MTU 1010 x JGL 11727	LS
JGL 21041	MTU 1010 x JGL 11727	LS
JGL 21051	MTU 1010 x JGL 11727	LS
JGL 21057	MTU 1010 x JGL 11470	MS
JGL 21062	MTU 1010 x JGL 11470	LS
JGL 21066	MTU 1010 x JGL 11470	LS
JGL 21071	MTU 1010 x JGL 11470	LS
JGL 21075	MTU 1010 x JGL 11470	LS
JGL 21078	MTU 1010 x JGL 11470	LS
JGL 21087	MTU 1010 x JGL 11470	LS
JGL 21088	MTU 1010 x JGL 11470	MS
JGL 21099	MTU 1010 x JGL 3844	LB
JGL 21106	MTU 1010 x JGL 3844	MS
JGL 21126	MTU 1010 x JGL 3855	LS
JGL 21129	MTU 1010 x JGL 3855	LS
JGL 21133	MTU 1010 x JGL 3855	LB
JGL 21136	MTU 1010 x JGL 3855	MS
JGL 21146	MTU 1010 x JGL 3855	LS
JGL 21163	MTU 1010 x JGL 384	LS
JGL 21164	MTU 1010 x JGL 384	LB
JGL 21166	MTU 1010 x JGL 384	LB
JGL 3855	Released variety from RARS, Jagtial	SS
MTU 1001	Released variety from APRRI, Maruteru	LB
MTU 1010	Released variety from APRRI, Maruteru	LS

intentionally delayed by 4 weeks than normal with a view to get natural occurrence of gall midge to screen against the insect.

Each culture was planted in 7.5 m² area by adopting row to row spacing of 15 cm and hill to hill 15 cm with 1-2 seedlings per hill. All the recommended package of practices were followed to ensure healthy crop growth. The data was recorded on 10 random plants per plot for effective bearing tillers per hill, plant height, panicle length, number of grains per panicle. Incidence of gall midge was recorded as percent tillers affected with silver shoots (IRRI, 2002) on 10 random hills and averaged. However, days to flowering, grain yield were recorded on whole plot basis (7.5 m²), whereas random sample was taken for estimation of test weight.

Statistical analysis

The data was subjected to analysis of variance (Panse and Sukhatme, 1985). The coefficient of variations (Burton, 1952), heritability in broad sense (Lush, 1940), genetic advance (Johnson *et al.*, 1955), correlations (Robinson *et al.*, 1951), direct and indirect effects (Dewey and Lu, 1959) were calculated as per standard statistical methods. Multivariate analysis was done as per Mahalanobis D² statistic described by Rao (1952) and the genotypes were grouped into different clusters following Tocher's method. Contribution of each character for genetic divergence was estimated from the number of times it appeared in first rank. These parameters were estimated using Windostat software version 8.1.

RESULTS AND DISCUSSIONS

Variability estimates

The analysis of variance revealed significant amount of variability among the cultures studied for all the eight characters (Table 2). The high level of significance for environments indicated that the performance of cultures vary from year to year depending on the existing climatic conditions.

The genotypic coefficient of variance (GCV) and phenotypic coefficient of variance

(PCV) were high for gall midge incidence (103.61, 114.99), number of grains per panicle (19.46, 24.88) and test weight (19.11, 19.61) whereas low for panicle length (5.91, 6.90), plant height (6.57, 8.57), effective bearing tillers per hill (7.58, 13.01), days to flowering (7.77, 8.19). Narrow difference between corresponding estimates of GCV and PCV for days to flowering, panicle length, test weight and plant height suggested that the environment had little role and predominance of additive gene effects in the expression of these traits. The results were in conformity with Sangam Kumar *et al.* (2011) for number of grains per panicle, test weight and Prajapati *et al.* (2011) for days to flowering and panicle length. Low PCV & GCV estimates for days to flowering and panicle length have also been reported by Shinha *et al.* (2004), Sangam Kumar *et al.* (2011) and Patil *et al.* (2003), respectively. However, PCV were considerably high than GCV estimates for number of grains per panicle, effective bearing tillers per hill and grain yield, indicating the existence of environmental role in expression and predominance of non-additive gene effects.

The heritability (broad sense) estimates were high for test weight (0.95), days to flowering (0.90), gall midge incidence (0.81) and panicle length (0.73), whereas low for effective bearing tillers per hill (0.34). Moderate heritability values were observed for number of grains per panicle (0.61), plant height (0.59) and grain yield (0.58). The results are in agreement with the findings of Sangam Kumar *et al.* (2011), Thomas and Gabriel (2012) for test weight, Ramanjaneyulu *et al.* (2014) for days to flowering and panicle length. Genetic advance as percent of mean was high for gall midge incidence (192.31) whereas moderate for test weight (38.35), number of grains per panicle (31.36) and low for effective bearing tillers per hill (9.10), plant height (10.39), panicle length (10.44) and grain yield (15.01). The results were in accordance for panicle length, grain yield, effective bearing tillers per hill, number of grains per panicle and contrary for test weight, plant height with Thomas and Gabriel (2012).

Heritability values along with the estimates of genetic advance should jointly be considered to arrive at a more reliable conclusion (Johnson *et al.*, 1955). Since

Table 2. Analysis of variance and genetic parameters for grain yield and its component characters in rice.

	DF	Days to Flowering	Effective Bearing Tillers/m ²	Plant Height (cm)	Panicle Length (cm)	Test Weight (g)	Number of grains/panicle	Grain Yield (Kg/plot)	Gall midge incidence (percent tillers)
Replications	1	9.30	749.31	129.77	4.96 *	0.71	47.09	0.20	1.33
Environments	1	62.88 **	106651.7 **	5183.2 **	148.09 **	117.07 **	2191.84 **	10.68 **	2.60
Interactions	1	1.14	125.64	15.12	1.49	11.47 **	22.35	1.50 **	2.16
Total	3	24.44 **	35842.21 **	1776.04 **	51.51 **	43.08 **	753.76	4.13 **	2.03
Treatments	42	221.52 **	3846.15 **	228.69 **	9.93 **	69.52 **	5054.53 **	1.35 **	23.48 **
Error	126	5.89	1258.35	34.05	0.82	0.92	691.43	0.21	1.29
Character Mean		94.5	336	106	25.5	21.67	170	5.58	2.27
Character Range		84 - 113	276 - 396	90 - 122	22.6 - 28.8	12.45 - 29.34	118 - 316	4.44 - 6.80	0.0 - 9.86
GCV		7.77	7.58	6.57	5.91	19.11	19.46	9.59	103.61
PCV		8.19	13.01	8.57	6.90	19.61	24.88	12.62	114.99
h ² (Broad Sense)		0.90	0.34	0.59	0.73	0.95	0.61	0.58	0.81
Genetic Advance as % of Mean 5%		15.20	9.10	10.39	10.44	38.35	31.36	15.01	192.31

** Significant at 1% level; * Significant at 5% level; GCV- Genotypic coefficient of variation; PCV-phenotypic coefficient of variation

Table 3. Genotypic (G) and Phenotypic (P) correlation coefficients among yield and yield contributing traits in rice.

		Effective Bearing Tillers/m ²	Plant Height (cm)	Panicle Length (cm)	Test Weight (g)	Number of grains/ panicle	Gall midge incidence (percent tillers)	Grain Yield (Kg/plot)
Days to Flowering	G	-0.2781 **	0.7899 **	0.4707 **	-0.2572 **	0.4127 **	-0.2173 **	0.2673 **
	P	-0.1186	0.6449 **	0.3730 **	-0.2353 **	0.3303 **	-0.2070 **	0.2270 **
Effective Bearing Tillers/m ²	G	1.0000	-0.3247 **	0.0444	0.1318	-0.3730 **	0.4118 **	-0.0174
	P	1.0000	-0.0777	-0.0367	0.0970	-0.2167 **	0.1851 *	0.0219
Plant Height (cm)	G		1.0000	0.5362 **	-0.0786	0.1820 *	-0.1737 *	0.3920 **
	P		1.0000	0.3649 **	-0.0211	0.1059	-0.1521 *	0.2706 **
Panicle Length (cm)	G			1.0000	0.1043	-0.0236	-0.2294 *	0.0481
	P			1.0000	0.0974	-0.0033	-0.1532 *	-0.0094
Test Weight (g)	G				1.0000	-0.8267 **	0.4815 **	0.3173 **
	P				1.0000	-0.6466 **	0.4180 **	0.2582 **
Number of grains/panicle	G					1.0000	-0.5303 **	-0.1493
	P					1.0000	-0.3579 **	-0.0894
Gall midge incidence (percent tillers)	G						1.0000	0.1383
	P						1.0000	0.1096

Gen: R² = 0.4074; RESIDUAL EFFECT = 0.7698Phe: R² = 0.2041; RESIDUAL EFFECT = 0.8921

Table 4. Genotypic (G) and Phenotypic (P) path coefficient analysis of various component characters on grain yield in rice.

		Days to Flowering	Effective Bearing Tillers/m ²	Plant Height (cm)	Panicle Length (cm)	Test Weight (g)	Number of grains/panicle	Gall midge incidence (percent tillers)	Grain Yield (Kg/plot)
Days to Flowering	G	0.0265	-0.0716	0.5075	-0.1754	-0.1792	0.1694	-0.0101	0.2673
	P	0.2603	-0.0038	0.1194	-0.0766	-0.0867	0.0188	-0.0043	0.2270
Effective Bearing Tillers/m ²	G	-0.0074	0.2574	-0.2086	-0.0165	0.0918	-0.1532	0.0192	-0.0174
	P	-0.0309	0.0324	-0.0144	0.0075	0.0358	-0.0123	0.0038	0.0219
Plant Height (cm)	G	0.0210	-0.0836	0.6425	-0.1998	-0.0548	0.0747	-0.0081	0.3920
	P	0.1679	-0.0025	0.1851	-0.0750	-0.0078	0.0060	-0.0031	0.2706
Panicle Length (cm)	G	0.0125	0.0114	0.3445	-0.3726	0.0726	-0.0097	-0.0107	0.0481
	P	0.0971	-0.0012	0.0675	-0.2054	0.0359	-0.0002	-0.0031	-0.0094
Test Weight (g)	G	-0.0068	0.0339	-0.0505	-0.0388	0.6966	-0.3394	0.0224	0.3173
	P	-0.0613	0.0031	-0.0039	-0.0200	0.3685	-0.0369	0.0086	0.2582
Number of grains/panicle	G	0.0110	-0.0960	0.1169	0.0088	-0.5759	0.4106	-0.0247	-0.1493
	P	0.0860	-0.0070	0.0196	0.0007	-0.2383	0.0570	-0.0074	-0.0894
Gall midge incidence (percent tillers)	G	-0.0058	0.1060	-0.0616	0.0555	0.3354	-0.2177	0.0465	0.1383
	P	-0.0539	0.0060	-0.0281	0.0315	0.1540	-0.0204	0.0205	0.1096

gall midge resistance is a qualitative trait high heritability and genetic advance was observed and selection for such trait is easier for improvement. High to moderate values of heritability and genetic advance were observed for test weight, number of grains per panicle revealed the predominance of additive gene effects and simple selection would be rewarding for improvement of the traits. However, moderate heritability with low genetic advance values for plant height, grain yield indicating the preponderance of non-additive gene effects and improvement through selection for such trait may not be useful. These results were contrary to the findings of Thomas and Gabriel (2012), Tandekar *et al.* (2010) for plant height, grain yield. Low heritability and genetic advance for effective bearing tillers per hill revealed that selection would be difficult for improvement of the trait.

Correlation and path coefficient analysis

Correlation coefficients were calculated to assess the relationship among seed yield and its component traits and presented in Table 3. Genotypic and phenotypic correlations were in perfect agreement with each other and relatively higher magnitude of former indicated the masking effect of the environment. Similar results were reported by Zahid *et al.* (2006) Khan *et al.* (2009). Grain yield recorded significantly positive correlation with plant height, test weight and days to flowering. The results clearly indicated that long duration genotypes with more height and bolder grains contribute for more grain yield. The results are in consonance with Ramanjaneyulu *et al.* (2014) for plant height and test weight. However, the finding agrees to statement of Cyprien and Kumar (2011) for days to flowering and contrary for test weight.

Test weight had significant positive correlations with gall midge incidence indicating fine grain varieties were relatively tolerant and bold grain varieties were susceptible. Positive correlation between effective bearing tillers per hill and gall midge incidence might be due to the fact that the gall midge induces more tillers. The result agrees with the findings of Ogunbayo *et*

al. (2010) and contrary to Bashir *et al.* (2013). However, number of grains per panicle, panicle length, days to flowering, plant height were significantly and negatively associated with gall midge incidence. Whereas, grain yield was found to be not associated with gall midge incidence significantly. Similar finding were reported by Bashir *et al.* (2013) for grain yield. Days to flowering showed significant positive correlation with plant height, panicle length, number of grains per panicle, whereas significant negative correlation with test weight and effective bearing tillers per hill. Plant height and panicle length were positively and significantly correlated. Ravindra Babu *et al.* (2012) reported positive correlation between plant height, panicle length and days to flowering. Test weight had highly significant negative correlation with number of grains per panicle.

Path coefficient analysis allows separating the direct and indirect effects through other attributes by apportioning the correlations (Wright, 1921) for better interpretation of cause and effect relationship. The results clearly showed significant difference in genotypic and phenotypic direct and indirect effects indicating the predominance of environmental influence in expression of the traits (Table 4). Perusal of results obtained in path analysis revealed that maximum direct effect on grain yield was exhibited by test weight followed by plant height, number of grains per panicle. However, panicle length showed highest negative direct effect on grain yield. These results were contrary to the reports of Ravindra Babu *et al.* (2012). Even though number of grains per panicle had positive direct effect on grain yield, it had high level of negative indirect effect through test weight resulting in negative correlation between grain yield and number of grains per panicle. It was primarily because of highly significant negative correlation between test weight and number of grains per panicle. Similarly days to flowering influence grain yield with high indirect positive effect via plant height besides having direct positive effect. Direct negative effect of panicle length on grain yield was nullified by indirect positive effect through plant height.

Table 5. Distribution of 43 rice genotypes into different clusters based on 8 traits.

Cluster	No. of genotypes	Genotypes
Cluster 1	27	JGL 20621, JGL 20624, JGL 20634, JGL 20644, JGL 20670, JGL 20756, JGL 20769, JGL 20773, JGL 20776, JGL 20777, JGL 20778, JGL 21031, JGL 21034, JGL 21037, JGL 21051, JGL 21071, JGL 21075, JGL 21078, JGL 21087, JGL 21126, JGL 21129, JGL 21133, JGL 21136, JGL 21146, JGL 21163, JGL 21164, JGL 21166
Cluster 2	7	JGL 20668, JGL 20779, JGL 21057, JGL 21062, JGL 21088, JGL 21106, JGL 3855
Cluster 3	1	JGL 21005
Cluster 4	5	JGL 20616, JGL 20753, JGL 21066, JGL 21099, Vijetha
Cluster 5	1	JGL 21002
Cluster 6	1	MTU 1010
Cluster 7	1	JGL 21041

Genetic divergence

On the basis of D^2 values, 43 genotypes were grouped into 7 clusters (Table 5). Cluster I was the largest comprised of 27 genotypes followed by cluster II with 7 genotypes and cluster IV with 5 genotypes. However, cluster III, V, VI and VII were consisted with single genotype each. The genotypes derived from 5 different pedigrees viz., JGL 20668, JGL 20779, JGL 21057, JGL 21088 were grouped in same cluster. It can be inferred that in majority of the breeding programs selection would be targeted towards plants with moderate height, medium early duration with good plant type. Hence, irrespective of pedigree of the genotype involving diverse parental lines, over the process of advancement through segregating generations, the diversity had been narrowed especially with reference to yield contributing traits.

In contrary, the genotypes derived from same pedigree viz., JGL 21002, JGL 21005, JGL 21041, JGL 21031, JGL 21037, JGL 21051 were grouped into 4 different clusters indicated the effect of directional selection for various traits in advancement of segregating population.

The intra cluster distance ranged from zero to 3.58 (Table 6). Even though cluster I comprised highest number of genotypes the intra cluster distance was only 3.26 indicating the similarity among the genotypes. However, inter cluster distance ranged from 7.2 to 8.69. Highest inter cluster distance (8.69) was observed

between cluster II & V followed by cluster II & III (7.87), cluster II & IV (7.65), cluster II & VII (7.62) suggesting wide diversity between traits. However, lowest inter cluster distance was noticed between cluster III & V (1.72) followed by cluster III & VI (2.49) and cluster V & VI (3.22) indicating that the genotypes of the cluster III, V & VI had genetic resemblance.

For the selection of genotypes and clusters considerable emphasis should be given to the characters contributing most to the divergence. Among the traits studied, test weight and days to flowering contributed considerably, accounting for 70.75% of total divergence indicating the importance of these traits for effective selections (Table 7). However, similar finding were reported by Karthikeyan (2002), Bhadru *et al.* (2012), Ramanjaneyulu *et al.* (2014) and Pandey *et al.* (2009) for test weight. Nevertheless, for days to flowering the results were contrary to the findings of Pandey *et al.* (2009). Number of grains per panicle, plant height and effective bearing tillers per hill contributed least towards divergence. The results are in agreement for number of grains per panicle and effective bearing tillers per hill and contrary for plant height with the findings of Pandey *et al.* (2009). The data on cluster means for eight characters (Table 7) revealed that the genotype (JGL 21005) in cluster III was recorded with highest grain yield and least days to flowering. Genotypes in cluster II were found to be good with respect to number of grains per panicle, grain slenderness and gall midge resistance.

Table 6. Average intra (diagonal) and inter cluster (above diagonal) distance values in rice.

Cluster No	I	II	III	IV	V	VI	VII
I	3.26	5.53	4.14	5.07	4.78	4.71	4.16
II		3.27	7.87	5.79	8.69	7.65	7.62
III			0.00	6.04	1.72	2.49	4.11
IV				3.58	6.21	5.89	5.29
V					0.00	3.22	4.08
VI						0.00	5.29
VII							0.00

Table 7. Cluster mean values and character contribution towards genetic divergence in 43 rice genotypes.

Cluster	Days to Flowering	Effective Bearing Tillers/m ²	Plant Height (cm)	Panicle Length (cm)	Test Weight (g)	Number of grains/panicle	Grain Yield (Kg/plot)	Gall midge incidence (percent)
I	91.2	333	104	25.4	22.55	163	5.56	2.14
II	98.0	337	109	25.1	14.70	223	5.29	1.20
III	90.5	372	102	24.2	27.44	146	6.80	5.40
IV	108.9	331	115	26.8	21.99	157	5.68	2.19
V	93.0	318	106	23.8	29.34	136	6.39	4.83
VI	92.5	374	107	24.1	25.54	118	5.97	9.56
VII	93.8	374	112	28.8	27.86	151	5.01	0.92
Times Ranked								
1st	218	12	11	66	448	2	24	122
Contribution %	24.14	1.33	1.22	7.31	49.61	0.22	2.66	13.51

The genotype (JGL 21002) in cluster V was recorded highest test weight and high grain yield whereas, the genotype (MTU 1010) in cluster VI had least number of grains per panicle and was found to be susceptible to gall midge. Hybridization program should always be formulated in such a way that the parents belonging to different clusters with maximum divergence to get desirable transgressive segregants.

Based on the inter cluster distances and means of cluster groups, the present investigation suggests that the genotypes grouped in cluster II could be crossed with JGL 21002 and JGL 21005 of cluster III with a view to derive transgressive segregants for

improvement of grain yield, number of grains per panicle and test weight. The genotypes JGL 21041 of cluster VII having least gall midge incidence (0.92%) could be utilized in hybridization program for development of gall midge resistant rice varieties.

CONCLUSION

Variability estimates infer that for number of grains per panicle, effective bearing tillers per hill and grain yield PCV were considerably high than GCV estimates indicating the existence of environmental role in expression and predominance of non-additive gene effects

whereas for other traits environmental influence was very less. The results of correlation and path coefficient studies conclude that improvement in grain yield might be possible by selecting plants with longer duration, more height and bolder grains. Genetic diversity studies suggested that the genotypes of cluster II, cluster V and cluster III may be crossed with each other to derive transgressive segregants for desirable varieties having more grain yield, grain number with super fine/ bold grains. The genotype, JGL 21041 could be exploited as donor for incorporating gall midge resistance through various breeding programs.

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