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Genetic Parameters and Divergence Studies for Gall Midge Incidence and Yield Components in Rice (*Oryza sativa* L.)

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ABSTRACT

The present investigation was carried out with 30 genotypes of rice (*Oryza sativa* L.) to study the variability and genetic divergence for yield contributing characters and gall midge incidence at Regional Agricultural Research Station, Warangal, Telangana during *kharif,* 2021 (July–November) in RBD replicated twice for eight quantitative traits. The phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV) for all traits, indicating that environmental influences affect the expression of these traits. High heritability coupled with high genetic advance as % of the mean values were observed for 1000 grain weight and number of grains panicle^{-1} suggesting that selection for the improvement of these traits may be rewarding. The PCA analysis showed that first three principal components accounted for about 91.57%. Based on D^2 studies, 30 genotypes were grouped into seven clusters with the cluster I (13) containing maximum number of genotypes followed by cluster III (9) and cluster II (4). Highest inter cluster distances were observed between the clusters IV and VII (1272.49) followed by IV and V (1097.39), VI and VII (1013.83) and II and VII (944.20) indicating the importance of the genotypes present in these clusters for exploiting heterosis for the desirable traits of these clusters. Days to 50% flowering (27.58%),1000-grain weight (27.36%) and plant height (27.36%) were found to be the most contributing traits towards total genetic diversity, which could be given due importance by the breeders for development of superior rice genotypes under crop improvement programme.

KEYWORDS: Gall midge incidence, D^2 statistics, rice, yield, PCA, variability, heritability

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1. INTRODUCTION

Rice (*Oryza sativa* L.), one of the most important food crops, supplies more than 20% of the global dietary energy and feeds more than half of the world's population (Birla et al., 2017). Owing to a fast-growing population, global rice consumption is projected to increase from 450 mt in 2011 to approximately 490 mt in 2020, and 40% more rice production is needed by 2050 to meet people's demand for food (Cheng et al., 2021). Most of the world's rice is cultivated and consumed in Asia, which constitutes more than half of the global population (Nithya et al., 2020). Many biotic and abiotic stresses often limit rice production. The Asian gall midge, *Orseoliaoryzae* (Wood-Mason) is one of the serious insect pests of rice responsible for causing an estimated annual yield loss worth more than US$700 million (Herdt, 1991). It is endemic in Central Telangana region of South India. In India gall midge damage causes an average annual yield loss of about 477 tt of grain or 0.8% of the total production amounting to US$ 80 million (Bentur et al., 2003). In India, it is rated as third most important pest of rice in terms of spread and severity of damage and yield loss (Bentur, 2015), next to stem borers and plant hoppers. Breeding of resistant rice varieties has proved to be a viable and ecologically acceptable approach for management of this pest.

The knowledge of the accessible genetic variability and complex relationships between the traits of interest are essential for all the crop improvement techniques (Dhanuja et al., 2021). The nature and magnitude of the genetic variation governing the inheritance of quantitative characters in rice is essential for a plant breeder (Singh et al., 2021). Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection (Singh and Narayanan, 2006). High genetic advance coupled with high heritability offers most effective condition for selection of a specific character (Devi et al., 2022). Variability through various genetic parameters in rice populations have been studied by several workers like Srinivas et al. (2016), Devi et al. (2020), Singh et al. (2020), Akshay et al. (2022) etc.

Genetic divergence determines the inherent potential of a cross for hybrid vigour and frequency of desirable recombinants in subsequent generations. The pace and magnitude of genetic improvement are generally dependent on the amount of genetic diversity present in a population (Kumbhar et al., 2015, Prasad et al., 2021, Raju et al., 2021, Siddi, 2020, Srinivas et al., 2016, Mohan et al., 2015). For rational use of genetic resources, information on genetic diversity within and among closely related crop varieties is required (Raju et al., 2021). Murthy and Arunachalam (1966) emphasized the importance of genetic diversity existing in the germplasm. Several workers viz. Ramanjaneyulu et al. (2014), Mohan et al. (2015), Srinivas et al. (2016) and Naik et al. (2021) used D^2 statistics for estimation of genetic divergence in the populations. The crosses among parents with maximum genetic divergence are better responsive in genetic improvement (Govindaraj et al., 2014). Therefore, knowledge about the genetic diversity present in the germplasm for different yield traits and pest tolerance is the key information for any breeder for initiation of breeding programme for crop improvement. Keeping this in view, present study was undertaken to estimate the variability and genetic diversity present among the genotypes for various yield components and identifying the high yielding and gall midge resistant genotypes for further crop improvement.

2. MATERIALS AND METHODS

The experimental material for present study was comprised of 30 rice cultivars (Table 1) developed through pedigree method of breeding at Regional Agricultural Research Station (RARS), PJTSAU, Warangal, Telangana, India which is located at 18°01'N Latitude, 79°60'E Longitude and at an elevation of 270 m above mean sea level (MSL). The material was laid out in a randomized block design during *kharif,* 2021 (July–November) at RARS, Warangal. 25 days age old seedlings of each entry was transplanted in 7.0 m^2 area with two replications by adopting spacing of 20×15 cm^2 between the rows and within the row. Two seedlings were planted at each hill. The crop was grown with the application of N, P and K fertilizer @ 120, 60 and 40 kg ha^{-1} respectively. All recommended package of practices and need based plant protection measures were followed to raise a good crop. Data were recorded at maturity on 10 random plants for each entry in each replication for number of productive tillers m^{-2}, plant height (cm), panicle length (cm) and number of grains $panicle^{-1}$. Days to 50% flowering and grain yield kg ha^{-1} were recorded on whole plot basis, whereas, random sample was used to estimate 1000 grain weight (g) for each entry in each replication. Central Telangana Zone is the hot spot for gall midge incidence where natural screening of this pest could result in identification of resistance genotypes. Moreover, as gall midge incidence is severe in late sown conditions, the experimental material was sown late for obtaining more incidence and gall midge incidence data was recorded as % tillers affected with silver shoots (following Standard Evaluation System for Rice, IRRI, 2002) on 10 random hills and averaged. The mean data after computing for each trait was subjected to analysis of variance (Panse and Sukhatme, 1995), genotypic and phenotypic coefficients of variation (Falconer, 1981), heritability (h^2) in the broad sense (Allard, 1960) and genetic advance (Burton, 1952) following standard procedures. The analysis of genetic divergence was done using Mahalanobis (1936) D^2 statistics. Grouping of genotypes into clusters was carried out following Tocher's method (Rao, 1952). Intra and inter cluster distances and mean performances of clusters for all the traits were also computed. 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 9.1 (Table 1).

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

Sl. No.	Genotype	Pedigree	Source	Grain type
1.	WGL 1775	HKR-08-62/RP-2068-18-3-5	RARS, Warangal	LS
2.	WGL 1776	HKR-08-62/RP-2068-18-3-5	RARS, Warangal	LS
3.	WGL 1777	HKR-08-62/JGL 19618	RARS, Warangal	LS
4.	WGL 1778	WGL 1100/Aganni	RARS, Warangal	LS
5.	WGL 1779	WGL 1100/ RP-2068-18-3-5	RARS, Warangal	LS
6.	WGL 1780	WGL 1100/ RP-2068-18-3-5	RARS, Warangal	LS
7.	WGL 1781	WGL 1100/ RP-2068-18-3-5	RARS, Warangal	LS
8.	WGL 1782	WGL 1100/ RP-2068-18-3-5	RARS, Warangal	LS
9.	WGL 1783	WGL 1100/ RP-2068-18-3-5	RARS, Warangal	LS
10.	WGL 1784	WGL 1100/ RP-2068-18-3-5	RARS, Warangal	LS
11.	WGL 1785	WGL 1100/ RP-2068-18-3-5	RARS, Warangal	LS
12.	WGL 1786	WGL 1100/ RP-2068-18-3-5	RARS, Warangal	LS
13.	WGL 1787	WGL 1100/ RP-2068-18-3-5	RARS, Warangal	LS
14.	WGL 1788	WGL 1100/ RP-2068-18-3-5	RARS, Warangal	LS
15.	WGL 1789	WGL 1100/JGL 19618	RARS, Warangal	LS
16.	WGL 1790	WGL 1100/JGL 19618	RARS, Warangal	LS
17.	WGL 1791	WGL 1100/JGL 19618	RARS, Warangal	LS
18.	WGL 1792	WGL 1100/JGL 19618	RARS, Warangal	LS
19.	WGL 1793	BPT 5204/RP 5332-54	RARS, Warangal	MS
20.	WGL 1794	BPT 5204/JGL 19618	RARS, Warangal	LS
21.	WGL 1795	WGL 915/MTU 1010	RARS, Warangal	LS
22.	WGL 1796	WGL 915/MTU 1010	RARS, Warangal	LS
23.	WGL 1797	WGL 915/MTU 1010	RARS, Warangal	LS
24.	WGL 1798	WGL 1100/ RP 5332-54	RARS, Warangal	LS
25.	WGL 1799	MTU 1162/ RP-2068-18-3-5	RARS, Warangal	MS
26.	WGL 1800	MTU 1156/ RP-2068-18-3-5	RARS, Warangal	LS
27.	WGL 1801	MTU 1156/ RP-2068-18-3-5	RARS, Warangal	MS
28.	RNR 15048	Released variety	RRC, Rajendranagar	SS
29.	KNM 118	Released variety	ARS, Kunaram	LS
30.	SOMNATH	Released variety	RARS, Warangal	MS

LS: Long slender; MS: Medium slender; LB: Long bold; SS: Short slender

3. RESULTS AND DISCUSSION

Analysis of variance (Table 2) revealed significant differences among the genotypes for all the characters studied indicating the presence of considerable amount of variability among the genotypes for gall midge incidence and yield and its component traits. Significant genetic variation in various component characters might be effective. Mean data (Table 3) on various characters revealed that WGL

Table 2: Mean squares corresponding to various sources of variation for 8 characters in rice

Source of variation	Degrees of freedom	Mean sum of squares							
		Days to 50% flowering	No. of productive tillers m^{-2}	Plant height (cm)	Panicle length (cm)	No. of grains panicle^{-1}	1000 grain weight (g)	Grain yield (kg ha^{-1})	Gall midge incidence (%)
Replications	1	0.067	1570.817	1.233	1.601*	3.75	0.081	213010.4	2.886**
Treatments	29	55.221**	1154.334**	230.415**	2.963**	3528.05**	34.69**	1217525.0**	12.669**
Error	29	0.377	377.299	1.641	0.368	316.405	0.596	435153.78	0.282

*Significant at (p=0.05) level; **at (p=0.01) level

Table 3: Mean values of 8 characters for 30 rice genotypes

Genotype	Days to 50% flowering	No. of productive tillers m^{-2}	Plant height (cm)	Panicle length (cm)	No. of grains panicle^{-1}	1000 grain weight (g)	Grain yield (kg ha^{-1})	Gall midge incidence (%)
WGL 1775	97	320	149.6	30.8	217	21.9	6071	6.35
WGL 1776	98	305	142.2	29.2	253	22.5	5103	1.32
WGL 1777	92	322	158.9	30.4	244	18.4	4985	4.55
WGL 1778	94	358	147.4	29.2	169	23.8	5566	0.50
WGL 1779	96	340	124.9	27.1	172	25.6	5284	3.68
WGL 1780	97	340	129.9	30.0	210	25.0	5936	5.31
WGL 1781	101	297	127.7	28.4	218	25.0	5103	3.33
WGL 1782	88	322	131.4	29.1	154	30.7	5793	0.40
WGL 1783	101	337	120.6	27.5	200	25.0	3907	3.04
WGL 1784	92	292	151.4	29.6	192	26.7	4151	6.62
WGL 1785	95	350	129.3	28.5	181	24.3	5086	2.72
WGL 1786	91	348	146.9	28.4	213	24.2	4985	2.66
WGL 1787	92	310	124.8	27.2	173	23.2	5035	2.85
WGL 1788	94	254	131.2	28.7	160	23.9	3890	3.87
WGL 1789	108	337	127.6	28.3	195	23.7	6206	0.00
WGL 1790	108	337	121.7	26.7	219	22.4	5835	0.00
WGL 1791	105	345	126.4	27.9	249	23.8	7426	3.06
WGL 1792	94	350	133.6	27.9	203	26.1	5717	0.36
WGL 1793	101	337	148.8	28.4	238	14.3	5557	4.25
WGL 1794	92	320	129.9	30.0	191	24.6	5465	6.94
WGL 1795	93	355	133.0	30.5	186	26.2	6778	6.30
WGL 1796	92	373	132.9	30.2	205	23.1	6812	5.36
WGL 1797	91	333	134.9	29.1	200	22.9	5052	7.12
WGL 1798	93	333	143.6	28.5	234	23.2	5039	0.00
WGL 1799	92	332	143.6	29.1	268	16.9	5785	1.18
WGL 1800	90	350	131.1	27.7	248	19.5	5431	0.00
WGL 1801	98	330	146.7	29.3	242	14.9	6227	1.33
RNR 15048	96	350	135.8	27.0	307	11.6	5751	7.18
KNM 118	90	368	119.4	26.3	144	22.8	5481	6.97

Table 3: Continue...

Genotype	Days to 50% flowering	No. of productive tillers m^{-2}	Plant height (cm)	Panicle length (cm)	No. of grains panicle^{-1}	1000 grain weight (g)	Grain yield (kg ha^{-1})	Gall midge incidence (%)
Somnath	102	328	117.3	26.9	325	16.0	5524	5.64
Mean	95.60	332.38	135.75	28.57	213.51	22.76	5499	3.43
CV	0.64	7.82	0.95	2.12	8.33	3.45	11.99	15.48
SEm±	0.43	18.40	0.90	0.42	12.57	0.54	466.45	0.37
CD (*p*=0.05%)	1.25	-	2.61	1.24	36.38	1.57	1349.16	1.08

1782, WGL 1800 and KNM 118 recorded least maturity durations, whereas, WGL 1789 and WGL 1790 recorded highest flowering durations among all the genotypes. WGL 1775 (30.8 cm) and WGL 1795 (30.5 cm) were characterized by bearing long panicles. Long Slender grain genotype WGL 1782 exhibited highest 1000 grain weight (30.70 g) and least was recorded for short slender grain genotype RNR 15048 (11.60 g), WGL 1793 (14.30 g) and WGL 1801 (14.90 g). Somnath and RNR 15048 which have medium slender and short slender grain types respectively recorded highest number of grains panicle^{-1}, whereas, KNM 118 recorded least. Highest gall midge incidence (7.18) was exhibited by RNR 15048 and the genotypes WGL 1789, WGL 1790, WGL 1798 and WGL 1800 were characterized by zero gall midge incidence. Maximum grain yield was observed for WGL 1791 (7426 kg ha^{-1}) followed by WGL 1796 (6812 kg ha^{-1}), whereas, low yield (3890 kg ha^{-1}) was observed for WGL 1788.

The extent variability with respect to studied quantitative characters was measured in terms of mean, range, PCV, GCV, heritability and genetic advance (Table 4). Higher phenotypic coefficient of variation (PCV) values than genotypic coefficient of variation (GCV) indicating the role of environmental forces in the inheritance of these traits. Similar findings were earlier reported by Devi et al. (2022), Mahesh et al. (2022), Srinivas et al. (2016), Nirmaladevi et al. (2015) and Mohan et al. (2015). Higher PCV and GCV values were observed for gall midge incidence (74.20, 72.56) followed by number of grains panicle^{-1} (20.53, 18.77) which could be improved through selection in desirable direction. whereas, moderate values for 1000 grain weight (18.77, 18.45) and grain yield kg ha^{-1} (16.53, 11.37) and low values for number of productive tillers m^{-2} (9.10, 4.65), Plant height (7.99, 7.94), days to 50% flowering (5.51, 5.47) and Panicle length (4.52, 3.99). Narrow difference between corresponding estimates of GCV and PCV for days to 50% flowering, panicle length, number of productive tillers m^{-2} and plant height suggested that the environment had little role and predominance of additive gene effects in the expression of these traits. whereas, in case of gall midge incidence more difference indicated susceptibility of this trait to environmental fluctuations. These results are in agreement with findings of Srinivas et al. (2016), Mohan et al. (2015) for gallmidge incidence and number of grainspanicle^{-1}, Singh et al. (2020) for number of productive tillers m^{-2} and plant height, Devi et al. (2022) and Hossain

Table 4: Mean, coefficient of variation, heritability (broad sense), genetic advance and genetic advance as per cent of mean for 8 characters in rice

Character	Mean	Range		GCV	PCV	h^2 (b) (%)	Genetic advance	Genetic advance as % of mean (5%)
		Minimum	Maximum					
Days to 50% flowering	95.0	88	108	5.47	5.51	98.6	10.71	11.20
Number of productive tillers m^{-2}	332.0	254	374	4.65	9.10	26.0	16.23	4.88
Plant height (cm)	134.75	117.0	158.9	7.94	7.99	98.6	21.87	16.23
Panicle length (cm)	28.57	26.3	30.8	3.99	4.52	77.9	2.07	7.24
No. of grains panicle^{-1}	213.51	144.0	324.5	18.77	20.53	83.5	75.45	35.33
1000 grain weight (g)	22.37	11.55	30.65	18.45	18.77	96.6	8.36	37.36
Grain yield kg ha^{-1}	5499.0	3890.0	7425.50	11.37	16.53	47.3	886.48	16.12
Gall midge incidence (%)	3.4297	0.00	7.18	72.56	74.20	95.6	5.014	146.18

h^2 (b)=Heritability in broad sense; GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation et al. (2020) for number of grains panicle^{-1}, for grain yield kg ha^{-1} and 1000 grain weight, Aditya and Bhartiya (2013) and Devi et al. (2022) for days to 50% flowering, plant height and panicle length; Singh et al. (2020) and Devi et al. (2020) for days to 50% flowering.

The heritability (broad sense) estimates (Table 4) were high for plant height (98.6%), days to 50% flowering (98.6%), 1000 grainweight (96.6%), gall midge incidence (95.6%), number of grains panicle^{-1} (83.5%) and panicle length (77.9%), whereas low for number of productive tillers m^{-2} (26.0%). Moderate heritability values were observed for grain yield kg ha^{-1} (47.3%). The results are in agreement with the findings of Akshay et al. (2022) for number of grainspanicle^{-1} and plant height, Nithya et al. (2020) for number of productive tillers m^{-2}, Singh et al. (2020b) for panicle length and 1000 grain weight, Devi et al. (2022) for days to 50% flowering and Mohan et al. (2015) for grain yield kg ha^{-1}. Selection of best genotypes based on both heritable estimates and genetic advance values is more reliable than selecting based on heritable values alone, because observed variation in a population is due to both factors i.e., genetics and environmental whereas, genetic variability is the only heritable in nature so the heritability alone does not give an idea about the expected gain in the next generation therefore it has to be considered in combination with the genetic advance (Srinivas et al., 2016). The characters those exhibit maximum heritability and high genetic advance as % of mean could be used as powerful tool in selection process, such characters are controlled by the additive genes and less influenced by the environment (Panse and Sukhatme, 1995). In the present investigation, high heritability estimates coupled with high genetic advance values were observed for 1000 grain weight and number of grains panicle^{-1} which indicated that these traits were predominantly governed by the additive genes which could be improved through simple selection procedures. Similar results were reported by Akshay et al. (2022), Devi et al. (2022) and Devi et al. (2020). High heritability and low values of genetic advance were recorded for panicle length, whereas, number of productive tillers per hillexhibited moderate levels of heritability estimates and low genetic advance value indicating that these traits are under control of non-additive genes and improvement of these traits through mere selection is not useful, therefore, breeder should go for heterosis breeding and recurrent selection methods for improvement of these characters. These results are in conformity with the findings of Devi et al. (2020), Pratap et al. (2018) and Mohan et al. (2015). High to moderate values of heritability and genetic advance were observed for days to 50% flowering and plant height revealed the predominance of additive gene effects and simple selection would be rewarding for improvement of these traits. These results are in accordance with the findings of Singh et al. (2020) for days to flowering and Devi et al. (2022) for plant height. Moderate heritability and moderate genetic advance as a % of mean were observed for grain yield indicating that simple selection would be effective. The trait gall midge incidence expressed high heritability and high genetic advance as % of mean which indicated the predominance of additive genes in governing the inheritance of this trait. There for the selection of this trait would be very effective for breeding programmes. Mohan et al. (2015) reported that gall midge resistance is a qualitative trait high heritability and genetic advance was observed and selection for such trait is easier for crop improvement. In contrary, Srinivas et al. (2016) reported that the trait gall midge incidence expressed moderate heritability and high genetic advance which indicated the predominance of additive genes in governing the inheritance of this trait and selection based on phenotype could be done in the negative direction to eliminate or reduce the trait in successive breeding populations.

D^2 statistics grouped the 30 rice genotypes into seven different clusters based on genetic distances (Figure 1). The composition of the various clusters obtained from the D^2 analysis is presented in Table 5. Cluster I was the largest comprised of 13 genotypes followed by cluster III with 9 genotypes and cluster II with 4 genotypes (Figure 1). According to Siddi (2020) total 32 genotypes were grouped into 12 clusters of which cluster I was the largest consisting of 12 genotypes followed by cluster II and III having 9 and

Table 5: Distribution of 30 rice genotypes into different clusters based on 8 traits

Cluster	No. of genotypes	Genotypes grouped
Cluster I	13	WGL 1779, WGL 1780, WGL 1781, WGL 1783, WGL 1785, WGL 1787, WGL 1788, WGL 1792, WGL 1794, WGL 1795, WGL 1796, WGL 1797, WGL 1800
Cluster II	4	WGL 1789, WGL 1790, WGL 1791, SOMNATH
Cluster III	9	WGL 1775, WGL 1776, WGL 1777, WGL 1778, WGL 1784, WGL 1786, WGL 1798, WGL 1799, WGL 1801
Cluster IV	1	WGL 1793
Cluster V	1	KNM 118
Cluster VI	1	RNR 15048
Cluster VII	1	WGL 1782

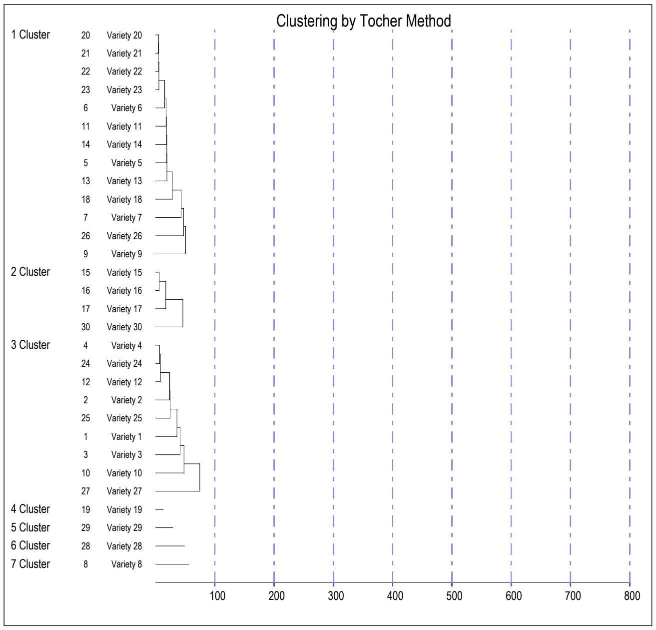

Figure 1: Dendrogram representing the grouping of 30 rice genotypes by Tocher's Method

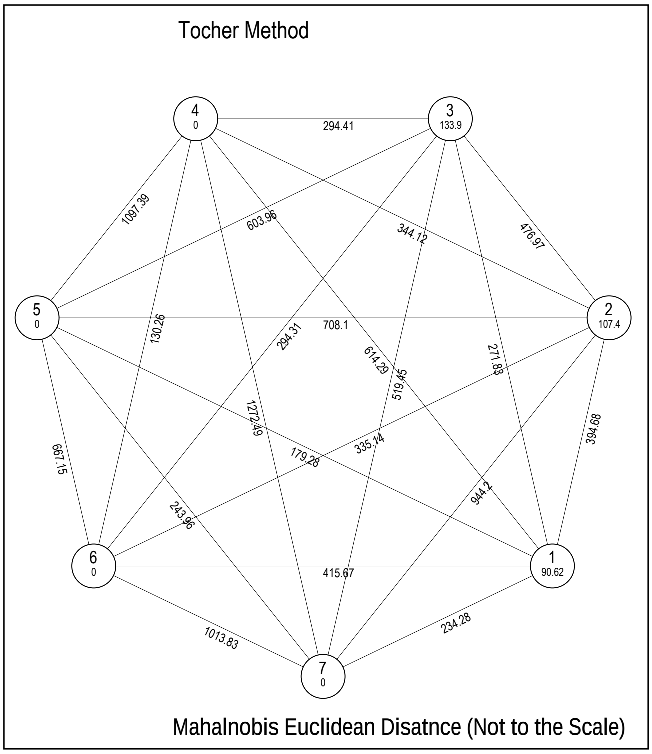

Figure 2: Cluster diagram depicting intra and inter-cluster distances between 30 rice genotypes

2 genotypes, respectively. Researchers had grouped 30 low land rice genotypes in to four distinct clusters. Sing et al. (2021) grouped 112 rice genotypes into 7 clusters, wherein cluster I had the highest number of genotypes (73) followed by cluster III with 22 genotypes. Similar results were also reported by Prasad et al. (2021). However, cluster IV, V, VI and VII were consisted with single genotype each. It might be due to their different genetic makeup from that of other germplasm lines in the present study. Similar results of greater genetic diversity for the genotypes in the mono-genotypic clusters were also reported by Prasad et al. (2021), Raju et al. (2021), Siddi (2020), Srinivas et al. (2016) and Mohan et al. (2015).

The average intra and inter-cluster distances is presented in Table 6 and diagrammatically represented in Figure 2. The intra cluster distance ranged from 0–133.9 Even though cluster I comprised highest number of genotypes the intra cluster distance was only 90.62 indicating the similarity among the genotypes. However, inter cluster distance ranged from 130.26–1272.49. Highest inter cluster distance (1272.49) was observed between cluster IV & VII followed by cluster IV & V (1097.39), cluster VI & VII (1013.83), cluster II & VII (944.20) (Figure 2) which indicated the existence of high genetic diversity among genotypes in these clusters, and therefore crosses between the genotypes of these clusters could yield desirable transgressive segregants. Similar explanation was given by Amegan et al. (2020), Singh et al. (2020b) and Prasad et al. (2021). Higher genetic distance was noticed between mono-genotypic cluster IV (WGL 1793) and other mono-genotypic cluster VII (WGL 1782). These genotypes may be used for developing early and medium duration genotypes. Moreover, it was interesting to note that in most of the cases, cluster VII produced the highest inter cluster value with all other

Table 6: Average intra (diagonal) and inter cluster distances (Tocher's method) for 30 rice genotypes

Cluster	I	II	III	IV	V	VI	VII
I	90.62	394.68	271.83	614.29	179.29	415.67	234.28
II		107.40	476.97	344.62	708.10	335.14	944.20
III			133.90	294.41	603.96	294.31	519.45
IV				0.00	1097.39	130.26	1272.49
V					0.00	667.15	243.96
VI						0.00	1013.83
VII							0.00

clusters. This suggests that genotype (WGL 1782) of cluster VII has the potential to be used for hybridization programme to produce breeding material with high yield and other maximum probability of desirable traits as well. These results are in consonance with Siddi (2020) and Singh et al. (2020b). However, lowest inter cluster distance was noticed between cluster IV & VI (130.26) followed by cluster I & V (179.29), cluster I & VII (234.78) and cluster V & VII (243.96) indicating that the genotypes of the cluster I, V, VI & VII had genetic resemblance. The genotypes derived from different pedigrees were grouped in the same cluster viz. I, II and III indicated that selection would be targeted towards desirable plant types in the majority of the breeding programmes for rice crop improvement. Hence, the diversity had been narrowed irrespective of pedigree of the genotype over the process of advancement through segregating generations (Siddi, 2020).

In contrary, the genotypes derived from same pedigree viz., WGL 1779, WGL 1780, WGL 1781, WGL 1782, WGL 1783, WGL 1784, WGL 1785, WGL 1786, WGL 1787, WGL 1788 were grouped into 3 different clusters indicated the effect of directional selection for various traits in advancement of segregating population.

Principal Component Analysis is (PCA) showed two most informative principal components with eigen values of 2191.75 and 1325.14, respectively (Table 7), which together accounted 81.18% of the total variance for all the characters. According to first principal component, traits such as days to 50% flowering (0.52), plant height (0.21), number of grains panicle^{-1} (0.13) and number of productive tillers m^{-2} (0.11) had relatively higher contributions (50.59%) to the total variation, while principal component 2 accounted for 30.59% of the total variation with days to 50% flowering (0.52) and number of productive tillers m^{-2} (0.12) giving the highest contribution. The analysis of eigenvectors recorded the information of morphological traits for % of variation to the third principle component, which was 10.38 with 1000-grain weight (0.56), days 50% flowering (0.26) and plant height (0.22) and had higher contribution. Similarly, Siddi (2020) reported the first two principal components accounting for 90.15% of total variation for all the characters studied. The PCA analysis showed that the first eight principal components accounted for about 85.4% of the total variation and exhibited very high correlation among them reported by Naik et al. (2021).

Table 7: Eigenvectors and eigen values of the first three principal components of 8 traits in rice

Variable	Eigenvectors		
	PC1	PC2	PC3
Eigene value	2191.75	1325.14	449.95
Variation (%)	50.59	30.59	10.38
Cumulative Var. Exp.	50.59	81.18	91.57
Days to 50% Flowering	0.52	0.50	0.26
Number of productive tillers m^2	0.108	0.115	0.037
Plant height (cm)	0.213	-0.779	0.215
Panicle length (cm)	0.024	0.006	0.053
Number of grains panicle^{-1}	0.132	-0.314	-0.115
1000 grain weight (g)	-0.735	0.065	0.564
Grain yield kg ha^{-1}	0.046	-0.138	0.051
Gall midge incidence (%)	-0.320	0.049	-0.738

PC: Principal component

Cluster means of all the characters is presented in Table 8. The cluster mean values varied in all the clusters for all the 8 quantitative traits studied. Cluster II recorded the highest mean values for grain yield kg ha^{-1} (6297.4) and more incidence of gall midge (2.18%), whereas cluster III genotypes characterized highest for panicle length (29.36). Further, the clusters IV, V, VI recorded the highest mean values for one trait each viz., plant height (148.0), number of productive tillers m^{-2} (368.0) and number grains per panicle (307.0) respectively. Cluster VII genotype (WGL 1782) was characterized with gall midge resistance (0.40%), early in flowering (88.0 days) and 1000 grain weight (30.5 g) including good grain yield (5793.0 kg ha^{-1}), hence this genotype could be used for obtaining gall midge resistant, high yielding, early duration, and long slender grain varieties. The results indicated the existence of high genetic diversity among genotypes in these clusters, therefore, genotypes in these clusters can be used for specific trait improvement in plant breeding programmes. Also, such crosses are likely to yield considerable heterotic effect. Similar results were explained by Siddi (2020) and Prasad et al. (2021).

The % contribution of each trait (Table 8) towards total divergence showed that days to 50% flowering (27.58%), 1000 grain weight (27.36%) and plant height (27.36%) contributed considerably, accounting for 82.30% of total divergence indicating the importance of these traits for effective selections whereas, remaining traits viz. gall midge incidence (15.63%), grain yield kg ha^{-1} (1.15%), number of productive tillers m^{-2} (0.46%), panicle length (0.23%) and number of grains panicle^{-1} (0.23%) contributed least towards divergence which are of less importance in selection of diverse parents. Similar results were reported by Naik et al. (2021) and Singh et al. (2020b) for days to 50% flowering, Banumathy et al. (2010) and Panday et al. (2009) for plant height, Siddi (2020), Srinivas et al. (2016) and Mohan et al. (2015) for days to 50% flowering and 1000 grain weight. In contrary to this, the contribution of number of grains panicle^{-1} was high towards genetic divergence reported by

Table 8: Cluster mean values and character contribution towards genetic divergence in 30 rice genotypes

Cluster	Days to 50% flowering	No. of productive tillers m^2	Plant height (cm)	Panicle length (cm)	No. of grains panicle^{-1}	1000 grain weight (g)	Grain yield (kg ha^{-1})	Gall midge incidence (%)
I	94.15	331.46	129.52	28.65	195.77	24.16	5345.69	3.91
II	105.63	336.75	123.25	27.44	246.88	26.44	6297.63	2.18
III	94.06	326.61	147.81	29.36	225.61	21.36	5323.44	2.72
IV	101.00	337.00	148.80	28.35	237.50	14.30	5557.00	4.25
V	90.0	368.00	119.40	26.30	144.00	22.75	5481.50	6.97
VI	96.0	349.50	135.80	26.95	307.00	11.55	5750.50	7.18
VII	88.0	321.50	131.40	29.10	154.00	30.65	5793.00	0.40
Times ranked first	120	2	119	1	1	119	5	68
Contribution %	27.58	0.46	27.36	0.23	0.23	27.36	1.15	15.63

Prasad et al. (2021). Since, Days to 50% flowering (27.58%), 1000 grain weight (27.36%), Plant height (27.36%) and gall midge incidence (15.63%) exhibited more contribution to the divergence, the present experimental material could be used for developing high yielding rice varieties with desirable grain types and maturity durations.

4. CONCLUSION

High PCV and GCV for gall midge incidence (%) and number of grains panicle^{-1} indicated wide range of variations. Crosses between the genotypes of clusters IV and VII, IV and V, VI and VII, II and VII are expected to manifest high heterosis along with, accumulation of favourable genes in subsequent segregating generations. The genotype, WGL 1782 could be exploited as donor for incorporating gall midge resistance through various breeding programs.

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