Genetic Divergence Studies for Gall Midge Incidence, Earliness, Yield and Yield Components in Rice (*Oryza sativa* L.) Genotypes in Telangana State

Sreedhar Siddi[1*]

[1]*Professor Jayashankar Telangana State Agricultural University, Rice Breeding Scheme, Agricultural Research Station, Kunaram, 505 174, Peddapalli, Telangana, India.*

ABSTRACT

The study was carried out with 32 genotypes of rice (*Oryza sativa* L.) under irrigated system in RBD design with three replications at Agricultural Research Station, Kunaram in Telangana State during the rainy season of 2017. In general, major problem is high incidence of gall midge (Biotype 3) in rainy season under early as well as late planting conditions in Northern Zone of Telangana State. Hence, all the 32 genotypes were evaluated with an aim to know the divergence among them for gall midge incidence, earliness, yield and yield components. Based on D^2 analysis, 32 genotypes were distributed into twelve clusters with the cluster I (12) containing maximum number of genotypes followed by cluster II (9). Highest inter cluster distances were observed between the clusters X and XII (2469.5) followed by III and XII (2283.3), and VII and XII (2173.6) suggesting wide diversity between the traits. Cluster mean analysis revealed that genotype, WGL 1119 from the cluster V would be used in breeding programme to develop gall midge resistant, high yielding, early duration, non lodging, medium slender grain genotypes as it recorded very low incidence of galls (0.9%) with high yield (4869.7 kg/ha), early duration (84.7 days), short stature (93.7 cm) and less 1000-grain weight (14.8 g). The genotypes, KNM 2305 and MTU 1001 from the clusters *viz.,* VIII and X, respectively were identified as potential lines for developing high yielding, early and medium

___

Corresponding author: E-mail: siddu.35@gmail.com;

duration, long bold or long slender grain varieties. Among the traits studied, days to 50% flowering (55.8%) and 1000-grain weight (31.9%) manifested highest contribution towards total divergence, thus, these traits could be given due importance by the breeders for development of superior rice genotypes under crop improvement programme.

1. INTRODUCTION

More than half of the world's population use rice as an important staple food and Asian countries produce and consume 80% of the world's rice [1]. It has been referred to as "Global grain" after maize and wheat. In Northern Zone of Telangana State, rice has been occupied larger area, accounts for nearly 5 lakh ha among the cereals during every rainy season. The Asian rice gall midge, *Orseolia oryzae* (Wood-Mason) is one of the important insect pests in the Northern Telangana region of South India. Recently, gall midge incidence has been increased which results in annual yield loss, amounting to Rs.3300 million in South India alone [2]. Hence, breeding for development of gall midge resistant varieties has been an important strategy with more yield and acceptable grain quality [3].

Knowledge on the nature and magnitude of genetic variation in plant breeding programmes is essential for improving yield and its components and provides promising genotypes that can be selected to develop new varieties or breeding materials. Kumbhar et al. [4] reported that the pace and magnitude of genetic improvement is generally dependent on the amount of genetic diversity present in a population. The breeders are interested to evaluate genetic diversity based morphological traits because they are inexpensive, rapid, and simple to score. It was proved in many cases that wide the divergence between parents, more choice for obtaining wide segregants to enable scope for selection of superior plants with desirable trait combinations [5]. Hence, the selection of desirable segregants from segregating populations could be achieved through the inclusion of most divergent parents in the breeding programmes. Multivariate analysis is an important tool for estimation of genetic divergence in the populations which was reported by several workers [6,7,8,9,10,11,12]. Keeping in view of the importance, present study was undertaken to estimate the genetic diversity present among the genotypes to enable for selection of more divergent, high yielding and gall midge resistant genotypes for further crop improvement.

2. MATERIALS AND METHODS

The material comprised of 32 rice genotypes were evaluated under irrigated system during the rainy season of the year, 2017 at Agricultural Research Station, Kunaram (Table 1). The experiment was laid out in the randomized block design with three replications. The farm is located at 18.6°N Latitude, 79°E Longitude and at an elevation of 231 m asl. The soil is silty loam with pH 7.43 and EC 0.26 dS/m. The recommended agronomic practices and plant protection measures were followed to raise a good crop. The variables measured for quantitative traits were days to 50% flowering, plant height (cm), panicle length (cm), number of productive tillers per m^2, number of grains per panicle, 1000 grain weight (g) and grain yield (kg/ha) for each entry in each replication. The incidence of gall midge was recorded in percent tillers affected with silver shoots (following Standard Evaluation System for Rice, IRRI, 2002) on 10 tagged random plants. The mean data after computing for each trait was subjected to analysis of variance [13]. Multivariate analysis was done as per the Mahalanobis D^2 statistics described by Rao [14] and the genotypes were grouped into different clusters following Tocher's method. Intra and inter-cluster distances and mean performances of clusters for all the traits were also computed.

3. RESULTS AND DISCUSSION

In the present investigation, analysis of variance (Table 2) was carried out to test the significance of variance among 32 diverse genotypes for all the eight traits. Analysis of variance revealed significant differences (P>0.01) among the material, indicating the presence of wide spectrum of variability among the genotypes for gall midge incidence, yield and its component traits for selecting desirable genotypes by the plant breeder.

Table 1. List of genotypes studied along with pedigree and status

S.No.	Genotype/Variety	Pedigree	Status
1	JGL 24497	JGL 17004 x NLR 3042	Not released
2	RDR 1162	JGL 11727 x JGL 17004	Not released
3	RNR 15048	MTU 1010 X JGL 3855	Released
4	JGLH 169	IR 62030-54-1-2-2R x IR 42266-29-4-2-2-2-2R	Not released
5	RNR 23595	Yamini x BM 71	Not released
6	RDR 1188	JGL 11118 x RNR 2465	Not released
7	IBT R9	Tellahamsa* 2 x GPP2	Not released
8	MTU 1010	Krishnaveni x IR 64	Released
9	JGL 20776	MTU 1010 x JGL 13595	Not released
10	WGL 1119	WGL 32100 // B95-1 x Abhaya	Not released
11	IET 26241	-	Not released
12	KNM 2305	JGL 11470 x Himalaya 741	Not released
13	IBT R4	Tellahamsa* 2 x GPP2	Not released
14	WGL 962	BPT 5204 x GEB 24 // BPT 5204 x Shatabdi	Not released
15	KMPS 6251	MTU 1001 x NLR 145	Not released
16	KNM 2307	JGL 11727 x JGL 17004	Not released
17	US 314	Private company hybrid	Released
18	IBT R8	Tellahamsa* 2 x GPP2 // Tellahamsa* 2 x NLR 145	Not released
19	KNM 118	MTU 1010 x JGL 13595	Released
20	JGL 23746	JGL 3855 x C 28	Not released
21	WGL 1150	Tellahamsa // B95-1 x Abhaya	Not released
22	RNR 21225	MTU 1075 x Kavya	Not released
23	IET 26224	-	Not released
24	Krishna	Chandan x BPT 5204	Released
25	RNR 17500	Sumathi x Kavya	Not released
26	WGL 1021	WGL 32183 x Sheetal	Not released
27	Pusa 1121	Pusa 614-1-2 x Pusa 614-2-4-3	Released
28	RNR 15435	RNR 17818 x Vasumathi	Not released
29	Sumathi	Chandan x Pak Basmathi	Released
30	MTU 1001	MTU 5249 x MTU 7014	Released
31	JGL 18629	JGL 7046 x Swarna // BPT 5204	Not released
32	JGL 11470	JGL 418 x Gedongibeton	Released

Table 2. Mean squares corresponding to various sources of variation for eight traits in rice

	Source of variation		
	Replications	**Treatments**	**Error**
Degrees of freedom	2	31	62
Days to 50% flowering	0.07	346.26**	0.29
Plant height (cm)	8.83	641.77**	3.19
Panicle length (cm)	1.33	16.99**	0.69
Number of productive tillers per m^2	339.29	1821.46**	241.79
Number of grains per panicle	275.69	12506.50**	681.64
1000- grain weight (g)	1.79**	65.08**	0.14
Grain yield (kg per ha)	693712.50	2560828.47**	286063.15
Gall midge incidence (%)	88.09	972.83**	36.86

* Significant at (P>0.05), ** significant at (P>0.01)

In the present investigation, D^2 analysis was carried out as the chi-square test indicated that the population of rice was divergent. Based on the relative magnitude of D^2 values, 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 2 genotypes, respectively. However, the remaining clusters comprised of only one genotype each (Fig. 1).
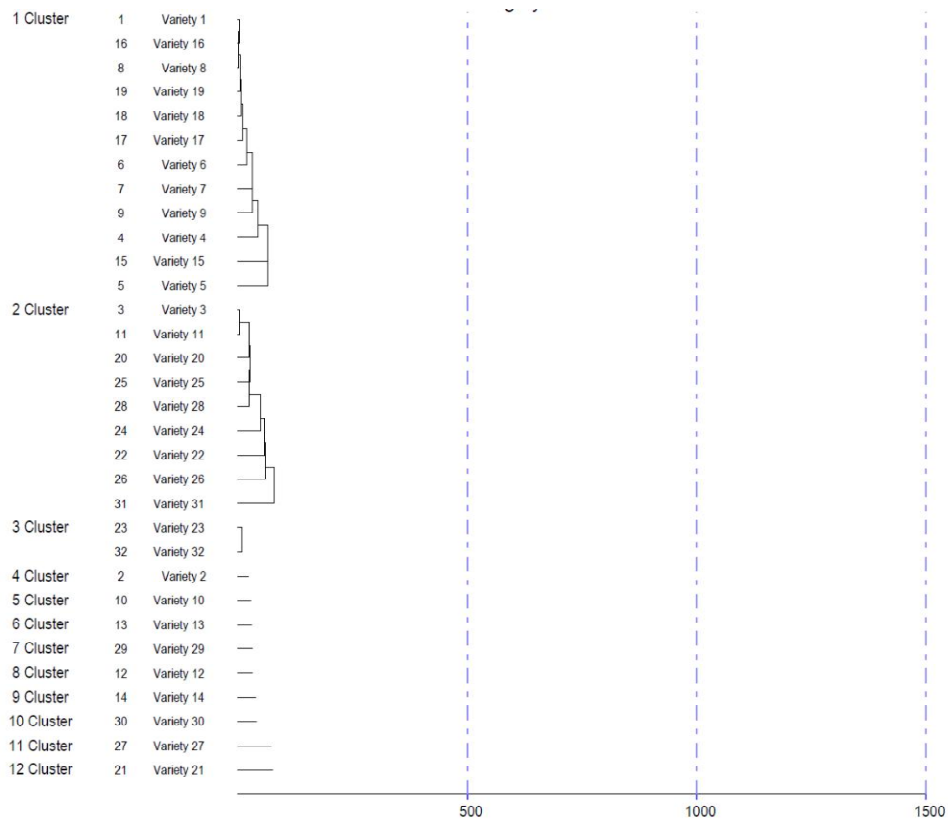
Fig. 1. Clustering 32 rice genotypes by the Tocher's method

According to Akter et al. [15], the maximum eight entries were grouped into the cluster II followed by seven in cluster IV. Similarly, fifty red rice germplasm with fifteen agro morphological traits were grouped into five clusters [16]. In other study of Ahamdikhah et al. [17], 58 rice varieties were clustered into four groups based on 18 morphological traits. From the pattern of clustering it could be inferred that sufficient divergence was present to enable the formation of individual clusters. The clustering pattern could be utilized in selection of better parents for crossing and deciding the best cross combinations which may generate highest possible variability for the desirable traits. A total of 12 genotypes were grouped in to cluster I namely JGL 24497, KNM 2307, MTU 1010, KNM 118, IBT R 8, US 314, RDR 1188, IBT R9, JGL 20776, JGLH 169, KMPS 6251, RNR 23595; nine genotypes in cluster II namely Telangana Sona, IET 26241, JGL 23746, RNR 17500, RNR 15435, Krishna, RNR 21225, WGL 1021, JGL 18629 and two genotypes in the cluster III namely IET 26224, JGL 11470. The genotypes derived from different pedigrees were grouped in the same clusters *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. The genotypes RDR 1162,WGL 1119, IBT R4, Sumathi, KNM 2305, WGL 962, MTU 1001, Pusa 1121 and WGL 1150 maintained their separate identities by making mono-genotypic groups, that is, clusters, IV,V,VI,VII,VIII, IX,X,XI and XII while forming clusters. It might be due to their different genetic makeup from that of other gemplasm lines in the present study (Table 3). Similar results of greater genetic diversity for the genotypes in the monogenotypic clusters were also reported [18,19].

Principal Component Analysis is (PCA) showed two most informative principal components with eigen values of 5144.09 and 2066.31, respectively, which together accounted 90.15% of the total variance for all the characters. According to first principal component, traits such as days to 50% flowering (0.89) and plant height (0.23) had relatively higher contributions

(64.32%) to the total variation, while principal component 2 accounted for 25.83% of the total variation with number of grains Panicle^{-1} (0.12) giving the highest contribution. The analysis of eigenvectors recorded the information of morphological traits for percentage of variation to the third principle component, which was 7.35 with days 50% flowering (0.27), grain yield (0.23) and 1000-grain weight (0.21) had higher contribution (Table 4). Similarly, Rajiv et al. [20] reported the first two principal components accounting for 68.6% of total variation in drought stress and 82.1% in control.

The values of intra and inter cluster distances for the 32 rice genotypes based on phenotypic traits was determined (Table 5). According to Pattnaik [21], higher intra-cluster distance also indicated greater heterogeneity of the genotypes. Considerable variation occurred in intra cluster distances ranged from zero to 162, indicating wider diversity prevailing among the gemplasm lines within clusters. The maximum intra cluster distance was in cluster II (162.0) followed by clusters I (109.8) and III (19.8), while it was zero for the remaining clusters. Hence, germplasm under the cluster II and I was most heterogeneous and germplasm under cluster III was comparatively homogeneous or less divergent. Genotypes falling in the clusters II, I and III which were having high degree of divergence would produce more desirable segregates to achieve greater genetic divergence, having ample scope to select superior genotype for the trait of interest . Since the cluster I and cluster II consisted of 21 genotypes with highest values of intra-cluster distances, presence of high heterogeneity among the germplasm within these two clusters is expected. Hence, the sub clustering of clusters I and II is an approach towards the effective selection of desired parents for hybridization programme within these clusters.

Table 3. Distribution of 32 rice genotypes in different clusters

Cluster number	Number of genotypes	Genotypes
I	12	JGL 24497, KNM 2307, MTU 1010, KNM 118, IBT R 8, US 314, RDR 1188, IBT R9, JGL 20776, JGLH 169, KMPS 6251, RNR 23595
II	9	Telangana Sona, IET 26241, JGL 23746 , RNR 17500, RNR 15435, Krishna, RNR 21225, WGL 1021, JGL 18629
III	2	IET 26224, JGL 11470
IV	1	RDR 1162
V	1	WGL 1119
VI	1	IBT R4
VII	1	Sumathi
VIII	1	KNM 2305
IX	1	WGL 962
X	1	MTU 1001
XI	1	Pusa 1121
XII	1	WGL 1150

Table 4. Eigenvectors and eigen values of the first three principal components

Variable	Eigenvectors		
	PC1	PC2	PC3
Eigen value	5144.09	2066.31	588.39
Variation (%)	64.32	25.83	7.35
Cumulative (%)	64.32	90.15	97.51
Days to 50% flowering	0.89	0.05	0.27
Plant height (cm)	0.23	-0.25	-0.90
Panicle length (cm)	0.07	-0.02	-0.01
Number of Productive tillers m$^{2-1}$	-0.17	0.01	-0.12
Number of grains Panicle^{-1}	-0.17	0.12	-0.01
1000 - grain weight (g)	0.01	-0.94	0.21
Grain yield (kg ha^{-1})	-0.24	-0.18	0.23
Gall midge incidence (%)	-0.13	-0.06	-0.05

PC: Principal components

Table 5. Average intra (diagonal) and inter cluster distances (Tocher's method) for 32 rice genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	109.8	533.1	1097.6	326.1	439.2	250.7	921.8	260.5	391.0	1097.0	501.4	376.4
II		162.0	286.0	713.3	616.5	709.7	344.1	521.1	323.6	500.6	442.8	1358.1
III			19.8	1283.8	970.4	1223.3	390.9	975.6	577.4	347.8	962.6	2283.3
IV				0.00	75.5	76.8	1607.0	920.7	169.3	1860.3	1108.7	283.8
V					0.00	83.1	1492.5	1006.0	102.8	1632.9	1215.2	519.8
VI						0.00	1477.6	744.5	223.9	1628.7	1019.8	228.9
VII							0.00	450.0	1013.2	108.6	288.6	2173.0
VIII								0.00	806.2	538.4	233.2	936.6
IX									0.00	1171.4	887.4	763.7
X										0.00	606.3	2469.5
XI											0.00	1257.4
XII												0.00

Table 6. Cluster means and percent contribution of each character towards total divergence of 32 rice genotypes for eight quantitative characters

Cluster	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Number of Productive tillers m$^{2-1}$	Number of grains Panicle^{-1}	1000-grain weight (g)	Grain yield (kg ha^{-1})	Gall midge incidence (%)
I	83.5	113.9	25.6	245.9	160.6	23.4	4542.1	60.1
II	98.4	125.2	27.8	240.1	235.2	16.5	4414.6	46.6
III	109.7	101.6	24.9	229.9	275.9	14.8	3744.5	45.2
IV	79.7	108.5	25.0	246.4	213.9	15.5	5564.7	40.8
V	84.7	93.7	24.4	284.5	225.2	14.8	4869.7	0.9
VI	80.0	94.5	24.3	299.2	118.7	19.9	3521.7	5.3
VII	105.0	137.9	30.8	202.4	154.3	22.3	3268.0	45.6
VIII	91.0	122.4	27.8	243.5	160.7	27.9	6377.7	54.1
IX	90.3	104.4	20.9	264.0	236.1	13.5	3847.3	58.7
X	110.0	112.1	25.1	226.6	170.3	23.9	5633.0	32.3
XI	91.0	158.7	30.2	257.4	83.9	23.7	3049.0	33.1
XII	68.3	110.6	25.4	244.2	87.7	23.7	3684.7	18.3
% Contribution of character	55.8	11.1	0	0.40	0.20	31.9	0.60	0

Table 7. Mean performance of eight characters for 32 rice genotypes

Genotype	Days to 50 % flowering	Plant height (cm)	Panicle length (cm)	Number of productive tillers m$^{2-1}$	Numbers of grains panicle^{-1}	1000- grain weight (g)	Grain yield (kg ha^{-1})	Gall midge incidence (%)
JGL 24497	82.3	114.4	25.7	281.6	122.9	24.6	5096.3	59.6
RDR 1162	79.7	108.5	25.0	246.4	213.9	15.5	5564.7	40.8
RNR 15048	98.0	127.1	26.8	266.9	306.8	12.6	3903.4	67.3
JGLH 169	90.3	115.7	28.1	211.2	165.8	23.9	3093.4	81.4
RNR 23595	85.0	122.5	27.5	225.9	289.2	17.0	4002.9	59.7
RDR 1188	77.3	115.1	25.5	228.8	160.1	27.1	3608.2	35.0
IBT R9	87.7	111.1	24.0	243.5	75.5	25.5	3941.8	53.6
MTU 1010	81.7	107.2	24.6	272.8	102.5	25.3	5004.0	62.7
JGL 20776	88.3	122.6	26.4	234.7	204.5	23.4	5433.6	56.3
WGL 1119	84.7	93.7	24.4	284.5	225.2	14.8	4869.7	0.9
IET 26241	98.3	128.0	26.2	258.1	228.2	12.2	3868.3	62.2
KNM 2305	91.0	122.5	27.8	243.5	160.7	27.9	6377.7	54.1
IBT R4	80.0	94.4	24.3	299.2	118.7	19.9	3521.7	5.3
WGL 962	90.3	104.4	20.9	264.0	236.1	13.5	3847.4	58.7
KMPS 6251	83.0	117.3	24.7	258.1	216.9	17.3	5040.2	61.7
KNM 2307	82.3	112.2	24.7	240.5	131.3	25.2	5223.0	67.8
US 314	82.7	112.4	26.4	234.7	179.2	22.2	4528.3	65.3
IBT R8	80.7	112.9	24.4	269.9	146.5	23.5	3923.5	69.3
KNM 118	81.0	104.0	24.9	249.3	133.2	26.0	5609.8	48.6
JGL 23746	95.3	124.0	29.8	265.1	203.0	17.9	5549.7	41.2
WGL 1150	68.3	110.6	25.4	244.2	87.7	23.7	3684.7	18.3
RNR 21225	102.0	115.2	26.0	215.6	205.3	19.7	5445.0	40.8
IET 26224	110.3	99.7	24.5	215.6	245.6	15.8	3390.3	54.0
Krishna	100.0	101.4	24.1	222.2	267.3	15.6	4201.1	50.9
RNR 17500	92.0	141.6	30.2	215.6	205.3	16.9	3988.1	47.5
WGL 1021	100.3	139.4	30.9	217.8	278.0	19.6	5492.5	36.9
Pusa 1121	91.0	158.6	30.3	257.4	83.9	23.7	3049.2	33.1
RNR 15435	91.7	139.5	30.2	279.4	174.2	17.7	3027.2	34.2
Sumathi	105.0	137.9	30.8	202.4	154.3	22.3	3268.1	45.6
MTU 1001	110.0	112.1	25.1	226.6	170.3	23.9	5633.0	32.3
JGL 18629	108.0	110.8	26.0	220.0	248.7	16.5	4255.6	38.6

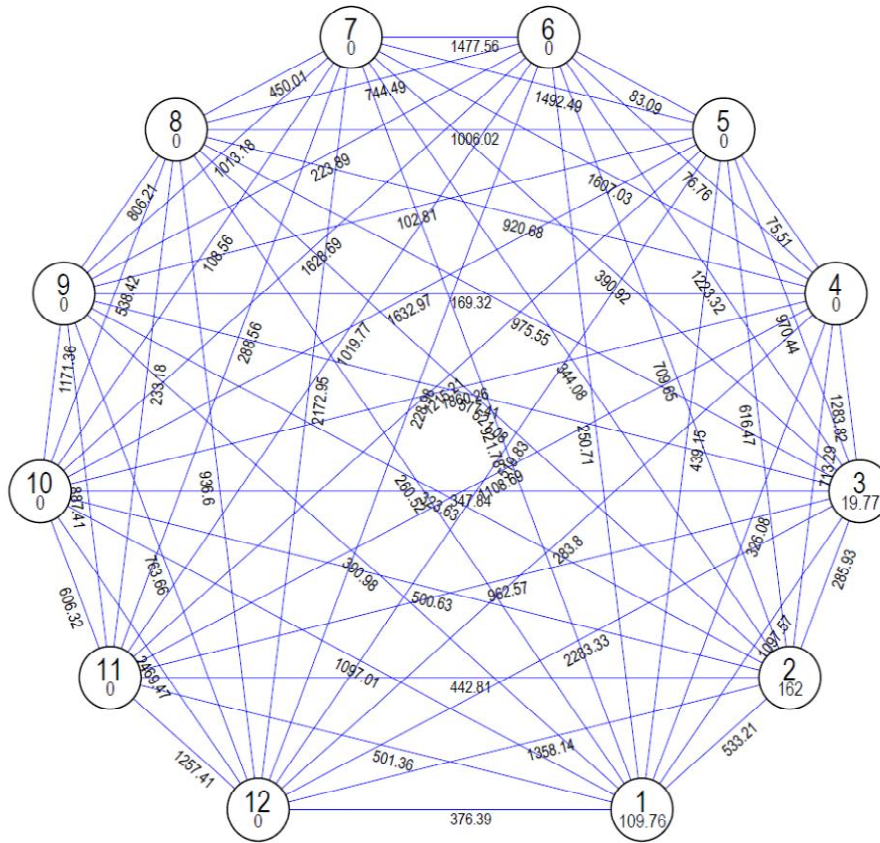| Genotype	Days to 50 % flowering	Plant height (cm)	Panicle length (cm)	Number of productive tillers m$^{2-1}$	Numbers of grains panicle^{-1}	1000- grain weight (g)	Grain yield (kg ha^{-1})	Gall midge incidence (%)
JGL 11470	109.0	103.6	25.4	244.2	306.3	13.8	4098.9	36.4
Mean	90.9	116.9	26.3	244.9	188.9	20.1	4423.2	47.5
C.V.	0.6	1.5	3.2	6.3	13.8	1.9	12.1	12.8
C.D. (5%)	0.9	2.9	1.4	25.4	42.6	0.6	872.9	9.9
C.D. (1%)	1.2	3.9	1.8	33.7	56.7	0.8	1160.5	13.2

Fig. 2. Mahalonobis Euclidean distance through Tocher's metod among 32 rice genotypes

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 the earlier reports [7,19]. From the inter cluster distance values, it is clear that highest divergence occurred between cluster X and XII (2469.5) followed by cluster III and XII (2283.3) and cluster VII and XII (2173.0) indicating the presence of greater diversity between genotypes of these groups which could be exploited in crop improvement. Higher genetic distance was noticed between mono-genotypic cluster X (MTU 1001) and other mono-genotypic cluster XII (WGL 1150). These genotypes may be used for developing early and medium duration bold grain genotypes since both genotypes are bold grained. Moreover, it was interesting to note that in most of the cases, cluster XII produced the highest inter cluster

value with all other clusters. This suggests that genotype of cluster XII 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 similar with other findings in rice crop [15]. De Reddy et al. [22] and Maurya et al. [9] reported genotypes belonging to clusters separated by high cluster distance could be used in breeding programme for obtaining high heterosis and wide spectrum of variation among the segregants. In contrary to this, lowest inter cluster distance was noticed between cluster IV and V (75.5) indicating that the genotypes of these clusters had genetic resemblance (Fig. 2).

Based on morphological data of eight quantitative traits, it was noticed that there is a considerable amount of variation existing among the cluster means (Table 6) indicating the presence of plenty diversity for these traits in 32 rice genotypes under study. Genotype, WGL

1119 in the mono-genotypic cluster V was characterized with very low incidence of gall midge (0.9%), early in flowering (84.7 days), short stature (93.7 cm), more number of grains per panicle (225.2), effective bearing tillers (284.5) and grain slenderness (14.8 g) including good grain yield (4869.7 kg/ha), hence this genotype could be used for obtaining gall midge tolerant, high yielding, early duration, medium slender grain, non lodging genotypes. Genotypes KNM 2305 and MTU 1001 in the mono-genotypic clusters VIII and X, respectively were found to be accumulated with maximum good characters such as 1000-grain weight (27.9 g and 23.99 g) and number of grains per panicle (160.7 and 170.3) and as a result higher grain yield (6377.7 kg/ha and 5633.0 kg/ha) was obtained in these clusters. However, these genotypes KNM 2305 (54.6%) and MTU 1001 (32.3%) recorded medium incidence of gall midge. Therefore, they could be used as a parents for developing high yielding early and medium duration long slender or long bold rice varieties. Genotype RDR 1162 from cluster IV was characterized by good yield (5564.7 kg/ha), early in flowering (79.7 days) and lesser 1000-grain weight (15.5 g) with the medium incidence of gall midge (40.8%); hence, this genotype could be used for obtaining early duration medium slender grain varieties (Table 7). Considerable emphasis should be given to the characters contributing most to the divergence. The traits, 1000-grain weight (31.9%) and days to flowering (55.8%) contributed considerably, accounting for 87.7% of total divergence among all the traits indicating the importance of these traits for effective selections, whereas, panicle length (0.0) and gall midge incidence (0.0) recorded zero contribution towards total divergence which are of less importance in selection of diverse parents. Similarly, according to Mohan et al. [7] and Thippaswamy et al. [23] higher contribution of days to flowering and 1000- grain weight was reported towards total divergence in rice. In contrary to this, the contribution of percent filled grains per panicle was high towards genetic divergence [19]. Least contribution of effective tillers, plant height and panicle length towards total divergence was noticed [12] and panicle length had a good contribution towards total divergence [24]. Since, days to 50% flowering (55.8%), 1000-grain weight (31.9%), plant height (11.1%) and grain yield (0.60%) exhibited more contribution to the divergence, the present experimental material could be used for developing high yielding rice varieties with desirable grain type, maturity duration and plant height (Table 6).

4. CONCLUSION

It is assumed that the maximum amount of heterosis will be expressed in cross combinations involving the parents that belong to most divergent clusters. In the present investigation, maximum distances existed between the clusters X and XII, III and XII and VII and XII would exhibit high heterosis as well as high level of yield potential. Based on the cluster means in the genetic diversity study, gall midge susceptible genotype namely KNM 2305 was identified as a potential genotype for developing early duration, long bold or long slender grain varieties. In view of increasing demand for medium slender fine grain varieties, gall midge resistant genotype WGL 1119 from the cluster V would be used in breeding programme to develop early duration varieties of medium slender, fine grain gall midge resistant varieties as it exhibited earliness, lower test weight and very less damage against gall midge. Further, D^2 statistics identified days to 50 % flowering, 1000-grain weight, plant height and grain yield similar to PCA in various principal components playing a major role in developing high yielding rice varieties with desirable grain type, maturity duration and plant height.

ACKNOWLEDGEMENTS

COMPETING INTERESTS

Author has declared that no competing interests exist.

REFERENCES

1. Bhat FM, Riar CS. Effect of amylose, particle size and morphology on the functionality of starches of traditional rice varieties. International Journal of biological macromolecules. 2016;92:637-644.
2. Bentur JS, Pasalu IC, Sharma NP. Gall midge resistance in rice. Current status in

India and future strategies. DRR Research Paper Series 01/2003. Directorate of Rice Research, Rajendranagar, Hyderabad, India.

3. Henrichs EA, Pathak PK. Resistance to the rice gall midge (*Orseolia oryzae*) in rice. International Journal of Tropica Insect Science. 1981;1(2):123-132.

4. Kumbhar SD, Kulwal PL, Patil JV, Sarawate CD, Gaikwad AP, Jadhav AS. Genetic diversity and population structure in land races and improved rice varieties from India. Rice Science. 2015;22(3):99-107.

5. Manonmani S, Fazlullah Khan. Analysis of genetic diversity for selection of parents in rice. Oryza. 2003;40:54-56.

6. Ramanjaneyulu AV, Gouri Shankar V, Neelima TL, Shashibhushan D. Genetic analysis of rice (*Oryza sativa* L.) genotypes under aerobic conditions on alfisols. SABRAO Journal of Breeding and Genetics. 2014;46(1): 99-111.

7. Mohan YC, Thippeswamy S, Bhoomeshwar K, Madhavilatha B, JameemaSamreen. Diversity analysis for yield and gall midge resistance in rice (*Oryza sativa* L.) in northern telangana zone, India. SABRAO Journal of Breeding and Genetics. 2015;47(2):160-171.

8. Islam MZ, Khalequzzaman M, Bashar MK, Ivy NA, Haque MM, Mian MAK. Variability assessment of aromatic and fine rice germplasm in Bangladesh based on quantitative traits. The Scientific World Journal. 2016;16.

9. Maurya BK, Singh PK, Verma OP, Mandal DK. Genetic variability and divergence analysis in rice (*Oryza sativa* L.) under sodic soil. International Journal of Current Microbiology and Applied Sciences. 2017;6(10):2865-2869.

10. Ram BJ, Babu GS, Lavanya GR, Spandana B, Kumar KM. Genetic divergence studies of elite germplasm accessions of rice (*Oryza sativa* L.). Plant Archives. 2017;17(2): 821-824.

11. Rusdiansyah, Subiono T, Sunaryo W, Suryadi A, Sulastri, Anjasmara S. The genetic diversity and agronomical characters of local cultivars of tidal rice in East Kalimantan, Indonesia. Biodiversitas. 2017;18(4):1289-1293.

12. Sowmiya CA, Venkatesan M. Studies on Genetic Diversity in Rice (*Oryza sativa* L.).

13. Panse VG, Sukhatme PV. Statistical methods for agricultural workers, 2nd edition ICAR, New Delhi; 1985:361.

14. Rao CR. Advance Statistical Methods in Biometrical Research. John Wiley & Sons, New York; 1952.

15. Akter N, Begum H, Islam MZ, Siddique MA, Khalequzzaman M. Genetic diversity in AUS rice (*Oryza sativa* L.) genotypes of Bangladesh. Bangladesh Journal of Agricultural Research. 2018:43(2):253-266.

16. Islam MZ, Khalequzzamen M, Prince MFRK, Siddiue MA, Rashid ESMH, Ahmed MSU, Pittendrigh BP, Ali MP. Diversity and population structure of red rice germplasm in Bangladesh. PLoS ONE. 2018;13(5): 0196096.
DOI: 10.1371/journal.pone.0196096

17. Ahamdikhah A, Nasrollanejad S, Alishah O. Quantitative studies for investigating variation and its effect on heterosis of rice. International Journal of Plant Production. 2008;2(4):297-308.

18. Archana RS, Sudha Rani M, Vishnu Vardhan KM, Fareeda G. Genetic diversity studies among rice (*Oryza sativa* L.) Genotypes for grain yield, yield components and nutritional traits in rice. International Journal of Chemical Studies. 2018;6(6);134-137.

19. Pragnya K, Radha Krishna KV, Subba Rao LV, Suneetha K. Studies on genetic divergence analysis in soft rice (*Oryza sativa* L.) genotypes. International Journal of Pure & Applied Bioscience. 2018;6(2): 968-975.

20. Rajiv S, Thivendran P, Deivanai S. Genetic divergence of rice on some morphological and physiochemical responses to drought stress. Pertinaka Journal. 2010;32(2):315-328.

21. Pattnaik LK. Genetic variability and character association in low-land rice cultures (M.S. thesis), Orissa University of Agriculture and Technology, Odisha, India; 1992.

22. De Reddy RN, Surya JN, Rao AV, Mohanty KK. Genetic divergence in early rice under two situations. Indian Journal of Genetics and Plant Breeding. 1992;52:225-229.

23. Thippaswamy S, Chandramohan Y, Srinivas B, Padmaja D. Selection of

diverse parental lines for heterotic hybrid development in rice (*Oryza sativa* L.). SABRAO Journal of Breeding and Genetics. 2016;48(3):285-294.

24. Kumar S, Singh PK, Bisen P, Loitongbam B, Rai VP, Siha B. Genetic Diversity Analysis of Rice (*Oryza sativa* L.) Germplasm through Morphological Markers. International Journal of Agriculture, Environment and Biotechnology. 2018;953- 957.