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Genetic diversity analysis for yield and quality traits in elite rice (*Oryza sativa* L.) germplasm

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Abstract

The present investigation was carried out with 39 rice genotypes at the Field Experimentation Centre, Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology & Sciences Prayagraj during *Kharif*-2018. The study included Analysis of variance, assessment of variability, Heritability, Genetic advance, Genetic Diversity. The experimental material was sown in a randomized block design with three replications and observations were recorded on five randomly selected plants for 13 yield and yield components. The presence of large amount of variability might be due to diverse source of materials taken as well as environmental influence affecting the phenotypes. All the character's showed significant at 5% level of significant. Higher difference between GCV and PCV were depicted for number of tillers per plant, harvest index, grain yield per plant. High heritability coupled with high genetic advance in the present set of genotypes was recorded for number of spikelet per panicle followed by days to 50% flowering and days to maturity, indicating the predominance of additive gene effects and the possibilities of effective selection for the improvement of these characters. The 39 genotypes were grouped into 4 clusters cluster III with 21 genotypes emerged as the cluster followed by cluster I includes 15 genotypes, cluster II comprised 2 genotypes and cluster IV includes one genotypes. The pattern of group constellation proved the existence of significant amount of variability. Maximum intra cluster distance was recorded for cluster III followed by I and II whereas minimum intra cluster distance recorded for IV. The inter cluster D^2 value was maximum between cluster I and IV.

Keywords: Variability, heritability, genetic advance, genetic diversity

Introduction

Rice is the most important cereal crop of the world especially in East, South and South East Asia and has been referred to as "Global Grain" (Shalini and Tulasi, 2008) [19]. It is probably the most important grain and staple food for more than 100 countries of the world providing nutrition for more than 60 per cent of the global population meeting more than 1/5th of the calories consumed worldwide by the human species. 'Rice is life' was the theme of International year 2004 denoting its over whelming importance as an item of food and commerce (Pandey *et al.*, 2010) [13]. Rice is inseparable from our day-to-day life since time immemorial as evident from its use in almost all rituals of our culture. The crop is grown in a diverse geographical and climatic conditions ranging from a below sea level in kuttanad (Kerala) to high altitude in Kashmir valley. Rice is cultivated in a hydrology rang of moisture stress upland condition to water-logged ecology.

The nutrient contents of rice are 80% carbohydrates, 7-8% protein, the amino acid profile shows that it is rich in Glutamic acid and aspartic acid, highest quality cereal protein being rich in lysine (3.8%), 3% fibre, iron 1. Mg and zinc 0.5mg (Juliano *et al.*, 1985). Rice is the major crop in Uttar Pradesh and is grown in about 5.9 m ha. The cropping intensity is 153%. The state ranks 1st in the country in production of rice. The production is 44.01 and productivity of the state is round 2.2t/ha thus it is understood that there is an extreme need to enhance the rice productivity in Uttar Pradesh, which will be achieved only by developing high yielding hybrid varieties (Agriculture statistics,2018) Current population in India is 120 cores by 2025 it will be around 150 cores. So there is need to develop high yielding varieties. In the present scenario the rice productivity has reached a plateau. In order to achieve the expected targets, we have to develop the varieties with higher yield potential by breaking the existing yield plateau and by utilizing more diversified parents in breeding programmes. The success of any plant breeding programme largely depends on the existence of diversity among the genotypes (Beevi and Venkatesan, 2015) [1]. This helps in the choice of parents for hybridization in yield improvement programmes. The rice germplasm is a rich reservoir of valuable genes that plant breeders can harness for crop improvement. A thorough understanding of the genetic structure and diversity of rice varieties is crucial for efficient utilization of rice genetic resources. The amount of genetic advance under selection mainly depends on the amount of genetic variability (Jayasudha and Sharma, 2010) [6].

Mahalanobis D^2 statistics for estimating genetic divergence had been emphasized by many workers (Roy and Panwar, 1993; Ramya and Senthilkumar, 2008) [17]. Recognizing the Importance of genetic diversity and variability in plant breeding experiments, present research work was undertaken with Rice (*Oryza sativa* L.) to select divergent parents for future hybridization programmes.

Materials and Methods

Present investigation was carried out in the Field Experimentation Centre of Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, U.P during *Kharif*-2018. The experimental materials for the present study consisted of 39 germplasm of rice received from IRRI(Philippines), include local check (JAYA) received from Department of Genetics and Plant Breeding, SHUATS, Allahabad conducted during *Kharif*-2018. The data was recorded on five randomly selected plants from each genotype in each replication leaving the first two border rows from all the four sides, in order to avoid sampling error. The observation recorded as per the following procedure. Reading from five plants was averaged replication-wise and the mean data was used for statistical analysis for 13 quantitative characters.

1. Analysis of Variance (Fisher, 1936)
2. Variability parameters (Burton, 1952) [2]
3. Heritability (Burton and Devane, 1953) [3]
4. Genetic Advance (Johanson *et al.* 1955) [7]
5. Genetic divergence (Mahalanobis, 1936) [12]

The genetic divergence among 39 genotypes was estimated by Mahalanobis (1936) [12] D^2 statistics for 13 quantitative characters. The D^2 values were arranged in an increasing order of magnitude. The grouping of the genotypes into cluster was done by using Tocher's method (Rao, 1952) [16]. The two most closely associated genotypes were chosen and then a third genotype was found which had the smaller average D^2 from the first there and so on. At certain stage, D^2 values did not fit in the formed group and therefore, taken in other cluster. The square root of average D^2 value was worked out to calculate the average intra and inter-cluster D values. Average intra and inter-cluster (D) = $\sqrt{D^2}$ value.

Results and Discussion

Analysis of variance showed significant differences to all 13 quantitative characters under study at 5% level of significant. This indicates that there was a sample scope for selection of promising lines from the present gene pool for yield and its components. The presence of large amount of variability might be due to diverse source of materials taken as well as environmental influence affecting the phenotypes. Phenotypic variance was higher than genotypic variance for all the yield and yield attributing characters that indicates the influence of environmental factors on these traits. Similar findings were reported by Singh *et al.* (2011) [20], Prajapati *et al.* (2011) [15], Lingaiah *et al.* (2014) [11], Harsh *et al.* (2015) [5] and Shaikh *et al.* (2017) [18], for grain yield per plant, plant height, number of spikelet's per panicle and biological yield. A wide range of phenotypic coefficient of variation (PCV) was observed for the character ranging from 5.50 (Plant height) to 22.063 (number of spikelet per panicle). Genotypic coefficient of variation (GCV) ranged from 4.24 (Plant height) to 21.045 (number of spikelet per panicle). The heritability estimates were high (>60%) for traits days to 50% flowering (95.24),

days maturity (95.24), test weight (92.89), number of spikelet per panicle (90.93), panicle length (85.03), number of panicle per plant (80.78), flag leaf length (80.55), number of tiller per plant (71.75), flag leaf width (68.65). Moderate heritability (>30% to <60%) was found in harvest index (36.01), biological yield (38.69), panicle height (59.46), grain yield per plant (51.80).%, low heritability (<30%) not found in any character. Kumar *et al.* (2012) recorded high heritability estimates for most of the character. According to Panse and Sukhatme (1957) such characters governed predominantly by additive gene action and can be improved through individual plant selection. High heritability coupled with high genetic advance as per cent mean day to 50% flowering, number of spikelet per panicle, days to maturity, High heritability coupled with low genetic advance (<10) test weight (92.89 & 2.54), panicle length (85.03 & 3.30), number of panicle per plant (80.78 & 2.83), flag leaf length (80.55 & 7.77). Similar findings were reported by Kumar and Senapati (2013) [9, 10].

The cluster formation was done by Tocher's method suggested by Rao (1952) [16]. The distribution of thirty nine genotypes in different clusters was presented in table below. On the basis of magnitude of D^2 values, thirty nine genotypes were grouped in 4 clusters. Cluster III with 21 genotypes emerged as the largest cluster followed by cluster I includes 15 genotypes, cluster II comprised 2 genotypes and cluster IV includes 1 genotype. The pattern of group constellation proved the existence of significant amount of variability. The average intra cluster distance was ranged from 0.00 to 168.862. The maximum intra cluster distances were recorded for cluster III (168.862) followed by cluster I (123.425), cluster II (19.169) whereas minimum intra cluster distance recorded for cluster IV.

The inter cluster D^2 value was maximum between cluster I and IV (411.843) followed by cluster III and IV (352.222), cluster II and IV (321.843), cluster I and III (170.243) and cluster II and III (137.262). Suggesting that the genotypes present in these clusters may be used as parents for hybridization programme to develop desirable types as heterosis can be best exploited and chance of getting transgressive segregants are maximum when generating diverse lines are crossed.

Hybridization programme involving genetically diverse parents belonging to different clusters would provide an opportunity for bringing together gene constellations of diverse nature, promising hybrid derivatives probably due to complementary interaction of different genes in parents.

The total percent contribution of thirteen characters to total genetic divergence is presented in table 4.7. High contribution in the manifestation of genetic divergence was exhibited by grain yield per ha (36.84) followed by test weight (g) (32.65) and No of spikelet's per panicle (7.28) suggesting scope for improvement in these characters. In other words, selection for these characters may be rewarding. The contribution of flag leaf width (0.2699), panicle length (0.4049), biological yield (1.2146) and days to 50% flowering (1.3495) was least to genetic diversity among all thirteen characters.

Summary and Conclusion

Analysis of variances indicated highly significant difference among the genotypes for all the traits. This indicates that there was an ample scope for selection of promising lines from the present gene pool for yield and its components. The presence of large amount of variability might be due to diverse source of materials taken as well as environmental influence affecting the phenotypes. An estimate of GCV and PCV revealed that phenotypic coefficient of variation was higher than genotypic coefficient of variation, which indicates the presence of

environmental effect on expression of character studied. Higher difference between GCV and PCV were depicted for number of tillers per plant, harvest index, grain yield per plant. High heritability coupled with high genetic advance in the present set of genotypes was recorded for number of spikelet per panicle (90.93 & 66.83) followed by days to 50% flowering (95.24 & 11.06) and days to maturity (95.24 & 11.06), indicating predominance of additive gene effects and the possibilities of effective selection for the improvement of these characters. Genetic advance as per cent of mean was highest for number of spikelet's per panicle

(41.33), number of panicles per plant (32.18), number of tillers per plant (26.92). The 39 genotypes were grouped into 4 clusters cluster III with 21 genotypes emerged as the cluster followed by cluster I includes 15 genotypes, cluster II comprised 2 genotypes and cluster IV includes one genotype. Cluster I and IV, cluster III and IV, Cluster II and IV had the high inter cluster distances, were most diverse from each other and the genotypes present in these clusters provide a broad spectrum of variability in segregating and may be used as parents in future hybridization program to develop desirable genotypes, for yield improvement in rice genotypes.

Table 1: List of Germplasm

S.NO	Name of the germplasm	Grain type	Grain colour
1.	TP 30596	Long slender	Yellow
2.	TP 30597	Medium slender	Yellow
3.	TP 30598	Medium slender	Yellow
4.	TP 30599	Long slender	Yellow
5.	TP 30600	Medium slender	Yellow
6.	TP 30601	Medium slender	Yellow
7.	TP 30602	Medium slender	Yellow
8.	TP 30603	Long slender	Yellow
9.	TP 30604	Short Bold	Yellow
10.	TP 30606	Medium slender	Yellow
11.	TP 30607	Short Bold	Yellow
12.	TP 30608	Long slender	Yellow
13.	TP 30614	Medium slender	Yellow
14.	TP 30616	Medium slender	Yellow
15.	TP 30484	Long slender	Yellow
16.	TP 30617	Medium slender	Yellow
17.	TP 30618	Medium slender	Yellow
18.	TP 30619	Medium bold	Yellow
19.	TP 30620	Long slender	Yellow
20.	TP 30621	Long slender	Yellow
21.	TP 30622	Long slender	Yellow
22.	TP 30623	Long Bold	Yellow
23.	TP 30624	Long slender	Yellow
24.	TP 30625	Medium slender	Yellow
25.	TP 16228	Medium bold	Yellow
26.	TP 21654	Medium slender	Yellow
27.	TP 24370	Long slender	Yellow
28.	TP 24362	Long slender	Yellow
29.	TP 18154	Medium slender	Yellow
30.	TP 26777	Medium slender	Yellow
31.	TP 30754	Medium bold	Yellow
32.	TP 30755	Medium slender	Yellow
33.	TP 24172	Long slender	Yellow
34.	TP 24360	Long slender	Yellow
35.	TP 26717	Long slender	Yellow
36.	TP 25175	Long slender	Yellow
37.	TP 30757	Medium slender	Golden Yellow
38.	TP 30758	Medium slender	Yellow
39.	JAYA(Check)	Medium Bold	Yellow

Source: International Rice Research Institute, Philippines and Department of Genetics and Plant Breeding, SHUATS, Prayagraj.

Table 2: Estimation of genetic parameters for grain yield and other components in rice germplasm

Parameters Characters	σ^2_g	σ^2_p	GCV	PCV	(h ² %)	GA	GA as % of Mean
Days to 50% flowering	30.28	31.79	6.05	6.20	95.24	11.06	12.17
Plant height	24.17	40.65	4.24	5.50	59.46	7.81	6.74
Number of tiller per Plant	2.44	3.40	15.43	18.21	71.75	2.72	26.92
Number of panicle per plant	2.33	2.89	17.38	19.34	80.78	2.83	32.18
Panicle length	3.02	3.56	5.97	6.48	85.03	3.30	11.34
Flag leaf length	17.68	21.95	11.08	12.34	80.55	7.77	20.48
Flag leaf width	0.02	0.03	8.75	10.56	68.68	0.24	14.94
Number of spikelet's per panicle	1157.55	1272.93	21.04	22.06	90.93	66.83	41.33
Days to maturity	30.28	31.79	4.55	4.66	95.24	11.06	9.15
Biological yield per plant	23.26	60.13	5.95	9.57	38.69	6.18	7.63

Harvest index	9.37	26.01	6.96	11.59	36.01	3.78	8.60
Test weight	1.64	1.77	5.50	5.71	92.89	2.54	10.92
Grain yield per plant	14.18	27.37	10.58	14.71	51.80	5.58	15.69

Table 3: Distribution of the genotypes into different clusters

Cluster No.	No. of genotypes	Genotypes included
I	15	1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 26, 28,
II	2	23 33
III	21	14, 15, 16, 17, 18, 19, 20, 21, 22, 24, 25, 27, 29, 30, 31, 32, 34, 35, 36, 37, 38
IV	1	39

Table 4: Intra (diagonal) and inter cluster average distances (D²) for 13 different quantitative characters in rice

Cluster No.	I	II	III	IV
I	123.425 (11.11)	98.969 (9.948)	170.243 (13.048)	411.843 (20.294)
II		19.169 (4.378)	137.262 (11.716)	321.843 (17.94)
III			168.862 (12.995)	352.222 (18.768)
IV				0

The values in the brackets are D values

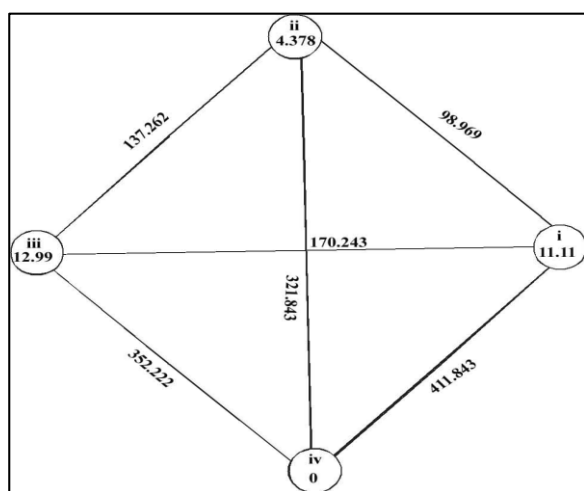


Fig 1: Cluster Diagram

Table 5: Per cent contribution of different quantitative characters towards genetic divergence in genotypes

S. No.	Source	RANK	Contribution %
1	Days to 50% flowering	10	1.3495
2	Plant height	13	1.7544
3	Flag Leaf Length	19	2.5641
4	Flag Leaf width	2	0.2699
5	No. of tillers	19	2.5641
6	No of Panicles	18	2.4291
7	Panicles length	3	0.4049
8	No of Spikelet's per Panicle	54	7.2874
9	Days to maturity	53	7.1525
10	Biological yield per plant	9	1.2146
11	Harvest index	26	3.5088
12	Test Weight	242	32.6586
13	Grain yield	273	36.8421
	Total	741	100

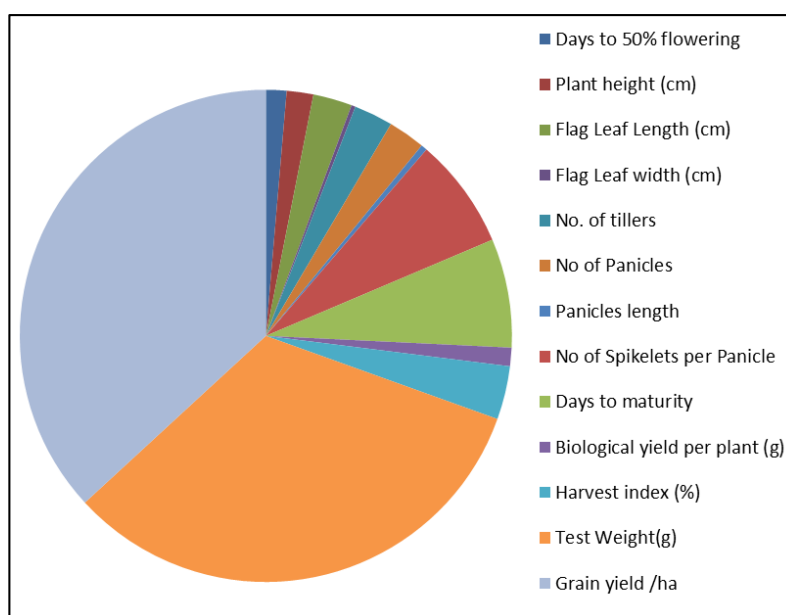


Fig 2: Percent contribution of different quantitative characters towards genetic divergence in genotypes

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