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

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### Abstract

In the present investigation, thirty four genotypes of rice were evaluated to assess the genetic divergence among them. The experiment was carried out in Randomized Block Design with three replications at Field Experimentation Centre, Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture Technology and Sciences, Prayagraj (Allahabad), during *kharif*-2018. The data were recorded for thirteen quantitative characters to study genetic variability, heritability, genetic advance and genetic divergence. Analysis of variance among 34 rice genotypes showed highly significant differences for all the characters under study indicated the presence of substantial amount of genetic variability. High estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for panicles per plant followed by tillers per plant indicating that these characters could be used as selection for crop improvement. High heritability coupled with high genetic advance was recorded for spikelets per panicle. Based on relative magnitude of  $D^2$  values, the genotypes were grouped into seven clusters by Euclidean methods of divergence study. Cluster I constituted maximum number of genotypes with twenty eight genotypes and clusters II,III,IV,V,VI,VII had one genotype each. Maximum inter-cluster distance ( $D^2$ ) was observed between cluster VII and IV, followed by cluster VII and I, suggesting that the genotypes from these clusters can be selected to yield superior segregants and further genetic improvement. Maximum genetic divergence was exhibited by days to maturity (25.49%), followed by spikelets per panicle (15.69), and biological yield per plant (15.33), days to 50% flowering (10.16), grain yield per plant (7.31). Therefore, days to maturity, plant height, spikelets per panicle, biological yield, days to 50% flowering, grain yield per plant contributing to 73.98% of the total divergence need to be focused in selection of parents for hybridization programme.

**Keywords:** Genetic diversity, germplasm, *Oryza sativa* L.

### Introduction

*Oryza* of family Poaceae. About half of the world's population depends on rice for their survival (Bhati *et al.*, 2015) [4]. It contributes significantly in Indian Economy and also serves as staple food for more than 70 per cent of the people dwelling in Asia. The slogan 'Rice is life' aptly describes the importance of rice in food and nutritional security. Rice is being cultivated in around 113 countries of the world. Globally it is cultivated in an area of 161.8 m ha with an annual production of about 748.0 million tones and an average productivity of 4.6 t ha<sup>-1</sup> (FAO, 2018) [6].

Rice is the most important food crop of India covering about one-fourth of the total cropped area and providing food to about half of the Indian population. India has the largest area 43.39 mt under rice cultivation with a production of 104.32 million tons and a productivity of 2404 kg per hectare. In Uttar Pradesh, rice is grown in an area of 5.87 million hectares with a production of 12.22 million tons and productivity of 2082 kg per hectare. (Ministry of Agriculture, 2016-2017).

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) [3]. 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.

Genetic variability helps to choose desirable genotypes. The genetic variation and genetic gain obtained by selection are studied by predicting the heritability and genetic advance. Genetic parameters such as genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) are useful in detecting the amount of variability present in the germplasm.

Genetic variability for quantitative traits is the key component of breeding programme for broadening the gene pool of rice and other crops. High magnitude of variability in a population provides the opportunity for selection to evolve a variety having desirable characters.

Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. The genetic coefficient of variation together with heritability estimate would give the best picture of the amount of advance to be expected from the selection. The amount of genetic advance under selection mainly depends on the amount of genetic variability.

Genetic diversity is a pre requisite for any crop improvement program as it helps in the development of superior recombinants. The crosses between parents with maximum genetic divergence are responsive for genetic improvement. Characterization and quantification of genetic diversity has long been a major goal in evolutionary biology and plant breeding (Manohara and Singh, 2013) [12]. Recently diversity in rice has been well utilized with respect producing high yielding genotypes along with another desirable back ground to solving the food problems.

Mahalanobis  $D^2$  statistics for estimating genetic divergence had been emphasized by many workers (Roy and Panwar, 1993) [19]. The multivariate analysis developed by Mahalanobis (1936) has been found to be most suitable in quantifying the degree of divergence in germplasm. 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

The experiment 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, India. The experimental materials for the present study consisted of 34 genotypes of rice including 1 local check. The experiment were laid out in a Randomized Block Design (RBD) with three replications. The experimental material was planted in three replications. Each replication consisted of 34 rice genotypes randomized and replicated within each block. Twenty five days old seedlings were transplanted 20cm apart between rows and 15 cm within the row. All necessary precautions were taken to maintain uniform plant population in each treatment per replication. All the recommended package of practices were followed along with necessary prophylactic plant protection measures to raise a good crop. Observations were recorded and the data was subjected to statistical analysis. The variability was estimated as per procedure for analysis of variance suggested by Panse and Sukhatme (1985) [15], PCV and GCV were calculated by the formula by Burton (1952) heritability in broad sense ( $h^2$ ) by Burton and De Vane (1953) [5] and genetic advance i.e., the expected genetic gain were calculated by using the procedure given by Johnson et al. (1955).

### Results and Discussion

Analysis of variance showed significant difference among all the 13 quantitative characters indicating the presence of sufficient genetic variability among the genotypes and revealing the scope for selection of suitable parents for future

hybridization and yield improvement in rice genotypes. These findings were in accordance with the findings of Shaikh *et al.* (2013), Beevi and Venkatesan (2015) [3]. Mean value for Days to 50% flowering for the varieties ranged from 74.33 to 101.00 days with a mean of 88.94 days. Out of 34 varieties, genotype SONAM took the longest period for 50% flowering (101.00 days). Plant height ranged from 98.80 cm to 142.05 cm with a mean of 114.53 cm. The highest plant height was recorded in KANZI SARIF (142.05 cm). Flag leaf length varied from 28.76 cm to 49.40 cm with a mean of 38.99. Maximum flag leaf length was observed in IRRI-181 (49.40 cm). Flag leaf width varied from 1.26 cm to 2.24 cm with a mean of 1.49 cm. Maximum flag leaf width was observed in IRRI-181 (2.24 cm). Number of tillers per plant varied from 6.60 to 18.40 with a mean value of 11.49. The genotype KANZI SARIF (18.40) had the highest number of tillers per plant. The number of spikelets per panicle among the genotypes varied from 104.33 to 260.06 with a mean of 130.81. The genotype SHIATS DHAN-1 (260.06) had the highest number of spikelets per panicle. The days to maturity varied from 117.00 days to 134.00 days with mean of 126.20 days. The genotype IRRI-156 (134.00) had maximum days to maturity. The Biological yield per plant ranged from 31.73 g to 83.33 g with mean of 62.48 g. The genotype TP-29409 (83.33) exhibited highest biological yield. Grain yield per plant varied from 13.60 g to 35.40 g with mean of 24.57 g. The maximum grain yield was observed in TP-29409 (35.40). Wide range of phenotypic ( $VP$  or  $\sigma^2_p$ ) and genotypic variance ( $VG$  or  $\sigma^2_g$ ) were observed in the experimental material for the traits studied. The highest variance ( $\sigma^2_g$  and  $\sigma^2_p$ ) was recorded for spikelets per panicle (747.23 and 774.42) followed by biological yield per plant (174.03 and 191.24) and Plant height (91.99 and 104.87), while moderate value were recorded for days to 50% flowering (33.49 and 36.39) days to maturity (32.79 and 35.00), flag leaf length (30.43 and 37.02), grain yield per plant (22.26 and 23.62), harvest index (17.15 and 24.65). Whereas, panicle length (10.36 and 13.91), tillers per plant (10.01 and 11.06), panicles per plant (8.06 and 8.66) and test weight (4.92 and 5.95) showed low variance. The least genotypic and phenotypic variance was observed in flag leaf width (0.04 and 0.05). Phenotypic variance was higher than genotypic variance for all the yield and yield contributing characters which indicates the influence of environmental factors on these traits. 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) [22], Prajapati *et al.* (2011) [16], Lingaiah *et al.* (2014) [11], Harsh *et al.* (2015) [8] and Shaikh *et al.* (2017) [21], for grain yield per plant, plant height, number of spikelets per panicle and biological yield. A wide range of phenotypic coefficient of variation (PCV) was observed for the character ranging from (4.68) for days to maturity to (33.62) for panicles per plant. Higher magnitude of phenotypic coefficient of variation was recorded for panicle per plant (33.62), followed by tillers per plant (28.94), biological yield per plant (22.13), spikelets per panicle (21.27). Moderate estimates of PCV were recorded for grain yield per plant (19.78), flag leaf length (15.60), flag leaf width (14.62), panicle length (13.64), harvest index (12.44), test weight (11.09). Lowest magnitude of PCV was recorded for plant height (8.94) days to 50% flowering (6.78), followed by days to maturity (4.68). In this regards, (Nath and Singh, 2013) [13] reported high PCV and GCV for grain yield per plant, (Kumar *et al.*, 2017) [9] for spikelets per panicle, (Harsh

*et al.*, 2015)<sup>[8]</sup> for grain yield per plant and (Sahu *et al.*, 2017)<sup>[20]</sup> for grain yield and biological yield in rice crop. Genotypic coefficient of variation (GCV) ranged from (4.53) for days to maturity to (32.44) for panicles per plant. Higher magnitude of genotypic coefficient of variation was recorded for panicles per plant (32.44), followed by tillers per plant (27.53) biological yield per plant (21.11), spikelets per panicle (20.89). Moderate estimates of GCV were recorded for grain yield per plant (19.20), flag leaf length (14.14), flag leaf width (13.58), panicle length (11.77), harvest index (10.38), test weight (10.09). Lowest magnitude of GCV was recorded for days to maturity (4.53), followed by days to 50% flowering (6.57), plant height (8.37). Similar findings were also reported by Krishna *et al.* (2014), Harsh *et al.* (2015)<sup>[8]</sup>, Sahu *et al.* (2017)<sup>[20]</sup> and Kumar *et al.* (2017)<sup>[9]</sup>. The heritability estimates were high (>0.60) for spikelets per panicle (96.49%), grain yield per plant (94.24%), days to maturity (93.69%), panicles per plant (93.08%). High heritability coupled with high genetic advance (>30) in the present set of genotypes was recorded for spikelets per panicle (96.49% and 55.31), indicating predominance of additive gene effects and the possibilities of effective selection for the improvement of these characters. Similar findings were reported by Nath and Singh (2013)<sup>[13]</sup>. High heritability coupled with moderate genetic advance (>10 to <30) for biological yield (91.03% and 25.93), plant height (87.52% and 18.50), days to 50% flowering (92.02% and 11.43), and days to maturity (93.69% and 11.41), flag leaf length (82.19% and 10.30) suggesting the greater role of non-additive gene action in their inheritance. Heterosis breeding could be used to improve these characters. High heritability coupled with low genetic advance (<10) for grain yield (94.24% and 9.43), harvest index (69.58% and 7.11), tillers per plant (90.50% and 6.20), panicle length (74.48% and 5.72), panicle per plant (69.00% and 5.64), test weight (82.75% and 4.15) and flag leaf width (86.21% and 0.41). It is indicative of additive gene action. Genetic advance as per cent of mean was highest for panicles per plant (64.47), tillers per plant (53.96), spikelet per panicle (42.28), biological yield per plant (41.49), grain yield per plant (38.40), flag leaf length (26.42), flag leaf width (25.97), panicle length (20.93). Similar findings were reported by Kumar and Senapsati (2013)<sup>[10]</sup>. Moderate genetic advance as per cent of mean were recorded for test weight (18.92), harvest index (17.84), plant height (16.15), days to 50% flowering (12.85) and. Low genetic advance as per cent of mean was recorded for days to maturity (9.04). Mahalanobis D<sup>2</sup> statistics was used for the quantitative assessment of genetic divergence for all the 13 characters

The 34 genotypes taken for genetic divergence analysis differed significantly with regard to characters studied (Table 1) and displayed marked divergence when subjected to Wilk's criterion taking all the twelve characters together. In the present study, genetic divergence was assessed by Mahalanobis D<sup>2</sup> statistics and Tocher's method. In the present

study, 34 genotypes were grouped into seven clusters by Non-Hierarchical Euclidean cluster analysis. Cluster I evolving the maximum genotype TP-30022, TP-30431, TP-30082, TP-29632, TP-30047, TP-29631, TP-30441, TP-30438, TP-30439, TP-30432, IRRI-179, TP-30430, TP-30035, TP-29737, TP-30433, TP-29651, TP-30015, IRRI-174, TP-29637, TP-29759, TP-29654, DESI SONAM, IRRI-105, SONAM, IRRI-181, TP-30011, TP-30436, IRRI-156, cluster II comprised one genotype (NDR-359), cluster III one genotype (TP-30025), cluster IV only one genotype (IRRI-104), cluster V only one genotype (KANJI SARIF), cluster VI only one genotype (TP-29409) and cluster VII only one genotype (SHIATS DHAN-1). Cluster I comprised of Twenty eight genotypes with semi dwarf plant height (114.32 cm). Cluster II consists of one genotype with low mean values for flag leaf length (28.76 cm), Cluster III consists of one genotype with high mean values of panicle length (28.05 cm), Cluster IV contained only one genotype and was characterized for high mean value of harvest index (45.86), Cluster V contained only one genotype with high mean values of semi dwarf plant height (142.05 cm), Cluster VI contained only one genotype with highest mean values of days to maturity (133.00), Cluster VII contained only one genotype and was characterized for highest mean values for days to flowering (97.00). The intra and inter cluster average distances among seven clusters were variable. The maximum intra-cluster (D<sup>2</sup>) was registered for, cluster I (71.21). The minimum intra-cluster distance was observed in cluster II, III, IV, V, VI and VII (0.000). The inter-cluster distance (D<sup>2</sup>) was found maximum between cluster VII and IV (693.74) followed by distance between cluster VII and I (463.45). The lowest inter-cluster distance was observed between cluster V and II (72.28) followed by cluster VI and III (83.32).

The inter distances in all the clusters were higher than the intra cluster distances indicating wider genetic diversity among genotypes of different groups. Therefore, the genotypes from the clusters having maximum inter-cluster distances can be selected to yield superior segregants and further genetic improvement. The results were in agreement with Priyanka *et al.* (2015)<sup>[17]</sup> and Ashok *et al.* (2017)<sup>[1]</sup> and Priya *et al.* (2017)<sup>[18]</sup>. The percent contribution of thirteen characters towards total genetic divergence is presented in.

The selection and choice of parents mainly depends upon contribution of characters towards divergence (Nayak *et al.*, 2004)<sup>[14]</sup>. The highest contribution in the manifestation of genetic divergence was exhibited by days to maturity (25.49%) followed by spikelets per panicle (15.69%) and biological yield per plant (15.33%). Grain yield per plant (7.31%), tillers per plant (5.17%), harvest index (4.81%), plant height (3.74), test weight (3.21%), flag leaf width (3.03%), panicles per plant (3.03%), panicle length (1.6%), flag leaf length (1.43%), contributed least among all the character towards genetic diversity.

**Table 1:** Analysis of variance for 13 characters in 34 rice genotypes during Kharif-2018

S. No	Character	Mean squares		
		Replication (df=2)	Treatment (df = 33)	Error (df = 66)
1	Days to 50% flowering	6.12	103.383**	2.91
2	Plant Height (cm)	36.94	288.860**	12.88
3	No. of tillers/ plant	0.35	31.082**	1.05
4	No. of panicles/ plant	0.53	24.799**	0.60
5	Panicle length (cm)	8.51	34.632**	3.55
6	Flag leaf length (cm)	4.81	97.897**	6.60
7	Flag leaf width (cm)	0.01	0.149**	0.01



8	No. of Spikelets/ panicle	80.42	2268.896**	27.19
9	Days to maturity	4.39	100.592**	2.21
10	Biological yield per plant (g)	2.62	539.435**	17.16
11	Harvest Index (%)	0.872	58.968**	7.50
12	Test weight (g)	0.12	15.804**	1.03
13	Grain Yield per Plant (g)	0.81	68.167**	1.36

**Table 2:** Genetic parameters for 13 quantitative characters in 34 rice

S. NO.	Characters	Vg	Vp	Coefficient of variation		h <sup>2</sup> % (B.S)	GA	GA as % of mean
				GCV	PCV			
1	Days to 50% Flowering	33.49	36.39	6.50	6.78	92.02	11.43	12.85
2	Plant Height (cm)	91.99	104.87	8.37	8.94	87.72	18.50	16.15
3	Flag Leaf Length (cm)	30.43	37.02	14.14	15.60	82.19	10.30	26.42
4	Flag Leaf Width (cm)	0.04	0.05	13.58	14.62	86.21	0.41	25.97
5	Panicle Length (cm)	10.36	13.91	11.77	13.64	74.48	5.72	20.93
6	Tillers per Plant	10.01	11.06	27.53	28.94	90.50	6.20	53.96
7	Panicle per Plant	8.06	8.66	32.44	33.62	93.08	5.64	64.47
8	Spikelets per Panicle	747.23	774.42	20.89	21.27	96.49	55.31	42.28
9	Days to Maturity	32.79	35.00	4.53	4.68	93.69	11.41	9.04
10	Harvest index %	17.15	24.65	10.38	12.44	69.58	7.11	17.84
11	Biological Yield (g)	174.03	191.24	21.11	22.13	91.03	25.93	41.49
12	Test Weight (g)	4.92	5.95	10.09	11.09	82.75	4.15	18.92
13	Grain Yield per Plant (g)	22.26	23.62	19.20	19.78	94.24	9.43	38.40

### Conclusion

The present investigation concluded that presence of adequate amounts of variability and highest yield and recorded in. TP-29409 (6.7 t/ha), followed by SHIATS DHAN-I (6.5 t/ha), TP-29759 (6.4 t/ha) recorded to be the best performer for grain yield.

The estimate of genotypic variance ( $\sigma^2g$ ) and phenotypic variance ( $\sigma^2p$ ) revealed that 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. 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 flag leaf length flag leaf width, panicle length, tillers per plant, panicles per plant, harvest index and biological yield respectively

The heritability estimates were high for spikelets per panicle, grain yield per plant, days to maturity, panicles per plant, days to 50% flowering, biological yield, tillers per plant respectively. High heritability coupled with high genetic advance in the present set of genotypes was recorded for spikelets per panicle, 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 panicles per plant, tillers per panicle, and spikelets per panicle.

The selection of divergent genotypes from the clusters having maximum inter-cluster distances (cluster VII and IV) would produce a broad spectrum of variability for yield, which can be used for further selection and genetic improvement.

Considering the importance of genetic distance and relative contribution of characters towards total divergence, the present study indicated that genotypes in in cluster IV can be selected for harvest index and cluster V for maximum plant height, tillers per plant and cluster VI can be used for maximum grain yield cluster VII for panicles per plant, spikelets per panicle could be used in future hybridization programme to identify desired segregants.

Since one year data is not sufficient to conclude results. So, further experimentation is required to corroborate the results.

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