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Studies on Variability, Heritability, Genetic Advance and Divergence for Earliness, Yield and Yield Components in Rice (*Oryza sativa* L.) Genotypes

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Abstract

Thirty one genotypes derived through pedigree method of breeding were studied for estimation of genetic variability and divergence at Agricultural Research Station, Kunaram. The GCV and PCV were high for number of grains panicle^{-1} and 1000-grain weight, whereas, low for panicle length and plant height. Additive gene action was predominant for 1000-grain weight, number of grains panicle$^{-1,}$ days to 50 % flowering and grain yield as they registered high heritability coupled with high genetic advance values. Based on D^2 analysis, 31 genotypes were distributed into five clusters with the cluster II containing maximum number of genotypes followed by cluster I. Highest inter cluster distances were observed between the clusters III and V followed by I and IV, and IV and V suggesting wide diversity between the traits. Cluster mean analysis revealed that genotypes from the clusters IV and III would be used in breeding programme to develop varieties of medium slender fine grain varieties as they recorded more number of grains panicle^{-1} and low 1000-grain weight and also these genotypes were characterized by early and medium duration flowering duration. The genotype, RDR 1156 was identified as a potential genotype for developing early duration, long bold or long slender grain varieties. Among the traits studied, days to 50% flowering and 1000-grain weight manifested highest contribution towards total divergence, thus, these traits could be given due importance for further crop improvement in the present material.

Keywords: Rice, PCV, GCV, heritability, genetic advance, genetic divergence

1. Introduction

Rice is the most important staple food crop in the world particularly in South East Asia. Though enormous progress has been made in recent past in improving yield levels with the use of high yielding varieties, still there is a pressing need for improving productivity in long bold or long slender and medium slender fine grain rice varieties of various maturity groups by exploiting available variability in the rice germplasm. Hence, presence and magnitude of variability in the germplasm and its critical analysis is a pre-requisite for initiating rice crop improvement programme and for adopting of appropriate selection techniques. The available variability in a population can be partitioned into heritable and non-heritable parts with the aid of genetic parameters such as coefficient of variation, heritability and genetic advance (Miller et al., 1958). As demand has been increasing for high yielding long bold or long slender and medium slender fine grain varieties of desired maturity groups, once genetic variability is ascertained in the population, crop improvement through appropriate selection can proceed for development of these varieties in rice.

Heritability is the heritable portion of a character from parents their offspring (Falconer, 1981).The estimates of heritability help the plant breeders to provide information on the proportion of variation that is transmissible to the progenies in the subsequent generations and selection of elite genotypes from genetic populations. Moreover, heritability estimates in conjunction with genetic advance are normally more helpful in predicting the gain under selection. The pace and magnitude of genetic improvement are generally dependent on the amount of genetic diversity present in a population (Kumbhar, 2015). The study of genetic divergence is of great interest for plant breeder to formulate successful breeding programme and 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. Hence, selection of desirable segregants from segregating populations could be achieved through the inclusion of most divergent parents in breeding programme. Multivariate analysis is an important tool for estimation of genetic divergence in the populations by several workers such as Bose et al. (2005); Ramanjaneyulu et al. (2014); Mohan et al. (2015); Islam et al. (2016); Maurya et al. (2017); Ram et al. (2017); Rusdiansyah et al. (2017); Sowmiya and Venkatesan (2017); Tripathi et al. (2017). Therefore, knowledge about the genetic diversity present in the germplasm for various yield traits is the key information for any breeder for initiation of breeding programme for crop improvement.

Keeping in view of the importance, present study was undertaken to assess the variability, heritability and genetic advance and to estimate the genetic diversity present in the experimental material to enable for selection of more divergent high yielding long bold or long slender and medium slender fine grain genotypes of various maturity groups for further improvement.

2. Materials and Methods

The experimental material for present investigation was consisted of 31 rice genotypes developed through pedigree method of breeding. The seed was raised on nursery beds and 25 days old seedlings of each entry was transplanted in 10.53 m^2 area under irrigated system with two replications in a RBD design during *kharif*, 2015 at Agricultural Research Station, Kunaram by adopting spacing of 15x15 cm^2 between the rows and within the row. All the recommended package of practices and need based plant protection measures were followed to raise a good crop. Data was recorded at maturity on 5 random plants for each entry in each replication for plant height (cm), panicle length (cm), number of productive tillers m$^{2-1}$ and number of grains panicle^{-1}. However, days to 50% flowering and grain yield (kg plot^{-1}) were recorded on whole plot basis, whereas, random sample was used to estimate 1000 grain weight (g) for each entry in each replication. Number of productive tillers plant^{-1} values were converted in to the number of productive tillers m$^{2-1}$and grain yield values recorded from the net plot (kg plot^{-1}) were converted in to hectare (kg ha^{-1}). The mean data after computing for each trait was subjected to analysis of variance (Panse and Sukhatme, 1985), genotypic coefficient of variation (GCV), phenotypic coefficients of variation (PCV) following the formula suggested by (Falconer, 1981), heritability (h^2) in the broad sense as suggested by (Allard,1960) and genetic advance (Burton, 1952) following standard procedures. Multivariate analysis was done as per the Mahalanobis D^2 statistics described by the Rao (1952) and the genotypes were grouped in to different clusters following Tocher's method, and intra and inter cluster distances and mean performances of clusters for all the traits were also computed. Contribution of each trait for genetic divergence was estimated from the number of times it appeared in first rank.

3. Results and Discussion

In the present study, analysis of variance (Table 1) revealed highly significant differences among the genotypes for all the traits studied indicating the presence of considerable amount of variability among the genotypes for earliness, yield and its components.

Table 1: Mean squares corresponding to various sources of variation for seven traits in rice

Source of variation	Degrees of freedom	Days to 50% flowering	Plant height (cm)	No. of productive tillers m$^{2-1}$	Panicle length (cm)	No. of grains panicle^{-1}	1000-grain weight (g)	Grain yield (kg ha^{-1})
Replications	1	1.95	6.20	724.90	1.71	373.63	0.34	21293.56
Treatments	30	300.82^{**}	209.90^{**}	4860.10^{**}	9.41^{**}	5275.57^{**}	46.35^{**}	1681795.43^{**}
Error	30	0.62	4.04	940.77	0.70	567.10	0.36	219122.40

$^{*}p< 0.05$; $^{**}p<0.01$.

The mean performances (Table 2) of 31 genotypes for seven traits revealed that days to 50 per cent flowering varied from 78.0 to 114.0 days with a grand mean of 93.4 days. The released variety, MTU 1001 (114.0 days) had the longest days to flowering and RDR 1153 (78.0 days) was the earliest in this regard followed by RNR 19416 (78.5 days) and RDR 1150 (79.0 days). The trait, plant height ranged from 83.10 to 137.3 cm with a grand mean of 107.3 cm. The tallest genotype being KNM 626 (137.3 cm), while, the shortest genotype was the released variety, BPT 5204 (83.1 cm) followed by the genotype, JGL 24438 (90.2 cm). The genotype, WGL 915 (28.10 cm) possessed longest panicles followed by KNM 626 (27.9 cm) and KNM 736 (27.5 cm), while, minimum length was observed in the released variety, BPT 5204 (18.3 cm) with a grand mean of 24.2 cm. The maximum number of productive tillers m$^{2-1}$ were observed in the genotype, RDR 1140 (413.5) followed by RNR 17859 (400.5) and RDR 1150 (365.5) with an overall mean value of 302.3. The highest grains panicle^{-1} was observed in the medium slender genotypes, JGL 3844 (304.5) followed by JGL 23714 (293.2) and the released variety, JGL 11470 (282.6), while, minimum value was recorded in the long bold grain genotype, RDR 1156 (90.2) in this regard which was varied from 90.2 to 304.5. Long bold grain genotype, RDR 1156 recorded maximum test weight (31.5 g) followed by other long bold genotypes, WGL 915 (29.9 g) and KNM 736 (26.6 g) and minimum was observed for the medium slender grain genotypes, JGL 23714 (13.0 g) followed by JGL 11470 (14.1g) and KNM 733 (14.4 g). Highest grain yield was found to register for long bold grain type genotypes, KNM 736 (7283.5 kg/ha) followed by RNR 19399 (7236 kg/ha) and JGL 20777 (7051.5

Table 2: Mean performance of seven characters for 31 rice genotypes

Genotype	Days to 50 % flowering	Plant height (cm)	Panicle length (cm)	No. of productive tillers m^{2-1}	No.of grains panicle^{-1}	1000- grain weight (g)	Grain yield (kg ha^{-1})
KNM 604	79.0	111.7	26.1	339.0	190.8	22.4	6821.5
WGL 739	90.5	104.4	23.7	312.5	201.1	21.4	6199.0
MTU 1010	86.5	102.7	24.9	343.0	136.9	25.0	6754.0
RDR 1140	79.0	114.7	26.8	413.5	143.0	25.5	6961.5
JGL 23666	89.5	102.4	21.2	259.5	134.0	24.5	6274.0
RNR 17497	90.5	101.2	22.4	286.0	166.4	16.9	3873.0
RDR 1150	79.0	101.7	25.9	365.5	109.4	24.2	5708.5
KNM 626	108.0	137.3	27.9	286.0	170.9	23.2	7044.5
JGL 24423	84.5	103.5	24.3	352.0	158.0	23.9	5908.0
RDR 1156	84.0	119.1	25.2	343.0	90.2	31.5	5225.0
JGL 3844	90.0	105.3	24.5	317.0	304.5	16.7	6517.5
KNM 736	84.0	121.0	27.5	325.5	218.2	26.2	7283.5
WGL 505	108.5	115.9	22.3	352.0	223.6	14.8	5948.5
RDR 1153	78.0	104.1	26.4	299.5	113.4	25.6	5494.5
RNR 19416	78.5	104.6	24	304.0	151.6	24.7	5255.0
KNM 733	84	93.1	22.7	330.0	200.9	14.4	6805.5
RNR 17859	84.5	96.5	23.8	400.5	135.2	24.5	6382.5
WGL 705	112.0	111.9	23.4	237.5	145.5	25.2	6160.0
JGL 20777	107.0	105.9	24.3	237.5	176.2	25.1	7051.5
RNR 19399	107.0	112.0	25.0	259.5	150.6	23.3	7236.0
WGL 697	110.5	112.5	24.7	224.5	202.8	22.5	6359.5
MTU 1001	114.0	110.4	23.4	299.5	139.8	24.8	6505.0
RNR 11718	107.0	99.9	21.9	268.5	167.3	19.1	4818.5
WGL 915	108.5	116.4	28.1	198.0	197.8	29.9	6665.5
JGL 23714	108.0	108.7	22.9	317.0	293.2	13.0	5313.5
RNR 17441	84.0	109.6	25.1	316.5	126.4	24.7	5888.0
BPT 5204	86.5	83.1	18.3	281.5	167.3	14.9	6788.5
WGL 725	88.5	115.7	25.7	268.0	182.0	17.6	5772.0
JGL 11470	88.5	98.5	23.9	250.5	282.6	14.1	6331.5
JGL 24438	108.0	90.2	20.3	286.0	211.1	15.8	3785.5
RNR 17947	89	114.2	25.5	299.0	140.4	21.4	4534.5
Mean	93.4	107.3	24.2	302.3	175.2	21.8	6053.7
C.V.	0.8	1.9	3.4	10.1	13.6	2.8	7.7
SEm±	0.6	1.4	0.6	21.7	16.8	0.4	331.0
CD (*p*=0.05)	1.6	4.1	1.7	62.6	48.6	1.2	956.0
CD (*p*=0.01)	2.2	5.5	2.3	84.3	65.5	1.7	1287.3

kg ha^{-1}), whereas, medium slender grain type genotype, JGL 24438 showed less grain yield (3785.5 kg ha^{-1}).

The variability estimates (Table 3) for yield and its contributing traits revealed that genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for number of grains panicle^{-1} and 1000-grain weight indicated the presence of high degree of variation for these traits among the genotypes which could be improved through selection in desirable direction. These results are in agreement with the findings were obtained by Mohan et al. (2015); Srinivas et al. (2016) for both number of grains panicle^{-1}and 1000-grain weight and, Ahmed et al. (2010); Das et al. (2015) for 1000-grain weight, and Ram et al. (2017) for grain yield, whereas, low levels of PCV and GCV were observed for panicle length and plant height suggesting the less variability among the genotypes for these traits. Similar reports were concluded by Das et al. (2015); Akinwale et al. (2011); Sangram Kumar et al. (2011). Moderate levels of PCV and GCV for number of productive tillers plant^{-1}, grain yield and days to 50% flowering indicated the considerable level of variability in these traits and suggested the possibility of improving these traits through selection. In contrary to this, Akinwale et al. (2011); Ramanjaneyulu et al. (2014) reported moderate GCV and high PCV values for grain yield. High estimates of PCV were observed than GCV for all the traits studied indicating the role of environmental forces in the inheritance of these traits. Similar findings were earlier reported by Vanisree et al. (2013); Ketan and Sarkar (2014); Mohan et al. (2015); Bagati et al. (2016); Hefena et al.(2016); Srinivas et al. (2016); Rusdiansyah et al.(2017). Narrow differences between the corresponding estimates of PCV and GCV were observed for days to 50% flowering, plant height, panicle length and 1000-grain weight indicated the presence of high genetic variability and less interference of environment on expression of these traits which may facilitate selection (Yadav, 2000). However, estimates of PCV were considerably higher than GCV for number of productive tillers m$^{2-1}$, number of grains panicle^{-1} and grain yield, indicating the sensitive nature of these traits to environmental fluctuations and predominance of non-additive gene effects. Similar findings are in accordance with the earlier reports of Vanisree et al. (2013); Ketan and Sarkar (2014); Das et al. (2015); Mohan et al. (2015); Rusdiansyah et al. (2017); Tripathi et al. (2017).

Table 3: Genetic parameters for yield and yield contributing traits in rice

Character	Mean	Range		GCV	PCV	h² (Broad Sense)	GA in % over mean
		Min	Max				
Days to 50% flowering	93.4	78.0	114.0	13.1	13.1	99.6	26.9
Plant height (cm)	107.3	83.1	137.3	9.5	9.6	96.2	19.1
Panicle length (cm)	24.2	18.3	28.1	8.6	9.3	86.6	16.6
Number of productive tillers m$^{2-1}$	302.3	198.0	413.0	14.6	17.8	67.6	24.8
Number of grains panicle^{-1}	175.2	90.2	304.5	27.7	30.9	80.6	51.2
1000- grain weight (g)	21.8	13.0	31.5	21.9	22.2	98.4	44.9
Grain yield (kg ha^{-1})	6053.7	3785.5	7283.5	14.1	16.1	76.9	25.5

GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation

The heritability (broad sense) estimates (Table 3) were high for all the traits except number of productive tillers m$^{2-1}$ indicated that these traits could be improved through selection based on their phenotype, whereas, in case of number of productive tillers m$^{2-1}$which had relatively moderate estimates, improvement through selection could be relatively low when compared with other traits due to masking effect of environment on the expression of this trait. Similarly, moderate heritable values were reported by Sangramkumar et al. (2011), Thomas and Gabriel (2012) for test weight, Ramanjaneyulu et al. (2014) for days to flowering and panicle length. The traits those exhibit high heritability and high genetic advance as % of mean could be used as powerful tool in selection process, such traits are controlled by the additive genes and less influenced by the environment (Panse and Sukhatme, 1995). In the present investigation, high heritability coupled with high genetic advance values were observed for 1000-grain weight, number of grains panicle^{-1}, days to 50% flowering and grain yield 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 Toshimenla and Changkija (2013); Srinivas et al. (2016); Chandramohan et al. (2016); Islam et al. (2016); Ram et al. (2017); Tripathi et al. (2017) for 1000-grain weight. Similarly, high heritability coupled with moderate genetic advance estimates were recorded by the researchers Ketan and Sarkar (2014); Chandramohan et al. (2016) for plant height and panicle length suggested the role of both additive and non-additive gene effects in their inheritance, therefore, adoption of breeding procedures which could exploit both the gene actions would be a prospective approach.

On the basis of D^2 values (Table 4), 31 genotypes were grouped into 5 clusters of which cluster II was the largest consisting of 15 genotypes followed by cluster I included 8 genotypes, however, the clusters III, IV and V comprised of 3, 4 and 1 genotypes, respectively. Intra and inter cluster distance values among 31 genotypes were presented in Table 5. The intra cluster distances ranged from zero (cluster V) to 9.48 (cluster II). Genotypes in the clusters II, I and III which were having high degree of divergence would produce more

Table 4: Distribution of 31 rice genotypes in different clusters

Cluster no.	No. of genotypes	Genotypes
I	8	WGL 705, MTU 1001, WGL 697, RNR 19399, JGL 20777, RNR 11718, WGL 915, KNM 626
II	15	RDR 1156, RNR 19416, RDR 1153, RDR 1140, JGL 24423, RNR 17441, RNR 17859, MTU 1010, KNM 604, KNM 736, JGL 23666, RNR 17947, WGL 739, RNR 17497, WGL 725
III	3	WGL 505, JGL 23714, JGL 24438
IV	4	JGL 3844, JGL 11470, KNM 733, BPT 5204
V	1	RDR 1156

Table 5: Average intra (diagonal) and inter cluster distances (Tocher method) for 31 rice genotypes

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	9.75	26.67	17.52	32.08	26.28
Cluster II		9.48	25.68	17.66	16.97
Cluster III			8.65	23.09	33.03
Cluster IV				7.99	31.57
Cluster V					0.00

desirable segregates to achieve greater genetic divergence. From the inter cluster distance values, it was clear that highest divergence occurred between cluster III and V (33.03) followed by cluster I and IV (32.08) and cluster IV and V (31.57) indicating the presence of greater diversity between genotypes of these groups. Hence, crossing between genotypes belonging to these clusters may result in high heterosis, which could be exploited in crop improvement. Genotypes belonging to clusters separated by high cluster distance could be used in breeding programme for obtaining wide spectrum of variation among the segregants as reported by De Reddy et al. (1992); Maurya et al. (2017). However, lowest inter cluster distance was noticed between cluster II and V (16.97) indicating that the genotypes of the cluster II and V had genetic resemblance.

For all the traits studied, considerable amount of variation among the cluster means (Table 6) was observed indicating the presence of ample diversity for these traits in experimental material. Genotypes in cluster IV were characterized with early in flowering, moderate plant height, good number of grains panicle^{-1}, grain slenderness and more grain yield, hence these genotypes could be used for obtaining high yielding, early duration, medium slender grain, on lodging genotypes, despite less number of productive tillers m$^{2-1}$ were observed. Cluster V genotype, RDR 1156 was found to be good with respect to days to 50% flowering, 1000-grain weight and number of productive tillers m$^{2-1}$ and, therefore, it could be used as a parent for developing early duration long slender or long bold rice varieties. Genotypes from cluster III were characterized by highest number of grains panicle^{-1} and lesser 1000-grain weight; hence, these genotypes could be used for obtaining medium slender grain varieties.The traits, 1000-grain weight and days to flowering contributed considerably, accounting for 83.01% of total divergence among all the traits indicating the importance of these traits for effective selections, whereas, panicle length (0.43), number of productive tillers m$^{2-1}$(0.43) and number of grains panicle^{-1} (0.22) recorded least contribution towards total divergence which are of less importance in selection of diverse parents. Similarly, researchers Bose and Pradhan (2005); Srinivas et al. (2016); Chandramohan et al. (2016) reported higher contribution of days to flowering and 1000- grain weight towards total divergence in rice , whereas, least contribution of effective tillers, plant height and panicle length towards total

Table 6: Cluster means and percent contribution of each character towards total divergence of 31 rice genotypes for seven characters

Cluster	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	No. of Productive tillers m$^{2-1}$	No. of grains panicle^{-1}	1000- grain weight (g)	Grain yield (kg ha^{-1})
Cluster I	109.25	113.25	24.81	251.38	168.86	24.11	6480.06
Cluster II	84.33	107.17	24.81	325.60	153.79	23.21	5940.63
Cluster III	108.17	104.92	21.80	318.33	242.63	14.50	5015.83
Cluster IV	87.25	94.99	22.31	294.75	238.83	15.00	6610.75
Cluster V	84.00	119.05	25.15	343.00	90.20	31.45	5225.00
% Contribution of character	57.85	8.17	0.43	0.43	0.22	25.16	7.74
No. of times ranked first	269	38	2	2	1	117	36

divergence was noticed by Garg et al. (2011); Chandramohan et al. (2016); Sowmiya and Venkatesan (2017). Since, days to 50 % flowering, 1000-grain weight, plant height and grain yield 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.

4. Conclusion

Variability studies suggest that PCV estimates were considerably higher than GCV estimates for number of productive tillersm$^{2-1}$, number of grains panicle^{-1} and grain yield. Based on the genetic diversity study, genotype RDR 1156 was identified as a potential genotype for developing early duration, long bold or long slender grain varieties. Genotypes from the clusters III and IV would be used in breeding programme to develop early and medium duration varieties of medium slender, fine grain varieties.

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