Genetic Diversity and Correlation Studies for Early Mature Yield and Quality Traits in Elite Rice (*Oryza sativa* L.) Germplasm

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Abstract: *The presence of sufficient genetic variability, the knowledge of nature of association among different characters and relative contribution of different characters to yield is a pre-requisite to any breeding programme. The aim of the present study was to estimate genetic parameters of thirteen yield attributing traits in thirty seven rice cultivars with a view to select better yield attributes in rice. Genotypes IRRI 5 was found to be superior for grain yield per hill among 37 rice genotypes of rice followed SHIATS DHAN 2, SHIATS DHAN 1 and SHIATS DHAN 3. The higher value of phenotypic co-efficient of variation (PCV) compared to the corresponding genotypic coefficient of variation (GCV) for all the studied traits indicated that there was an influence of the environment High to moderate GCV and PCV were recorded for grain yield per hill, number of spikelet's per panicle, panicles per hill, tillers per hills, biological yield per hill and test weight respectively suggesting that there was preponderance of additive gene action. High estimates of heritability coupled with high genetic advance as percent of mean was observed for number spikelet per panicle (99.5%, 37.73%), grain yield per hill (92.0%, 37.69%), biological yield per plant (94.7%, 31.00%) respectively suggesting that there was preponderance of additive gene action governing the inheritance of this character and offers the best possibility of improvement through simple selection. At both genotypic and phenotypic levels, significant positive correlations were observed for grain yield per plant with Grain yield indicated significant positive correlation with harvest index, biological yield, number of spikelet's per panicle, days to 50 percent flowering, days to maturity, number of panicles/ hill, flag leaf length, number of tillers per hill, test weight and plant height, flag leaf width. All the37 Rice genotypes were classified using Mahalanobis D^2 statistics involving 17 quantitative traits through this method. Based on D^2 values 37 genotypes grouped into 5 clusters. Among 5 clusters cluster I had more number of genotypes (30) followed by cluster II (4 genotypes), remaining all clusters had (1 genotype) each. The maximum intra cluster distance were observed in cluster II and highest inter cluster distance observed between cluster IV and cluster V and cluster III and cluster IV crosses involving genotypes from these clusters would give wider and desirable recombination's. Therefore, genotypes present in these clusters are suggested to provide a broad spectrum of variability and may be used as parent for future hybridization programme to develop desirable genotypes.*

Keywords: Rice Cultivars, genetic variability, coefficient of variation, heritability, correlation, genetic divergence

1. Introduction

Rice (*Oryza sativa* L.) is one of the most important staple cereal food crop in the world and belongs to the genus *Oryza* of family Graminae (Poaceae). The genusincludes24 species out of which 22 are wild and two viz., *Oryza sativa* and *Oryza glaberimma* are cultivated. The basic chromosomes number (n) of the genus *Oryza sativa* is 12 (2n=24). The cropis cultivated round the year in one or the other parts of the country under diverse ecologies spread about 44 million hectares. In order to feed the increasing population, the production of rice has to match with the consumption growth, where rice is the staple food crop. In the past fifty years, the growth in production has originated from technological progress in rice cultivation in irrigated and favourable rain fed low land areas. Irrigated rice production supplies 75 to 80 percent of global rice requirements Genetic variability refers to the presence of difference among the individuals of the plant population. The large spectrum of genetic variability in segregating population depends on the amount of the genetic variability among genotypes and offer better scope for selection. Correlation is the measure of the mutual relationship between two variables. The study of correlations may help the plant breeder to know how the improvement of one character will bring simultaneous improvement in other characters. Genetic diversity is one of the useful tools to select appropriate genotypes/lines for hybridization. Genetic diversity is estimated by the D2 analysis, metroglyph and principle component analysis using morphological traits. This analysis provides a measurement of relative contribution of different components on diversity both at intra and inter-cluster level and genotypes drawn from widely divergent clusters are likely to produce heterotic combinations and wide variability in segregating generation.

2. Materials and Methods

The experimental materials for the present study consisted of 37 Rice varieties and one check variety. Rice varieties are being received from department of Genetics and Plant Breeding, SHUATS during *kharif*-2020. The experiment was laid in Randomized Block Design (RBD) with 37 genotypes under three replications. Observations were recorded on the various morpho-agronomic, yield and quality traits in order to study the magnitude of genetic variability and level of genetic divergence in the material. Five competitive representative plants were selected at random from each experimental plot in each replication and tagged for recording the biometrical observations. Observations on five randomly selected plants were recorded for days to 50% flowering, plant height (cm), number of tillers per hill, number of panicles per hill, panicle length (cm), flag leaf length (cm), flag leaf width (cm),

number of spikelet per panicle, days to maturity, biological yield per plant (gm), harvest index, test weight (gm), grain yield per plant (gm).The data for days to 50 per cent flowering and days to maturity were recorded on whole plot basis. Mean values for all the characters and median values for days to 50 per cent flowering and maturity were worked out. Observations were recorded in the field at the appropriate developmental stages of plant growth and morphological characters.

3. Results and Discussion

Analysis of variance 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. The estimate of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) revealed that phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the characters that indicate the influence of environmental factors on these traits. Higher estimates of PCV were observed for number of tillers per hill (20.71%) and number of panicles per hill (21.56%) and higher GCV is not observed in the experiment. Moderate estimate of GCV and PCV observed for grain yield per hill (19.08%, 19.89%) followed by spikelet's per panicle (18.36%, 18.41%), panicles per hill (16.52%), biological yield per hill (15.46%, 15.89%), tillers per hill (13.95%), test weight (10.74%, 12.25%) and flag leaf length (10.13%, 12.73%). While harvest index (10.95%) and flag leaf width (11.86%) were also observed moderate PCV. Lowest estimates of GCV and PCV observed for days to maturity (4.71%, 4.71%) followed by days to 50% flowering (5.51%, 6.08%), panicle length (5.23%, 6.63%), plant height (9.88%, 7.91%). While harvest index (9.15%) and flag leaf width (9.88%) were also observed moderate GCV.

3.1 Correlation Coefficient

Correlation coefficient analysis at phenotypic level revealed that days to 50 percent flowering (0.54**), plant height (0.28**), tillers per plant (0.34**), panicles per plant (0.41**), flag leaf length (0.35**), flag leaf width (0.26**), spikelet's per panicle (0.56**), days to maturity (0.51**), biological yield (0.79**), harvest index (0.87**) and test weight (0.31**) showed positive significant correlation with grain yield. Whereas panicle length (0.19), showed positive but non-significant association with grain yield. Correlation coefficient analysis at genotypic level revealed that Days to 50percent flowering (0.56**), Plant height (0.28**), Number of tillers per hill (0.42**), Number of panicles per hill (0.42**), Flag leaf length (0.39**), Flag leaf width (0.39**), Spikelet's per panicle (0.57**), Days to maturity (0.53**), Biological yield (0.82**), Harvest index (0.89**) and Test weight (0.32**) showed positive significant association with grain yield, whereas panicle length (0.14*), showed positive but non-significant association with grain yield.

3.2 Genetic Diversity

Based on D^2 values 37 genotypes grouped into 5clusters. Among 5 clusters cluster I had more number of genotypes (30) followed by cluster II (4genotypes), remaining all clusters had (1 genotype) each. The intra cluster values ranged from 0 to 47.24. The maximum intra cluster distance were observed in cluster II (47.24) followed by cluster I (43.16).The minimum intra cluster distance for cluster III, IV, V exhibited zero. The inter cluster distance differ from 109.1 (between I and III) to 470.06 (between IV and V). Other inter cluster distance were between these values. The highest inter cluster distance observed between cluster IV and cluster V (470.06) followed by cluster III and cluster IV (388.95), cluster I and cluster IV (284.33), cluster II and cluster V (194.34), cluster III and cluster V (183.83). The minimum inter cluster distance observed between cluster I and III (109.1), cluster II and cluster IV (111.64), cluster I and cluster II (120.51). Clusters is essential to judiciously combine all the targeted traits. The selection and choice of parents mainly depend upon the contribution of characters towards divergence. From the characters taken under study spikelets per panicle (71.67%), days to maturity (10.59%) and biological yield for plant (10.34%) were the major contributors towards divergence and accounted for about 92.60% of contribution towards total divergence need to be stressed in selection of parents for hybridization.

Table 1: Analysis of variance for 13 quantitative characters in 37 rice genotypes

S. No	Characters	Mean Sum of Squares		
		Replications (df=2)	Treatments (df=36)	Error (df=72)
1	Days to 50% flowering	18.4860	129.194**	44.266
2	Plant height	168.1350	360.591**	100.331
3	Number of tillers/ hill	0.240	8.93**	0.748
4	Number of panicles hill	0.4760	5.656**	0.566
5	Panicle length	3.0450	16.244**	4.109
6	Flag leaf length	20.8880	113.886**	9.474
7	Flag leaf width	0.010	0.073**	0.009
8	No. of spikelets per panicle	147.8490	3407.655**	116.218
9	Days to maturity	12.2290	125.941*	69.506
10	Biological yield	40.1220	250.085**	23.389
11	Harvest index	50.091**	90.438**	7.389
12	Test weight	1.4750	18.997**	2.007
13	Grain weight per hill.	2.090	107.183**	3.774

Table 2: Distribution of 37 Rice genotypes into different clusters

Cluster No.	No. of Genotypes	Genotypes included in the cluster
I	30	IRRI-1, IRRI-2, IRRI-4, IRRI-5, IRRI– 6, IRRI– 7, IRRI–8, IRRI–9, IRRI–10, IRRI–11, IRRI-12, IRRI– 14, IRRI-16, IRRI–17, IRRI–20, IRRI-21, IRRI-22, IRRI– 23, IRRI –24, IRRI-25, IRRI-26, IRRI-29, IRRI– 30, IRRI-31, IRRI-36, IRRI –37, IRRI –39, IRRI-150.
II	4	SHIATSDHAN-3, SHIATSDHAN-4, SHIATSDHAN-5, NRC-369
III	1	SHIATSDHAN-2
IV	1	SHIATSDHAN-1
V	1	IRRI-3

Table 3: Intra (diagonal) and Inter-cluster average distances for different quantitative characters in Rice

Cluster Distances					
	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5
Cluster1	43.16	120.51	109.1	284.33	173.76
Cluster2		47.24	176.21	111.64	194.34
Cluster3			0	388.95	183.83
Cluster4				0	470.06
Cluster5					0

Table 4: Cluster Mean Values for 13 Quantitative characters in 37 Rice genotypes

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of Primary Branches	Number of Secondary Branches	Total number of pods per plant	Number of effective pods per plant	Biological yield per plant (g)	Seed index (g)	Harvest index (%)	Seed yield per plant (g)
1 Cluster	**81.935**	120.933	36.120	2.003	5.465	12.733	10.732	**22.453**	19.733	48.606	**10.987**
2 Cluster	81.733	**121.067**	38.200	2.269	**5.732**	18.201	15.387	20.573	20.267	47.491	10.293
3 Cluster	80.721	119.278	**39.248**	2.058	5.611	23.556	19.378	21.933	17.333	**54.529**	12.138
4 Cluster	80.611	111.333	39.011	2.168	4.779	**28.555**	**23.877**	15.244	23.167	47.693	7.476
5 Cluster	80.083	118.250	37.450	2.251	5.001	17.50'0	14.167	13.417	21.583	46.197	6.216
6 Cluster	85.420	111.500	35.517	**2.581**	4.585	24.583	20.417	17.367	**25.750**	48.311	8.616

Table 5: Percent contribution of different characters to genetic diversity

S. No.	Character	Contribution (%)	Times ranked first
1.	Days to 50% flowering	0.25	1
2.	Plant Height	0	0
3.	Number of tillers per hill	0.25	1
4.	Number of panicles per hill	0.25	1
5.	Panicle Length	0	0
6.	Flag leaf length	0.25	1
7.	Flag leaf width	0	0
8.	Number of spike lets per panicle	71.67	291
9.	Days to maturity	10.59	43
10.	Biological yield	10.34	42
11.	Harvest Index	1.48	6
12.	Test Weight	1.97	8
13.	Grain yield per hill	2.96	12

4. Conclusion

The experiment results concluded that the genotype IRRI 5 (43.2 g) was found to be superior for grain yield per hill among 37 rice genotypes of rice followed by SHIATS DHAN 2, SHIATS DHAN 1 and SHIATS DHAN 3.Highto moderate estimate of GCV and PCV were recorded for grain yield per hill, number of spikelet per panicle, panicles per hill, tillers per hills, and biological yield per hill and test weight. Grain yield per plant was positively and significantly associated with harvest index, biological yield, number of spikelet per panicle, days to 50 percent flowering, days to maturity, number of panicles/hill, flag leaf length, number of tillers per hill, test weight and plant height, flag leaf width at both genotypic and phenotypic levels. Based on D^2 values 37 genotypes grouped into 5 clusters. Among 5 clusters cluster I had more number of genotypes (30) followed by cluster II (4 genotypes), remaining all clusters had (1genotype)each. The maximum intra cluster distance were observed in cluster II and highest inter cluster distance observed between cluster IV and cluster V and cluster III and cluster IV crosses involving geno types from these clusters would give wider and desirable recombination's. Therefore, genotypes present in these clusters are suggested to provide a broad spectrum of variability and may be used as parent for future hybridization program to develop desirable genotypes.

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