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Quantitative Analysis Of Rice Genotypes (*Oryza Sativa L.*)

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Abstract:

Genetic variability, genotypic and phenotypic coefficients of variation, heritability and genetic advance for eleven characters in one hundred and fifty genotypes including five check varieties of rice were studied. The analysis of variance revealed that there were highly significant differences for all the characters Leaf Length, Panicle Length, 100-seed Wt, Germination % and Coleoptiles Length. The estimates of genotypic and phenotypic coefficients of variation (GCV and PCV) were high for all the characters except days to 50% flowering and panicle length. Heritability and genetic advance were high for all the traits except Yield/ Plant and Fertile Grains/ Panicle and Radical length which had a moderate magnitude of genetic advance, which had moderate genetic advance along with high heritability indicating the involvement of additive type of gene action in controlling these characters.

Key words: Rice, Genetic variability, Heritability, Genetic advance

1.Introduction

Rice is the world's most important food crop and a primary source of food for more than half the world's population and forms the cheapest source of food, energy and protein. In India, rice is cultivated by different methods under diverse environmental conditions. Genetic diversity determines the inherent potential of a cross for heterosis and frequency of desirable recombinants in advanced generations. For the same, genetic distance plays a vital role, as the parental diversity in optimum magnitude is required to obtain superior genotypes in segregating population (Varshney et al 2008). A systematic evaluation and characterization of germplasm lines not only helps in the identification of superior and genetically divergent germplasm lines (Nayak et al, 2003).

The breeders are interested to evaluate genetic diversity based on morphological traits because they are inexpensive, rapid, and simple to score. The study of these traits needs neither sophisticated method nor complicated equipments, and also these traits can be inherited without either specific biochemical or molecular techniques. Until now scientific classification of plant was based on morphological traits (Kumar 1999). Characterization of accessions provides the information on morphological and agronomic aspects of the material that is essential for the gene bank management. Therefore, the present investigation was undertaken to assess the nature and magnitude of genetic diversity among the genotypes for further utilization in breeding programmes.

2.Materials And Methods

A set of 470 rice germplasm accessions collected from different parts of the country were tested for their cold tolerance in a phytotron. Five checks AK Dhan, N-22, Prasanna, RP-Bio and Vikas were used. The seeds of the germplasm lines were allowed to germinate at 35°C in a growth chamber for 3 days. 30 uniformly germinated seeds from each accession were sown in germination trays and cultured in a growth cabinet where the temperature was maintained at 25°C with 70% relative humidity. At one-leaf stage the seedlings were subjected to cold stress at 6°C during night time and 8°C during the day with a relative humidity of 70% for 7 days after which the temperature was adjusted gradually back to 25°C. The survived lines at 20th day were transferred to field to evaluate their agronomic performance and tolerance to heat during reproductive phase. A field experiment was conducted by using augmented design during Rabi, 2012 at DRR farm, ICRISAT Campus Patancheru, Hyderabad, India. Situated at 17.53°N latitude, 78.27° E

longitude and altitude of 545m above mean sea level. The augmented experimental design introduced (Federer 1956) was used for the experiment.

An Augmented Experimental Design (AED) is usually useful for testing a large number of genotypes in early generations when valid statistical analyses are needed particularly when seed supplies are too limited to permit replication. Seedlings were transplanted at 21 days old with a spacing of 20X20 cm. The field experiment was carried out in summer with maximum temperatures crossing 40°C. One seedling was transplanted per hill and the inter-plot spacing was 40 cm. A plot size of 1.2x5 m with 6 rows was used for each accession in the field. Recommended cultural practices are followed. Morphological data were collected for nineteen quantitative characters at the appropriate growth stage of rice plant following the descriptor for Rice *Oryza sativa* L. (IRRI, 1980). The plot means were analysed using standard statistical analysis suggested by Federer (1956) and elaborated by Sharma (1998). The phenotypic and genotypic coefficient of variability (PCV and GCV), heritability and genetic advance were computed as per methods of Burton (1952) & Johnson *et al.* (1955).

3.Results and Discussion

Greater variability in the initial breeding material ensures better chances of producing a desired form of a crop plant. Thus the primary objective of germplasm conservation is to collect and preserve the genetic variability in an indigenous collection of crop species to make it available to present and future generations. The analysis of variance indicated the existence of highly significant differences among genotypes for the characters like Leaf Length , Panicle Length , 100-seed Wt , Germination % and Coleoptiles Length (Table 1). A wide range of variation was observed in the rice germplasm for all the quantitative characters and yield (Table 2). However, widest range of variability was recorded for Seed vigor (-637.52 to 4842.5) followed by Fertile Grains/ Panicle (-36.84 to 254.3). The range of variation obtained for leaf width (0.52 to 2.2) and 100-seed weight (0.05 to 3.5) was least when compared to all the other characters. Seed vigor and germination% exhibited high genotypic and phenotypic variances, followed by Sterility% . Similar results were obtained earlier by Sawant *et al.* (1994).

Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for all the characters under study were less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits. The magnitude of the PCV was lower than the corresponding GCV for the characters suggesting the influence of environment on the expression of these traits. The characters like Effective Tillers/ Plant, Plant Height , Pollen Viability, and Seed vigour showed high PCV and GCV estimates. Observations for Days to 50% Flowering, Seed Density and Pollen Viability (Table 2). Low PCV and GCV estimates were obtained for days to 50% flowering and panicle length. These results are in conformity with those obtained for days to 50% flowering by Sinha *et al.* (2004) .

The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore, high heritability helps in the effective selection for a particular character. In the present study, all the characters exhibited high heritability, which ranged from -1.01to 0.98 (Table 2). The genetic advance is a useful indicator of the progress that can be expected as a result of exercising selection on the pertinent population. The genetic advance expressed as a percentage of mean ranged from -75.25 to 868.5 and the important characters like Seed vigour (868.5), Germination % (59.54) and Leaf Length (18.92) recorded higher estimates.

	Block (Ignoring Treatments)	Treatment (Eliminating Blocks)	Checks	Checks+Var Vs. Var.	ERROR
d.F	4	474	4	14.203	5.4 to 36.4
Tillers/Plant	966.46 ***	23.59 ***	6.7	5.797	-0.560 to 20.4
Effective Tillers/ Plant	106.65 ***	14.46	3.34	101.868	46.2 to 150.4
Plant Height cm	2512.62***	219.40 *	1351.70 ***	55.915	20.4 to 98.2
Leaf Length cm	551.92 ***	139.06 ***	405.50***	1.149	0.52 to 2.2
Leaf Width cm	0.35***	0.04	0.11*	25.785	15.7 to 37.1
Panicle Length cm	131.77***	12.01***	64.97***	80.415	0.6 to 109
Sterility %	2882.25***	381.75*	5394.24***	5.638	-3.16 to 49.8
Yield/ Plant	189.71**	32.67	564.93***	2.038	-0.05 to 3.5
100-seed Wt	0.36**	0.18**	0.26**	83.789	5.08 to 101.8
Seed Density	775.70***	141.36	357.46*	119.622	43.48 to 289.6
Grains/ Panicle	7676.18*	1215.72	2603.06	29.672	-36.84 to 254.3
Fertile Grains/ Panicle	6675.63	1528.31	15504.14**	71.209	47.24 to 97.8
Pollen Viability	423.21***	71.98*	491.04***	104.976	92.52 to 110.9

	Block (Ignoring Treatments)	Treatment (Eliminating Blocks)	Checks	Checks+Var Vs. Var.	ERROR
Days to 50% Flowering	123.06**	14.93	15.26	74.596	3.88 to 102
Germination %	1000.55***	908.5***	12.26	6.154	-1.49 to 37.9
Coleoptiles Length (cm)	12.57	31.72**	25.6	6.496	-4.06 to 18.7
Radical Length (cm)	17.36	22.66	15.97	12.651	-5.37 to 49.3
Seed Growth (cm)	51.79	98.61	67.35	1105.261	-637.52 to 4842.5
Seed vigor	399585.16	1053480.1	618118	14.203	5.4 to 36.4

Table 1: Analysis Of Variance For Different Traits In Rice Germplasm

Based upon variability and heritability estimates, it could be concluded that improvement by direct selection in rice is possible for traits like Seed vigour and Leaf Length. In general, the character that shows high heritability with high genetic advance are controlled by additive gene action (Panse and Sukatme, 1957) and can be improved through simple or progeny selection methods. Selection for the traits having high heritability coupled with high genetic advance is likely to accumulate more additive genes leading to further improvement of their performance.

	Variance components		Coefficient of variability		Heritability (Broad Sense)	Genetic Advance	Gen. Adv. as % of Mean	Mean	Range
	Genotypic	Phenotypic	Genotypic	Phenotypic					
Tillers/Plant	25.4	30.3	35.42	38.68	0.83	9.51	66.81	14.20	5.4 to 36.4
Effective Tillers/ Plant	5.8	14.8	42.04	66.63	0.39	3.15	54.65	5.79	-0.560 to 20.4
Plant Height cm	113.3	213.1	10.43	14.31	0.53	15.98	15.67	101.86	46.2 to 150.4
Leaf Length cm	101.1	120.9	17.91	19.59	0.83	18.92	33.72	55.91	20.4 to 98.2
Leaf Width cm	0.2	0.03	9.67	17.18	0.31	0.12	11.21	1.14	0.52 to 2.2
Panicle Length cm	9.7	11.5	12.0	13.13	0.84	5.89	22.820	25.78	15.7 to 37.1
Sterility %	125.5	294.6	13.88	21.26	0.42	15.07	18.66	80.41	0.6 to 109
Yield/ Plant	-9.1	24.2	-54.46	88.80	-0.37	-3.81	-68.81	5.63	-3.16 to 49.8
100-seed Wt	0.12	0.1	17.56	20.53	0.73	0.63	30.94	2.03	-0.05 to 3.5
Seed Density	66.37	142.7	9.72	14.25	0.46	11.4	13.65	83.78	5.08 to 101.8
Grains/ Panicle	-628.13	1138.9	-21.05	28.35	-0.55	-38.34	-32.20	119.62	43.48 to 289.6
Fertile Grains/ Panicle	-1314.11	1293.9	-124.81	-123.84	-1.01	-75.25	-259.10	29.67	-36.84 to 254.3
Pollen Viability	33.67	63.1	8.16	11.16	0.53	8.74	12.29	71.2	47.24 to 97.8
Days to 50% Flowering	-9.79	15.7	-2.98	3.77	-0.62	-5.09	-4.84	104.9	92.52 to 110.9
Germination %	851.14	867.1	39.22	39.58	0.98	59.54	80.05	74.5	3.88 to 102
Coleoptiles Length (cm)	19.80	30.54	72.50	90.04	0.64	7.38	120.27	6.15	-1.49 to 37.9
Radical Length (cm)	-0.83	21.86	-14.1	72.28	-0.03	-0.36	-5.69	6.49	-4.06 to 18.7
Seed Growth (cm)	36.095	94.91	47.65	77.27	0.38	7.63	60.53	12.65	-5.37 to 49.3
Seed vigor	423871.7	1010714.5	59.159	91.3	0.41	868.5	78.9	1105.26	-637.52 to 4842.5

Table 2: Range, Mean, Genotypic And Phenotypic Variance Components, Coefficient Of Variability, Heritability And Genetic Advance For Different Traits In Rice Germplasm

In the present investigation, high heritability along with high genetic advance was noticed for all the traits except Yield/ Plant and Fertile Grains/ Panicle, Grains/ Panicle and Radical length which had moderate magnitude of genetic advance. The characters showing high heritability along with moderate or low genetic advance can be improved by intermating superior genotypes of segregating population developed from combination breeding (Deb Choudhary PK and PK Das (1998).

In the present study, eleven superior genotypes, viz., GP8181, GP 8308 , GP 8437 , GP 8507 , GP 8571 , GP 4495 and GP 3428 were found to be potential enough to be used as parents in heterosis breeding. These genotypes recorded higher values for one or the other yield contributing characters and hence their utilization in combination breeding may help in generating high yielding varieties/ hybrids by pyramiding all the favourable genes.

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