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GENETIC VARIABILITY STUDIES FOR YIELD ATTRIBUTING AND QUALITY TRAITS IN RICE (*ORYZA SATIVA* L.)

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Abstract

Genetic variability study was conducted with twelve parents and their 66 F_1's crosses for the genetic parameters for yield, yield attributing, quality and characters in rice. A two years study was carried out during *kharif* 2011-12 and 2012-13 with 78 genotypes of rice and all the genotypes were evaluated in a Randomized Block Design with three replications at Crop Research Center of Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut. Analysis of variance revealed significant differences for all the traits under study. High phenotypic and genotypic coefficient of variation was observed for grain yield per plant followed by harvest index, number of productive tillers per plant, number of grains per panicle, plant height, biological yield per plant, L/B ratio, kernel elongation after cooking and kernel length suggesting that selection may be carried out on the basis above mentioned traits and grain yield as well as quality of rice genotypes can be enhanced.

Key words : GCV, PCV, grain yield, quality traits, rice.

Introduction

Rice (*Oryza sativa* L.) belongs to family gramineae. Morphologically, rice is an annual grass and one of the most important crops. Globally, it is grown extensively in tropical and sub-tropical regions of the world. More than half of the people on the globe depend on rice as their basic diet and, generally extensively consumed in the producing countries. It is expected that the world population increase by about 2 billion in the next two decades and half of this increase will in Asia, where rice is the staple food (Gregory *et al.*, 2000). To feed this increasing population, 35% more rice will be required than the present level of rice production globally (Duwayrie *et al.*, 1999). The chief rice production countries are; China, India, Indonesia, Bangladesh, Vietnam, Thailand, Myanmar, Philippine, Brazil, Japan, U.S.A and Pakistan. China is the prime producer of rice.

Development of high yielding varieties requires the knowledge of existing genetic variability. Hence, rice breeders are interested in developing varieties with improved yield and other desirable agronomic characters. Genetic variability for agronomic traits is the key component of breeding programs for broadening the gene poolof rice. Plant breeders commonly select for yield components which indirectly increase yield. The present study was made with an objective to estimate genetic variability of yield and its component characters in rice genotypes. Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in detecting the amount of variability present in the germplasm (Idris *et al.*, 2012).

Materials and Methods

The investigations were conducted at the Experimental Farm, Crop Research Centre of Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut (U.P.), India. The experimental material consisted of twelve parents and their 66 F_1's crosses for 18 yield and quality component characters. The two years study was carried out during *kharif* 2011-12 and 2012-13 with 78 genotypes of rice were obtained from the genetic stock available at Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut. The first nursery was prepared with seed of 78 lines during season 2012. The seedlings of 21 days old were transplanted in field in 2 m long rows with spacing of 25 × 15 cm between and within rows, respectively. The experiment was carried out in

Randomized Block Design with three replications. Observations were recorded on ten randomly selected plants in the three replications for eighteen traits *viz*., days to 50% flowering, days to maturity, plant height, number of productive tillers per plant, panicle length, number of branches per panicle, number of grains per panicle, biological yield per plant, grain yield per plant, harvest index, 1000-grain yield, hulling %, kernel length, kernel breadth, L/B ratio, kernel elongation after cooking, kernel elongation ratio and amylose content were subjected to the statistical/biometrical analyses. Analysis of variance was carried out as suggested by Panse and Sukhatme (1978), GCV and PCV methods suggested by Burton (1952) and Singh and Chaudhary (1979).

Results and Discussion

Analysis of variance revealed highly significant differences among genotypes for all traits (table 1). All the genetic material studied under present investigation revealed sufficient variability for all the eighteen characters. High amount of genetic variability for many of these traits has also been reported earlier by Shinha *et al.* (2004), Patil *et al.* (2003), Devi *et al.* (2006), Padmaja *et al.* (2008) and Yadav *et al.* (2008). The above mentioned variation supported by highly significant differences in respect of each trait studies suggests that parents selected for study were genetically divergent.

Coefficient of Variation (GCV and PCV)

Selection which is the basis of every breeding programme operates only on variation, which is of genetic nature (Johnsen, 1909). A wide range of variability present in any crop always provides the better chances of selecting desired types (Vavilov, 1951). The success of plant improvement lies in careful management of variability and techniques to be employed in each case will depend upon clear understanding of the extent and nature of variability. Mean, range, phenotypic coefficient of variation and genotypic coefficient of variation for various yield components and quality traits in rice are presented in table 2 showing huge amount of genetic variability. High PCV was observed for grain yield per plant followed by harvest index, number of productive tillers per plant, number of grains per panicle, plant height, biological yield per plant, L/B ratio, kernel elongation after cooking and kernel length. Remaining characters *viz*., 1000-grain weight, panicle length, number of branches per panicle, kernel breadth, amylose content, days to 50% flowering, kernel elongation ratio, hulling

Table 1 : Analysis of variance for yield components and quality traits in rice.

Source of variation	**D.F.**	**Days to 50% flowering**	**Days to maturity**	**Plant height (cm)**	**No. of productive tillers/plant**	**Panicle length (cm)**	**No. of branches/ panicle**	**No. of grains/ panicle**	**Biological yield per plant (g)**	**Grain yield per plant (g)**
Replication	2	0.75	0.26	0.02	0.26	0.18	0.03	1.63	1.19	0.34
Treatments	77	90.75**	7.48**	1118.27**	20.57**	11.06**	0.89**	2443.19**	786.12**	114.00**
Error	154	0.44	0.36	0.35	0.24	0.30	0.34	0.72	0.49	0.40
Total	233	30.29	2.71	369.79	6.96	3.86	0.52	807.90	260.13	37.95

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Source of variation	**D.F.**	**Harvest index (%)**	**1000-grain weight (g)**	**Hulling (%)**	**Kernel length (mm)**	**Kernel breadth (mm)**	**L/B ratio**	**Kernel elongation after cooking (mm)**	**Kernel elongation ratio**	**Amylose content (%)**
Replication	2	0.012	0.024	0.125	0.038	0.003	0.006	0.016	0.001	0.568
Treatments	77	100.72**	14.09**	2.84**	2.14**	0.02**	1.24**	4.97**	0.008**	3.65**
Error	154	0.45	0.19	0.18	0.06	0.005	0.07	0.006	0.002	0.34
Total	233	33.58	4.78	1.06	0.75	0.009	0.45	1.64	0.004	1.44

**significance level at 1%.

Table 2 : Mean, range, phenotypic coefficient of variation and genotypic coefficient of variationfor yield components and quality traits in rice.

Characters	Mean	Range	Coefficient of variation	
			PCV	GCV
Days to 50% flowering	109.42	99.33-120.67	5.05	5.01
Days to maturity	150.18	147.33-153.33	1.10	1.03
Plant height (cm)	117.50	74.39-166.16	16.44	16.43
No. of productive tillers per plant	14.47	8.40-25.77	18.31	17.99
Panicle length (cm)	28.67	21.77-32.09	6.88	6.61
No. of branches per panicle	11.53	9.40-12.87	6.30	3.72
No. of grains per panicle	161.50	91.67-207.87	17.68	17.67
Biological yield per plant (g)	101.70	59.66-138.92	15.93	15.91
Grain yield per plant (g)	26.04	9.42-44.85	23.76	23.63
Harvest index (%)	25.88	12.02-38.28	22.49	22.34
1000-grain weight (g)	23.73	20.21-30.83	9.25	9.07
Hulling (%)	79.36	75.73-80.83	1.30	1.19
Kernel length (mm)	7.83	5.53-9.31	11.10	10.64
Kernel breadth (mm)	1.63	1.49-1.83	5.94	4.01
L/B ratio	4.84	3.10-5.82	13.97	12.89
Kernel elongation after cooking (mm)	10.82	7.43-12.62	11.90	11.88
Kernel elongation ratio	1.38	1.29-1.56	4.43	3.16
Amylose content (%)	21.00	18.33-23.33	5.73	5.00

% and days to maturity recorded low phenotypic coefficient of variation. High GCV was observed for grain yield per plant followed by harvest index, number of productive tillers per plant, number of grains per panicle, plant height, biological yield per plant, L/B ratio, kernel elongation after cooking and kernel length. Whereas, 1000-grain weight, panicle length, days to 50% flowering, amylose content, kernel breadth, number of branches per panicle, kernel elongation ratio, hulling % and days to maturity recorded low genotypic coefficient of variation.

According to Fisher (1918), the continuous variation exhibited by quantitative traits with which most of the plant breeders have to deal with, includes the heritable and non-heritable components. The heritable component is the consequence of genotypes and the non-heritable part is mainly due to unknown environmental factors. As it is very difficult to assess the genotypes directly, it is possible only through the assessment of phenotypic expression (which is an outcome of genotype and environmental interaction) in the existing material. Therefore, the study of phenotypic variability for various traits under investigation is of great importance.

A thorough screening of the material studied under present investigation revealed sufficient variability for twelve characters *viz.,* number of productive tillers per plant, panicle length, number of branches per panicle, grain yield per plant, harvest index, 1000-grain weight, hulling, kernel length, kernel breadth, L/B ratio, kernel elongation ratio and amylose content. The genotypic and phenotypic variances are of little meaning as they do not have any clear limit or ceiling and at the same time, the categorization of the genotypic variance as low or high is difficult, rendering them unsuitable for comparison of two populations with desired precision when expressed in absolute values. To overcome this difficulty, the genotypic and phenotypic coefficients of variation, which are free from the unit of measurement, can be conveniently employed for making comparison between populations and different metric traits of population.

In this context, results from the present study indicated thathigh phenotypic and genotypic coefficient of variationwas observed for grain yield per plant followed by harvest index, number of productive tillers per plant, number of grains per panicle, plant height, biological yield per plant, L/B ratio, kernel elongation after cooking and kernel length. Further, the present findings revealed that the estimates of PCV were generally higher than their corresponding GCV for all the characters studied. The present study indicated moderate contribution of towards genetic variability and thereby suggesting that the parents chosen on the basis of these characters may be utilized in the crossing programme for obtaining good transgressive segregants. Earlier researchers, Pandey *et* *al*. (2012), Kiran *et al*. (2012) and Seyoum *et al*. (2012) have also reported similar findings with respect to PCV and GCV.

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