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Estimation of genetic variability, heritability and genetic advance for grain yield components in rice (*Oryza sativa* L.)

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Abstract

The present investigation consists of 23 rice genotypes and the experiment was conducted during *Kharif*-2016 in Randomized Block Design with three replications. The data were recorded for 13 quantitative characters to study genetic variability, heritability, genetic advance, correlation coefficient analysis and path analysis. On the basis of mean performance, high seed yield per plant were exhibited by the genotypes LSD-1, TP29654, and TP29737. Analysis of variance among 23 genotypes showed significant difference for all characters studied. Highest genotypic coefficient of variation (GCV) & phenotypic coefficient variation (PCV) was observed for seed yield per plant followed by flag leaf length, number of spikelets per panicle, biological yield per plant and panicles per plant indicating that these characters could be used as selection for crop improvement. High estimates of heritability were observed for plant height, flag leaf length, biological yield per plant, spikelets per panicle, panicles per plant. High genetic advance were observed for number of spikelets per panicle and plant height, indicating predominance of additive gene effects and possibilities of effective selection for the improvement of these characters.

Keywords: Rice, Genetic variability, Heritability and Genetic Advance.

Introduction

Rice (*Oryza sativa* L.) is principal food crop of India as well as one of the pivotal staple cereal crops feeding more than one-third of the world's population. Rice is the staple food of about 65% of Indian population. Our rice requirement by the year 2020 is estimated to be around 122 million tons as against the present production of about 100 million tons, thus leaving a gap of about 22 million tons rice.

It accounts for about 43% of total food grain production and 46% of total cereal production in the country (FAO 2015). Low productivity of rice in India is a major concern for food and nutritional security of more than 60% population which is dependent on rice. The slogan "Rice is life" is most appropriate for Indian as this crop plays a vital role in our national food security and a means of livelihood for millions of rural people of India. Rice occupies a pivotal place in Indian agriculture and it contributes to 15 per cent of annual GDP and provides 43 per cent calorie requirement for more than 70 per cent of Indians.

The country witnessed an impressive growth in rice production due to adoption of semi dwarf varieties coupled with intensive input based management practices. In order to keep pace with growing population the estimated rice requirement by 2025 is about 130 million tones (Viraktamath, 2013).

The success of breeding program depends upon the quantum of genetic variability available for exploitation and the extent to which the desirable characters are heritable (Tiwari *et al.*, 2011) [14]. Variability refers to the presence of differences among the individuals of plant population. Variation results due to difference either in genetic constitution of the individual of a plant population or in environment, they have grown. The existence of variability is essential for improvement of genetic material. Selection is also effective when there is significant amount of genetic variability among the individuals in breeding materials.

Materials and Methods

The material for the present investigation consists of 23 (including 1 check) rice genotypes of which 20 genotypes were received from IRRI-International Rice Research Institute (Philippines) and 3 other genotypes were collected from Department of Genetics and Plant Breeding. These were grown in Randomized block design with three replications during *kharif*-2016 at the Central Research Farm of the Department of Genetics and Plant Breeding, Naimi Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad, Twenty five days old seedlings raised in nursery were transplanted at 20 cm x 15 cm spacing. Five representative plants for each genotype in each replication were

randomly selected to record observations on plant height (cm), flag leaf length (cm), flag leaf width (cm), total tillers per plant, productive tillers per plant, panicle length, spikelets per panicle, and biological yield, harvest index, test weight, and seed yield per plant (g). Days to 50% flowering and days to maturity were computed on plot basis and data was subjected to statistical analysis. The variability was estimated as per procedure for analysis of variance suggested by Panse and Sukhatme (1967) [15] PCV and GCV were calculated by the formula given by Burton (1952) [3] heritability in broad sense (h^2) by Burton and De Vane (1953) [4] and genetic advance i.e. the expected genetic gain were calculated by using the procedure given by Johnson *et al.* (1955) [10].

Results and Discussion

Genetic variability in any crop is pre-requisite for selection of superior genotypes over the existing cultivars. The analysis of variance for different characters indicated the existence of highly significant differences for all 13 characters under study at 1% level of significance suggesting each and every genotype are genetically divergent from each other and there is ample scope for selection of characters from these diverse sources for yield and its components (Table 1). These findings were in accordance with the findings of Bekele *et al.*, (2013)

and Sandhya *et al.* (2015) [19].

A wide range of variance was observed for all the characters. Phenotypic variance was higher than genotypic variance for all the yield and its contributing characters indicate the influence of environmental factors on these traits. The highest variability (V_g & V_p) was recorded for number of spikelet's per panicle (808.37 and 821.61) followed by plant height (117.24 and 117.96), biological yield per plant (112.41 and 113.60), Similar results were also reported by Anjaneyulu *et al.*, (2010) [1], Idris *et al.* (2012) [8] and Sandhya (2014) [18]. Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV (table 2) among the all traits grain yield per plant (21.47 and 21.98), exhibited high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) followed by flag leaf length (20.61 and 20.71), number of spikelets per panicle (19.58 and 19.74), high values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for these traits suggested the possibility of yield improvement through selection of these traits. Close relationship between GCV and PCV was found in all the characters and PCV values were slightly greater than GCV, revealing very little influence of environment for their expression.

Table 1: Analysis of variance for 13 quantitative characters in 23 rice genotypes

S. No.	Characters	Mean squares		
		Replication (d.f=2)	Treatments (d.f=22)	Error (d.f=44)
1	Days to 50% flowering	0.05	37.25**	0.43
2	Plant height	0.65	352.45**	0.72
3	Flag leaf length	0.15	139.78**	0.43
4	Flag leaf width	0.0004	0.03**	0.0006
5	Panicle length	0.55	14.37**	0.40
6	Tillers / plant	0.14	10.58**	0.09
7	Panicles / plant	0.04	9.70**	0.06
8	Spikelets / panicle	9.04	2438.37**	13.23
9	Days to maturity	0.17	36.94**	0.35
10	Biological yield	1.32	338.44**	1.18
11	Harvest index	3.64	31.39**	3.87
12	Test weight	0.001	9.32**	0.12
13	Grain yield / plant	1.34	75.94**	1.20

** Significant at 1% level of significance

Table 2: Estimation of components of variance and genetic parameters for 13 characters in rice genotypes

S. No.	Characters	σ^2_g	σ^2_p	Coefficient of variation		h^2 (bs) (%)	GA	GA as % of mean
				GCV	PCV			
1	Days to 50% Flowering	12.27	12.71	3.89	3.96	96.56	7.09	7.87
2	Plant Height	117.24	117.96	10.51	10.54	99.39	22.237	21.59
3	Flag Leaf Length	46.45	46.88	20.61	20.71	99.07	13.974	42.26
4	Flag Leaf Width	0.01	0.011	7.59	7.82	94.22	0.203	15.18
5	Panicle Length	4.65	5.06	8.48	8.84	92.00	4.263	16.76
6	Tillers/ Plant	3.49	3.59	16.10	16.32	97.35	3.800	32.74
7	Panicles/ Plant	3.21	3.28	17.03	17.21	98.01	3.656	34.75
8	Spikelets/ Panicle	808.37	821.61	19.58	19.74	98.39	58.096	40.02
9	Days to Maturity	12.19	12.55	2.90	2.95	97.17	7.091	5.90
10	Biological Yield/ Plant	112.41	113.60	18.25	18.35	98.96	21.727	37.41
11	Harvest Index	9.17	13.04	7.65	9.13	70.29	5.230	13.22
12	Test Weight	3.06	3.18	7.66	7.81	96.15	3.537	15.48
13	Grain Yield/ Plant	24.91	26.12	21.47	21.98	95.37	10.041	43.19

σ^2_g = Genotypic variance. σ^2_p = Phenotypic variance. h^2 = Heritability (broad sense), GCV = Genotypic coefficient of variation. PCV = Phenotypic coefficient of variation.

The amount of genetic variation considered alone will not be of much use to the breeder unless supplemented with the information on heritability estimate, which gives a measure of the heritable portion of the total variation. It has been

suggested by Burton and Devane (1953) [4] that the GCV along with heritability estimate could provide a better picture of the amount of advance to be expected by phenotypic selection. Since genetic advance is dependent on phenotypic

variability and heritability in addition to selection intensity, the heritability estimates in conjunction with genetic advance will be more effective and reliable in predicting the response to selection (Johnson *et al.*, 1955) [10]. Heritability in broad sense includes both additive and non-additive gene effects. While, narrow sense heritability includes only additive components (Johnson *et al.*, 1955) [10]. In the present study, heritability in broad sense was estimated. Highest broad sense heritability was recorded in the case of plant height, flag leaf length, biological yield and spikelets per panicle Fiyaz *et al.* (2011) [6], Dhanwani *et al.*, (2013) [4]. Maximum genetic advance was recorded for spikelets per panicle (58.096) followed by plant height, Tiwari *et al.* (2011) [14]. In general heritability along with genetic advance can be useful in selection programmes. The characters number of spikelets per panicle Anjaneyulu *et al.*, (2010) [1], plant height and biological yield per plant have shown high genetic advance as percent of mean along with high heritability. High heritability with high genetic advance as percent of mean indicates that these characters are largely controlled by additive gene action, which indicates that improvement in these characters is possible through mass selection and progeny selection.

Conclusion

In the present investigation which included 23 genotypes of rice was carried out in order to study the nature and amount of variability, heritability and genetic advance for 13 quantitative characters. On the basis of mean performance, high seed yield per plant were exhibited by the genotypes LSD-1, TP29654, and TP29737. Analysis of variance among 23 genotypes showed significant difference for all characters studied. Highest genotypic coefficient of variation (GCV) & phenotypic coefficient variation (PCV) was observed for seed yield per plant followed by flag leaf length, number of spikelets per panicle, biological yield per plant and panicles per plant indicating that these characters could be used as selection for crop improvement. High estimates of heritability were observed for plant height, flag leaf length, biological yield per plant, spikelets per panicle, panicles per plant. High genetic advance were observed for number of spikelets per panicle and plant height, indicating predominance of additive gene effects and possibilities of effective selection for the improvement of these characters.

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