

Original Research Article

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Studies on Genetic Variability, Heritability and Genetic advance for Yield and Quality Components in Rice (*Oryza sativa* L.) Germplasm

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ABSTRACT

The present investigation consists of 39 rice genotypes used for studying genetic variability parameters, correlation and path analysis which was carried out at Field Experiment Centre, Department of Genetics and Plant Breeding during *Kharif* 2018 in Randomized Block Design with three replications. The data were recorded for 13 quantitative characters to study genetic variability, heritability, genetic advance, correlation and path analysis. Analysis of Variance showed significant differences for all characters under study at 1% and 5% Level of Significance, indicated that presence of ample genetic variation among genotypes. On the basis of *Per se* performance of grain yield per plant was exhibited by TP 30614 followed by TP 30601, TP 30607, TP 30600. High estimates of GCV and PCV was recorded for spikelet's per panicle followed by grain yield per plant and biological yield per hill. High heritability coupled with high genetic advance as percent mean is recorded for number of spikelet's per panicle followed by number of panicles per plant and number of tillers per plant indicating predominance of additive gene effects and possibilities of effective selection for the improvement of the characters.

Keywords

Rice (*Oryza sativa* L.), Variability, Heritability, Genetic advance

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Introduction

Rice (*Oryza sativa* L.) is the second most widely cultivated cereal in the world, after wheat, and is staple food for over half the world's population, especially in Asia. It is mainly cultivated by small farmers in holdings of less than one hectare. Rice is vital for the nutrition of much of the population in Asia, as

well as in Latin America and the Caribbean and in Africa; it is central to the food security of over half the world population. Developing countries account for 95% of the production, with China and India alone responsible for nearly half of the world output. Global rice production and trade in 2017-18 are forecasted to be decrease by 0.41% and 0.1% over previous year respectively. The world

consumption is also anticipated to up about 0.20%. Slight change/ decrease (0.80%) has been forecasted in global carry over stock in 2017-2018 (DAC, 2018). In 2018, global paddy production is estimated to be 769.9 million tonnes (FAO, 2018). Rice is grown in almost all the states in the country however the major 5 states in rice production are West Bengal, UP, Andhra Pradesh and Tamil Nadu. As a result of near normal rain fall during monsoon 2017 and various policy initiatives taken by the government, country has witnessed record 111.01 million tonnes this crop year. Rice production is expected to climb to a record food grain production in the current year, 1.2% higher than last year's output. Rice is the most important agricultural crop in India, contributing to more than 40% of the country's total food grain production (D&ES, 2018). 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. The magnitude of heritable variation in the traits studied has immense value in understanding the potential of the genotype for further breeding programme. Variability results due to difference either in the genetic constitution of the individuals of a population or in the environment in which they are grown (Mohammad *et al.*, 2002).

Materials and Methods

The experiment was carried out in the Field Experimentation Centre of Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, U.P, India. The experimental materials for the present study consisted of 39 genotypes of rice including 1 local check. The experiment was laid out in a

Randomized Block Design (RBD) with three replications. The experimental material was planted in three replications. Each replication consisted of 39 genotypes randomized and replicated within each block. Twenty five days old seedlings were transplanted 20cm apart between rows and 15 cm within the row. All necessary precautions were taken to maintain uniform plant population in each treatment per replication. All the recommended package of practices was followed along with necessary prophylactic plant protection measures to raise a good crop. Observations were recorded and the data was subjected to statistical analysis. The variability was estimated as per procedure for analysis of variance suggested by Panse and Sukhatme (1985), PCV and GCV were calculated by the formula by Burton (1952) heritability in broad sense (h^2) by Burton and De Vane (1953) and genetic advance i.e., the expected genetic gain were calculated by using the procedure given by Johnson *et al.*, (1955).

Results and Discussion

Analysis of variance revealed significant differences for all the characters indicating sufficient variability among the genotypes. This indicated that the genotypes were possessing inherent genetic variance among themselves with respect to the characters studied (Table 1) (Bekele *et al.*, 2013) [5]. On the basis of mean performance highest grain yield per hill was observed by the genotypes TP 30614, TP 30601, TP 30607, TP 30600. In the present investigation, as expected, the PCV estimates were higher than the GCV estimates the variation due to environment as well as variation due to interactions. However, there was a close correspondence between the estimates of PCV and GCV for the characters, viz., plant height, days to maturity, days to 50% flowering, panicle length, flag leaf length, flag leaf width, number of spikelet's per panicle, test weight and grain yield per hill

under study indicating the fact that these characters were less influenced by the environmental factors as evidenced from the less differences in magnitude of PCV and GCV. In this study, highest PCV is accompanied with highest GCV for number of spikelet's per panicle, number of panicles per plant, number of tillers per plant (Singh *et al.*, 2011). In contrast, other characters, viz., biological yield per hill, number of tiller per hill, number of panicle per hill and harvest index were highly influenced by environment as evidenced from high magnitudinal difference between the estimates of PCV and GCV. Hence, selection for these characters sometimes may be misleading. These environmental factors could be due to the heterogeneity in soil fertility status and other unpredictable factors (Reddy *et al.*, 2012).

In the present study, the heritability in broad sense (h^2) ranges from 36.01% in harvest index to 95.24% in days to 50% flowering (Table 2). High estimate of heritability (above 60%) recorded for flag leaf width (68.68%), number of tillers per hill (71.75%), flag leaf length (80.55%), number of panicle per hill (80.78%), panicle length (85.03%), number of spikelet's per panicle (90.93%), days to 50% flowering (95.24%), days to maturity (9.14%) and test weight (92.89%). while moderate estimate of heritability (30-60%) was found in harvest index (36.01%), biological yield per hill (51.80%), plant height (59.46%), grain yield per hill (51.80%). None of the characters showed low estimates of heritability (below 10%).

It showed that the phenotypic variability of none characters had greater share of environmental. In the present study, the GA % M ranged from 6.74% (plant height) to (41.33%) number of spikelet's per panicle. It was low (below 10%) for plant height (6.74%), biological yield per hill (7.63%) harvest index (8.60%), days to maturity

(9.15%) and moderate GA% M (10-20) for *via*; test weight (10.92%), days to 50% flowering (12.17%), panicle length (11.34%), flag leaf width (14.94%), and grain yield per hill (15.69 %) while high GA % M (above 20%) recorded in flag leaf length (20.48%), number of tiller (26.92%), number of panicle per hill (32.18%), number of spikelet's per panicle (41.33%). Many of characters showed high heritability coupled with high GA % M was observed for number of spikelet's per panicle, flag leaf length, number of panicles per plant number of tillers per plant (Prajapathi *et al.*, 2011) whereas high heritability coupled with moderate GA% M was observed for days to flowering, panicle length, flag leaf width and test weight respectively suggesting that there was preponderance of additive gene actions for the expression of these characters. Hence selection of these characters can bring enhancement in Rice production and productivity.

From the present investigation it is concluded that among 39 genotypes of rice on the basis of mean performance TP 30614 was found to be superior in grain yield over the check followed by TP 30601, and TP 30607 showed higher yield over the check. 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. High to moderate estimates of GCV and PCV were recorded for number of spikelet's per panicle, grain yield per hill, biological yield per hill, number of panicle per hill, number of tiller per hill, flag leaf length.

Table.1 Analysis of variance for 13 characters of 39 rice genotypes during *kharif*-2018

Characters	Mean Sum of Squares		
	Replications	Treatments	Error
	(df= 2)	(df= 38)	(df=76)
Days to 50% Flowering	1.724	82.356**	1.512
Plant Height	20.776	88.991**	16.480
No of Tillers/ plant	0.02	8.27*	0.96
No of Panicles/ Plant	0.202	7.549*	0.555
Panicle Length	0.592	9.603**	0.532
Flag Leaf Length	4.462	57.315**	4.270
Flag Leaf Width	0.003	0.066*	0.009
No of spikelet's per Panicle	0.923	3588.142**	0.502
Days to maturity	2.824	92.356**	0.912
Biological yield	102.268	106.648**	36.864
Harvest Index	27.289	44.741**	16.642
Test weight	0.231	5.044*	0.126
Grain Yield/Plant	0.853	55.718*	13.191

** Significant at 1% Level of Significance, * Significant at 5% Level of Significance

Table.2 Estimation of genetic parameters for grain yield and other components

Parameters Characters	σ^2_g	σ^2_p	GCV	PCV	Heritability	GA	GA as per se Mean
Days to 50 % flowering	30.28	31.79	6.05	6.20	95.24	11.06	12.17
Plant height	24.17	40.65	4.24	5.50	59.46	7.81	6.74
Number of tillers	2.44	3.40	15.43	18.21	71.75	2.72	26.92
Number of panicles	2.33	2.89	17.38	19.34	80.78	2.83	32.18
Panicle length	3.02	3.56	5.97	6.48	85.03	3.30	11.34
Flag leaf length	17.68	21.95	11.08	12.34	80.55	7.77	20.48
Flag leaf width	0.02	0.03	8.75	10.56	68.68	0.24	14.94
Number of spikelet's per panicle	1157.55 9	1272.93 7	21.040	22.06 3	90.936	66.83 5	41.331
Days to maturity	31.28	32.89	4.55	4.66	94.14	12.06	9.15
Biological yield	23.26	60.13	5.95	9.57	38.69	6.18	7.63
Harvest index	9.37	26.01	6.96	11.59	36.01	3.78	8.60
Test weight	1.64	1.77	5.50	5.71	92.89	2.54	10.92
Grain yield	14.18	27.37	10.58	14.71	51.80	5.58	15.69

Vg = genotypic variance, Vp = phenotypic variance, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, GA = Genetic advance

High heritability coupled with high genetic advance as per cent mean in the present rice genotypes was recorded for No. of spikelet's per panicle and followed by No. of panicles per plant, No. of tillers per plant, flag leaf length indicating predominance of additive gene effects and possibilities of effective selection for the improvement of the characters.

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