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Genetic variability, heritability and genetic advance for yield and its contributing traits in rice (*Oryza sativa* L.)

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Abstract

The experiment on 125 genotypes (20 lines, 5 tester and 100 F₁'s) including a check *viz.*, Pusa Basmati 6 of rice (*Oryza sativa* L.) was conducted to work out the genetic variability, heritability and genetic advance effects of their various attributes on grain yield. The mean squares due to treatments, parents and crosses were highly significant for all the fifteen characters indicated the presence of sufficient variability in the study materials. PCV was higher than the genotypic GCV for all the traits. High heritability (>60%) were recorded for characters *viz.*, grains per panicle, spikelets per panicle, L:B ratio, kernel length, panicle length, kernel breadth, flag leaf area, grain yield per plant, plant height, panicle bearing tillers per plant, 1000-grain weight, harvest-index and spikelet fertility. The high genetic advance in percent of mean (>20) was recorded for grains per panicle followed by spikelet's per panicle and L:B ratio for this parameter. High heritability coupled with high genetic advance in per cent of mean were observed for the characters like grains per panicle, spikelets per panicle, and L:B ratio. High heritability and genetic advance account that the additive nature of gene action and so that these characters are directly selecting for further advancement of rice crop.

Keywords: Genetic variability, heritability, genetic advance

Introduction

Rice is central to the lives of billions of people around the world. Possibly the oldest domesticated grain (~10,000 years), rice is the staple food for 2.5 billion people and growing rice is the largest single use of land for producing food, covering 9% of the earth's arable land. Rice provides 21% of global human per capita energy and 15% of per capita protein. Calories from rice are particularly important in Asia, especially among the poor, where it accounts for 50-80% of daily caloric intake. As expected, Asia accounts for over 90% of the world's production of rice, with China, India and Indonesia producing the most. Only 6-7% of the world's rice crop is traded in the world market. Rice belongs to the family of grasses *i.e.*, Gramineae (*Poaceae*). The cultivated rice belongs to genus *Oryza* and there are about 24 species of rice distributed in tropical, sub-tropical and warm temperate regions of the world. Out of these, most commonly cultivated species are *Oryza sativa* and *Oryza glaberrima*. The *Oryza sativa* is divided into three sub-species, namely, *indica*, *japonica* and *javanica*. Rice is rich in genetic diversity, with thousands of varieties grown throughout the world. Rice farming is practiced in several agro-ecological zones in India. Globally rice is cultivated approximately on an area of 158 million hectares, with production of more than 700 million tons annually. Out of the total production nearly 640 million tons of rice is grown in Asia alone, representing 90% of global production. India has highest acreage of 44 million hectares under rice with production and productivity of 108.8 million tonnes and 2.47 tonnes per hectare respectively (Anonymous, 2016) [4]. The world rice requirement by 2050 will be 943.6 million-tonnes which require an annual increase of 5.8 million tonnes from the present level of production (FAO, 2017) [7]. To achieve this target, it is essential to develop varieties with high yield potential. The presence of desirable variability in germplasm collections enables breeders to recombine favourable phenotypes of different traits to develop improved genotypes capable of producing high and stable yield. Therefore, it becomes imperative to evaluate the available germplasm and assess the existing genetic variability for agronomically important traits so that breeders may know which few of the numerous accessions available in the germplasm collections would be useful for serving the breeding objective.

In absence of such information, it would be very difficult to launch a systematic breeding programme consuming optimum time and resources. Therefore, an attempt was made to evaluate a germplasm collection of aromatic rice and examine the level of genetic variability to work out an efficient selection criterion. The available variability in a population can be partitioned into heritable and non-heritable components with the aid of genetic parameters such as coefficients of variation, heritability and genetic advance to serve as basis for selection of some outstanding genotypes than existing ones.

Materials and Methods

This investigation was conducted at Crop Research Centre of Sardar Vallabhbhai Patel University of Agriculture and Technology, Modipuram, Meerut. The experimental material for this study consisted 20 lines and 5 testers and their 100 crosses which attempted through line x tester mating design during *Kharif*, 2017. The 100 crosses along with 25 parental lines including a check *viz.*, Pusa Basmati 6 were evaluated during *Kharif*, 2018. Single row plots of 3m length were used for transplanting single seedling per hill for each genotype (treatment) in each replication following intra and inter-row spacing of 15 cm and 20 cm. The experiment was laid out in Randomized Block Design. The observation were recorded on fifteen different characters *viz.*, days to 50% flowering, plant height (cm), flag leaf area (cm), panicle bearing tillers per plant, panicle length(cm), spikelets per panicle, grains per panicle, spikelet fertility (%), 1000-grain weight (g), biological yield per plant (g), harvest-index (%), kernel length (mm), kernel breadth (mm), L:B ratio and grain yield per plant (g). The certain selected statistical approaches were used for data analysis. Analysis of variance was carried out for each of the characters studied as per Panse and Sukhatme (1967) [12], Phenotypic (PCV) and genotypic (GCV) coefficients of variation for different characters were estimated by formulae suggested by Burton and de Vane (1953) [6]. Heritability in broad sense (h²_b) was calculated as suggested by Hanson *et al.*, (1963) [8]. The expected genetic advance (Ga) was estimated using formula suggested by Johnson *et al.*, (1955) [10].

Results and Discussion

Analysis of variance for fifteen characters to test the significance of differences among various treatments and is presented in (Table 1). The mean squares due to treatments, parents and crosses were highly significant for all the fifteen

characters indicated the presence of sufficient variability in the study. The knowledge of nature of association among different characters and relative contribution of different characters to yield is a prerequisite to any breeding programme. The similar results were found by Sandeep *et al.*, (2018) [14]. A wide range of phenotypic coefficient of variation (7.05 -21.51%) and genotypic coefficient of variation (5.11-20.88%) was observed for the traits studied (Table 2). Phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the traits, but little difference was recorded between PCV and corresponding GCV for all the traits. Grains per panicle, spikelets per panicle, grain yield per plant and L:B ratio displayed moderate phenotypic and genotypic coefficient of variance. The similar results were found by Warkad *et al.*, (2013) [17]; Bhati *et al.*, (2015) [5]; Shrivastava *et al.*, (2015) [15]; Adhikari *et al.*, (2018) [2]; Saha *et al.*, 2019 [13]. High heritability (>60%) were recorded for characters *viz.*; grains per panicle (94.17), spikelets per panicle (93.15), L:B ratio (91.26), kernel length (76.44), panicle length (73.85), kernel breadth (73.63), flag leaf area (73.05), grain yield per plant (72.31), plant height (71.41), panicle bearing tillers per plant (71.24), 1000-grain weight (69.96), harvest-index (63.70) and spikelet fertility (60.55). Estimates of moderate heritability (30-60%) were recorded biological yield per plant (57.10) and days to 50% flowering (52.51). High or moderate heritability estimates for most of the traits studied, have been reported earlier by Venkanna *et al.*, (2014) [16]; Paikhomba *et al.*, (2014) [11] and Adhikari *et al.*, (2018) [2]. High heritability coupled with high genetic advance in per cent of mean were observed for the characters like grains per panicle, spikelets per panicle, and L:B ratio, indicated that additive genetic control in the inheritance of these traits and selection pressure could be profitably applied on these characters for yield improvement. Similar findings also reported earlier by Akhtar *et al.*, (2011) [3]; Hefena *et al.*, (2016) [9]; Abebe *et al.*, (2017) [1]; Adhikari *et al.*, (2018) [2]; Saha *et al.*, (2019) [13]. High heritability coupled with moderate genetic advance in per cent of mean were observed for the characters like kernel length, flag leaf area, grain yield per plant, plant height, panicle bearing tillers per plants, 1000 grain weight, harvest-index and spikelet fertility the importance of dominance and epistatic effects in the inheritance of these traits and selection for these characters would be less effective and also reported by Paikhomba *et al.*, (2014) [11]; Venkanna *et al.*, (2014) [16]; Adhikari *et al.*, (2018) [2].

Table 1: Analysis of variance for 15 characters in parents and their F₁ s.

Source of variation	d.f.	Day of 50% flowering	Plant height (cm)	Flag leaf area (cm)	Panicle bearing tillers /plant	Panicle length (cm)	Speklets per panicle	Grains per panicle	Speklet fertility (%)
Replication	2	14.99	14.92	13.10	5.02	1.90	628.37	478.81	27.61
Treatment	124	93.36**	221.21**	32.50**	5.79**	19.34**	4237.86**	3715.27**	106.36**
Error	248	21.62	26.06	3.56	0.69	2.04	101.42	75.14	18.98

Source of variation	d.f.	1000 grain weight (g)	Biological yield per plant (g)	Harvest index (%)	Kernel length (mm)	Kernel breadth (mm)	L: B Ratio	Grain yield / plant (g)
Replication	2	2.19	7.85	12.31	3.97	0.090	0.228	1.00
Treatment	124	11.29**	55.51**	22.82**	2.49**	0.166**	1.204**	13.41**
Error	248	1.41	11.12	3.64	0.23	0.018	0.037	1.52

*, ** significant at 5% and 1% level, respectively

Table 2: Estimation of genetic parameters of variability for various traits studied in rice

Characters	Mean	Min	Max	Heritability (%)	Genetic Advance	GA as % means	GCV (%)	PCV (%)
Day of 50% flowering	95.66	78.67	106.00	52.51	7.30	7.63	5.11	7.05
Plant height (cm)	110.55	91.70	142.76	71.41	14.04	12.70	7.30	8.63
Flag leaf area (cm)	35.75	26.02	42.18	73.05	5.47	15.30	8.69	10.17
panicle bearing tillers /plant	15.79	10.36	17.69	71.24	2.27	14.36	8.26	9.78
panicle length (cm)	26.35	21.07	35.64	73.85	4.25	16.14	9.12	10.61
Spkelets per panicle	200.15	82.59	288.33	93.15	73.82	36.88	18.55	19.22
Grains per panicle	166.86	61.98	235.19	94.17	69.63	41.73	20.88	21.51
Spkelet fertility (%)	83.07	64.60	90.89	60.55	8.65	10.42	6.50	8.35
1000 grain weight (g)	25.61	19.51	30.31	69.96	3.13	12.21	7.09	8.47
Biological yield /plant (g)	62.85	49.52	71.64	57.10	5.99	9.53	6.12	8.10
Harvest index (%)	37.65	31.38	47.10	63.70	4.16	11.04	6.72	8.42
Kernel length (mm)	9.66	6.88	12.34	76.44	1.56	16.17	8.98	10.27
Kernel breadth (mm)	2.42	1.96	2.86	73.62	0.39	16.26	9.20	10.72
L: B Ratio	4.04	2.51	5.77	91.26	1.23	30.37	15.43	16.15
Grain yield / plant (g)	23.65	17.20	28.15	72.31	3.49	14.75	8.42	9.90

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