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Studies on variability and genetic parameters for yield and its contributing traits in rice (*Oryza sativa* L.)

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Abstract

The present study was carried out using 29 parents (25 lines x four testers) and 100 hybrids with the aim of determining the genetic variability and genetic parameters for yield and yield related traits along with 16 traits in rice. The 29 parental genotypes and their 100 F₁'s were evaluated for yield and its associated traits during *Kharif* 2018. The analysis of variance revealed highly significant mean sum of squares due to treatments, parents and crosses for all the sixteen characters. PCV was higher than the genotypic GCV for all the traits. High heritability coupled with high genetic advance was observed for leaf area, spikelets per panicle, grains per panicle, L:B ratio and grain yield per plant indicated that additive genetic control in the inheritance of these traits and selection pressure could be profitably applied on these characters for yield improvement in rice.

Keywords: Variability, correlation coefficients, heritability, genetic advance, rice

Introduction

Rice (*Oryza sativa* L.) is a monocotyledonous angiosperm belonging to the family Graminae, sub-family Bamboosoideae and tribe Oryzeae (Sarla and Swamy, 2005) [23]. It is diploid with 12 chromosomes (2n=24) (Garrise *et al.*, 2005) [8]. The small genome of rice (430 Mb) made it a model plant for studying cereal genetics. After maize and sugarcane, it is the third (FAOSTAT, 2015) highly preferred potent staple food crop all over the world and is the most widely consumed staple food for nearly half of the world's population (FAO, 2017) [6] especially in Asian region. Over 2 billion people in Asia alone derive 80% of their energy needs from rice, which contains 80% carbohydrates, 7-8% protein, 3% fat, and 3% fibre (Juliano, 1985) [12]. Minerals such as calcium, magnesium and phosphorus are present in addition to some traces of iron, copper, zinc and manganese. In addition, rice is a good source of niacin, thiamine and riboflavin (Oko *et al.*, 2012) [18]. India stands the fourth position in rice production having 110.15 million tones of rice (Anonymous, 2017) [2].

Due to continuous increment in the population throughout the world, the demand for rice will continue to increase in near future; therefore, rice breeders across the world aim at enhance the grain yield in rice (Song *et al.*, 2007) [27]. Grain yield is a complex polygenic quantitative trait which controlled by several genes and is highly influenced by the environment (Ashfaq *et al.*, 2012) [3]. A better understanding of the relationship between grain yield and its component traits becomes necessary for making an efficient selection for the development of new varieties with improved economically important traits (Kumar *et al.*, 2014) [14]. Any successful hybridization programme for varietal improvement mainly depends on the selection of parents having high variability, so that desired character combination may be selected to improve grain quality and higher grain yield. Moreover, knowledge of heritability is essential for selection based improvement as it indicates the transmissibility of a character into future generations. Johnson *et al.*, 1955 [11] suggested that heritability estimates along with genetic advance would be more useful in predicting grain yield under phenotypic selection than heritability estimates alone. Keeping in consideration, the above background information, this study was undertaken with an attempt to estimate the genetic variability, heritability for yield and its component traits in rice.

Materials and methods

Experimental material

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 25 lines and 4 testers and their 100 crosses which attempted through line x tester mating design during *Kharif*, 2017. The 100 crosses along with 29 parental lines check varieties Pusa Basmati 1509 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, respectively. Recommended cultural practices were followed to raise a good crop. Sixteen characters included in the study *viz.*, days to 50% flowering, days to maturity, plant height (cm), flag leaf area (cm²), panicle bearing tillers per plant, panicle length (cm), spikelets/panicle, grains/panicle, spikelet fertility (%), 1000-grain weight (g), biological yield/plant (g), harvest-index (%), kernel length (mm), kernel breadth (mm), L:B ratio and grain yield/plant (g).

Statistical analysis

The mean values of the observation recorded were subjected to statistical analysis. SPSS (version 16) software was used for the descriptive statistical analysis and analysis of variance (ANOVA) of yield and its component traits. Analysis of variance was carried out for each of the characters studied as per Panse and Sukhatme (1967) [19]. For computation of genotypic and phenotypic coefficient of variations (GCV & PCV) was according to Burton and de Vane (1953) [4]; for heritability in broad sense Hanson (1963) [9] and genetic advance and the genetic advance in per cent of mean Johnson *et al.* (1955) [11] were followed.

General mean (\bar{X}) = Sum of observations of selected plants in each genotype/Number of plants selected

Range = the minimum and maximum values for each trait within a genotype

Anova

The analysis of variance was supported the subsequent linear model of Fisher (1918) [7].

$$y_{ij} = \mu + g_i + r_j + e_{ij}$$

Where, $i = 1, 2, \dots, r$ (replication), $j = 1, 2, \dots, t$ (treatment), Y_{ij} = phenotypic observation of the i th genotype in the j th replication, μ = general mean, g_i = effect of i th genotype, r_j = effect of j th replication, e_{ij} = random error associated with the i th genotype in the j th replication

GCV and PCV

$$GCV\% = (\sigma_g / \bar{X}) \times 100$$

$$PCV\% = (\sigma_p / \bar{X}) \times 100$$

where, σ_g = genotypic standard deviation σ_p = phenotypic standard deviation, \bar{X} = general mean of the characters. The PCV and GCV are classified as follow as suggested by Sivasubramanian and Madhavamenon (1973) [26]. It is as follows > 25 % - high, 10-25 % - moderate and < 10 % - low.

Heritability

Heritability in a broad sense is the ratio expressed in the percent of genetic variation to total phenotypic variance.

$$h^2_b (\%) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where, σ_g^2 = Genotypic variance and σ_p^2 = Phenotypic variance. The estimates of heritability in broad sense were categorized according to Johnson *et al.* (1955) [11]. It is as follows: <30% - low, 30-60% - moderate and >60% and above - high.

Genetic advance and Genetic advance as per cent of mean

The expected genetic advance (GA) and Genetic advance as per cent of mean (GAM) were estimated using formula suggested by Johnson *et al.* (1955) [11] as; $GA = h^2_b \times \sigma_p \times k$

and $GAM = GA / \bar{X} \times 100$, Where, h^2_b = heritability in broad sense, σ_p = phenotypic standard deviation, k = selection differential ($k=2.06$) at 5% selection intensity (Lush, 1949)

[15], GA = expected genetic advance and \bar{X} = mean of the character. The range of genetic advance as percent of mean is classified as suggested by Johnson *et al.*, (1955) [11]. It is as follows: 0-10% - low, 10-20% - moderate and 20% and above - high.

Results and Discussion

The 25 lines and 4 testers along with their 100 hybrids were evaluated for yield and its component traits during the year 2018. The analysis of variance revealed highly significant mean sum of squares due to treatments, parents and crosses for all the sixteen characters indicating the existence of significant amount of variability among the characters studies. The presence of significant amount of variability in the initial breeding material assures the production of component traits (Table 1). The similar results were found by Sandeep *et al.* (2018) [22]. Very wide range of variation in mean performance of genotypes was observed for all the 16 characters under study *i.e.* days to 50% flowering (82.00-94.00), days to maturity (109.00-124.00), plant height (90.37-132.68cm²), Flag leaf area (23.05-49.08cm²), panicle bearing tillers/plant (11.66-17.70), panicle length (23.16-32.77cm), spikelets/panicle (109.95-274.57), grains/panicle (82.44-230.69), spikelet fertility (71.83-91.95%), 1000 grain weight (20.33-31.21), biological yield/plant (44.35-73.98g), harvest index (31.05-46.65%), kernel Length (7.95-11.98mm), kernel Breadth (2.20-3.11mm), L : B ratio (2.62-5.44) and grain yield/plant (16.15-29.85g). The comparison of mean performance of rice genotypes for 16 traits using critical differences revealed existence of very high level of variability in the rice genotypes evaluated in the present study.

A wide range of phenotypic coefficient of variation (3.03 – 18.04%) and genotypic coefficient of variation (2.52 – 17.97%) 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 were recorded between PCV and corresponding GCV for all the traits. Grains per panicle, spikeletes per panicle, grain yield per plant, flag leaf area and L:B ratio displayed moderate phenotypic and genotypic coefficient of variance. The similar results were found by Devi *et al.* 2017; Pragnya *et al.* 2018 and Manjunatha *et al.* 2019 [5, 20, 16].

Table 1: Analysis of variance for 15 characters in parents and their F₁ generation of rice

Source of Variation	d.f.	Days to 50% Flowering	Days to Maturity	Plant Height	Flag leaf Area	Panicle bearing Tillers/Plant.	Panicle Length	Spikelets/Panicle	Grains/Panicle
Replication	2	7.02	7.02	4.64	0.25	0.08	0.42	15.55	3.27
Treatment	128	18.45**	18.45**	183.42**	82.23**	3.92**	13.70**	3846.63**	2969.00**
Error	256	2.24	2.24	1.66	0.13	0.22	0.17	6.39	7.38

Source of variation	d.f.	Spikelet fertility	1000 grain weight	Bio. yield/Plant	Harvest index	Kernel Length	Kernel Breadth	L/B ratio	Grain yield/Plant
Replication	2	2.88	0.41	49.02	21.97	0.008	0.001	0.006	3.14
Treatment	128	42.68**	11.97**	109.69**	28.26**	1.995**	0.107**	0.737**	26.10**
Error	256	2.28	0.10	16.47	11.64	0.019	0.002	0.009	2.74

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

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

Characters	Mean	Range (Min - Max)	GCV (%)	PCV (%)	Heritability (%)	Genetic Advance	GA as % means
Days to 50% flowering	85.69	82.00-94.00	2.71	3.23	70.69	4.03	4.70
Days to maturity	116.26	109.00-124.00	2.52	3.03	68.98	5.01	4.31
Plant height	112.06	90.37-132.68	6.95	7.04	97.37	15.83	14.12
Flag leaf area	38.43	23.05-49.08	13.61	13.65	99.52	10.75	27.97
Panicle bearing tillers/plant.	14.82	11.66-17.70	7.49	8.14	84.59	2.10	14.19
Panicle length	27.82	23.16-32.77	7.63	7.78	96.36	4.30	15.44
Spikelets/ panicle	208.6	109.95-274.57	17.15	17.19	99.51	73.53	35.24
Grains/ panicle	174.84	82.44-230.69	17.97	18.04	99.27	64.49	36.88
Spikelet fertility	83.69	71.83-91.95	4.39	4.74	85.55	6.99	8.36
1000 grain weight	26.47	20.33-31.21	7.52	7.61	97.59	4.05	15.29
Bio. yield/plant	57.75	44.35-73.98	9.65	11.94	65.36	9.28	16.08
Harvest index	40.44	34.05-46.65	5.82	10.25	52.25	2.75	6.81
Kernel Length	9.33	7.95-11.98	8.70	8.83	97.24	1.65	17.68
Kernel Breadth	2.55	2.20-3.11	7.33	7.56	93.89	0.37	14.63
L : B ratio	3.68	2.62-5.44	13.38	13.63	96.36	1.00	27.06
Grain yield/plant (g)	23.22	16.15-29.85	12.02	13.98	73.94	4.94	21.29

Heritability of a trait is an index of transmission of characters from parents to its progeny. The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic population, hence prior knowledge about the heritability of the traits is a prerequisite for the selection programme (Singh *et al.*, 2011) [24]. Broad sense heritability describes both fixable (additive) and non-fixable (dominant and epistatic) variances which helps in estimating the inheritance of a character (Nirmala devi *et al.*, 2015) [17]. The present study in this context exhibited that an estimate of heritability (broad sense) was high (> 60%) for all traits flag leaf area, (99.52), spikelets per panicle (99.51), grains per panicle (99.27), 1000-grain weight (97.59), plant height (97.37), kernel length (97.24), panicle length (96.36), L:B ratio (96.36), kernel breadth (93.89), spikelet fertility (85.55), panicle bearing tillers per plant (84.59), grain yield per plant (73.94), days to 50% flowering (70.69), days to maturity (68.98) and biological yield per plant (65.36) except harvest index (52.25) which exhibited moderate heritability. High or moderate heritability estimates for most of the traits studied, have been reported earlier by Venkanna *et al.* (2014), Kahani and Hittalmani (2015), Hefena *et al.* (2016) and Abebe *et al.* (2017) [29, 13, 10, 1].

For an effective selection, the knowledge alone on the estimates of heritability is not sufficient and genetic advance if studied along with heritability is more useful. High heritability coupled with high genetic advance was observed for leaf area, spikelets per panicle, grains per panicle, L:B ratio and grain yield per plant 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 Sala Santhi *et al.* (2016), Devi *et al.* (2017) and Pragnya *et al.*

(2018) [21, 5, 20]. High heritability with moderate or low genetic advance for days to 50% flowering, plant height, panicle bearing tillers per plant, panicle length, 1000 grain weight, biological yield per plant, kernel length and kernel breadth 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 Singh and Singh (2005) [25] and Venkanna *et al.* (2014) [29].

Conclusion

Presence of genetic variability in a crop is a foremost requirement for the improvement of economically important traits like yield in rice. From this study, we conclude that the genotypes possessed adequate amounts of variability for yield and its associated traits. High heritability coupled with high genetic advance was observed for leaf area, spikelets per panicle, grains per panicle, L:B ratio and grain yield per plant indicated that additive genetic control in the inheritance of these traits and selection pressure could be profitably applied on these characters for yield improvement.

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