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Genetic variability studies in rice (*Oryza sativa* L.)

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Abstract
Genetic variability was assessed in rice (*Oryza sativa* L.) germplasms with 50 genotypes of rice collected from various sources which were evaluated in RBD at ZARS, Igatpuri during *kharif* 2020. The analysis of variance for eleven characters indicated the appreciable amount of variability was present in the material under study. Genotypic coefficient of variation (GCV) was lower than the phenotypic coefficient of variation (PCV) for all the characters under study. The high GCV and PCV was observed for plant height, panicle length, number of panicles plant^{-1}, number of spikelets panicle^{-1}, number of fertile spikelets panicle^{-1}, number of infertile spikelets panicle^{-1}, test weight and grain yield plant^{-1}. The characters such as plant height, number of spikelets panicle^{-1} and number of fertile spikelets panicle^{-1} exhibited high heritability coupled with high genetic advance indicating that most likely heritability is due to additive gene effect and selection may be effective for these characters. High heritability coupled with moderate genetic advance was observed in days to 50% flowering, days to physiological maturity, number of infertile spikelets plant^{-1}, spikelet fertility and grain yield plant^{-1} indicating that additive and non-additive both gene action were present.

Keywords: Rice, genetic variability, heritability, genetic advance

Introduction
Rice (*Oryza sativa* L.) is one of the most important staple food crops for more than 60% of the world population and it has been the cheapest source of food, energy and protein. It belongs to family Poaceae (Gramineae) that includes other cereals such as wheat and corn. It provides 43% of calories of human diet in India; and contributes 20-25% of agricultural income due to its intensive cultivation. In Asia, majority of the population consumes rice in meal every day. In many countries, rice accounts for more than 70% of human calorific intake.

In India, rice is cultivated in an area of 43.79 mha with the production and productivity levels of 116.42 Mt and 2659 kg/ha, respectively (Anonymous, 2018), while in Maharashtra, rice is cultivated in an area of 1.54 mha with the production of 3.51 Mt (Anonymous, 2019). West Bengal has the highest rice production, while Punjab has the highest productivity of rice in India.

Any breeding programme to be successful it depends upon the degree of genetic variability available in the crop species, the efficiency of selection technique implemented by plant breeder. Grain yield is a complex phenotypic character which gets influenced by several quantitative traits, these are governed by polygenes. An implementation of biometrical techniques in plant breeding has helped to better understand the genetics of quantitative characters and has proved useful to the plant breeder for systematic analysis at genetic level.

Robinson *et al.* (1949) [11] stated that heritability is the main concern to breeder, since it indicates that improvement can be achieved through selection. Heritability together with genetic advance would bring out the genetic gain expected from selection (Johnson *et al.,* 1955) [7]. The knowledge of the source of genetic variability for the different characters is considered of great importance, since the target of the plant breeder is to improve the yield and the quality by evolving superior varieties. With this available background information, the present studies have been initiated with an objective to understand the variability for grain yield and yield contributing characters in rice.

Material and Methods
For the present study, 50 genotypes of rice originating from different geographic regions and showing phenotypic variability for different Agronomic yield characters were used from the germplasm maintained by Zonal Agricultural Research Station, Igatpuri. The genotypes were sown in June, 2020 in a Randomized Block Design with two replications. 3-4 grains were dibbled hill^{-1} to ensure better crop stand and a single seedling was kept hill^{-1} after thinning of seedlings.

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Observations were recorded on randomly selected five plants for twelve characters *viz.* days to 50% flowering, days to physiological maturity, plant height (cm), panicle length (cm), number of panicles plant[-1], number of spikelets panicle[-1], number of fertile spikelets panicle[-1], number of infertile spikelets panicle[-1], spikelet fertility (%), test weight (g), grain yield plant[-1] (g) and grain type.

The analysis of variance was done as suggested by Panse and Sukhatme (1985) [10]. The genotypic and phenotypic variance was calculated as per the formulae (Burton and Devane, 1953) [5]. Genotypic coefficient of variation (GCV) was estimated by formula suggested by Burton (1952) [4].

$$GCV\ (\%) = \frac{\sqrt{\sigma_g^2}}{X} x\ 100$$

Where, σ_g^2 = Vg = Genotypic variance, X = General mean of the character Phenotypic coefficient of variation (PCV) was also estimated by the formula suggested by Burton (1952) [4].

$$PCV\ (\%) = \frac{\sqrt{\sigma_P^2}}{X} x\ 100$$

Where, σ_p^2= V_p = Phenotypic variance

GCV and PCV were classified as suggested by Robinson *et al.* (1949) [11].

Heritability estimates in broad sense (h[2]) were computed by the formula suggested by Burton (1952) [4]. Heritability was classified as, (Robinson *et al.* 1949) [11]. From heritability estimates the genetic advance was estimated by the formula given by Burton (1952) [4]. In order to estimate the relative utility of genetic advance among characters, genetic advance as percent for mean is usually calculated. The range of genetic advance as percent of mean was classified as per suggestion by Johnson *et al.* (1955) [7].

Results and Discussion

The analysis of variance for eleven characters has been presented in Table 1. It revealed that, the mean sum of square due to treatments for all characters studied is found to be significant. It indicated that appreciable amount of diversity is present in the material under study. The parameters range, GCV and PCV, heritability in broad sense and genetic advance as per cent of mean have been presented in the Table 2. The estimates for genotypic coefficients of variation (GCV) were lower than the phenotypic coefficients of variation (PCV) for all characters under trial. The character number of fertile spikelets panicle[-1] exhibited the highest GCV (36.22)

and PCV (37.56). The highest difference between GCV and PCV values was observed for number of infertile spikelets panicle[-1] followed by grain yield plant[-1]. However, the lowest GCV and PCV difference was observed for days to 50% flowering. The high GCV and PCV was observed for plant height, panicle length, number of panicles plant[-1], number of spikelets panicle[-1], number of fertile spikelets panicle[-1], number of infertile spikelets panicle[-1], test weight and grain yield plant[-1], indicating the presence of large variation among the genotypes for these characters. The character panicle length exhibited moderate GCV and PCV. Seven characters exhibited high GCV and PCV, one character recorded moderate GCV and PCV, while three characters recorded low GCV and PCV. Days to 50% flowering, days to physiological maturity and spikelet fertility recorded low GCV and PCV.

The characters *viz.* days to 50% flowering, days to physiological maturity and spikelet fertility registered low estimate of GCV and PCV which indicate that low degree of variation found in these characters in the present experimental material, thus gives little scope for future improvement of these characters. Similar types of findings were reported by Lingaiah *et al.* (2020) [20] for days to 50% flowering.

Highest heritability was shown by plant height (98.65). All heritability figures were more than 60% so all characters have been classified under high heritability. Heritability as well as genetic advance are regarded as an important selection parameter. Burton (1952) [4] suggested that "genetic variation along with heritability estimate would give a better idea about the efficiency of selection." From the present study, it can be concluded that high heritability values were recorded for all the characters, these estimates indicate the least effect of environment on these characters. These findings were in consonance with the report made by Tuwar *et al.* (2013) [12] for days to 50% flowering, days to maturity, plant height and panicle length, Lingaiah *et al.* (2020) [20] for test weight.

Plant height, number of spikelets panicle[-1] and number of fertile spikelets panicle[-1] exhibited high heritability with high genetic advance indicating that probably heritability is due to additive gene effect and selection could be effective for these characters. Similar results were observed by Abdul *et al.* (2011) [1] for number of spikelets panicle[-1], Lingaiah *et al.* (2014) [8] for plant height. High heritability with moderate genetic advance was observed in days to 50% flowering, days to physiological maturity, number of infertile spikelets plant[-1], spikelet fertility and grain yield plant[-1]which indicate that additive and non-additive both gene actions were present. Similar results were obtained by Devi *et al.* (2020) for test weight and grain yield plant[-1].

Table 1: Analysis of variance for eleven characters of 50 rice genotypes

Sr. No.	Character	Replication	Genotypes	Error
	DF	1	49	49
1	Days to 50%flowering	0.64	111.82**	2.88
2	Days to physiological maturity	1.21	130.31**	4.70
3	Plant height (cm)	0.61	905.18**	6.14
4	Panicle length (cm)	2.82	24.85**	1.37
5	Number of panicles plant[-1]	0.09	17.48**	0.60
6	Number of spikelets panicle[-1]	1.44	6705.14**	238.97
7	Number of fertile spikelets panicle[-1]	50.41	6897.87**	250.21
8	Number of infertile spikelets panicle[-1]	68.89	192.21**	28.34
9	Spikelet fertility (%)	7.25	110.23**	9.57
10	Test weight (gm)	0.19	36.50**	1.13
11	Grain yield plant[-1]	6.46	92.81**	5.02

*Significant at 5% level
**Significant at 1% level

Table 2: Different parameters of variability in 50 genotypes of rice

Sr. No.	Character	Mean	Range	GCV (%)	PCV (%)	ECV (%)	Heritability (b.s.) (%)	Genetic Advance	Genetic Advance as per cent of Mean
1	Days to 50% flowering	108.92	94.00 – 120.00	6.78	6.95	1.56	94.97	14.82	13.60
2	Days to physiological maturity	142.03	128.00 – 157.00	5.58	5.79	1.53	93.04	15.75	11.09
3	Plant height	83.95	50.40 - 134.10	25.38	25.55	2.97	98.65	43.38	51.92
4	Panicle length	21.54	14.00 – 27.70	15.91	16.81	5.44	89.54	6.68	31.01
5	No. of panicles plant^{-1}	11.09	5.50 - 17.50	26.20	27.11	6.99	93.36	5.78	52.15
6	No. of spikelet panicle^{-1}	187.90	92.50 – 288.00	30.26	31.36	8.23	93.12	113.03	60.15
7	No. of fertile spikelet panicle^{-1}	159.17	70.00 - 261.50	36.22	37.56	9.94	93.00	114.53	71.96
8	No. of infertile spikelet panicle^{-1}	28.73	11.00 - 51.50	31.51	36.55	18.53	74.30	16.07	55.95
9	Spikelet fertility	83.26	58.81 - 94.23	8.52	9.30	3.72	84.03	13.40	16.09
10	Test weight	17.99	11.10 - 27.19	23.37	24.10	5.90	94.01	8.40	46.67
11	Grain yield plant^{-1}	19.79	9.71 - 34.61	33.48	35.35	11.33	89.73	12.93	65.33

Conclusion
The analysis of variance indicated that appreciable amount of variability is present in the material under study. High estimate of GCV and PCV indicate that high degree of variation found in these characters in the present experimental material, thus gives large scope for future improvement of these characters. It can also be seen that high heritability values were recorded for all the characters; these estimates indicate the least effect of environment on these characters. All high heritability values indicate transmission of characters from parents to their offspring which will be helpful for selection in future hybridization programme. High heritability coupled with moderate genetic advance as per cent of mean indicating additive gene action and selection would be effective for these characters.

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