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Variability and genetic parameters studies in rice (*Oryza sativa* L.)

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Abstract
The present investigation was carried out on genetic variability and heritability with 27 local and improved genotypes of rice in RBD with three replications at Research farm, RARS, Karjat during *kharif*, 2018. The results revealed that, analysis of variance indicated positively significance for all the characters under study. Considerable amount of genetic variability was observed for all the characters. Phenotypic coefficients of variation (PCV) was observed greater in magnitude over the respective genotypic coefficients of variation (GCV). The magnitude of phenotypic coefficient of variation was reported highest for straw yield per plant (43.74) followed by 1000 grain weight (g) (30.33), number of tillers per plant (27.513) and plant height (19.143). The magnitude of genotypic coefficient of variation was highest for straw yield per plant (34.77) followed by 1000 grain weight (g) (30.25), number of tillers per plant (26.87), plant height (18.98) and number of filled spikelets per panicle (14.86). High heritability coupled with high genetic advance was observed for plant height, number of spikelets per panicle, number of filled spikelets per panicle indicating that these characters can be improved through direct selection since the additive gene action is being involved in the inheritance of these characters. The characters number of spikelets per panicle expressed maximum genetic advance (46.39) followed by plant height (44.07), number of filled spikelets per panicle (41.65), days to maturity (12.54). Hence it is suggested that these characters could be of great importance for selecting better genotype in the rice improvement programme.

Keywords: Rice, GCV, PCV, GA, heritability, gene action and inheritance

Introduction
Rice (*Oryza sativa* L.) is one of the staple foods of the world and also staple food of more than 60% of Indian population. It accounts for about 43% of total food grain production and 46% of total cereal production in the country. Rice occupies pivotal place in Indian Agriculture. In order to meet the domestic demand of the increasing population the present day production of 112.15 million tons (Annonymous, 2017-18) [1] of milled rice has to be increased to 125 million tons by the year 2030. Since the yield of high yielding varieties (HYVs) of rice is plateauing, it is rather difficult to achieve this target with the present day inbred varieties. Therefore, to sustain the self-sufficiency in rice, additional production of 1.17 million tons is needed every year. There are a large number of indigenous rice varieties in India, which are still grown by the tribal people and small farmers of the remote areas where the modern agricultural practices, sufficient foods as well as healthcare systems are a dream. Nature has provided them some alternative ways. They have different indigenous rice varieties with its nutritional and medicinal values. The indigenous rice varieties cultivated by traditional farmers may contain a considerable genetic diversity that can serve as a source of germplasm for genetic improvements of cultivated varieties of rice. In rice varietal improvement programmes, indigenous rice varieties have proved to be useful donors for sources of resistance or tolerance to many stress environments and for imparting resistance to important pests and diseases. In general, diverse landraces traditionally cultivated by farmers around the centers of diversity and domestication of crops are as key natural resources important for maintaining the future food security in light of the changing climate. After considering this attributes, Regional Agriculture Research Station, Karjat has collected several local germplasm. These germplasm have more genetic diversity, high degree of tolerance for biotic and abiotic stresses and wide adaptability with meaningful nutrional quality.

Materials and Methods
The experiment was conducted at the Research Farm of Regional Agricultural Research Station, Karjat during *Kharif*, 2018. The experimental material for the present study consisted of twenty seven genotypes of rice (*Oryza sativa* L.) which was collected from different sources. The present experiment was carried out by adopting Randomized Block Design with

three replications. The direct sowing method was used for sowing the seed in 3.5x 1.2 sq m. Each genotype was planted in 5 rows of 20 cm apart. The fertilizer dose was 40:20:20 kg NPK /ha. Twenty one days old seedlings were transplanted with 20 cm distance between rows and 15 cm distance between plants within rows. All the recommended package of practices was followed along with necessary prophylactic plant protection measure raise. Data on five randomly selected plants in each genotype were collected for the traits viz., days to 50 per cent flowering, day to maturity, plant height at maturity (cm), number of tiller per plant, panicle length (cm), number of spikelets per panicle, number of filled spikelets per panicle, spikeletes fertility (%), 1000 grain weight (g), grain yield per plant (g), straw yield per plant (g), harvest index (%).The mean of the replications are used for statistical analysis. The variability was estimated as per procedure for analysis of variation suggested by Panse and Sukhatme (1985) [13]. PCV and GCV were calculated by the given formula by Burton and De Vane (1953) [3], broad sense heritability by Lush (1949) [12] and genetic advance i.e. the expected genetics were calculated by using the procedure given by Johnson *et al*. (1955) [6].

Result and Discussion

The analysis of variance revealed that the genotypes exhibited significant differences among all the genotypes for all the characters under studied. The phenotypic expression of the characters is the result of inter action between the genotype and environment. In the present study, estimates of phenotypic coefficient of variation for all the characters were higher than the estimates of genotypic coefficient of variation. It can be seen that magnitude of phenotypic coefficient of variation was highest for straw yield per plant (43.74) followed by 1000 grain weight (g) (30.33), number of tillers per plant (27.513) and plant height (19.143) The genotypic coefficient of variation was highest for straw yield per plant (34.77) followed by 1000 grain weight (g) (30.25), number of tillers per plant (26.87), plant height (18.98) and number of filled spikelets per panicle (14.86) indicating presence of high amount of variability for improvement of these characters Elisama *et al. (2018)* [4], Khaire *et al.* (2017) [7], Kunkerkar *et al*. (2017) [11] and Basavaraja *et al.* (2013) [2] also reported high variability for these traits. The high difference between PCV and GCV observed for straw yield per plant (g) indicated that this character was highly influenced by the environment. The similar results also reported by Karim *et al.* (2017) [8], Kunkerkar *et al*. (2017) [11] and Krishna *et al.* (2008) [10].

In present investigation, higher heritability estimates were obtained for all the characters except grain yield per plant (g) which has moderate heritability values. The genetic advance as percentage of mean was high for the traits grain yield per plant, number of spikelets per panicle, plant height (cm), number of filled spikelets per panicle and days to maturity. High heritability coupled with high genetic advance was observed for plant height, number of filled spikelets per panicle and number of spikelets per panicle indicating the role of additive gene action in the expression of these characters. High heritability estimates with low genetic advance was noticed for 1000 grain weight, number of tillers per plant, harvest index, panicle length and spikelet fertility indicating the role of non-additive gene action in the expression of these characters. These results are in accordance with that Khaire *et al*. (2017) [7], Kunkerkar *et al.* (2017) [11], Vincent *et al*. (2017) [15] and Priyanka *et al.* (2017) [14]; 1000 grain weight (g) exhibited high heritability and panicle length (cm) low genetic advance indicating the presence of both additive and non-additive gene action hence simple selection for these traits would be less effective. This results are in accordance with by Khaire *et al.* (2017) [7], Kunkerkar *et al.* (2017) [11], Ketan and Sarkar (2014) [9] and Jamal *et al.* (2009) [5].

Table 1: Estimates of Phenotypic Coefficient of Variance (PCV) and Genotypic Coefficient of Variance (GCV), genotypic, phenotypic and error variance, heritability in percentage, Genetic advance and Genetic advance expressed in percentage of mean for ten quantitative Characters of Rice (*Oryza sativa* L.)

Sr. No.	Characters	Mean	PCV	GCV	σ^2_P	σ^2_G	σ^2_E	Heritability (%)	Genetic advance	Genetic advance (%)
1.	Days to 50 per cent flowering	100.20	6.19	5.98	38.59	36.00	2.58	93.29	11.93	11.91
2.	Days to maturity	130.20	4.98	4.82	42.07	39.48	2.58	93.84	12.54	9.63
3.	Plant height (cm)	113.67	19.14	18.98	473.57	465.64	7.94	98.32	44.07	38.77
4.	Number of tillers per plant	8.37	27.51	26.87	5.31	5.06	0.24	95.38	4.52	54.06
5.	Panicle length (cm)	23.23	10.52	9.47	5.98	4.84	1.42	80.92	4.07	17.55
6.	Number of spikelets per panicle	184.48	15.89	13.93	860.05	660.47	199.5	76.79	46.39	25.14
7.	Number of filled spikelets per panicle	152.02	16.60	14.86	637.42	510.55	126.86	80.09	41.65	27.40
8.	Spikelet fertility (%)	82.44	5.57	4.73	21.10	15.22	5.88	72.12	6.82	8.28
9.	1000 grain weight (g)	19.85	30.33	30.25	36.29	36.10	0.18	99.48	12.34	62.16
10.	Grain yield per plant(g)	13.75	17.33	13.28	5.68	3.34	2.34	58.75	2.88	20.98
11	Straw yield per plant(g)	21.74	43.74	34.77	90.43	57.15	33.27	63.20	12.38	56.95
12	Harvest index (%)	44.60	9.03	8.84	16.23	15.57	0.66	95.88	7.95	17.84

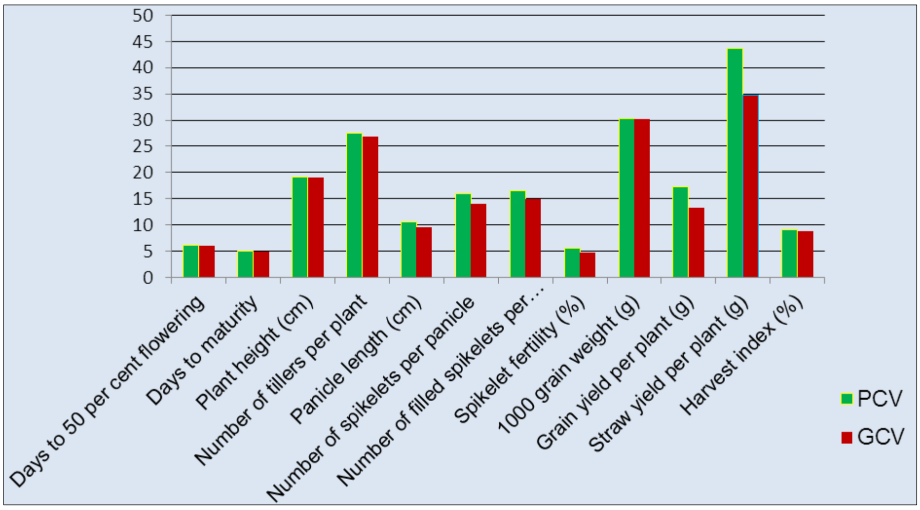

Fig 1: Phenotypic Coefficient of Varience (PCV) and Genotypic Coefficient of Variance (GCV) for ten quantitative characters of Rice (*Oryza sativa* L.)

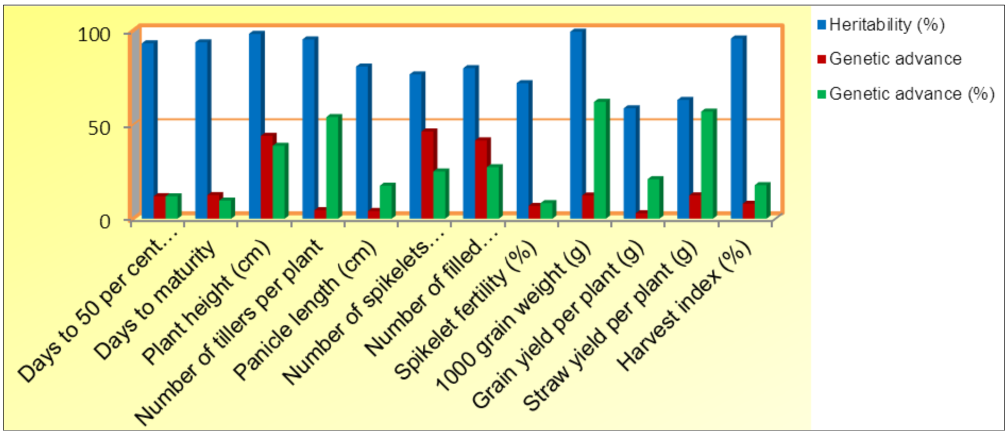

Fig 2: Genetic parameters for ten quantitative characters of Rice (*Oryza sativa* L.)

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