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## Genetic variability, heritability and genetic advance studies for quantitative and quality traits in basmati rice (*Oryza sativa* L.)

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**Abstract**

The present study was undertaken with an objective of estimation of genetic variability, heritability, genetic advance for yield components and quality parameters among thirty aromatic rice genotypes. The genotypes were evaluated in RBD and ANOVA results revealed the highly significant mean sum of squares among the genotypes for all the characters. PCV and GCV estimates were found high for almost all the traits of interest except for days to maturity, hulling percent and 100 kernel weight after cooking. High heritability was registered for all the traits except hulling percent, coupled with high genetic advance as percent of mean for all characters except days to maturity, 100 kernel weight after cooking and hulling percent, which indicates that these characters are largely controlled by additive gene action.

**Keywords:** Paddy, *Oryza sativa* L., variability, yield, quality

**Introduction**

Rice (*Oryza sativa* L.) is one of the pivotal staple cereal crops and central to the lives of billions of people around the world. Rice occupies an important place in the Indian agriculture and has been grown under diverse ecological conditions and gets exposed to different environmental stresses like salinity, alkalinity, drought, cold etc. Fiyaz *et al.* (2011) [6]. Considering the ever-rising population, the basic objective of the plant breeders heads towards yield improvement in staple food crops. For improvement of any crop the first and one of the major needs is of genetic diversity and variability. It gives an opportunity to a plant breeder to exploit all the diversity which is present for the crop improvement programme. Genetic Variability is a most important need when it comes to the survival and existence of a species. Genetic variability in a species provides it with ability to adjust as per the conditions prevailing. The extent of genetic variability is considered as an important factor and a must pre-requisite for a successful hybridization programme (Dhanwani *et al.* 2013) [4]. For any crop improvement programme to succeed, genetic variability is a basic requirement. The presence of genetic variability in any species for qualitative traits gives the breeders an opportunity to exploit it to the best. If genetic variability in a species is not considerable then our first objective in the crop improvement programme becomes the generation of diversity. This genetic variation is the source which is exploited to improve a species and as result new efficient cultivars are achieved. In populations genetic drift is a constant phenomenon due to which species gradually loose genetic Variation. This loss of variability hampers the potential of the species and therefore, there's a need for its conservation and determination as well.

If the amount of genetic variability in the natural population is less then it becomes important for a plant breeder to create it, for the sake of crop improvement. Along with this, it is equally important to conserve the genetic diversity which is already present. Usually the characters which are of interest to the plant breeder are complex and are the result of the interaction of a number of components. For improvement of a crop, along with the genetic diversity, the heritability of the character is equally important. Heritability in simple terms is the transmission of characters from one generation to another and is one of the most important factors in crop improvement programme. It is a parameter widely used in establishment of breeding programs and formation of selection indices (Falconer, 1985) [5]. The genetic variability present, if is not considerably heritable then improvement of a genotype for the trait of interest becomes tedious. The selection of parents for polygenic traits is quite difficult and hence for selection of superior parents for the crop improvement programme there is a need of good amount of genetic variation as well as the transmissibility of that variation. Genetic advance is the amount of improvement in the character. Heritability in combination with genetic advance helps in identifying the character type and the way of its improvement. The present study was carried out with an objective to understand the genetic background and

inheritance of the different traits in aromatic rice genotypes. Furthermore, the specific objective of this study is to estimate genetic variability, heritability, and genetic advance for the various quantitative traits of aromatic rice grown under *Tarai* conditions in order to aid the effective selection for successful breeding program. The findings of this study would help to identify the highly suitable genetic material and assist to design the subsequent breeding program to foster the varietal improvement programs in aromatic rice

### Materials and methods

Thirty improved genotypes of aromatic rice were evaluated at Research farm of R.M.P. P.G. College, Gurukul Narsan, Haridwar (Uttarakhand) for conducting the present study. The experimental farm of Gurukul Narsan is situated in the foothills of Shivalik range of Himalaya and falls in the humid sub-tropical climate Zone. The experimental material was planted in a plot of size 2 m<sup>2</sup> keeping 20x15 cm spacing utilizing randomized complete block design with three replications. The observations were recorded for 22 quantitative characters on a random sample of 10 plants from each plot. These characters included morphological characters viz., Days to 50% flowering, days to maturity, plant height (cm), number of tillers per plant, panicle length (cm), flag leaf length (cm), flag leaf width (cm), number of grains per panicle, grain weight per panicle (g), 100 grain weight (g) and quality parameters such as 100 kernel weight (g), hulling (%), kernel length before cooking (mm), kernel breadth before cooking (mm), kernel length after cooking (mm), kernel breadth after cooking (mm), L:B ratio, kernel elongation ratio, breadth increase ratio after cooking, 100 kernel weight after cooking (g), water absorb by 10 gm kernel (ml), grain weight per plant (g).

Genetic parameters viz., Mean, Range, Coefficients of variability (PCV, GCV and ECV) along with heritability in broad sense, genetic advance and genetic advance as percent of mean were estimated for the character studied. Analysis of variance, which was carried out as per methodology described by Panse and Sukhatme (1967) [12], permits estimation of phenotypic, genotypic and environmental coefficients of variability. PCV and GCV were calculated using the formula given by Burton (1952) [3], heritability in broad sense ( $h^2$ ) by

Burton and De Vane (1953) [2] and genetic advance i.e. the expected genetic gain was calculated by using the procedure given by Johnson *et al.* (1955) [8]. GCV and PCV values were categorized as low (0-10%), moderate (10-20%) and high (20 and above 20) as indicated by Sivasubramanian and Menon (1973) [15]. The heritability was categorized as low (0-30%), moderate (30-60%) and high (60 and above) as given by Robinson *et al.* (1949) [13]. Genetic advance as per cent mean was categorized as low (0-10%), moderate (10-20%) and high (20 and above) as given by Johnson *et al.* (1955) [8].

### Results and discussion

Genetic variability in any crop is pre-requisite for selection of superior genotypes over the existing cultivars. In present investigation the data was collected as per the requirement of the experimental objectives and was analyzed for the entire 22 yield and quality associated characters. The analysis of variance for different characters revealed that the mean sum of squares among the genotypes for all the characters was highly significant for all the 24 characters under study suggesting each and every genotype are genetically divergent from each other and there is ample scope for selection of characters from these diverse sources for yield and its components. These findings were in accordance with the findings of Bekele *et al.*, (2013) [1] and Sandhya *et al.* (2015) [14]. Knowledge about the amount of genetic variability present to act upon and its heritability among the agronomically important traits is the requirement to design a suitable plant breeding method. For a plant breeder, it's very important to have an accurate idea about the extent of genetic variability and the amount of heritable variation for important traits. It is very important to partition the total genetic variability into different components because sometimes due to the effect of environment the species either out-performs or under-performs leading to the experimental errors. Partitioning of variability helps us to have information regarding the nature and extent of actual variability present. The mean, range, phenotypic (PCV), genotypic (GCV), environmental (ECV), broad sense heritability ( $h^2_b$ ), genetic advance (GA) and genetic advance as percent of mean (GAM) were estimated and presented in Table 1.

**Table 1:** Mean, Range, Phenotypic (PCV), Genotypic (GCV) and Environmental (ECV) coefficient of variability, broad sense heritability ( $h^2_b$ ), genetic advance (GA) and genetic advance as percent of mean (GAM) of different characters in basmati rice

S. No.	Character	Mean	Range	PCV	GCV	ECV	$h^2$	GA	GAM
1	Days to flowering	91.76	78.00-111.00	10.45	10.35	1.51	97.91	19.35	21.09
2	Days to maturity	120.87	110.67-152.67	7.35	7.26	1.17	97.47	17.85	14.77
3	Plant height (cm)	120.46	77.33-152.33	12.95	12.91	0.92	99.49	31.96	26.53
4	Number of tillers per plant	6.58	4.40-8.80	19.96	19.32	5.02	93.68	2.54	38.60
5	Peduncle length (cm)	41.66	30.50-48.17	11.90	11.85	1.08	99.17	10.13	24.32
6	Flag leaf length (cm)	37.63	25.83-51.67	17.24	17.08	2.34	98.15	13.11	34.84
7	Flag leaf width (cm)	1.48	1.20-2.07	15.68	15.05	4.43	92.03	0.44	29.73
8	Number of grains per panicle	157.88	108.30-216.67	25.04	24.72	4.00	97.44	79.36	50.27
9	Grain weight per panicle (g)	3.84	2.57-5.28	22.85	22.38	4.62	95.91	1.74	45.31
10	Grain weight per plant (g)	13.68	5.09-20.53	30.62	30.32	4.33	97.99	8.46	61.84
11	100 grain weight (g)	2.52	1.92-3.50	16.43	16.26	2.33	97.99	0.83	39.94
12	100 kernel weight (g)	1.86	1.47-2.40	15.36	14.43	5.25	88.29	0.52	29.96
13	Hulling (%)	74.21	65.91-77.99	4.98	3.03	3.92	37.75	2.87	3.87
14	Kernel length before cooking (mm)	8.04	7.03-9.59	10.98	10.94	0.97	99.21	1.81	22.51
15	Kernel breadth before cooking (mm)	1.89	1.50-2.50	12.65	11.58	5.09	83.81	0.41	21.69
16	Kernel length after cooking (mm)	74.21	7.87-12.97	13.70	13.66	1.08	99.38	2.89	28.06
17	Kernel breadth after cooking (mm)	8.04	2.10-4.70	21.11	20.93	2.76	98.29	1.55	48.69
18	L.B. Ratio	1.89	2.89-4.95	15.82	14.80	5.58	87.58	1.24	28.64
19	Kernel elongation ratio	10.30	1.07-1.95	14.42	14.34	1.52	98.89	0.38	29.69
20	Breadth increase ratio after cooking	3.63	1.13-2.78	23.99	23.15	6.31	93.08	0.89	45.64
21	100 kernel weight after cooking (g)	4.33	4.30-6.30	9.83	9.61	2.07	95.56	0.98	19.25
22	Water absorbed by 10gm kernel (ml)	1.28	8.17-23.03	19.51	17.95	7.65	84.65	6.06	34.04

### Variability parameters

Days to 50% flowering ranged from 78-111 with a mean value of 91.76 and showed moderate PCV and GCV. Days to maturity ranged from 110.67-152.67 with mean value of 120.87 days. The low PCV and GCV were found for days to maturity. The range of plant height varied from 77.33-152.33 cm with a general mean 120.46 cm and observed with moderate PCV and GCV. The number of tillers per plant varied from 4.4-8.8 with moderate PCV and GCV around a mean of 6.58. Moderate PCV and GCV was seen with a range from 30.50-48.17 cm for peduncle length with general mean 41.66 cm. The range of flag leaf length was found to be 25.83-51.67 cm with a mean value of 37.63 cm and moderate PCV and GCV. The flag leaf width ranged from 1.20-2.07 cm with moderate PCV and GCV and the general means was found to be 1.48 cm. High PCV and GCV was recorded for number of grains per panicle with a range from 108.3-216.67 with the mean value of 157.77 grains per panicle. The range of grain weight per panicle was 2.57-5.28 g with high PCV and GCV around a mean value of 3.84 g. High PCV and GCV was exhibited by Grain weight per plant, which ranged from 5.09-20.53 g around the mean value was 13.68 g. Value of 100 grain weight ranged between 1.92-3.50 g with a mean value of 2.52 g and moderate PCV and GCV. The 100-kernel weight showed moderate PCV and GCV and ranged from 1.47-2.4 g with the mean of 1.86 g. Range of hulling was found between 65.91-77.99% with General mean of 74.21% and low PCV & GCV. The kernel length before cooking reported moderate PCV and GCV and ranged from 7.03-9.59 mm around the mean of 8.04 mm. Value of kernel breadth before cooking ranged between 1.50-2.50 mm with a mean value of 1.89 mm and moderate PCV and GCV. Kernel length after cooking ranged from 7.87-12.97 mm with moderate PCV and GCV and had the mean value of 10.30 mm. The range of kernel breadth after cooking was 2.10-4.70 mm with a mean value of 3.63 mm and exhibited marginally high PCV and GCV. Moderate PCV and GCV with a range varied from 2.89-4.95 was recorded for L.B. Ratio with the mean value of 4.33. The range of kernel elongation ratio varied from 1.07-1.95 with a general mean 1.28 and moderate PCV and GCV. High PCV and GCV was exhibited by breadth increase ratio after cooking and ranged from 1.13-2.78 with a mean of 1.95. Range of 100 kernel weight was found between 4.3-6.3 g with General mean of 5.09 g and low PCV and GCV. Value of water absorbed by 10 gm kernel ranged between 8.17-23.03 ml with a mean value of 17.80 ml and moderate PCV and GCV.

Critical perusal of the Table 1 revealed that the values of PCV and GCV were highest for Grain weight per plant followed by number of grains per panicle, breadth increase ratio after cooking, grain weight per panicle and kernel breadth after cooking, indicating the presence of great amount of variability between the genotypes for these traits, whereas, the values were found lowest for hulling percent followed by days to maturity and 100 kernel weight after cooking. However, the difference between PCV and GCV was found very low reflecting very few influences of environment in the expression of characters or lower sensitivity of genotypes to environment and greater role of genetic control governing the character is in agreement with the results explained by Karim *et al.* (2007) [10] and Sravan *et al.* (2012) [12]. Days to 50% flowering, plant height (cm), number of tillers per plant, panicle length (cm), flag leaf length (cm), flag leaf width (cm), 100 grain weight (g), 100 kernel weight (g), kernel length before cooking (mm), kernel breadth before cooking (mm), kernel length after cooking (mm), L:B ratio, kernel

elongation ratio, water absorb by 10 gm kernel (ml) recorded moderate GCV and PCV. The very low difference in the values of PCV and GCV for all the traits indicated that characters less affected by environment (Karad and Pol, 2008) [9] and selection on the basis of phenotype independent of genotype could be effective for the improvement of such traits. These findings are in agreement to earlier reports by Kumar and Verma (2015) [11], Sravan *et al.* (2016) [17] and Srivastava *et al.* (2017) [18].

### Heritability and genetic advance

High heritability was estimated for all the morphological characters such as days to 50% flowering, days to maturity, plant height (cm), number of tillers per plant, panicle length (cm), flag leaf length (cm), flag leaf width (cm), number of grains per panicle, grain weight per panicle (g), 100 grain weight (g) and quality parameters such as 100 kernel weight (g), kernel length before cooking (mm), kernel breadth before cooking (mm), kernel length after cooking (mm), kernel breadth after cooking (mm), L:B ratio, kernel elongation ratio, breadth increase ratio after cooking, 100 kernel weight after cooking (g), water absorb by 10 gm kernel (ml), grain weight per plant (g). except hulling percent. Heritability in broad sense ( $h^2_b$ ) was registered maximum for plant height followed by kernel length after cooking and kernel length before cooking whereas, it was found minimum for hulling percent. Genetic advance as percent of mean was recorded highest for number of grains per plant followed by number of grains per panicle and breadth increase ratio after cooking and lowest for hulling %. High heritability for all the characters except hulling %, moreover, the twelve out of 24 characters studied exhibited greater than 95% heritability, indicated the fixation of advance genotypes through selection for these traits. Genetic advance as percent of mean was also recorded high for all the characters except days to maturity, 100 kernel weight after cooking and hulling % for which moderate to low genetic advance was found.

Heritability in combination with genetic advance helps in calculating the advances in the trait of interest that can be achieved through simple selection. It also suggests the methodology to be applied for the improvement programme. With genetic variability and heritability, genetic advance of the trait under consideration is equally important. Genetic advance is improvement of the genotype for a character over its parent. In other words, is the expected response to selection and is denoted as GA and gives an implication of effectiveness of selection under a particular condition for trait of interest. In this study, high heritability and genetic advance were observed for grain yield and 20 yield components and quality characters indicating presence of additive genetic control also in agreement with Bekele *et al.* (2013) [1] and Islam *et al.* (2016) [7] during their study in aromatic and fine rice germplasm.

### Conclusion

It could be safely concluded from the present study that high PCV and GCV for Grain weight per plant, number of grains per panicle, breadth increase ratio after cooking, grain weight per panicle and kernel breadth after cooking, along with high heritability coupled with high genetic advance as percent of mean for all the characters except days to maturity, 100 kernel weight after cooking and hulling % suggested the ample scope of selection as well as desired improvement in these traits under which indicates that improvement in these characters is possible through mass selection and progeny

selection. It was noticed that the trait hulling percent registered lower values for all the parameters studied viz., phenotypic coefficient of variance, genotypic coefficient of variance, heritability in broad sense and genetic advance as percent of mean which indicated that the improvement of this trait is difficult to achieve and needs more attention.

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