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Genetic variability studies for yield components and quality traits in basmati rice (*Oryza sativa* L.)

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Abstract
The present investigation was carried out with an objective of assessing the genetic variability, heritability, genetic advance for twenty-two yield and quality characters of thirty rice genotypes evaluated in RBD with three replications. The results of ANOVA revealed that the mean sum of squares among the genotypes for all the characters were highly significant indicating the presence of ample amount of variability which can be exploited for selection of characters for crop improvement programme. The value of PCV and GCV was observed highest in case of flag leaf width .Genetic Advance as a percent of mean was maximum in case of grain yield per plant followed by number of grains per panicle, grain weight per panicle and water absorb by kernel while minimum for hulling percent and days to maturity. On the basis of study, the desirable donors for each character were identified. The most promising donors for grain yield were SKG-2017-19, SKG-2017-64, SKG-2017-40, SKG-2017-06 and SKG-2017-17. These genotypes can be used for further breeding programme to improve the yield potential of the variety.

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

Introduction
Rice is the most important cereal food crop of India. It occupies the largest area and ranks second in production next to China.According to the most recent official report of the United States Department of Agriculture (USDA) estimates that, the World Rice Production 2017-2018 will be 481.04 million metric tons (milled rice). During 2016-17, India produced 165 million tons of rice from 45 million hectares of land. Knowledge on the genetic architecture of genotypes is necessary to formulate efficient breeding methodology. The systematic breeding programme involves the steps like creating genetic variability practicing selection and utilization of selected genotypes to evolve promising varieties. Identification of better genotypes with desirable traits and their subsequent use in breeding programme and establishment of suitable selection criterion can helpful for successful varietals improvement programme. Analysis of variability among the traits would be of great importance in planning a successful breeding program. Information on the extent of genetic variability as well as heritability among the agronomically important traits is the requirement to design a suitable plant breeding method. Sometimes the trait of interest is influenced by the environmental conditions prevailing, especially in case of polygenic characters so it becomes important to partition the total variability components, to have information regarding the nature and extent of actual variability present. Heritability on the other hand is a parameter widely used in establishment of breeding programs and formation of selection indices (Falconer, 1985) [5] as it gives an idea about the transmissibility of the trait of interest. As it is difficult to select suitable parents for poly genetically controlled characters, therefore, for efficient selection of superior parents there's a need of adequate genetic variation as well as considerable heritability of the trait of interest. Heritability along with genetic advance helps in assessing the amount of improvement that can be achieved through selection and gives an idea about which type of crop improvement methodology would work. It gives an implication of effectiveness of selection under a particular condition for trait of interest.Therefore, development of high-yielding varieties requires through knowledge of the existing genetic variation for yield and its components. Therefore, the present investigation had been conducted to estimate the extent of variability, heritability and genetic advance for yield and its components in rice and to assess the nature and magnitude of inter-character correlation for different characters among basmati rice genotypes.

Materials and Methods
The present study was conducted at Research farm of R.M.P. P.G. College, Gurukul Narsan, Haridwar (Uttarakhand) with 30 improved genotype of basmati rice. The Gurukul Narsan is situated in the foothills of Shivalik range of Himalaya and falls in the humid sub-tropical climate Zone. The Material was planted in a randomized complete block design with three replications in the plot size of 2 m^2 keeping 20x15 cm spacing. The observations were recorded on a random sample of 10 plants from each plot for 22 quantitative 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 with (cm), number of grains per panicle, grain weight per panicle (g), 100 grain weight (g), 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, breath 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 and GCV) along with heritability in broad sense, genetic advance and genetic advance as percent of mean were estimated for the character studied. Analysis of variance permits estimation of phenotypic, genotypic and environmental coefficients of variability, which was carried out as per methodology advocated by Panse and Sukhatme (1967) [11]. When coefficient of variability is high the sample is less consistent or more variable and when it is low the sample is more consistent and less variable. PCV and GCV were calculated using the formula given by Burton (1952) [2], heritability in broad sense (h2) by Burton and De Vane (1953) [3], and genetic advance i.e. the expected genetic gain was calculated by using the procedure given by Johnson *et al.* (1955) [6]. 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) [6].

Results and Discussion
Genetic Variability is an absolute necessity for survival of a species. It facilitates genotypes with ability to adapt according to the conditions prevailing. The extent of genetic variability is considered as an important factor and a must pre-requisite for a successful breeding programme. If a species lacks the opportunity to adapt itself to new condition it will ultimately get vanished. 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. In present study the data was collected and was analyzed for 22 yield associated characters and quality parameters. The results of ANOVA revealed that the mean sum of squares among the genotypes for all the characters were highly significant, which indicated that the genotypes were genetically divergent. This implicated that there is a great scope of selection of promising genotypes from the present gene pool. In present investigation, General Mean, Range, Genotypic (GCV) and Phenotypic (PCV)

coefficients of variability, broad sense heritability (h^2$_b$) and genetic advance as percent of mean (GAM) were estimated and are presented in Table 1.

Days to flowering ranged from 64.67-110.00 days with a mean value of 89.66 days and had moderate PCV and GCV. The genotype Pusa Basmati-1121 was the earliest in days to 50% flowering. Days to maturity ranged from 110.00-125.67 days with a mean value of 118.56 days and had low PCV and GCV. The genotype SKG-2017-43 was earliest in days to maturity. The Plant height ranged from 68.68-155.33cm with mean value of 122.63cm. The PCV and GCV were found moderate. The shortest genotype was SKG-2017-19. The range of number of tillers per plant varied from 4.67–10.00 with a general mean 7.67. High phenotypic and genotypic coefficients of variation were observed. The genotype SKG-2017-64 exhibited maximum number of tillers, while genotype Pusa basmati 1121 had minimum number of tillers. The panicle length varied from 24.67-64.23 cm with a mean of 39.67cm. High PVC and GCV was recorded for panicle length. The longest panicle was observed in the genotype SKG-2017-54, shortest panicle was found in the genotype SKG-2017-12. Range of flag leaf length was observed from 31.00-52.10cm with general mean 41.73cm and had moderate PCV and GCV. Range of flag leaf width was observed from 1.20-9.47cm with general mean 2.00cm. Moderate PCV but low GCV was estimated for this trait. The range of number of grains per panicle was found to be 111.00-294.67 with a mean value of 171.73. High PCV and GCV were observed and the genotype SKG-2017-51 exhibited maximum number of grains per panicle. The grain weight per panicle ranged from 2.20-8.53g and the general means was found to be 4.08g, with high PCV and GCV. The genotype SKG-2017-02 recorded maximum grain weight per panicle. Range of grain weight per plant varied from 6.44-19.27g with the mean value of 11.93g. High values of PCV and GCV were recorded for grain weight per plant. The genotype SKG-2017-19 reflected maximum grain weight per plant followed by SKG-2017-64, SKG-2017-40, SKG-2017-06 and SKG-2017-17. The range of 100 grain weight was 1.67-3.50g with a mean value of 2.64g with marginally high PCV and GCV. The genotype SKG-2017-05 had highest 100 grain weight. 100 kernel weight ranged from 1.23-2.57g and the mean value was 1.91g with marginally high PCV and GCV. The genotype SKG-2017-16 attained maximum 100 kernel weight. Hulling (%) ranged from 68.55-84.27% and the mean value was 72.62% with low PCV and GCV. The genotype SKG-2017-19 exhibited maximum hulling (%).

Value of kernel length before cooking ranged between 4.80-9.50 mm with a mean value of 7.61 mm with moderate PCV and GCV. The genotype SKG-2017-16 showed maximum kernel length before cooking and genotype SKG-2017-55 showed minimum kernel length before cooking. Range of kernel width before cooking was found between 1.50-2.50mm with general mean of 1.96mm. Moderate PCV & GCV was found and the genotype SKG-2017-54 reflected maximum kernel width before cooking while genotype SKG-2017-26 showed minimum kernel width before cooking. Range of kernel length after cooking was found between 7.00-13.00mm with general mean of 9.81mm with moderate PCV and GCV. The genotype SKG-2017-46 attained maximum kernel length after cooking, while genotype SKG-2017-51 had minimum kernel length after cooking. Range of kernel width after cooking was found between 2.10-4.63mm with general mean of 2.59mm and marginally high PCV and GCV. The genotype SKG-2017-46 attained maximum kernel width after cooking

while genotype SKG-2017-26 attained minimum kernel width after cooking. Range of L:B Ratio was found between 2.28-4.89 with General mean of 3.93. It showed moderate PCV and GCV. The genotype SKG-2017-02 showed maximum L:B Ratio and genotype SKG-2017-55 reflected minimum L:B Ratio. Range of kernel elongation ratio was found between 1.11-1.63 with general mean of 1.29 and moderate PCV and GCV. The genotype SKG-2017-64 attained maximum kernel elongation ratio and genotype SKG-2017-02 showed minimum kernel elongation ratio. Range of breath increase ratio after cooking was found between 1.09-2.32 with general mean of 1.33 and marginally high PCV and moderate GCV. The genotype SKG-2017-46 had maximum breath increase ratio after cooking and genotype SKG-2017-51 attained minimum breath increase ratio after cooking. Range of kernel weight after cooking was found between 3.40-6.30g with General mean of 4.88g and moderate PCV and GCV. The genotype SKG-2017-46 attained maximum kernel weight after cooking, while genotype Pusa basmati 1121 recorded minimum kernel weight after cooking. Range of water absorption by 10g kernel was found between 6.97-24.70ml with general mean of 16.19ml and High PCV and GCV estimates.

The variability among genotypes indicates ample scope for selection for different quantitative characters for rice improvement. Earlier workers also observed significant variability for yield and its components in rice. The magnitude of phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters which may be due to higher degree of interaction of genotypes with the environment. These findings are in accordance with the earlier reports by Singh et al. (2011) [14], Tiwari et al. (2011) [18], Paul et al. (2011) [12], Kumar et al. (2013) [9] and Srivastava et al. (2017) [17].

Heritability along with genetic advance becomes more useful tool for the prediction of the method of improvement to be applied, rather than heritability alone. As per results heritability in broad sense was ranging from high to moderate, whereas genetic advance as a percent of mean was ranging from high to low, which signified the ineffective of simple selection measures for the improvement of genotypes. Use of inter- and intra-population improvement methods will be more beneficial. suggested that heritability and genetic advance when calculated together would prove more useful in predicting the resultant effect of selection on phenotypic expression Based in this consideration as reported by Johnson et al. (1995) [6], high heritability coupled with high genetic advance as percentage of mean was registered for plant height, number of tillers per plant, panicle length, flag leaf length, number of grains per panicle, grain weight per panicle, grain weight per plant, 100 grain weight, 100 kernel weight, kernel length before cooking, kernel length after cooking, kernel width after cooking, L:B Ratio, kernel elongation ratio, breath increase ratio, kernel weight after cooking and water absorption by kernel, suggesting preponderance of additive gene action in the expression of these characters. Therefore, selection may be effective through these characters. Whereas days to maturity and hulling %, recorded high heritability but low genetic advance as percent of mean which revealed the non-additive gene action in the expression of these characters, hence in this case selection may not be effective. These findings were in agreement with the findings of earlier researcher Akinwale et al. (2011) [1], Kumar et al. (2011) [10], Krishnamurthy and Kumar (2012) [7], Kumar and Verma (2015) [8], Sravan et al. (2016) [16], Devi et al. 2017 [4] and Tripathi et al. (2018) [19].

Table 1: Mean, Range, Phenotypic (PCV) and Genotypic (GCV) Coefficients of Variation, heritability (h^2),Genetic advance (GA) and Genetic advance as percent of mean (GAM) for yield and its components in basmati rice

Character	GM	Range	PCV	GCV	h^2	GA	GAM
Days to 50% flowering	89.66	64.67-110.0	12.08	10.37	73.70	16.44	18.34
Days to Maturity	118.56	110.00-125.67	4.38	4.19	91.34	9.78	8.25
Plant height (cm)	122.63	68.68-155.33	17.47	14.91	72.81	32.14	26.21
Number of tillers per plant	7.67	4.67-10.00	21.38	21.25	98.76	3.34	43.51
Panicle length (cm)	39.67	24.67-64.23	24.76	24.67	99.34	20.09	50.66
Flag leaf length (cm)	41.73	31.00-52.10	11.99	11.67	94.85	9.78	23.42
Flag leaf with (cm)	2.00	1.20-9.47	12.24	6.39	27.53	0.35	17.50
Number of grains per panicle	171.73	111.00-294.67	32.89	32.63	98.38	114.49	66.67
Grain weight per panicle (g)	4.08	2.20-8.53	35.78	35.66	99.32	2.98	73.20
Grain weight per plant (g)	11.93	6.44-19.27	29.36	29.32	99.76	7.19	60.33
100 grain weight (g)	2.64	1.67-3.50	20.50	20.14	96.58	1.08	40.78
100 kernel weight (g)	1.91	1.23-2.57	20.48	19.98	95.18	0.77	40.16
Hulling (%)	72.62	68.55-84.27	5.34	4.34	65.95	5.27	7.26
Kernel length before cooking (mm)	7.61	4.80-9.50	16.34	16.29	99.38	2.55	33.46
Kernel breadth before cooking (mm)	1.96	1.50-2.50	10.06	9.39	87.10	0.35	18.04
Kernel length after cooking (mm)	9.81	7.00-13.00	16.70	16.69	99.84	3.37	34.35
Kernel breadth after cooking (mm)	2.59	2.10-4.63	21.06	20.93	98.77	1.11	42.84
L.B. ratio	3.93	2.28-4.89	18.38	17.83	94.08	1.40	35.63
Kernel elongation rations	1.29	1.11-1.63	11.64	11.57	98.77	0.31	23.68
Breath increase ratio after cooking	1.33	1.09-2.32	21.59	19.36	80.40	0.47	35.77
100 kernel weight after cooking (g)	4.88	3.40-6.30	12.13	11.97	97.23	1.19	24.31
Water absorb by 10 gm kernel (ml)	16.19	6.97-24.70	31.38	30.31	93.30	9.76	60.30

Conclusion

The present study revealed that plant height, number of tillers per plant, panicle length, flag leaf length, number of grains per panicle, grain weight per panicle, grain weight per plant, 100 grain weight, 100 kernel weight, kernel length before cooking, kernel length after cooking, kernel width after cooking, L:B Ratio, kernel elongation ratio, breath increase ratio, kernel weight after cooking and water absorption by kernel exhibited high heritability coupled with high genetic advance as percentage of mean, indicating preponderance of

additive gene action in the expression of these morphological and quality characters. These characters could be used for selection, which will be helpful in crop improvement. On the basis of study, the desirable donors for each character were identified. The most promising donors for grain yield were SKG-2017-19, SKG-2017-64, SKG-2017-40, SKG-2017-06 and SKG-2017-17. These genotypes can be used for further breeding programme to improve the yield potential of the variety.

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