Madhubala Kurmanchali
Department of Genetics and
Plant Breeding, GBPUAT,
Pantnagar, Uttarakhand, India

Neelam Kurmanchali
Department of Seed Science and
Technology, HNBGU, Srinagar
Garhwal, Uttarakhand, India

Akshit Kukreti
Silviculture & FM Division,
Forest Research Institute,
Dehradun, Uttarakhand, India

Naveen Sihag
Department of Genetics and
Plant Breeding, GBPUAT,
Pantnagar, Uttarakhand, India

Himanshu Chaudhary
Department of Genetics and
Plant Breeding, GBPUAT,
Pantnagar, Uttarakhand, India

Mukesh Kumar Karnwal
Department of Genetics and
Plant Breeding, GBPUAT,
Pantnagar, Uttarakhand, India

Correspondence
Neelam Kurmanchali
Department of Seed Science and
Technology, HNBGU, Srinagar
Garhwal, Uttarakhand, India

Study of genetic variability, heritability and genetic advance for various yield attributing and quality traits in basmati rice (*Oryza sativa* L.)

Madhubala Kurmanchali, Neelam Kurmanchali, Akshit Kukreti, Naveen Sihag, Himanshu Chaudhary and Mukesh Kumar Karnwal

Abstract
Twenty four genotypes of rice were studied for genetic variability for seventeen economically important characters during *kharif* 2016 and *kharif* 2017 in Norman E. Borlaug crop research centren at Govind Ballabh Pant University of Agriculture and Technology, Pantnagar. The values of mean square were found significant for all the characters. Estimates of PCV were higher than the GCV and ECV values for all the characters, suggesting that these characters were relatively much influenced by the environment. The broad sense heritability estimates were high for grain breadth (99.89) followed by l/b ratio (99.65), grain length (99.11), gel consistency (97.95) and 1000 grain weight (95.64) whereas, gel consistency (28.51), plant height (18.97) and days to 50% flowering (16.11) revealed high genetic advance. The presence of high heritability and genetic advance in many of the traits indicates the presence of additive gene action, suggesting that these traits can be improved through direct selection. So, the overall result indicates the presence of enough variability in all the genotypes for development of improved rice varieties and the studied traits can be used for selection.

Keywords: genetic variability, heritability, genetic advance, yield, quality, basmati rice

1. Introduction

Rice (*Oryza sativa*) is a staple food for 2.5 billion people mainly in Asian and African countries. Asia is a major continent accounts for over 90% of the world's production of rice. In India rice is a paramount cereal and staple food crop which occupies an area of 43.97 million ha which is the largest in the world, with an annual production of around 106.3 million tones second largest in the world after China. Rice plays a pivotal role in food security of India because it contributes 46% of the total cereal production and 43% of total food grain production and feed more than 70% population of the country. Among all the Asian countries, India is gifted with a great diversity of rice germplasm in its vast provincial land areas accounting for about 20% of all world rice production. Among cultivars of aromatic rice, basmati rice from Indian sub-continent assured a premium status because of its distinct grain characteristics. Basmati rice is the exclusive one among other aromatic long grain rice varieties. India produces about 70% of the world's total basmati production and approximately two third of the total production is exported to other countries. It is being cultivated mainly in the foothills of the Himalayas, Uttar Pradesh, Punjab and Haryana. Basmati rice grain quality has a direct impact on consumer preference which leads to sales and consumption of the basmati rice product. According to the researches main rice quality parameters are grain dimension (Rabiei *et al.*, 2004) [13], aroma (Kovach *et al.*, 2009) [10], amylose content (Ward *et al.*, 2006) [24], gelatinization temperature (Cuevas *et al.*, 2010) [4], gel consistency and cooked rice texture (Meullenet *et al*., 2000) [11]. Rice aroma is a trait which is predominantly associated with special rice (Singh *et al.*, 2000) [19]. Rice quality plays a dominant role in both domestic and global markets (Unnevehr *et al.,* 1992) [23]. With increasing demand for aromatic rice in the local and international market, high attention has been laid on the development and improvement of basmati types. In spite of traditional high quality basmati varieties in India, the investigation is continued for the development and expansion of many new basmati and hybrid varieties of rice having high yield with better quality, disease and insect resistance and agronomic characters to meet the farmers and consumer demand. Genetic enhancement is one of the essential tool to improve upon the productivity and quality of

basmati rice. The technology to enhance genetic potential of crop species, hybrid technology has been extensively acclaimed and accepted in various species. High magnitude of variability in a population offers the opportunity for selection in order to evolve a variety having desirable features. The genotypic, phenotypic and environmental coefficients of variations are helpful in understanding and exposing the clear picture of existing variability in the populations. Thus, in a given crop species the knowledge of genetic variability for characters under improvement is important in any plant breeding programme. Heritability with genetic advance is more helpful in anticipating the gain under effective selection. Genetic parameters *viz.;* genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in determining the amount of variability exists in the genotypes (Idris *et al.,* 2012) [6]. In the present study it was assessed with respect to yield and quality traits in order to know the variability present in crosses of basmati rice derived from line × tester mating scheme with respect to yield, yield contributing and quality traits. Line × Tester mating design consists of 'l' lines used as female parent and 't' testers used as male parent, each of the male parents is crossed with each of the female parent, thus, producing l × t full sib progenies. Then the full sib progenies along with the parents are tested in replicated trial adapting suitable design for various quantitative and qualitative traits.

2. Material and Methods
The present investigation was carried out during *kharif* 2016 and *kharif* 2017 in Norman E. Borlaug crop research centreat Govind Ballabh Pant University of Agriculture and Technology, Pantnagar. A total of 36 genotypes including 8 parental lines, 3 testers and their 24 F₁ crosses were used. The lines used were UPR-3801-3-2-1, Lal Basmati, Pant Sugandh Dhan 15, Pant Basmati 1, Basmati 370, UPR-3709-8-1-2, Pant Sugandh Dhan 17 and Pant Basmati 2 whereas, the testers were Pant Sugandh Dhan 25, UPR 3506-7-1-1 and Pant Sugandh Dhan 27. Crosses were generated undertaking line × tester mating scheme. A total of 24 crosses among three testers and eight lines were made. The experimental material consisted of 35 genotypes. The complete set was evaluated with three replications in the Randomized complete Block Design during *kharif* season of 2017 at Norman E. Borlaug Crop research Centre. The observation were recorded on seventeen characters *viz*; days to 50% flowering, plant height (cm), panicle length (cm), no. of effective tillers per plant, no. of grains per panicle, 1000 grain weight (gm), grain yield per plant (gm), hulling recovery (%), milling recovery (%), head rice recovery(%), grain length (mm), grain width (mm), l/b ratio, alkali digestion value, gel consistency (mm), amylose percentage (%) and kernel elongation ratio.

3. Results and Discussion
3.1 Variability Parameters
Significant differences were found among all the genotypes for different traits under study, which revealed presence of adequate variability among the genotypes, so selection would be effective to develop the varieties with desired forms of crop plants [Table 1]. Since the adequate genetic variability serves as a basic requirement for any crop improvement, therefore confirming the sufficient genetic variability for the traits is an essential step. Among quantitative characters the highest value of range was obtained forplant height from 85.83 cm (Lal Basmati × Pant Sugandh Dhan 25) to 127 cm (Pant Sugandh Dhan 15 × Pant Sugandh Dhan 25) with a

general mean of 107.48 cm followed by number of grains per panicle from 72.33 (Pant Sugandh Dhan 15 × Pant Sugandh Dhan 27) to 101 (UPR3709-8-1-2) with mean value of 83.35, whereas among qualitative characters the value of range is highest for gel consistency from 45.66 (UPR3709-8-1-2 × UPR3506 7-1-1) to 94.33 (Pant Basmati 2) and had mean value of 70.49 followed by head rice recovery percentage from 25.93 (UPR3506 7-1-1) to 43.9 (Pant Basmati 1 × Pant Sugandh Dhan 27) with a general mean of 36.88 and milling recovery percentage from 61.17 (UPR3801-3-2-1 × UPR3506 7-1-1) to 75.3 (Pant Sugandh Dhan 15 × UPR3506 7-1-1) with a general mean of 67.23.

Table 1: Analysis of variance for RCBD for 17 characters in basmati rice genotypes

S.N.	Characters	Mean sum of squares		
		Replication	Treatment	Error
	d.f.	2	34	68
1	Days to 50% flowering	477.32	316.44**	44.00
2	Plant height (cm)	574.88	415.04**	51.72
3	Panicle length (cm)	3.43	22.82**	3.19
4	No. of effective tillers/ plant	10.35	71.84**	3.62
5	No. of grains/panicle	11.11	226.17**	9.73
6	1000 grain weight (gm)	0.20	29.11**	0.41
7	Grain yield/plant (gm)	22.11	77.73**	12.08
8	Hulling recovery (%)	0.39	32.62**	2.02
9	Milling recovery (%)	7.70	40.00**	2.40
10	Head rice recovery (%)	1.41	64.51**	2.16
11	Grain length (l) (cm)	0.00	0.87*	0.00
12	Grain breadth (b) (cm)	0.00	0.70*	0.00
13	l/b ratio	0.00	2.32**	0.00
14	Alkali digestion value	0.90	4.35**	0.39
15	Gel consistency (mm)	0.46	590.85**	4.09
16	Amylose percent (%)	0.37	9.60**	0.35
17	Kernel elongation	0.00	0.44*	0.00

** Significance at 1% level of probability,* Significance at 5% level of probability

Genotypic (GCV), phenotypic (PCV) and environmental (ECV) coefficient of variation were calculated for each character and presented in Table 2. The magnitude of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) and environment coefficient of variation (ECV) for all the characters under study. Among agronomical characters the highest estimates of GCV and PCV were reported for number of effective tillers/plant, 1000 grain weight and grain yield/plant and among quality characters for alkali digestion value, grain breadth (B) and L/B ratio whereas characters like panicle length, number of effective tillers/plant had high estimates of ECV denoting the prominent role of environment on the expression of these characters. The range of environment coefficient of variation was observed from 0.01 (for grain breadth) to 4.98 (for alkali digestion value). The difference between genotypic and phenotypic coefficient of variation was less for all characters studied except alkali digestion value, grain yield per plant and days to 50% flowering which was an indication of the more influence of the environment over these three characters. The characters studied in the present study exhibited low, moderate and high values of PCV and GCV. Among the yield characters the high percentage of PCV and GCV was recorded for number of effective tillers per plant (26.26 and 24.38) followed by 1000 grain weight (24.69 and 24.15) and lowest was recorded for no. of grains per panicle (10.85 and 10.19). Among the grain quality characters highest PCV and GCV was recorded for

alkali spreading value (40.79 and 35.81) followed by grain breadth (27.02 and 27.01), while the character hulling recovery percentage (4.56 and 4.16) recorded the lowest PCV and GCV values. Singh *et al.* (2011) [20], Subbaiah *et al.* (2011) [21] and Babu *et al.* (2012) [2] also reported high PCV and GCV for most of the yield attributing traits. The high magnitude of phenotypic variation were composed of high GCV and less of the ECV, indicatesthe presence of high genetic variability with less environmental influence. Therefore, on the basis of phenotype aloneselection can be effective for the improvement of these characters. Similar results for low to moderate values of PCV and GCV were also found by Ananadarao *et al.* (2011) [1].

3.2 Heritability and Genetic advance
In the present investigation heritability in broad sense was calculated for all the characters under study [Table 2]. The highest broad sense heritability belonged to grain breadth (99.89%) while grain yield per plant (64.41%) had the lowest. High heritability was observed for most of the characters except grain yield per plant (64.41), panicle length (67.20) and days to 50% flowering (67.35) which had low values of heritability. The heritability of a character has major impact on the methods chosen for population improvement, hybridization and other aspect of selection may be effective for the character with high heritability (Robinson, 1966) [14].The reliability of the phenotypic value highly depends on the estimates of heritability, therefore high heritability of these trait helps in the effective selection. Similar results for heritability was also reported by Saleem *et al.* (2008) [15], Tiwari *et al.* (2011) [22], and Ghara *et al.* (2014) [5].

Table 2: Summery table depicting phenotypic, genotypic and environment coefficient of variability (GCV and PVC), heritability (h^2_b), genetic advance for different characters in rice.

S. N	Character	Coefficient of variation			Heritability(h^2_b)%	Genetic advance
		PCV	GCV	ECV		
1.	Days to 50% flowering	13.06	10.72	2.34	67.35	16.11
2.	Plant height (cm)	12.23	10.23	2	70.07	18.97
3.	Panicle length (cm)	10.93	8.96	1.97	67.20	4.32
4.	No. of effective tillers/plant	26.26	24.38	1.88	86.24	9.12
5.	No. of grains/panicle	10.85	10.19	0.66	88.11	16.42
6.	Grain yield/plant (gm)	20.59	16.53	4.06	64.41	7.73
7.	1000 grain weight (gm)	24.69	24.15	0.54	95.64	12.75
8.	HR (%)	4.56	4.16	0.4	83.44	6.01
9.	MR (%)	5.74	5.26	0.48	83.89	6.67
10.	HRR (%)	12.98	12.35	0.63	90.54	8.93
11.	Grain length (L) (mm)	8.60	8.56	0.04	99.11	1.10
12.	Grain breadth (B) (mm)	27.02	27.01	0.01	99.89	0.99
13.	L/B ratio	23.65	23.61	0.04	99.65	1.81
14.	ADV	40.79	35.81	4.98	77.06	2.07
15.	Gel consistency (mm)	20.04	19.83	0.21	97.95	28.51
16.	Amylose content (%)	8.27	7.84	0.43	89.76	3.42
17.	KE	21.80	21.15	0.65	94.13	0.76

Notations:
HR- hulling recovery, MR- milling recovery, HRR- head rice recovery, L/B ratio- length/breadth ratio, ADV- alkali digestion value, KE- kernel elongation, PCV- phenotypic coefficient of variation, GCV- genotypic coefficient of variation, ECV- environment coefficient of variation.

The high, moderate and low estimates of genetic advance as percent of mean was recorded for the traits under study. The value of genetic advance as per cent of mean was highest for gel consistency (28.51) followed by plant height (18.97) whereas low for kernel elongation (0.76) followed by grain breadth (0.99) and grain length (1.10) and for rest of the characters it had moderate values. Genetic advance estimates are depicted in Table 2. The genetic advance provides more reliable information about the effectiveness of selection in improving the characters of the new population over the base or original population. Similar results were also reported by Sao (2002) [17] and Iftekharuddaula *et al.* (2001) [7].
As broad sense heritability comprises both additive and epistatic gene effects so it will be reliable only when accompanied by high value of genetic advance. Heritability estimates along with genetic advance is more useful, than heritability alone, in predicting the effectiveness of selection (Johnson *et al.* 1955) [9]. In the present study the characters which showed high heritability associated with high genetic advance were gel consistency, days to 50% flowering, plant height, no. of grains per panicle and 1000 grain weight. The traits that showed high heritability coupled with high genetic advance are under the control of additive gene action (Panse and Suhatme, 1957) [12] and can be improved through simple or progeny selection methods, while the characters which showed high heritability coupled with moderate or low genetic advance can be improved by intermating superior genotypes of segregating population developed from combination breeding (Samadhia, 2005) [16]. In the present study high heritability associated with high genetic advance for yield attributing characters was in accordance with the Jaiswal *et al.* (2007) [8] and Seyoum *et al.* (2012) [18] and for quality characters by Choudhary *et al.* (2004) [3].

Conclusion
The analysis of variance revealed highly significant difference among the genotypes for all the characters under study. From the result, it was concluded that among the yield and grain quality characters grain length, grain breadth, L/B ratio and kernel elongation could be easily inherited to their next generations due to high heritability, whereas the characters *viz*; days to 50% flowering, panicle length and grain yield per plant had low heritability which indicates that these characters are mainly influenced by environmental factors. Characters *viz.;* days to 50% flowering, plant height, grain yield per panicle and gel consistency showed maximum values of heritability and genetic advance, so for these characters direct selection can be adopted, whereas the characters viz;1000

grain weight, gel consistency, head rice recovery and plant height showed high values GCV, PCV, heritability and genetic advance. Thus one should select these characters for direct selection.

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