Plant Archives Volume 20 No. 2, 2020 pp. 5854-5858 **e-ISSN:2581-6063 (online), ISSN:0972-5210**

COEFFICIENT OF VARIATION, HERITABILITY AND CORRELATION COEFFICIENT IN BASMATI RICE HYBRIDS (*ORYZA SATIVA* L.) FOR YIELD AND QUALITY TRAITS

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Abstract

In the present investigation, variability, heritability and genetic advance in per cent of mean were estimated in F_1s obtained by crossing nine basmati rice varieties following half-diallel mating design. The results indicated that, F_1s possessed high heritability for all traits. But, genetic advance varied from low to high for different traits. High variability accompanied with high genetic advance was observed for most of the yield and quality traits including plant height, numbers of panicles per plant, numbers of grains per panicle, 100-grain weight, yield per plant, kernel length, kernel length/breadth ratio, kernel length after cooking, kernel breadth after cooking, elongation ratio, elongation index, alkali spreading value, amylose content and aroma. The difference between estimates of coefficient of variation (phenotypic or genotypic) was less in magnitude, indicating less influence of environment in inheritance of those traits. Yield per plant showed high positive correlation with days to fifty per cent flowering, panicle length, number of panicles per plant, number of grains per plant and 100-grain weight.

Key words: Basmati rice, coefficient of variation (phenotypic or genotypic), heritability, genetic advance and correlation

Introduction

Basmati is aromatic rice indigenous to North-western foot-hills of Himalayas (Northern India). Basmati rice holds strong domestic and international demand by virtue of its slender long kernel, pleasant aroma, cooked rice texture. Among the different types of rice traded in international market aromatic rice (Basmati from India and Pakistan; and Jasmine from Thailand) accounts for 4% of the total, but fetch far more premium price than non-aromatic rice. In view of importance of crop, there is need to develop more promising basmati varieties with increased yield and quality traits on par with minimum acceptable standards for basmati varieties.

In plant breeding program, a thorough insight of heritability and genetic advance of traits can facilitate in estimating genetic gain under selection and in predicting response of traits to artificial or natural selection. On the other hand coefficient of genetic and phenotypic variation facilitates in estimating the variability exist in the experimental material. A significant genetic correlation among traits indicates that the traits are co-inherited, thus by studying correlation among traits can facilitates in establishing inter-relationship among traits. Considering the aforementioned information a study was undertaken to estimate variability, heritability and correlation in 36 F_1s for 18 traits.

Materials and Methods

The field trial for the present study was conducted at Agricultural Research Farm, Institute of Agricultural Sciences, BHU, Varanasi, Uttar Pradesh under irrigated conditions of *Kharif* 2016 and 2017.

Experimental material for the present study was constituted of 36 crosses which were obtained by crossing nine basmati rice genotypes: Type-3, Basmati-370, Taraori Basmati, Ranbir Basmati, Pusa Basmati-1, CSR-30, Pusa Basmati-1121, HUBR10-9 and Pusa Basmati-1509 in half-diallel mating design in *Kharif* 2016. The F_1s were planted in 3 replications in randomized block design in *Kharif* 2017. Data was collected from randomly tagged 10 plants from each line from all the three replications on 18 traits: days to 50% flowering, days to maturity, plant height, main panicle length, number of panicles per plant, total number of grains per panicle, 100-grain weight, yield per plant, kernel length, kernel breadth, kernel length/

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breadth ratio, kernel length after cooking, elongation ratio, kernel breadth after cooking, elongation index, aroma, alkali spreading value and amylose content. Reading of data was carried out as specified in Standard Evaluation System of Rice, *IRRI*, (2013).

Analysis of variance was calculated according to Panse and Sukhatme (1967). Heritability in broad sense (h_2b) was calculated and classified into low (below 30%), medium (30- 60%) and high (above 60%) according to Johnson *et al*., (1955). Genetic advance in percent over mean (at 5%) were computed and categorized into low (0-10%), moderate (10-20%) and high (≥ 20%) as given by Johnson *et al*., (1955). Estimates of PCV and GCV was calculated following Burton and De Vane (1953) and Singh and Chaudhury (1985) and categorized into low (<10%), moderate (10-20%) and high (>20%) according to Sivasubramanian and Madhavamenon (1973).

Results and Discussion

ANOVA and mean values of F_1s

Significant ANOVA results were recorded in 36 F_1s for all the traits table 1. This suggested that there is an inherent genetic difference among the F_1s. Mean values of all eight yield traits of F_1s studied in the experiment were high in comparison to their parents in desirable direction. Similar findings have been observed in work of Bisne *et al*., (2009), Paikomba *et al*., (2014), Tripathi *et al*., (2018) and Singh and Verma (2018). When mean values of quality traits of F_1s and parents were compared, for three traits *viz*., kernel length, kernel breadth, kernel length/breadth ratio F_1s performance was higher than parents table 2. Other traits *viz*., kernel length after cooking, kernel breadth after cooking, elongation ratio and elongation index mean value of F_1s recorded lesser value than the parents. For traits *viz*., amylose content and alkali spreading value intermediate values are required *e.g.* for amylose content (20 to 25%) and for alkali spreading value (4 to 7). So, for these two traits performance of F_1s were estimated on the basis of intermediate values. For aroma, mean value of all F_1s recorded moderate range.

Coefficient of variation

Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) in general, although the difference between PCV and GCV was less which clearly indicates less influence of environmental effect in expression of phenotypes table 2. Genotypic and phenotypic coefficient of variation was low in traits *viz*., days to fifty per cent flowering, days to maturity, panicle length, kernel length, kernel breadth, kernel length/breadth ratio and amylose content. Moderate coefficient of variation was recorded for plant height, 100-grain weight, kernel length after cooking, kernel breadth after cooking, elongation ratio and elongation index. Whereas, high variability was observed for number of panicles per plant, number of grains per panicle, yield per plant, alkali spreading value and aroma. Aditya and Bhartiya (2013) and Tripathi *et al*., (2018) observed high variation for yield per plant, nevertheless moderate variation has been also reported by Adilaksmi *et al*., (2012) and Singh and Verma (2018). Low coefficient of variation for days to fifty per cent flowering, days to maturity, kernel length, kernel breadth and 100-grain weight has been reported by Tripathi *et al*., (2018), Singh and Verma (2018); Paikomba *et al*., (2014); Adilakshmi *et al*., (2012); and Aditya and Bhartiya (2013). However, these workers have reported low coefficient of variation for 100-grain weight, in present finding moderate range of variation has been observed for 100-grain weight.

Heritability in broad sense

High heritability was recorded for all the 18 traits. Genetic advance estimates varied from low, moderate to high table 2. High heritability following high genetic advance indicates role of additive gene action inheritance

Table 1: Analysis of variance of 36 crosses of basmati rice F_1s.

Traits	Source of variation		
	Replications (df=2)	**Hybrids (df=35)**	**Error (df=70)**
Days to fifty per cent flowering	0.29	43.14***	1.06
Days to maturity	0.40	60.91***	1.25
Plant height	0.14	1028.41***	2.54
Panicle length	0.10	13.17***	0.76
Numbers of panicle per plant	5.35	22.43***	0.83
Numbers of grain per panicle	447.98	1901.07***	84.28
100-grain weight	0.00	0.24***	0.00
Yield per plant	26.29	354.57***	2.95
Kernel length	0.05	0.59***	0.02
Kernel breadth	0.00	0.01***	0.00
Kernel length/breadth ratio	0.03	0.23***	0.01
Elongation ratio	0.01	0.15***	0.00
Kernel length after cooking	0.36	12.71***	0.19
Kernel breadth after cooking	0.02	0.22***	0.01
Elongation index	0.01	0.14***	0.00
Alkali spreading value	0.01	7.18***	0.04
Aroma	0.03	0.47***	0.03
Amylose content	0.37	7.97***	0.20

of such traits. In the present experiment, high heritability with high genetic advance was recorded in plant height, numbers of panicles per plant, numbers of grains per panicle, 100-grain weight, yield per plant, kernel length after cooking, kernel breadth after cooking, elongation ratio, elongation index, alkali spreading value, amylose content and aroma. Panicle length, kernel length and kernel length/breadth ratio showed high heritability with moderate genetic advance. Bisne *et al*., (2009) reported high genetic advance and heritability for number of grains

Table 2: Variability, heritability and genetic advance in 36 F_1s of basmati rice.

Traits	Mean Values		Range		Coefficient of variation		Herit-ability	Genetic Advance
	Parents	F_1s	Lowest value	Highest value	GCV (%)	PCV (%)	Broad sense (%)	in % of mean
Days to fifty per cent flowering	104.78	99.07	91	109	3.78	3.92	92.98	7.51
Days to maturity	138.37	133.40	126	146	3.34	3.45	94.11	6.68
Plant height	131.61	126.59	88.66	159.98	14.61	14.66	99.26	29.98
Panicle length	27.73	30.42	25.22	33.87	6.69	7.27	84.53	12.66
Number of panicles per plant	10.35	12.49	7.67	20.4	21.48	22.68	89.69	41.91
Number of grains per panicle	87.17	103.40	59.4	156.35	23.80	25.40	87.78	45.94
100-Grain Weight	2.49	2.61	2.17	3.16	10.66	10.94	94.98	21.40
Yield per plant	23.56	31.76	18.70	54.96	34.08	34.51	97.55	69.35
Kernel length	7.27	7.58	6.79	8.42	5.76	6.02	91.62	11.36
Kernel breadth	1.83	1.73	1.6	1.87	3.73	4.21	78.98	6.84
Kernel length/breadth ratio	3.98	4.40	3.78	4.93	6.20	6.61	87.89	11.97
Kernel length after cooking	14.13	13.38	10.56	17.64	15.28	15.62	95.71	30.79
Elongation ratio	1.93	1.77	1.4	2.17	12.70	12.95	96.25	25.67
Kernel breadth after cooking	2.32	2.54	2.06	2.85	10.53	10.96	92.31	20.84
Elongationindex	1.53	1.22	0.87	1.59	17.51	18.02	94.36	35.03
Alkali spreading value	5.64	4.23	1.85	6.78	36.49	36.81	98.26	74.50
Aroma	Highly aromatic	Moderately aromatic	Non-aromatic	Highly aromatic	24.57	26.81	83.99	46.39
Amylose content (%)	22.79	24.89	21.86	27.44	6.47	6.71	92.87	12.84

Table 3: Genotypic and phenotypic correlation between yield traits in 36 F_1s of basmati rice.

Traits		Days to fifty per cent flo-wering	Days to matu-rity	Plant height	Panicle length	Number of panicles per plant	Number of grains per panicle	100-Grain Weight
Days to fifty per cent flowering								
Days to maturity	r_g	0.760^{**}						
	r_p	0.741^{**}						
Plant height	r_g	0.056^{NS}	0.034^{NS}					
	r_p	0.053^{NS}	0.032^{NS}					
Panicle length	r_g	0.149^{NS}	0.013^{NS}	-0.134^{NS}				
	r_p	0.101^{NS}	0.003^{NS}	-0.124^{NS}				
Number of panicles per plant	r_g	0.408^{**}	0.206^{*}	-0.037^{NS}	0.178^{NS}			
	r_p	0.389^{**}	0.202^{*}	-0.033^{NS}	0.156^{NS}			
Number of grains per panicle	r_g	0.398^{**}	0.111^{NS}	-0.051^{NS}	0.748^{**}	0.380^{**}		
	r_p	0.361^{**}	0.107^{NS}	-0.045^{NS}	0.642^{**}	0.322^{**}		
100-Grain Weight	r_g	0.076^{NS}	-0.014^{NS}	0.124^{NS}	-0.118^{NS}	0.145^{NS}	-0.127^{NS}	
	r_p	0.081^{NS}	-0.016^{NS}	0.119^{NS}	-0.100^{NS}	0.121^{NS}	-0.107^{NS}	
Yield per plant	r_g	0.372^{**}	0.163^{NS}	-0.091^{NS}	0.556^{**}	0.674^{**}	0.738^{**}	0.225^{*}
	r_p	0.356^{**}	0.160^{NS}	-0.088^{NS}	0.506^{**}	0.625^{**}	0.697^{**}	0.219^{*}

r_g= genotypic correlation; r_p= phenotypic correlation; ** significant 1% level of significance; NS= non-significant.

Table 4: Genotypic and phenotypic correlation between quality traits in 36 F_1s of basmati rice.

Traits		Kernel length	Kernel breadth	Kernel length/ breadth rtaio	Kernel length after cooking	Elongation ratio	Kernel breadth after cooking	Elongation index	Alkali spreading value	Aroma
Kernel length										
Kernel breadth	r_g	0.089^{NS}								
	r_p	0.070^{NS}								
Kernel length/breadth ratio	r_g	0.821^{**}	-0.496^{**}							
	r_p	0.813^{**}	-0.477^{**}							
Kernel length after cooking	r_g	0.521^{**}	0.215^{*}	0.307^{**}						
	r_p	0.525^{**}	0.170^{NS}	0.321^{**}						
Elongation ratio	r_g	0.179^{NS}	0.235^{*}	-0.008^{NS}	0.931^{**}					
	r_p	0.168^{NS}	0.189^{*}	-0.002^{NS}	0.922^{**}					
Kernel breadth after cooking	r_g	-0.289^{**}	0.071^{NS}	-0.290^{**}	-0.055^{NS}	0.049^{NS}				
	r_p	-0.253^{**}	0.072^{NS}	-0.257^{**}	-0.047^{NS}	0.042^{NS}				
Elongation index	r_g	0.307^{**}	0.305^{**}	0.070^{NS}	0.766^{**}	0.763^{**}	-0.579^{**}			
	r_p	0.278^{**}	0.263^{**}	0.049^{NS}	0.745^{**}	0.751^{**}	-0.590^{**}			
Alkali spreading value	r_g	0.600^{**}	0.113^{NS}	0.454^{**}	0.477^{**}	0.314^{**}	-0.140^{NS}	0.323^{**}		
	r_p	0.564^{**}	0.101^{NS}	0.416^{**}	0.462^{**}	0.307^{**}	-0.128^{NS}	0.308^{**}		
Aroma	r_g	-0.293^{**}	-0.231^{*}	-0.104^{NS}	-0.248^{**}	-0.178^{NS}	0.323^{**}	-0.374^{**}	-0.405^{**}	
	r_p	-0.280^{**}	-0.199^{*}	-0.105^{NS}	-0.229^{*}	-0.157^{NS}	0.267^{**}	-0.321^{**}	-0.369^{**}	
Amylose content (%)	r_g	0.256^{**}	0.215^{*}	0.105^{NS}	0.148^{NS}	0.087^{NS}	-0.301^{**}	0.274^{**}	0.173^{NS}	-0.567^{**}
	r_p	0.233^{*}	0.195^{*}	0.095^{NS}	0.140^{NS}	0.080^{NS}	-0.269^{**}	0.250^{**}	0.157^{NS}	-0.497^{**}

r_g= genotypic correlation; r_p= phenotypic correlation; ** significant 1% level of significance; NS= non-significant.

per plant and yield per plant. Adilakshmi *et al*., (2012) have reported high heritability with high genetic advance for yield per plant, alkali spreading value, elongation ratio and amylose content. However, Singh and Verma have reported high heritability with moderate genetic advance for kernel length and 100-grain weight. Similarly, high heritability with low genetic advance indicates role non-additive gene action. Traits *viz*., days to fifty per cent flowering, days to maturity and kernel breadth although showed high heritability but genetic advance estimates were low for these traits, thus indicating role of non-additive gene action in inheritance of these traits. Low genetic advance for days to flowering and plant height has been reported by Singh and Verma (2018) and Tripathi *et al*., (2018).

Correlation coefficient

The study of correlation coefficient assists in understanding the association among yield and its attributing traits. Yield of a crop depends on combined effect of different yield attributing traits. In the present findings, genotypic and phenotypic correlation showed a highly positive correlation of yield per plant trait with days to fifty per cent flowering, panicle length, number of panicles per plant, number of grains per plant and 100-grain weight, thus indicating that these traits were positively contributing to the increase in yield of basmati rice crop table 3. Aditya and Bhartiya (2013), Prakash *et al*., (2018), Hossain *et al*., (2018), Mukesh *et al*., (2018) have reported significant high correlation of yield per plant with number of grains per panicle, days to maturity, plant height and days to fifty per cent flowering and reported non-significant correlation with 100-grian weight. However, in present finding yield per plant was positively correlated with 100-grain weight. Among quality traits, percentage of amylose content in rice kernel determines the texture of cooked rice. Amylose content was observed to be positively correlated with kernel length, kernel breadth and elongation index table 4. While, negative correlation of amylose content was observed with traits *viz*., kernel breadth after cooking and aroma. Alkali spreading value showed non-significant relation with amylose content.

Conclusion

Comprehensive study of variability, heritability, genetic advance and correlation among 18 traits of 36 F_1s, indicated presence of high variability, heritability and genetic advance for most of the yield attributing and quality traits. These traits can be improved through selection in segregating generations. However, for few traits, low genetic advance and variability have also been recorded indicating non-additive gene action which can be exploited by heterosis breeding. Yield per plant was found to be positively correlated with days to fifty per cent flowering, panicle length, number of panicles per plant, number of grains per plant and 100-grain weight. Thus in future breeding program selection of these yield attributing can be implemented to increase yield per plant.

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