Assessment of genetic variability in basmati and non-basmati cultivars of *Oryza sativa*

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Abstract: The experiment was conducted to reveal genetic variability and to study the parameter analysis in 24 aromatic and non-aromatic rice genotypes. Highly significant variations were determined and the phenotypic variance was relatively greater than genotypic variance for most of the traits, like plant height, number of spikelets per panicle and number of grains per panicle. Higher magnitude of phenotypic variance showed more effect of environment on expression of these traits. A few traits such as number of tillers per plant, spikelet fertility percentage, filled grains weight per panicle, 1000-grain weight and yield per plant indicated least differences between PV and GV, this phenomenon gave the information of gene control for expressivity of these traits. Highest GCV was observed for number of tillers per plant, then yield per plant, number of grains per panicle and filled grains weight per panicle, while spikelet fertility percentage showed lowest value of GCV. Sufficient amount of variability was observed for most of the traits. Filled grain weight per panicle exhibited high heritability but lowest genetic advance showing non-additive gene control. Moreover, number of grains per panicle, plant height and number of spikelets per panicle revealed high magnitudes of GCV %, PCV %, heritability % and genetic advance. These results suggested that the choice for better improvement considering these traits might be beneficial.
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Introduction

Cultivated rice (*Oryza sativa* L.) is a diploid species having 24 chromosomes (2n=24) and morphologically only identified as an annual grass but also have its recognition as cereal crop of paramount importance. Because, rice has wide range of geographical distribution in tropical and sub-tropical regions of the world, therefore its cultivation goes from 50° north to 35° south including low-lying basins to mountains top greater than 2000m (Rangare *et al.* 2012). Pakistan is the 11th largest rice producer and 5th largest rice exporting country (Masood *et al*., 2015ab; Rabbani *et al*. 2010) and produces sufficient quantity to fulfill both local demand and for export earnings and its production during 2011-12 was 6.16 million tons (27.7 % more than last year), covering area of 2.57 million hectares (8.7 % more than last year) and this significant increase in local production was due to increase in cultivation area and yield per hectare showed improved growth of 17.5 % as compared to -14.6 % last year (Economic Survey of Pakistan, 2011-12). In Pakistani economy, rice offers share of 4.9 % value added in agriculture and 1.0 % in gross domestic product (GDP), thus called as "Golden grain of Pakistan" (Shah *et al*. 1999). In Pakistan, it is also 2nd most important staple food after wheat and adds more than two million tones to national food necessity which is about 23% of the total foreign exchange

earnings (Zafar *et al*. 2004). Moreover, for people of the rural area, it is not only source of income but also predicts bright chances of employment (Jamal *et al*. 2009). Genetic parameters like genetic coefficients of variation, heritability and genetic advance (Sing and Chawdhury, 1985) can be exploited to partition the available amount of variation in a population into heritable and non-heritable components. However, the proposed study was carried out to evaluate the variability among the diverse cultivars in order to select best high yielding traits for future breeding programs.

Materials and methods

Twenty four genotypes of rice were evaluated in a field trial in the research area of the Department of Plant breeding and Genetics, University of Agriculture, Faisalabad, Pakistan during the kharif season 2011-12. The nursery was sown on 19-05-2011 by conventional dry method and transplanted into the field on 27-06-2011. Seed rate was 1-1.5 kg / Marla & 1-2 kg/ Marla for fine and coarse grain genotypes, respectively. Nearly 40 days old nursery was transplanted into the puddled field with plant to plant and row to row distance of 9 cm and laid out in randomized complete block design with three replications for each genotype. Five plants from each replication were randomly selected and data was

recorded on (i) number of tillers per plant, (ii) plant height, (iii) number of spikelets per panicle, (iv) number of grains per panicle, (v) filled grains weight per panicle, (vii) spikelet fertility percentage (vii) 1000-grain weight (viii) grain yield per plant. Steel *et al*., (1997) technique was adopted for variance and covariance analysis. Gneotypic and phenotypic variance, heritability, genetic advance and coefficients of variability were computed by the method presented by Sing and Chawdhury (1985).

Results and discussion
Analysis of variance & covariance
　　The conclusions found after the application of analysis of genotypic and phenotypic variances on various morphological traits are provided in Table 2. The data reports that all the basmati and non-basmati genotypes differ significantly from each other. The treatments sums of squares for 24 genotypes were

highly significant (p≤ 0.01). This means that all the varieties carried considerable amount of variability. This phenomenon offers, to utilize these genotypes in future breeding programs.

Analysis of variances and coefficients of variation
　　The phenotypic coefficients of variability for all traits had greater but close values to genotypic coefficients of variability (Table 3), eventually showing less influence of environment. This statement is supported by Sankar *et al*. (2006), Pandey *et al*. (2012), Rangare *et al*. (2012) and Sohrabi *et al*. (2012). However, close values of phenotypic and phenotypic variances (Table 1) were obtained for majority of the parameters, representing the stable nature of these traits. Similar, conclusions were forwarded by Fukrei *et al*. (2011). The results obtained from all these genotypes and various agronomic traits are discussed as under:

Table 1. Average, range, GV (Genotypic variance), PV (Phenotypic variance) & EV (Error variance) for 24 basmati and non-basmati cultivars of rice

Trait	Average	Range	GV	PV	EV	
No. of tillers/plant	21.84	9.60-33.60	49.06	49.29	0.23	
Plant height	135.87	97.60-175.60	636.73	638.39	1.66	
No. of spikelets/panicle	149.88	99.93-202.67	827.86	832.15	4.28	
No. of grains/panicle	117.87	81.93-163.00	609.10	613.80	4.69	
Spikelet fertility (%)	78.69	64.03-87.13	30.08	31.88	1.79	
Filled grains wt./panicle	2.64	1.57-3.53	0.25	0.26	0.01	
1000-grain weight	25.24	18.53-31.34	12.96	12.99	0.02	
Grain Yield per plant	26.25	16.01-39.71	42.29	42.80	0.51	

GV= Genotypic variance; PV= Phenotypic variance; EV= Error variance

Table 2. Analysis of variance for yield and yield related attributes for 24 basmati and non-basmati cultivars of rice

S.O.V	d.f	Mean sum of squares							
		No. Of tillers/ Plant	Plant height panicle	No. of spikelets/ panicle	No. of grains/ (%)	Spikelet Fertility panicle	Filled grains wt./ wt.	1000-grain plant	Grain yield/
Rep.	2	0.007	0.86	12.3 *	19.0*	9.06*	0.0156	0.1614*	0.57
Variety	23	147.88**	1915.17**	2496.5**	1841.4**	95.65**	0.8084**	38.97**	128.42**
Error	46	0.731	5.20	13.4	14.7	5.63	0.0326	0.0652	1.61
SE	0.023	0.006	0.006	0.007	0.029	0.318	0.045	0.025	

Rep. = Replication, SE = Standard error, ** = Significant at 5% probability level

Analysis of Genetic advance and Heritability
　　Genetic advance and heritability percentage (broad sense) are mentioned in Table 3. It is said that high heritability alone is not sufficient to make proper improvement in yield contributing parameters, because high heritability along with high genetic advance reveals the effect of additive gene; therefore selection would be beneficial for these types of characters. A suggestion was made by Johnson *et al.*

(1955) that genetic advance and heritability (percentage) when computed together would prove more fruitful in forecasting the resultant influence on expression of the phenotype. Furthermore, heritability (broad sense) was more than 90 % for all the traits studied in this experiment. Sankar *et al*. (2006) also noticed more than 90% heritability for all the traits under study. Ahmad *et al*. (2012); Ali *et al*. (2012); Ali *et al*. (2013ab); Ali *et al*. (2014abc); Imran *et al*.

(2014) reported that High heritability estimates for morphological traits shows that selection could be more effective for genetic improvement. High heritability illustrates the genetic improvement of these characters through selection. When high value of heritability couples with high amount of genetic advance, then it shows high additive gene control. This situation shows that these traits are best to select for breeding programs (Ali and Ahsan 2015; Ahsan *et al.* 2011 and Ahsan *et al.,* 2013).

Table 3. Variability parameters of yield and yield components for 24 basmati and non-basmati cultivars of rice

Trait	GCV%	PCV%	ECV%	Heritability%	GA%
No. of tillers/plant	32.06	32.14	2.21	99.5	9.78
Plant height	18.57	18.59	0.94	99.7	35.28
No. of spikelets/panicle	19.19	19.24	1.38	99.5	40.18
No. of grains/panicle	20.93	21.02	1.83	99.2	34.42
Spikelet fertility (%)	6.97	7.17	1.70	94.4	7.46
Filled grains wt./panicle	19.25	19.64	3.85	96.1	0.70
1000-grain weight	14.26	14.27	0.62	99.8	5.03
Grain yield per plant	24.76	24.91	2.73	98.8	9.05

Number of tillers per plant

The phenotypic variance (49.06) & phenotypic variance (49.29) had very minute difference while average value ranged from 9.60 to 33.60 (Table 1). Furthermore, the genotypic coefficient of variations and phenotypic coefficient of variation (32.06 & 32.14) although had high magnitude but carried minute difference, which shows that there was less influence of environment on expression of this trait along with presence of additive gene action for these traits. High amount of genetic variation was obtained for number of tillers per plant by Laxuman *et al.* (2011). The estimated heritability was more than 90 percent (99.5) and genetic advance value 9.78 was moderate (Table 3).

Plant height

The magnitudes of GCV and PCV for plant height were 18.57 and 18.59 respectively. Both coefficients of variation carried slight difference showing less influence of environment on the expression of this trait. Ghosal *et al.* (2010) also found very close values for GCV & PCV for this trait. The trait exhibited highest amount of genotypic variance and phenotypic variance (638.73 & 638.39) after number of spikelets per panicle and number of grains per panicle. Highest amount of heritability (99.7) and Genetic advance (35.28) was noticed for this character also reporting that selection based on this trait would be fruitful. Kole *et al.* (2008) and Ashfaq *et al.* (2012) observed high genetic variation for this trait in their experiments.

Number of spikelet per panicle

Variance analysis for this trait determined highly significant differences for the genotypes under study (Table 2). The average value ranged from 99.93 to 202.67. The magnitudes of GCV and PCV were 19.19 and 19.24 respectively. Heritability and genetic advance were 99.5 and 40.17, respectively and these values were highest amongst all the traits under examination. More expression of environment was involved, because phenotypic variance value was 832.15 greater than corresponding genotypic variance 827.86 values. These variances also achieved highest values amongst all the characters. Hence, this character will be best for improvement in rice genotypes. Highest values of genetic advance and heritability were found for this trait by Fiyaz *et al.* (2011) in his study.

Number of grains per panicle

The mean value for this trait ranged from 81.93-163.00. The PV (phenotypic variance) value was 613.805 and GV (genotypic variance) was 609.109 (Table 1). This information shows that there was more effect of environment on the expression of this character. The PCV and GCV were 21.02 and 20.93 respectively, indicating that environment played little role. The genetic advance and heritability were high i.e. 34.41 & 99.2. Sankar *et al.* (2006) provided similar findings.

Spikelet fertility percentage

The spikelet fertility percentage was more than 55 % but less than 95 % among all the genotypes (Table 1). Significant difference between genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was estimated, because PCV value 7.175 was greater than GCV value 6.970. The PV 31.883 was greater than GV 30.084. Hence, environment played dominant role in expression of this trait. Heritability was 94.4 and moderate genetic advance 7.45 was noticed for this character. . High magnitude of genetic divergence for this trait was seen by Saleem *et al.* (2005) and Pandey *et al.* (2012).

Filled grains weight per panicle

Mean sum of square for filled grains weight per panicle was highly significant, revealing more amount of genetic divergence among the genotypes for this trait. The average value for this trait was ranged from 1.57 to 3.53 (Table 1). The genotypic variance and phenotypic variances were very low in magnitude (0.25 & 0.26). When coefficients of variability were analyzed for this parameter then it was inferred that PCV (19.63) and GCV (19.25) both revealed minor difference, indicating less effect of the environment. Vange (2009) got very close difference for coefficients of variability for this character. High heritability (96.1) but lowest genetic advance (0.69) was observed for this trait, informing selection will not be useful after including this trait in breeding programs.

1000-grain weight

All the differences obtained during this study for all varieties for this trait were highly statistically significant. 1000-grain weight of the genotypes ranged from 18.53gm to 31.34gm. Very minor difference in GCV and PCV (14.26 & 14.27), GV and PV (12.96 & 12.99) depicted less contribution of environment on expression of this character along with predominance of genetic variation. Similar findings were reported by Masood *et al.*, (2014abc); Ahsan *et al.*, (2013); Fiyaz *et al.* (2011). High heritability (99.8) and lower value of genetic advance (5.03) was found for this character.

Grain yield per plant

The range of the yield per plant; 16.01gm was the minimum value and 39.71gm was the maximum value for this parameter. High GCV and PCV magnitudes were found (24.76 & 24.91, respectively) for this trait (Sankar *et al.* 2006) along with high values of PV and GV (42.80 & 42.29, respectively) and all the genotypes were highly significant for this character also (Table 2). Rasheed *et al.* (2002); Kumar *et al.* (2006); Kumar and Ramesh (2008); Abbas *et al.*, (2014) and Zafar *et al.*, (2015) also reported high genetic divergence for this character.

Conclusion

Significant differences were found for all the traits in all the genotypes under study. High heritability had coupled with high genetic advance for traits such as number of spikelets per panicle followed by plant height and number of grains per panicle indicating that these traits were under additive gene action and selection based on them would be fruitful. Number of tillers per plant, spikelet fertility percentage, 1000-grain weight, yield per plant and filled grains weight per panicle gave very minute differences between PV and GV, showing that expression of these traits was under additive gene action.

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