



P-ISSN: 2349-8528

E-ISSN: 2321-4902

IJCS 2017; 5(5): 309-312

© 2017 IJCS

Received: 16-07-2017

Accepted: 17-08-2017

**Mithilesh Kumar Singh**Department of Genetics and  
Plant Breeding, GBPUAT,  
Pantnagar, Uttarakhand, India**Surendra Singh**Department of Genetics and  
Plant Breeding, GBPUAT,  
Pantnagar, Uttarakhand, India**MK Nautiyal**Department of Genetics and  
Plant Breeding, GBPUAT,  
Pantnagar, Uttarakhand, India**ID Pandey**Department of Genetics and  
Plant Breeding, GBPUAT,  
Pantnagar, Uttarakhand, India**AK Gaur**Department of Molecular  
Biology and Genetic  
Engineering, GBPUAT,  
Pantnagar, Uttarakhand, India**Correspondence****Mithilesh Kumar Singh**Department of Genetics and  
Plant Breeding, GBPUAT,  
Pantnagar, Uttarakhand, India

## Variability, heritability and correlation among grain quality traits in basmati rice (*Oryza sativa* L.)

**Mithilesh Kumar Singh, Surendra Singh, MK Nautiyal, ID Pandey and AK Gaur**

### Abstract

Among 10 rice grain quality traits studied, phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits. High heritability (71 - 98) was found for all the traits. High heritability with high genetic advance was found for kernel L/B ratio (92 & 25.26), cooked kernel length (93 & 21.77) and alkali digestion value (98 & 43.48). Different rice grain quality traits were interrelated. Among various traits that were interrelated, strong association was found between kernel length and kernel length/breadth ratio ( $r=0.96$ ) and hulling and milling recovery ( $r=0.91$ ). Cooked kernel length was associated with most of the grain quality traits that could be given preference in selection criteria for improvement of multiple grain quality traits simultaneously.

**Keywords:** basmati rice, aromatic rice, correlation coefficient, variability, rice (*Oryza sativa* L.)

### Introduction

Among diverse rice forms cultivated in India, preference for fine grained aromatic rice has increased dramatically in past decades as purchasing power of consumer is steadily being improved. Increasing demand for basmati rice in international market and subsequent demand driven research interest in basmati rice improvement has made India a leading exporter of basmati and non-basmati aromatic rice (Singh *et al.*, 2015) [13]. During the year 2014-15 the country has exported 37, 02,260.12 metric tonnes of basmati rice and earned foreign exchange equivalent to ₹ 27,597.87 crores (APEDA, New Delhi, 2015). Consumer preference for quality rice commands incorporation of preferred grain quality parameters as the second most important objective after improvement in grain yield. Most frequently targeted rice grain quality parameters include hulling recovery, milling recovery, kernel length and breadth, kernel L/B ratio, cooked kernel length, elongation ratio, alkali digestion and amylose content (Rita and Sarawgi, 2008) [10]. Hence selection for improvement in these traits is crucial to meet consumers' preference and market demand. A wide range of variability has been reported for quality traits albeit their values are lower than that that observed for other agronomic traits. Existence of variability in germplasm provides basis for selection of elite germplasm that may be used either as end product in form of improved variety or can be used as starting material in several breeding programmes intended to accomplish diverse objectives. Genetic parameters such as GCV and PCV are indicator of extent of genetic variation present in germplasm and the extent to which genotype is influenced by environment. Heritability along with genetic advance reflects reliability of transmission of trait variation to the next generation. Genotypic correlation among grain quality trait is indicator of stable association between traits and helps in indirect selection. Towards this end, the present investigation was undertaken to estimate genetic variability, heritability and association among various grain quality traits.

### Materials and methods

The present investigation was carried out during *Kharif*, 2016 at G.B. Pant University of Agriculture and Technology, Pantnagar. Experimental materials consisted of 36 diverse basmati and non-basmati aromatic rice genotypes. Genotypes were grown in randomized complete block design with 3 replications. Each genotype was grown in single row (1.5 m) in a 6 m<sup>2</sup> plot with plant to plant spacing of 15 cm and row to row spacing of 20 cm. Recommended agronomic practices were followed to raise a healthy crop stand. Harvested seeds from individual genotypes were shade dried to 14% moisture level. The seeds were dehulled in a Satake laboratory huller to obtain data on hulling recovery (%).

Dehulled seeds were polished in a Satake Rice Polisher to obtain data on milling recovery (%). Polished rice kernels were used for recording data on 8 other quality traits *viz.*, kernel length and breadth (mm), kernel length/breadth ratio (kernel L/B ratio), 100-kernel weight (g), cooked kernel length (mm), elongation ratio, alkali digestion value and amylose content (%). Hulling and milling recovery were calculated by dividing the weight of dehulled kernel and milled kernel by the weight of initial paddy used for the purpose, respectively. Ten kernels at random from milled sample were used to measure kernel length and breadth and to calculate kernel L/B ratio. Average length of cooked kernel was divided by average length of same uncooked kernel to get elongation ratio. Alkali digestion value and amylose content (%) were estimated by the method as described by Little *et al.* (1958) [8] and Jennings *et al.* (1979) [5], respectively. Analysis of Variance (Fisher, 1946) [3], correlation coefficient (Searle, 1961) [12], PCV and GCV (Burton, 1952) [1], heritability in broad sense ( $h^2_{(b)}$ ) (Hanson *et al.*, 1956) [4] and genetic advance as percent of mean (Johnson *et al.*, 1955) [6] were estimated using Windostat software version 9.2.

### Results and discussion

The analysis of variance revealed highly significant differences among the genotypes for all the 10 quality traits that indicated the existence of ample amount of variability for these traits (Table 1).

**Table 1:** Analysis of variance for 10 rice grain quality traits.

Traits	Source of variation (mean sum of squares)		
	Replication	Treatment	Error
Hulling recovery	0.24	12.37**	0.23
Milling recovery	0.17	12.37**	1.12
Kernel length	0.01	1.32**	0.01
Kernel breadth	0.00	0.02**	0.00
Kernel L/B ratio	0.02	0.80**	0.02
Cooked kernel length	0.02	10.00**	0.02
Elongation ratio	0.01	3.09**	0.01
Alkali digestion value	0.05	4.49**	0.02
Amylose content	0.18	6.15**	0.07
100- kernel weight	0.86	14.95**	0.67

\*: 5% level of significance, \*\*:1% level of significance

**Table 2:** Estimation of genetic parameters for 10 rice grain quality traits.

Traits	HR	MR	KL	KB	L/B	CKL	ER	ADV	AC	100-KW
PCV	2.67	3.2	9.74	5.53	13.41	11.27	7.08	21.45	6.6	9.79
GCV	2.6	2.81	9.58	4.67	12.9	10.91	6.29	21.27	6.49	9.17
Heritability (broad sense)	94	76	0.96	0.71	0.92	0.93	0.78	0.98	0.96	0.87
Genetic advance (as % mean)	5.21	5.07	19.41	8.11	25.56	21.77	11.5	43.48	13.14	17.7

HR: hulling recovery, MR:milling recovery, KL:kernel length, KB:kernel breadth, L/B:kernel L/B ratio, CKL:cooked kernel length, ER: elongation ratio, ADV: alkali digestion value, AC: amylose content,100-KW:100-kernel weight

The estimates of heritability for different traits were high and ranged from 71% to 98%. Effectiveness of selection depends on heritability of trait but mere heritability may not always lead to genetic progress by selecting for the best individuals. This limitation can be addressed by combining genetic advance along with heritability estimates. Kernel L/B ratio (92% & 25.26%), cooked kernel length (93% & 21.77%) and alkali digestion (98% & 43.48%) recorded high heritability with high genetic advance as percent of mean. High heritability (>60%) with high genetic advance (>20%) for these traits would be more reliable in predicting gain under selection. High estimates of heritability and low estimates of genetic advance as percent of mean (<10%) was recorded for

The relative values of GCV and PCV provide important information on the magnitude of variability. PCV was higher than the GCV for all the studied traits and most portion of PCV was attributable to genetic component as good correspondence was observed between GCV and PCV for all the traits (Table 2). A wide range of PCV was observed ranging from 2.67% (hulling recovery) to 21.45% (alkali digestion value). Similarly, GCV showed wider range from 2.60% (hulling recovery) to 21.27% (alkali digestion value). High PCV and GCV (> 20%) were recorded only for alkali digestion value (21.45% & 21.27%). A similar finding for high GCV and PCV for alkali digestion value was also reported by Veerabathiran *et al.* (2009) [16]. The high magnitude of GCV and PCV for this trait suggested the presence of high degree of variability and hence, better scope for improvement through selection. Moderate values for PCV and GCV (10-20%) were observed for the L/B ratio (13.41% & 12.90%) and Cooked kernel length (11.27% & 10.91%). These results were consistent with the findings of Subbaiah *et al.* (2011) [14] for kernel L/B ratio and kernel length after cooking. This indicates the existence of comparatively moderate variability for these traits, which could be exploited for improvement through selection in advanced generations. Low GCV and PCV (<10%) were found for the traits *viz.*, hulling recovery (2.67% & 2.60%), milling recovery (3.20% & 2.81%), kernel length (9.74% & 9.58%), kernel breadth (5.53% & 4.67%), amylose content (9.86% & 9.88%), elongation ratio (7.08% & 6.29%), amylose content (6.60% & 6.49%) and 100-kernel weight (9.79% & 9.17%). Low GCV and PCV estimates for hulling recovery was also reported by Umadevi *et al.* (2010) [15] and for amylose content by Subbaiah *et al.* (2011) [14]. Lower GCV and PCV estimates indicates narrow genetic base for these traits. Improvement in these characters can be brought about by hybridization or induced mutagenesis to broaden genetic base followed by pedigree selection in advanced generations. Overall, the close correspondence between the estimates of GCV and PCV for all the traits indicated least environmental influence on the expression of these traits, which is in correspondence with high heritability values for these traits.

the traits *viz.*, hulling recovery (94% & 5.21%), milling recovery (76% and 5.07%) and kernel breadth (71% and 8.11%). This suggests that these traits are much influenced by environment. Sanjukta *et al.* (2007) [11] also observed similar results for hulling recovery and kernel breadth. These traits showing high heritability with low genetic advance indicated the presence of non-additive gene action. Hence, selection could be postponed for these characters. In other words these traits could be improved by inter-mating of superior genotypes in segregating population of suitable cross. The high estimate of heritability coupled with moderate estimate of genetic advance (10-20%) was observed for cooked kernel length (96% and 19.41%), elongation ratio (78% and

11.50%), amylose content (96% and 13.14%) and 100-kernel weight (87% and 17.70%). These results were in accordance with the findings of Chakraborty *et al.* (2009) [2]. Thus, these traits seem not to be suitable for improvement through selection.

Correlation analysis among grain quality traits; between quality traits and 100-kernel weight was calculated (Table 3). Correlation among traits helps in indirect selection. Hulling recovery showed significant and positive association with milling recovery cooked kernel length, elongation ratio and amylose content ( $r = 0.91, 0.35, 0.53$  &  $0.29$ ). Hulling recovery was not associated with any of any of the fine grain quality. Hulling and milling recovery enhances commercial success of a variety and strong association between hulling and milling recovery can bring simultaneous improvement of these two quality traits by selecting either of these two traits. Similar results were reported by Nayak *et al.* (2003) [9]. Genotypes with long slender grains are more prone to breakage than those possessing short bold grain. But, significant association of milling recovery with kernel length and kernel L/B ratio ( $r=0.25$  &  $0.26$ ) is not as per expectation. Cooked kernel length is one of the important cooking quality

attributes. Length wise expansion after cooking is an important criterion in designation of basmati rice. Cooked kernel length and elongation ratio are correlated ( $r = 0.47$ ). Selection for either of these traits will ultimately enhance the mean performance for both traits. The kernel breadth showed highly significant but negative correlation with L/B ratio ( $r=-0.82$ ) and cooked kernel length ( $r=-0.46$ ). Similar associations were reported by Khatun *et al.* (2003) [7]. Alkali digestion value showed positive significant correlation with kernel length ( $r = 0.3$ ), kernel L/B ratio ( $r=0.24$ ) and cooked kernel length ( $r=0.30$ ). Kernel L/B ratio was significantly associated with cooked kernel length ( $r = 0.78$ ). L/B ratio is a good indicator for linear expansion of rice kernel after cooking. The amylose content is a chemical quality trait that determines the texture of cooked rice. Varieties with intermediate amylose content are preferred by consumers. Amylose content was significantly associated with hulling recovery ( $r=0.29$ ), milling recovery ( $r=0.32$ ) and alkali digestion value ( $r=0.35$ ). Overall, cooked kernel length was associated with most of the rice grain quality traits and therefore, selection for this single trait could lead to simultaneous improvement in multiple traits in desired direction of consumer preference.

**Table 3:** Correlation coefficients for 10 rice grain quality traits.

Traits	MR	KL	KB	L/B	CKL	ER	ADV	AC	100-KW
HR	0.91**	0.06	-0.12	0.11	0.35**	0.53**	0.00	0.29**	-0.09
MR		0.25**	-0.14	0.26**	0.56**	0.61**	0.10	0.32**	0.04
KL			-0.65**	0.96**	0.83**	-0.11	0.30**	0.12	0.43**
KB				-0.82**	-0.46**	0.24**	-0.04	0.16	0.09
L/B					0.78**	-0.14	0.24**	0.04	0.29**
CKL						0.47**	0.30**	0.15	0.48**
ER							0.10	0.08	0.19*
ADV								0.35**	0.43**
AC									0.14

HR: hulling recovery, MR:milling recovery, KL:kernel length, KB:kernel breadth, L/B:kernel L/B ratio, CKL:cooked kernel length, ER:elongation ratio, ADV:alkali digestion value,AC:amylose content,100-KW:100-kernel weight, \*: 5% level of significance, \*\*:1% level of significance

## Conclusion

In the present study, it was concluded that the genotypes included in the study possessed adequate variability for various rice grain quality traits. Traits like, kernel L/B ratio, cooked kernel length and alkali digestion value showed high heritability with high genetic advance. Therefore, these traits should be given top priority during selection. Different quality traits are interrelated and among 10 studied traits cooked kernel length was associated with most of the quality traits (8) in desired direction of consumer preference. Therefore, such traits should be included in selection criteria while attempting indirect selection for other rice grain quality traits.

## Acknowledgment

The Corresponding author gratefully acknowledges Indian Council of Agricultural Research (ICAR) for providing him financial assistance as Senior Research Fellowship during the period of the study.

## References

- Burton GW. Quantitative inheritance in grasses. Proc. 6<sup>th</sup> Int. Grassld. Congr. 1952; 1:227-283.
- Chakraborty R, Chakraborty S, Dutta BK, Paul SB. Genetic variability and genetic correlation among nutritional and cooking quality traits in bold grained rice. *Oryza*. 2009; 46(1):21-25.
- Fisher RA. Statistical methods for research workers. (10<sup>th</sup> edition). Oliver and Boyd, Ed. In burg, 1946.
- Hanson GW, Robinson HF, Comstock RE. Biometrical studies of yield in segregating population of Korean lespedeza. *Agron. J.* 1956; 48:268-272.
- Jennings PR, Coffman WR, Kauffman MHE. Grain quality: Rice improvement. International Rice Research Institute, Philippines. 1979; 6:101-120.
- Johnson HW, Robinson HF, Comstock RE. Genotypic and phenotypic correlations in soybeans and their implication in selection. *Agronomy Journal*. 1955; 47:477-483.
- Khatun MM, Hazrat AM, Quirio D, Cruz ND. Correlation studies on grain physicochemical characteristics of aromatic rice. *Pakistan Journal of Biological Science*. 2003; 6(5):511-513.
- Little RR, Hilder GB, Dawson EH. Differential effect of dilute alkali on 25 varieties of milled white rice. *Cereal Chemistry*. 1958; 35:111-126.
- Nayak AR, Chaudhary D, Reddy JN. Genetic variability and correlation study among quality traits in scented rice. *Agri. Sci. Digest*. 2003; 23(3):175-178.
- Rita B, Sarawgi AK. Agro-morphological and quality characterization of Badshah bhog group from aromatic rice germplasm of Chhattisgarh. *Bangladesh Journal of Agriculture Research*. 2008; 33:479-492.

11. Sanjukta D, Subudhi HN, Reddy JN. Genetic variability in grain quality characteristics and yield in low land rice genotypes. *Oryza*. 2007; 44(4):343-346.
12. Searle SR. Phenotypic, genotypic and environmental correlations. *Biometrics*. 1961; 17:474-480.
13. Singh S, Sahu H, Sahu PK. Variability and genetic parameters for grain yield in CMS based rice hybrid (*Oryza sativa* L.). *Journal of Plant Development Sciences*. 2015; 7(3):247-250.
14. Subbaiah PV, Reddi SM, Reddy KHP, Eswara RNP. Variability and genetic parameters for grain yield and its components and kernel quality attributes in CMS based rice hybrids (*Oryza sativa* L.). *International Journal of Applied Biology and Pharmaceutical Technology*. 2011; 2(3):603-609.
15. Umadevi M, Veerabhadhiran P, Manonmani S, Shanmugasundaram P. Physico-chemical and cooking characteristics of rice genotypes. *Electronic Journal of Plant Breeding*. 2010; 1(2):114-123.
16. Veerabhadhiran P, Umadevi M, Pushpam R. Genetic variability, heritability and genetic advance of grain quality in hybrid rice. *Madras Agric. J.* 2009; 96(1-6):95-99.