GENETIC VARIABILITY ANALYSIS FOR VARIOUS YIELD ATTRIBUTING AND QUALITY TRAITS IN RICE (*O. SATIVA* L.)

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ABSTRACT
The analysis of variance was found to be highly significant for all the 13 Quantitative and 19 Quality traits in rice indicating that enough variability is present in the studied material. Among the desirable quantitative traits grain yield per plant (30.52%; 31.18%), filled grain per panicle (26.05%; 26.86%), were found to have high GCV and PCV while alkali spreading value (49.55%; 49.90%), gel consistency (42.72%; 43.67%), water uptake (24.59%; 25.33%) showed high GCV and PCV among quality traits of rice. Almost all the characters showed a little variation between PCV and GCV revealing little influence of the environment in the expression of these traits. The characters showing high GCV and PCV were found to be highly heritable coupled with high genetic advance. These characters are governed by additive gene action and one should go for direct selection for these traits.

INTRODUCTION

Rice is the most consumed cereal grain in the world, constituting the dietary staple food for more than half of the planet's human population. India being the second largest producer of rice still lacks behind. The rising demand, saturation of cultivable field and low gross domestic production of rice are likely to cause a supply shortage of a crop in the near future. By the year 2025, about 785 million tonnes of paddy which is 70 per cent more than the current production will be needed to meet the growing demand (Manomani and Khan, 2003).Therefore being the staple food of the population in India, improving its productivity has become a crucial importance (Subbaiah *et al.*, 2011). Knowledge on the nature and magnitude of the genetic variation governing the inheritance of quantitative character like yield and its components is essential for effecting genetic improvement. A critical analysis of the genetic variability is a prerequisite for initiating any crop improvement programme and for adopting of appropriate selection techniques. Improvement in grain quality that does not lower yield is the need of hour at present context in order to benefit all rice growers and consumers. Like grain yield, quality is not easily amenable to selection due to its complex nature. Lack of clear cut perception regarding the component traits of good quality rice is one of the important reasons for tardy progress in breeding for quality rice varieties. With increase in yield, there is also a need to look into the quality aspects to have a better consumer acceptance, which determine the profit margin of rice growers which in turn dictates the export quality and foreign exchange in India. Grain quality characteristics are very important in rice breeding as it is predominantly consumed as a whole grain. The milling per-

centage, hulling percentage, grain dimensions, cooking quality constitute the quality traits (Babu *et al.,* 2012). Keeping in view the above perspectives the present experiment was carried out to estimate the genetic variability parameters for various yield attributing and quality traits in rice.

MATERIALS AND METHODS

The present study was conducted at the Research Farm, Department of Plant Breeding and Genetics, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, C.G. The material comprises four parents *viz.*, R 1519-781-5-598-1, R 1540-1888-1278-1, R 1558-2423-3-1445-1, R 1529-1183-1-1041-1; used as female parents and six parents *viz.*, B6441-FMR-6-0-0, IR 42221-145-2-3-2, BR 240, IRBL 10, Swarna and Chaptigurmatia used as male parents. The material was planted in the *summer season* 2008 and crosses were made between four lines and six testers to obtain twenty four F_1 crosses in a line x tester design (Kempthrone, 1957). The above crosses were attempted in such a way that each seed parent *i.e.,* each lines was pollinated by all pollen parents. The F_1 seeds from each of twenty four crosses were collected separately and planted in the *kharif* 2008 along with parents in a Completely Randomised Block Design with two replications. The five competitive plants from each of the replication were tagged and observation were taken from these tagged plants at various stages of the crop plant growth and post harvest observations were taken at Rice quality Laboratory, Department of Genetics and Plant Breeding, IGKV, Raipur, C.G.. All the observations were taken as per the procedure given in Standard Evaluation System for Rice, IRRI, 2002. The observations were recorded for 13 field characters and 19 quality

characters. The variance analysis and test of significance was calculated as per the method of Fisher (1935). The genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) was calculated by the formula given by Burton (1952). Heritability in broad sense was calculated by the formula given by Hanson *et al.* (1956). From the heritability estimates, the genetic advance was calculated by the following formula given by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

Variability parameters

The analysis of variances indicated the existence of significant differences among the genotypes studied revealing that sufficient variability is present for the different characters and selection would be effective to develop the varieties with desired forms of crop plants. The result of analysis of variance is present in the Table 2. The difference between genotypic and phenotypic coefficient of variation was less for all characters studied except tiller number per plant and effective tiller number per plant, indication of the more influence of the environment over this two characters. The slight difference between GCV and PCV was also reported by Mustafa and

Table1: List of treatments used in the study

S.no.	Treatments
	Female parents
1	R 1519-781-5-598-1
2	R 1540-1888-1278-1
3	R 1558-2423-3-1445-1
4	R 1529-1183-1-1041-1
	Male parents
5	B 6441-FMR-6-0-0
6	IR 42221-145-2-3-2
7	BR 240
8	IRBL 10
9	Cheptigurmatia
10	Swarna
	Crosses
11	R 1519 -781-5-598-1 X B6441-FMR-6-0-0
12	R 1519- 781-5-598-1 X IR 42221-145-2-3-2
13	R 1519- 781-5-598-1 X BR 240
14	R 1519-781-5-598-1 X IRBL 10
15	R 1519-781-5-598-1 X Cheptigurmatia
16	R 1519-781-5-598 -1 X Swarna
17	R 1540-1888-1278-1 X IR 42221-145-2-3-2
18	R 1540-1888-1278-1 X B6441-FMR-6-0-0
19	R 1540-1888-1278-1 X BR 240
20	R 1540-1888-1278-1 X IRBL 10
21	R 1540- 1888-1278-1 X Cheptigurmatia
22	R 1540-1888-1278-1 X Swarna
23	R 1558-2423-3-1445-1 X B6441-FMR-6-0-0
24	R 1558 -2423-3-1445-1 X IR 42221-145-2-3-2
25	R 1558-2423-3-1445-1 X BR-240
26	R 1558-2423-3-1445-1 X IRBL 10
27	R 1558-2423-3-1445-1 X Cheptigurmatia
28	R 1558- 2423-3-1445-1 X Swarna
29	R 1529-1183-1-1041-1 X B6441-FMR-6-0-0
30	R 1529-1183-1-1041-1 X IR 42221-145-2-3-2
31	R 1529-1183-1-1041-1 X BR 240
32	R 1529-1183-1-1041-1 X IRBL 10
33	R 1529- 1183-1-1041-1 X Cheptigurmatia
34	R 1529- 1183-1-1041-1 X Swarna

Isheikh (2007), Kole *et al.* (2008) and Syoum *et al.* (2012) .The in the present investigation character studied exhibited low, moderate and high PCV and GCV values. Among the yield characters the high percent of GCV and PCV was recorded for the biological yield (32.54 and 33.78) followed by grain yield per plant (30.52 and 31.18) and lowest was recorded for days to 50% flowering (7.10 and 7.21).Among the grain quality characters highest GCV and PCV was recorded for alkali spreading value (49.55 and 49.90) followed by gel consistency (42.72 and 43.67) and water uptake (24.59 and 25.33) while the character hulling percentage (4.10 and 4.55) recorded the lowest GCV and PCV values. Singh *et al.* (2011), Subbaiah *et al.* (2011), Babu *et al.* (2012) also reported high GCV and PCV for most of the yield attributing traits. The moderate genotypic and phenotypic coefficient of variation were recorded for the characters, harvest index percentage (17.02 and 18.60), brown rice L/ B ratio (15.18 and 15.29), effective tiller number per plant (15.03 and 18.10), kernel L/B ratio (15.00 and 15.65), flag leaf area (14.37 and 14.84), paddy L/B ratio (13.73 and 14.14), plant height (13.66 and 13.75), tiller number per plant (12.87 and 15.35),kernel breadth after cooking (12.80 and 13.37), cooked rice L/B ratio (12.43 and 13.11), kernel length (12.05 and 12.11), panicle length (11.20 and 12.62) and kernel length after cooking (11.04 and 11.23). The high magnitude of phenotypic variation were composed of high genotypic coefficient of variations and less of the environment variations, which indicated high genetic variability for different traits and less influence of environment. Therefore selection on the basis of phenotype alone can be effective for the improvement of these traits. Similar results for low to moderate values of GCV and PCV were also found by Sarkar *et al.* (2007), Prajapati *et al.* (2011), Singh *et al.* (2011), Ananadarao *et al.* (2011).

Heritability

The reliability of the phenotypic value depends on the estimates of heritability for a particular character. Therefore high heritability helps in the effective selection for a particular character. In the present investigation heritability in broad sense was calculated for all characters under study and is presented in Table 3. Heritability is classified as high (above 60%), medium (30%-60%) and low (below 30%). High estimate of heritability were exhibited for all the character under study. Among the quality characters the length dimensions and there ratio recorded the high heritability value.The highest heritability for grain quality characters was recorded for kernel length (98.96) followed by brown rice length (98.74), brown rice L/B ratio (98.65), paddy length (98.63), alkali spreading value (98.58). While plant height (98.65), days to 50% flowering (96.90) and grain yield per plant (95.78), spikelet sterility percentage (95.29) were found to have high heritability among quantitative traits. Beside these filled grains per panicle, flag leaf area, paddy breadth, paddy L/B ratio, brown rice breadth, kernel length after cooking, elongation ratio, water uptake, gel consistency were also found to have high heritability. High heritability values indicate that the characters under study are less influenced by environment in their expression. The plant breeder, therefore adopt simple selection method on the basis of the phenotype of the characters which ultimately improves the genetic background of these traits. Similar results were also quoted by Li-Yun *et al.* (2003),

Table 2: Analysis of variance for yield and quality traits in rice

S. No.	Characters	Mean Sum of Squares		
		Replications d.f. = 1	Treatments d.f. = 33	Error d.f. = 33
1	Days to 50 % flowering	11.041**	86.886**	1.367
2	Plant height (cm)	0.059	304.894**	2.810
3	Tiller number per plant	0.132	10.719**	1.863
4	Effective tiller number per plant	0.115	10.161**	1.886
5	Panicle length (cm)	12.436**	19.238**	2.286
6	Flag leaf area (cm^2)	4.963	105.982**	3.429
7	Filled grains per panicle	84.711	2604.961**	80.095
8	Unfilled grains per panicle	24.241	305.788**	11.694
9	Spikelet sterility percentage	14.674**	64.317**	1.550
10	Hundred seed weight (g)	0.007	0.136**	0.009
11	Biological yield (g)	6.484	3020.070**	113.042
12	Grain yield per plant (g)	0.235	308.674**	6.656
13	Harvest Index (%)	1.033	78.983**	7.004
14	Paddy length (mm)	0.001	1.558**	0.011
15	Paddy breadth (mm)	0.007	0.068**	0.002
16	Paddy L/B ratio	0.004	0.480**	0.014
17	Brown rice length (mm)	0.000	0.974**	0.006
18	Brown rice breadth (mm)	0.005	0.053**	0.002
19	Brown rice L/B ratio	0.013	0.458**	0.003
20	Kernel length (mm)	0.011	0.932**	0.005
21	Kernel breadth (mm)	0.005	0.052**	0.002
22	Kernel L/B ratio (mm)	0.002	0.330**	0.014
23	Kernel length after cooking (mm)	0.073	1.811**	0.032
24	Kernel breadth after cooking (mm)	0.032	0.313**	0.014
25	Cooked rice L/B ratio	0.003	0.268**	0.014
26	Hulling percentage	33.882**	21.881**	2.307
27	Milling percentage	0.368	22.464**	2.095
28	Head rice recovery (%)	1.779	45.125**	3.870
29	Elongation ratio	0.004	0.045**	0.001
30	Water uptake (mL)	2,259.765	6022.724**	178.916
31	Alkali spreading value	0.210*	8.598**	0.061
32	Gel consistency (mm)	10.721	1027.011**	22.508

Choudhary *et al.* (2004), Satyanaryan *et al.* (2005), Jaiswal *et al.* (2007), Sarkar *et al.* (2007), Bisne *et al.* (2009), Verma (2010), Subbaiah *et al.* (2011) and Ananadarao *et al.* (2011).

Genetic advance

The estimates of genetic advance as per cent of mean provide more reliable information regarding the effectiveness of selection in improving the traits. Genetic advance denotes the improvement in the genotypic value of the new population over the original population. Genetic advance estimates are depicted in Table 3. Among the studied characters the high, moderate and low estimates of genetic advance as percent of mean was recorded. The genetic advance as percentage of mean was highest for biological yield (64.57) followed by grain yield (61.53) and lowest was recorded for days to 50% flowering among quantitative characters, whereas, in grain quality characters, alkali spreading value (101.34) recorded the highest followed by gel consistency (86.10) while the lowest was recorded for milling percentage. Similar results were also reported by Iftekharuddaula *et al.* (2001), Sao (2002).

Since broad sense heritability includes both additive and epistatic effects. It will be reliable only when accompanied by high genetic advance. Heritability estimates along with genetic advance is more useful than heritability alone in predicting the effectiveness of selection (Johnson *et al.* 1955). In the present study the characters which showed high heritability

associated with high genetic advance are alkali spreading value, gel consistency, water uptake, grain yield per plant biological yield per plant, filled grains per panicle, unfilled grains per panicle and spikelet sterility percent. The characters that show high heritability coupled with high genetic advance are controlled by additive gene action (Panse and Suhatme, 1957) 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 intermitting superior genotypes of segregating population developed from combination breeding (Samadhia, 2005). In the present investigation high heritability couple with high genetic advance for yield attributing characters is in accordance with the Satyanaryan *et al.* (2005), Hasib (2005), Jaiswal *et al.* (2007); Subbaiha *et al.* (2011) Syoum *et al.* (2012); for quality characters by Choudhary *et al.* (2004).

Therefore, it is concluded that the characters which showed high genotypic value coupled with high heritability and genetic advance should be considered for direct selection. Here grain yield per plant, biological yield per plant, filled grain per panicle, unfilled grain per panicle, spikelet sterility among field characters and alkali spreading value, gel consistency and water uptake showed high GCV, PCV, heritability and genetic advance. Thus one should select these characters for direct selection.

Table 3: Estimates of variability, heritability and genetic advance as percentage of mean

S. No.	Characters	PCV (%)	GCV (%)	Heritability(bs)(%)	Genetic advance (GA) as per cent of mean
1	Days to 50 % flowering	7.10	7.21	96.90	14.39
2	Plant height (cm)	13.66	13.75	98.65	27.94
3	Tiller number per plant	12.87	15.35	70.38	22.25
4	Effective tiller number per plant	15.03	18.10	68.98	25.72
5	Panicle length (cm)	11.20	12.62	78.76	20.48
6	Flag leaf area (cm²)	14.37	14.84	93.73	28.66
7	Filled grains per panicle	26.05	26.86	94.03	52.04
8	Unfilled grains per panicle	27.36	28.43	92.63	54.25
9	Spikelet sterility percentage	22.54	23.09	95.29	45.33
10	Hundred seed weight (g)	10.79	11.54	87.38	20.78
11	Biological yield (g)	32.54	33.78	92.78	64.57
12	Grain yield per plant (g)	30.52	31.18	95.78	61.53
13	Harvest Index (%)	17.02	18.60	83.71	32.07
14	Paddy length (mm)	9.66	9.72	98.63	19.76
15	Paddy breadth (mm)	6.94	7.18	93.59	13.84
16	Paddy L/B ratio	13.73	14.14	94.32	27.47
17	Brown rice length (mm)	10.21	10.28	98.74	20.91
18	Brown rice breadth (mm)	7.28	7.56	92.87	14.46
19	Brown rice L/B ratio	15.18	15.29	98.65	31.07
20	Kernel length (mm)	12.05	12.11	98.96	24.68
21	Kernel breadth (mm)	7.35	7.68	91.43	14.47
22	Kernel L/B ratio (mm)	15.00	15.65	91.77	29.59
23	Kernel length after cooking (mm)	11.04	11.23	96.56	22.34
24	Kernel breadth after cooking (mm)	12.80	13.37	91.64	25.24
25	Cooked rice L/B ratio	12.43	13.11	89.97	24.30
26	Hulling percentage	4.10	4.55	80.93	7.59
27	Milling percentage	3.87	4.47	74.88	6.90
28	Head rice recovery (%)	8.25	8.99	84.20	15.59
29	Elongation ratio	9.73	10.01	94.46	19.47
30	Water uptake (ml)	24.59	25.33	94.23	49.17
31	Alkali spreading value	49.55	49.90	98.58	101.34
32	Gel consistency (mm)	42.72	43.67	95.71	86.10

REFERENCES

Ananadrao, S. D., Singh, C. M., Suresh, B. G. and Lavanya, G. R. 2011. Evaluation of rice hybrids for yield and yield component characters under North East Plain Zone. *The Allahabad farmer.* **67(1):** 63-68.

Babu, V. R., Shreya, K., Dangi, K. S., Usharani, G. and Nagesh, P. 2012. Genetic variability studies for qualitative and quantitative traits in popular rice (*Oryza sativa* L.) hybrids of India. *International Journal of Scientific and Research Publication.* **2(6):** 1-5.

Bisne, R., Sarawgi, A. K. and Verulkar, S. B. 2009. Study of heritability, genetic advance and variability for yield contributing characters in rice. Bangladesh *J. Agric. Res.* **34(2):**175-179.

Burton, G. W. 1952. Quantitative inheritance in grasses. *Proc. 6th Int. Grassland Cong.* **1:** 127-83.

Choudhary, M., Sarawgi, A. K. and Motiramani, N. K. 2004. Genetic variability of quality, yield and yield attributing traits in aromatic rice (*Oryza sativa* L.). *Adv. Pl. Sci.* **17(2):** 484-90.

Fisher, R. A. 1935. The design of experiments. Oliver and Boyd. EdinburghHanson, W. D., Robinson, H. F. and Comstock, R. E. 1956. Biometrical studies of yield in segregating population Korean *Lespandeza. Agron. J.* **48:** 268-272.

Hasib, K. M. 2005. Genetic variability, interrelations and path analysis for panicle characters in scented rice. *Crop Res. J. Hissar.* **30(1):** 37-39.

Hanson, W. D., Robinson, H. F. and Comstock, R. E. 1956. Biometrical studies of yield in screening population. *Korean Lespandeza. Agron.*

J. **48:** 268-272.

Iftekharuddaula, K. M., Hassan, M. S., Islam, M. J., Badshah, M. A., Islam, M. R. and Akhter, K. 2001. Genetic evaluation and selection criteria of hybrids rice in irrigated ecosystem of Bangladesh. *Pakistan J. Biological Science.* **4:** 790-792.

Jaiswal, H. K., Shrivastava, A. K. and Dey, A. 2007. Variability and association studies in indigenous aromatic rice. *Oryza.* **44(4):** 351-353.

Johnson, H. W., Robinson, H. F. and Comstock, R. E. 1955. Estimates of genetic and environmental variability in soybean. *Agron. J.* **47:** 314-318.

Kempthrone, O. 1957. An introduction to genetic studies. John Willey and Sons Inc., New York, USA.

Kole, P. C., Chakrabarthy, N. R. and Bhat, J. S. 2008. Analysis of variability, correlation, path coefficients in induced mutants of aromatic non basmati rice. *Trop. Agric. Res. Exten.* **113:** 60-64.

Li, Y., Zhao. G. L., Zuo, Y. S. and Zhang, C. W. 2003. Studies on the combining ability of head rice milled rate under different environmental condition in three-line *Indica* hybrid rice. *Southwest China J. Agric. Sciences.* **16(2):** 22-25.

Manomani, S. and Fazlullah Khan, A. K. 2003. Studies on combining ability and heterosis in rice. *Madras Agric. J.* **90:** 228-231.

Mustafa, M. A. and Elsheikh, M. A. Y. 2007. Variability, correlation and path coefficient analysis for yield and yield components in rice. *Afri. Crop. Sci. J.* **15:** 183-189.

Panse, V. G. and Sukhatme, P. V. 1957. Genectics and Quantitative

characters in relation to plant breeding. *Indian J. Genetics*. **17**: 312-328.

Prajapati, M., Singh, C. M., Suresh, B. G., Lavanya, G. R. and Jadhav, P. 2011. Genetic parameters for grain yield and its component characters in rice. *Ele. J. Pl. Bred.* **2(2):** 235-238.

Samadhia, D. K. 2005. Genetic variability studies in Lasora(*Cordia myxa* Roxb.). *Indian J. Plant Genetic Resources*. **18(3):** 236-240.

Sao, A. 2002. Studies on combining ability and heterosis in F1 rice hybrids using cytoplasmic male sterile lines.M.Sc. (Ag.) Thesis, IGKV, Raipur, CG.

Sarkar, K. K., Bhutia, K. S., Senapati, B. K. and Roy, S. K. 2007. Genetic variability and character association of quality traits in rice (*Oryza sativa* L.). *Oryza*. **44(1):** 64-67.

Satyanaryana, P. V., Sriniwas, T., Reddy, P. R., Madhavilatha, L. and Suneetha, Y. 2005. Studies on variability, correlation and path coefficient analysis for restorer lines in rice (*Oryza sativa* L.). *Res*

Crops. **6**: 80-84.

Seyoum, M., Sentayehu, A. and Kassahum, B. 2012. Genetic variability, heritability, correlation coefficient and path analysis for yield and yield related traits in upland rice. *J. Plant Sciences*. **7(1):** 13-20.

Singh, S. K., Singh, C. M. and Gil, G. M. 2011. Assesment of genetic variability for yield and its component characters in rice. *Research in Plant Biology*. **1(4):** 73-76.

Subbaiah, P. V., Sekhar, M. R., Reddy, K. H. P. and Reddy, N. P. E. 2011. Variability and genetic parameters for grain yield and its components and kerenel quality attributes in CMS based rice hybrids (*Oryza sativa* L.). *International Journal of Applied Biology and Pharamaceutical Technology*. **2(3):** 603-609.

Verma, U. 201. Genetic diversity analysis in exotic rice genotypes. M.Sc. thesis, Deptt. Of GPB, SHITS, Allahabad.