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Research Article

Genetic variability and character association studies for quality attributing traits in rice (*Oryza sativa* L.)

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Abstract

Twenty rice genotypes were evaluated for quality attributing traits in the agricultural farm of Uttar Banga Krishi Viswavidyalaya, Pundibari, Cooch Behar, in *terai* region of West Bengal. The study was conducted in two different environments *pre-kharif* and *kharif* seasons during 2017-18. Statistical analysis was performed for the assessment of genotypic coefficient of variation (GCV), phenotypic coefficient variation (PCV), broad sense heritability and genetic advance as percentage of the mean (GAM) for the quality attributing traits *viz*., kernel length, kernel breadth, l:b ratio of the kernel, kernel length after cooking, kernel breadth after cooking, amylose content, l:b ratio of the cooked kernel and linear elongation ratio. Analysis of variance, GCV and PCV revealed significant variation for different characters under study. Except for kernel length and kernel length after cooking all the characters under study showed high heritability coupled with high GAM. The genotypic correlation study revealed that the l:b ratio of the cooked kernel had a significant positive correlation with linear elongation ratio (LER), while kernel breadth after cooking had a significant negative correlation with LER. Path analysis study revealed that among all the characters, l:b ratio of cooked kernel showed a significant positive correlation with LER and kernel breadth after cooking showed a significant negative correlation with LER. Among the set of 20 genotypes, three were identified as medium slender, seven had medium grain, seven with short medium type and three had short slender grain. Three genotypes namely, Phougak, Phaourin Nakuppi and Chakhao Sempak were found with aroma.

Key words: GCV, PCV, h^2, Genetic advance as percentage of mean, Correlation, Path, Grain quality traits, Rice

INTRODUCTION

Rice belongs to *Oryza* genus in the family *Poaceae*, containing nearly 20 species with a basic chromosome number of 12 of which *Oryza sativa* L., is the principle cultivated species. More than 90% of the world rice is grown and consumed in Asia. Grains vary in size and stickiness from long and fragrant Indian basmati and Thai Jasmine rice to the short sticky Japanese sushi and Italian aborio rice. There are several different rice colour existing in the market like brown, black, red, green, white or Vitamin A fortified golden rice (Finocchiaro *et al*., 2007; Dubock 2019). Rice contains Lysine (3.8%), the first limiting amino acid (Shobha Rani *et al*., 2006). Indian consumer normally prefers dry, flaky (non-sticky) rice yet consumer preference within the country itself varies enormously. So, the development of biologically superior and physiologically efficient genotypes with increased yield potential and quality grain is essentially required to meet the multi directional demand of ever-increasing consumers for the crop. Different quality characters play an important role in the selection and development of improved varieties, therefore study on these characters and understanding their genetic behavior has great importance. Attempts have been made in the current study to identify the genotypes of rice which have the potentiality to give good yield concomitantly encircled with other grain quality parameters concerned mainly with consumer preference and market demand. In this experiment, the conglomeration of different quality characters was assessed with the help of statistical analysis which includes analysis of variance, variability analysis, correlation studies, and path analysis. These quality parameters were deliberated to point out the existence of any relation out of these parameters with their genetic behavior which in future will help in constructing a suitable plant type combining desirable expression of different characters.

MATERIALS AND METHODS

The study on quality characters was carried out in two seasons, *pre-kharif and kharif* (2017-18). Department of Genetics and Plant Breeding, Faculty of Agriculture Uttar Banga Krishi Viswavidayalaya, Pundibari, Cooch Behar in *terai* region of West Bengal. Twenty rice genotypes *viz*., Phougak, Disang, Kakcheng Phou, Joymati, Satyaranjan, Chakhao sempak, Luit, Mahsuri, Borosolpana, Haripowa sali, Kanaklata, Kushal, Ranjit, Dhansiri, Piolee, Diphalu, Moniram, Bahadur, Teti Sali and Phourin Nakuppi were obtained from Regional Research station, Titabor, Jorhat, Assam. Genotypes were raised in the field using a randomized complete block design with three replications. Plot size was maintained at 2 x 1.5 m with a spacing of 20 cm x 15 cm. Soil type consisted of sandy loam with pH 5.74 and with organic carbon of (0.85%). Application of fertilizers to the crop was made from time to time as per standard recommendation. Intercultural operations were executed as and when necessary. The parameter studied under quality ascribed characters comprised of kernel length, kernel breadth, kernel l:b ratio, grain shape, kernel length after cooking, kernel breadth after cooking, l:b ratio of the cooked kernel, amylose content, linear elongation ratio, aroma content and gelatinization temperature. Grain shape (IRRI, SES, 1996) and presence of GT (Little *et al*., 1958) and presence of aroma (Juliano, 1971) were estimated and analysis of variance study was not executed. Genotypic variances, broad sense heritability, GAM, correlation and direct and indirect effect of various traits were estimated. Methods used include ANOVA by Panse and Sukhatme (1985), PCV and GCV by Burton (1952), simple correlation by Johnson *et al*. (1955), Path analysis by Dewey and Lu (1959). The genetic parameters (GCV, PCV, broad sense heritability and genetic advance as per cent of mean) along with correlation and path analysis was done only on the basis of the pooled data. The software used for statistical analysis were WINDOSTAT and GENRES.

RESULTS AND DISCUSSION

The presence of genetic variability is the fundamental basis for any plant breeding programme. The presence of adequate variability in quality traits is a crucial part for the overall development of a crop respective to genotype. For the assessment and for further improvement of the set of population, the current study was executed. Analysis of variance (**Table 1**) for two seasons showed significant variations in the set of genotypes for each and every parameter and pooled analysis data unfold that the genotypes differed significantly for each and every quality attributing traits except linear elongation ratio which revealed the good scope of qualitative improvement in high yielding rice genotypes. A similar kind of result

Table 1. Analysis of variance for eight quality characters in rice genotypes

Year	Sources of variation	Df	Mean Sum of Square (MSS)							
			Kernel length	Kernel breadth	l:b ratio of kernel	Kernel length after cooking	Kernel breadth after cooking	Amylose content	l:b ratio of cooked kernel	Linear elongation ratio (LER)
First Year	Replication	2	0.002	0.001	0.002	0.003	0.001	0.276	0.014	0.001
	Genotypes	19	0.910**	0.488**	1.237**	0.532**	0.440**	14.232**	0.503**	0.057**
	Error	38	0.003	0.001	0.003	0.006	0.003	0.131	0.020	0.0004
Second Year	Replication	2	0.010	0.004	0.013	0.013*	0.004	0.013	0.007*	0.005
	Genotypes	19	0.601**	0.459**	1.392**	0.410**	0.552**	15.630**	0.597**	0.176**
	Error	38	0.004	0.003	0.005	0.003	0.002	0.026	0.002	0.007
Pooled	Years	1	0.006	3.581**	7.793**	0.246*	0.015	0.660	0.076	5.242**
	Genotypes	19	1.395**	0.716**	2.023**	0.887**	0.930**	29.647**	1.038**	0.114
	G × Y	19	0.112	0.232	0.606	0.054	0.061	0.218	0.063	0.119
	Error	76	0.004	0.002	0.004	0.005	0.003	0.079	0.011	0.004

*, ** Significant at 5%, and 1% levels of probability, respectively.

was also observed by Roy *et al.* (2009). Genotypic coefficient of variation ranged from 4.83 to 30.69 per cent, whereas the phenotypic coefficient of variation ranged from 4.87 to 30.84 per cent among the eight quality attributing parameters. High magnitude of GCV and PCV (**Table 2**) was obtained only for amylose content and the rest of the characters had shown low GCV and PCV values. Sivasubramanian and Madhavamenon (1973) had classified the magnitude of GCV and PCV values in low (< 10%), moderate (10-20%) and high (> 20%). Very minimal differences between GCV and PCV values were noted for kernel length, kernel breadth, l:b ratio of the kernel, kernel length after cooking, kernel breadth after cooking and amylose content which signified that these characters were least influenced by the environment.

The broad sense heritability was high for each and every quality attributing character under the present study (**Table 2**). Categorization of heritability values suggested by Johnson *et al.* (1955). Low (< 30%), moderate (30-60%) and high (> 60%). But heritability estimation alone was not sufficient enough to give any conclusive result because it added the outcome of both the additive and non-additive gene action. Thus, genetic advance as a percentage of mean played a crucial part in selection in addition to the heritability effect. The assessment of high heritability coupled with high GAM was recorded for kernel breadth, kernel l:b ratio, kernel breadth after cooking, amylose content, l:b ratio of the cooked kernel and linear elongation ratio which revealed the prevalence of additive gene control on these characters and hence genetic advancement through selection can be worthwhile for these parameters. For kernel l:b ratio, kernel breadth after cooking and l:b ratio of cooked kernel similar results were reported by Dhanwani *et al.* (2013). For kernel breadth, amylose content and LER similar results were reported by Sahu *et al.* (2017).

The parameters *viz.*, kernel length and kernel length after cooking had revealed high heritability coupled with moderate and low GAM, respectively which indicated the influence of non-additive gene action on these characters. For kernel length similar results were also reported by Babu *et al.* (2012) and for KLAC similar results were also reported by Meghawal *et al.* (2015). Thus, for the development of these parameters complex breeding may be advocated. The range of heritability and GAM was classified as suggested by Johnson *et al.* (1955). Low (< 10%), moderate (10-20%) and high (> 20%). For the characters, gelatinization temperature (GT), aroma and grain shape, statistical analysis was not done. Based on GT, different genotypes were classified as high GT and intermediate GT. GT determine the water uptake and time required for cooking. It, also, may reflect the hardness of rice starch granules for cooking (Mady, 1994). As per consumer preference, intermediate GT is a good quality parameter. In this study, (**Table 3**) some genotypes had very high GT which includes Disang, Satyaranjan, Borosolpana, Haripowasali and Moniram and their ASV score was 2. And based on the ASV score (3-4) rest of the genotypes had shown intermediate GT. The similar result were also recorded by Khaled *et al*. (2016), Bansal *et al*. (2006) and Nirmaladevi *et al*. (2015). Madhan Mohan *et al*. (2021) recorded 4-5 ASV values. The existence of aroma in different rice genotypes were classified as mild and medium (**Table 4**). The aroma was absent in the maximum number of genotypes. Only three genotypes namely, Phougak, Phaourin Nakuppi (mild aroma) and Chakhao Sempak (medium aroma) were found with the presence of aroma. The genotypes on assessment on grain shape (**Table 5**) were classified based on SES, IRRI, (1996). Three genotypes had medium slender grain shape, whereas seven genotypes had the medium type of grain shape, seven genotypes had short medium type of grain shape and three genotypes had the short

Table 2. Mean, range, GCV, PCV, heritability and genetic advance for eight quality characters in rice genotypes

S. No.	Character	Mean	Range		GCV (%)	PCV (%)	Heritability % (broad sense)	Genetic advance as percentage of mean
			Minimum	Maximum				
1	Kernel length (mm)	5.49	4.77	6.50	8.76	8.79	99.37	17.99
2	Kernel breadth (mm)	1.94	1.07	2.41	17.76	17.82	99.29	36.46
3	l:b ratio of kernel	2.97	2.14	4.49	19.50	19.56	99.33	40.03
4	Kernel length after cooking (mm)	7.94	7.45	8.95	4.83	4.87	98.46	9.87
5	Kernel breadth after cooking (mm)	2.92	2.39	3.46	13.49	13.54	99.37	27.71
6	Amylose content (%)	7.23	3.03	11.57	30.69	30.84	99.08	62.94
7	l:b ratio of cooked kernel	2.79	2.21	3.49	14.84	15.06	97.17	30.14
8	Linear elongation ratio (LER)	1.24	1.03	1.61	10.88	11.44	90.52	21.33

Table 3. The scores of ASV in 20 rice genotypes

S. No.	Genotype	ASV score	GT
1	Phougak	3	High, Intermediate
2	Disang	2	High>74°c
3	Kakcheng Phou	3	High, Intermediate
4	Joymati	3	High, Intermediate
5	Satyaranjan	2	High>74°c
6	Chakhao Sempak	3	High, Intermediate
7	Luit	3	High, Intermediate
8	Mahsuri	3	High, Intermediate
9	Borosolpana	2	High>74c°
10	Haripowa sali	2	High>74°c
11	Kanaklata	3	High, Intermediate
12	Kushal	3	High, Intermediate
13	Ranjit	3	High, Intermediate
14	Dhansiri	3	High, Intermediate
15	Piolee	4	Intermediate (70- 74°c)
16	Diphalu	3	High, Intermediate
17	Moniram	2	High>74°c
18	Bahadur	3	High, Intermediate
19	Teti Sali	3	High, Intermediate
20	Phourin Nakuppi	3	High, Intermediate

Table 4. Assessment of aroma in 20 genotypes of rice

S. No.	Name of genotype	Scent	Judge 1	Judge 2	Judge 3
1	Phougak	*P*	+	+	+
2	Disang	*A*	-	-	-
3	Kakcheng Phou	*A*	-	-	-
4	Joymati	A	-	-	-
5	Satyaranjan	*A*	-	-	-
6	Chakhao Sempak	*P*	++	++	++
7	Luit	*A*	-	-	-
8	Mahsuri	*A*	-	-	-
9	Borosolpana	*A*	-	-	-
10	Haripowa sali	*A*	-	-	-
11	Kanaklata	*A*	-	-	-
12	Kushal	*A*	-	-	-
13	Ranjit	*A*	-	-	-
14	Dhansiri	*A*	-	-	-
15	Piolee	*A*	-	-	-
16	Diphalu	*A*	-	-	-
17	Moniram	*A*	-	-	-
18	Bahadur	A	-	-	-
19	Teti Sali	*A*	-	-	-
20	Phourin Nakuppi	*P*	+	++	+

***P**=Present, A=Absent*
Scoring: - + =Mild, ++ =Medium, +++ =Strong

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Table 5. Assessment of grain shape and size in 20 genotypes of Rice

S. No.	Name of genotype	Grain shape
1	Phougak	MS
2	Disang	MM
3	Kakcheng phou	SM
4	Joymati	MM
5	Satyaranjan	MM
6	Chakhao sempak	MM
7	Luit	MM
8	Mahsuri	SM
9	Borosolpana	MM
10	Haripowa sali	MM
11	Kanaklata	SM
12	Kushal	SM
13	Ranjit	SM
14	Dhansiri	SS
15	Piolee	SS
16	Diphalu	SS
17	Moniram	SM
18	Bahadur	SM
19	Teti sali	MS
20	Phourin nakuppi	MS

MS= Medium slender, MM= Medium medium, SM=Short medium, SS= Short slender

slender type of grain shape out of total twenty genotypes. Amudha and Thiyagarajan (2008) also recorded grain size and shape and distinct into medium, bold and slender. Madhan Mohan *et al*. (2021) were also reported short bold and medium slender type of grain shape. Sahu *et al*. (2017) recorded four types of grain shapes short slender, short bold, medium slender, long slender and long bold. Significant variation for every quality characters was noted which provided substantial opportunities for selection of lines of high quality for specific or combination of characters. The same finding was noted by Vanaja *et al.* (2006) on the improvement of rice quality parameters. The genotypic correlation coefficient among eight characters indicated a different degree of association between characters at the genotypic level (**Table 6**). A significant positive correlation was revealed by kernel length with kernel breadth and kernel length after cooking. Singh *et al*. (2017) and Kumar *et al.* (2019) reported a significant and positive correlation of kernel length with kernel length after cooking and the l:b ratio of kernel. Krishna *et al*. (2008) reported a significant and positive association of kernel length with kernel breadth and a significant negative association of kernel breadth with kernel l:b ratio. However, Meghawal *et al.* (2015) reported that kernel length before cooking, kernel length after cooking, kernel breadth after cooking showed a significant positive correlation with l:b ratio. Sabesan *et al.* (2009) reported a positive significant association of grain yield per plant with kernel length and kernel breadth. Kernel l:b ratio reported a significant positive correlation with amylose content. Although Kumar *et al.* (2019) reported a significant negative association between kernel l:b ratio and amylose content. Kernel length after cooking reported a significant positive correlation with kernel l:b ratio after

Table 6. Estimates of genotypic correlation coefficient among the eight quality attributing characters in rice genotypes

Character	Kernel breadth	l:b ratio of kernel	Kernel length after cooking	Kernel breadth after cooking	Amylose content	l:b ratio of cooked kernel	Linear elongation ratio (LER)
Kernel length	0.401**	-0.036	0.420**	0.010	-0.125	0.149	-0.183
Kernel breadth		-0.910**	-0.016	0.248	-0.517**	-0.196	0.051
l:b ratio of kernel			0.247	-0.261	0.486**	0.297	-0.074
Kernel length after cooking				-0.146	-0.057	0.452**	0.351
Kernel breadth after cooking (mm)					-0.348	-0.946**	-0.419**
Amylose content						0.259	0.093
l:b ratio of cooked kernel							0.482**

** significant at 1% probability level.

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Table 7. Genotypic path coefficient analysis showing the direct (diagonal) and indirect (off-diagonal) effects of quality attributing characters in rice genotypes

Character	Kernel length (mm)	Kernel breadth	l:b ratio of kernel	Kernel length after cooking	Kernel breadth after cooking	Amylose content	l:b ratio of cooked kernel	Correlation with Linear elongation ratio (LER)
Kernel length	**-2.224**	2.896	-0.223	3.227	-0.234	0.080	-3.706	-0.183
Kernel breadth	-0.891	**7.228**	-5.605	-0.122	-5.756	0.332	4.866	0.051
l:b ratio of kernel	0.080	-6.576	**6.161**	1.898	6.035	-0.312	-7.360	-0.074
Kernel length after cooking	-0.933	-0.114	1.520	**7.689**	3.378	0.037	-11.225	0.351
Kernel breadth after cooking	-0.022	1.796	-1.605	-1.121	**-23.166**	0.223	23.477	-0.419**
Amylose content	0.279	-3.739	2.995	-0.441	8.062	**-0.641**	-6.422	0.093
l:b ratio of cooked kernel	-0.332	-1.417	1.827	3.478	21.913	-0.166	**-24.820**	0.482**

Residual value = 0.54

cooking. Meghawal *et al.* (2015) reported a significant positive association between kernel length after cooking and grain l:b ratio. The l:b ratio of the cooked kernel also exhibited a significant positive correlation with LER. A similar result was also reported by Priyanka *et al*. (2020). Selection of this trait l:b ratio after cooking will serve as an improvement of LER. A significant negative correlation was revealed by the characters *viz*., kernel breadth with kernel l:b ratio and amylose content. A similar result was reported by Kumar *et al*. (2019) although they found a significant positive association between kernel breadth and amylose content. Also, kernel breadth after cooking showed a significant negative correlation with the LER and l:b ratio of the cooked kernel. Kumar *et al.* (2019) reported a significant positive association between cooked kernel breadth and LER. Correlation study reveals that l:b ratio of cooked kernel appeared to be the primary contributing character which could be helpful in for the selection of genotypes.

The straight and indirect effects of quality attributing characters on LER following path analysis executed at genotypic level (**Table 7**). The residual effect was high 0.54 which meant the requirement for consideration of additional characters under the experiment to draw more efficient and precise results. The parameters kernel breadth, kernel length after cooking and amylose content had a positive straight effect on the linear elongation ratio. A similar result was also reported by Priyanka *et al*. (2020) and Premkumar *et al*. (2016). Among all these characters l:b ratio of cooked kernel revealed a significant positive correlation with the linear elongation ratio. And kernel breadth after cooking had shown a significant negative correlation with LER. Though kernel length after cooking, kernel breadth and l:b ratio of kernel showed the highest direct effect on LER. The negative direct effects were observed for kernel length, kernel breadth after cooking, amylose content and l:b ratio of the cooked kernel. Naik *et al*. (2021) recorded a negative direct effect for amylose content and LER. But it showed a low correlation with LER and the positive effect may be negated by indirect negative contribution *via* kernel length, kernel breadth and l:b ratio of the cooked kernel. Makwana *et al*. (2009) also stated that the selection for kernel l:b ratio, water uptake, alkali score and cooking time could indirectly improve the cooking quality. Path analysis allows the division of the correlation coefficient into direct and indirect effects which help to identify effective traits for further improvement. In this study, path analysis revealed that kernel length after cooking and kernel breadth were reliable for the selection programme.

The present study in rice quality attributing traits may lead to accomplish result of practical value in the identification of superior genotypes and also for framing a breeding approach to bring concomitant improvement for quality parameters. The current investigation unveiled that for quality improvement, the focus should be given to gelatinization temperature, kernel breadth, l:b ratio of kernel, amylose content, aroma and kernel length after cooking. The study on variability, heritability and genetic advance also indicated the opportunity for the improvement of kernel breadth, l:b ratio of kernel and amylose content through selection in view of high heritability coupled with high genetic advance as percentage of the mean. The character l:b ratio of the cooked kernel was detected to be significantly and positively correlated with the linear elongation ratio. The result of path analysis exhibited a significant positive direct effect of l:b ratio of the cooked kernel on the linear elongation ratio. Kernel breadth after cooking had shown the significant negative direct effect on linear elongation ratio. These traits could be considered as key components to enhance the qualitative aspect with respect to individual genotypes.

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