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## Research Note

### Genetic variation and character association for grain yield and component traits in traditional rice (*Oryza sativa* L.) cultivars of Assam

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#### Abstract

An experiment was conducted with a view to obtain information of genetic parameters of variation and character association for 13 quantitative traits in a set of 64 rice cultivars of Assam. The study revealed significant differences for all the traits under study. Highest genotypic coefficient of variation was observed for the trait biological yield followed by harvest index and grain yield. More than 80% heritability was observed for all the traits except grain yield, effective tillers per plant and biological yield. Genetic advance as *per cent* of mean was highest for biological yield followed by harvest index, filled grains per panicle and grain yield. Higher magnitude of genetic advance along with considerably high heritability observed for harvest index, filled grains per panicle and biological yield indicated that these traits could be considered for selection to obtain high genetic gain. Character association studies indicated that direct selection of 100 - grain weight, grain length, grain breadth, biological yield and harvest index, would bring about improvement in grain yield. Non-significant association of grain yield with important yield attributes *viz.*, filled grain per panicle, tillers per plant and panicle length were due to their strong association with duration of genotypes, which in turn was negatively associated with grain yield. Recombination breeding and recurrent selection, therefore, could be suggested to break the negative linkage in order to achieve further genetic improvement.

**Keywords:** character association, genetic improvement, genetic variability, rice

Rice (*Oryza sativa* L.), is the principal food of more than 50 *per cent* of the global population. In South-East Asia 90 *per cent* of the people consume rice as their main source of energy (Anonymous 2018). In India, rice is grown in an area of 44 m ha, with a total production of 116 million tones and productivity of 2700 kg ha<sup>-1</sup> (Anonymous 2021). India is endowed with a large number of cultivated and

wild rice genotypes in different eco-geographical regions of its vast territorial land. Out of the different rice growing areas, Assam and adjoining states of northeast. India comprises a very rich region having enormous forms of cultivated rice. Altogether, there are 13 cultivated varietal groups of rice grown in the state of Assam, having a large array of diverse land races, which are reservoirs

of many economically important traits including yield and adaptation (Baruah and Das, 1995). Because of the ethnic preferences of traditional varieties having their specific indigenous uses, these varieties are still cultivated by the farmers despite their very low yield potential. Attempt for improvement of these land races have also been very much limited with the advent of modern high yielding semi-dwarf varieties. It is, therefore, utmost necessary to undertake yield improvement program in the traditional varieties. For any breeding program, the estimation of genetic parameter of variation is an essential component. The information thus obtained can be used in future crop improvement programs (Sarma *et al.*, 2022). Grain yield being a complex trait having contributions by many component traits, a detail study of interrelationship of different yield and yield contributing traits is necessary. This helps in identifying the traits that directly or indirectly influence the overall productivity of the crop and improves the efficiency of genetic selection in plant breeding programs (Pande *et al.*, 2006). Keeping, these in view, the present investigation was, carried out in order to assess the genetic parameters of variation and estimate the genotypic correlations amongst grain yield and associated traits in a set of traditional rice cultivars of Assam.

The materials for the present investigation consisted of a set of 64 rice cultivars collected from farmers' fields of North Bank Plain Zone, Upper Brahmaputra Valley Zone and Hill zones of Assam. The investigation was carried out at the experimental field of the Advanced Level Biotech Hub, Biswanath College of Agriculture, Biswanath Chariali, located at the latitude of 26° 15'N, 77° 45'S, the longitude of 92° 42'E, 95° 30'W and altitude of 104 m MSL. The crop for the present investigation was raised during *Kharif* season 2021. The experiment was laid down in a randomized block design with two replications. As per standard guidelines from IRRI, the germinated rice seedlings of all cultivars were first grown in well protected nursery beds and after 21 days, they were transplanted to well puddled experimental field. Each plot consisted of five rows of six meters in length with spacing 20 cm between plants and 25 cm between rows. Single seedling was transplanted per hill and the crop was raised following the recommended package of practices. Observations on 13 traits were recorded as per the standard evaluation system for rice by IRRI (IRRI, 2013). Data on days to 50 % flowering and days to maturity were recorded on plot basis. Five plants were randomly selected from each plot to record the observations on the traits, *viz.*, plant height, effective tillers per plant, panicle length, number of filled grains per panicle, 100 grain weight, grain yield per plant, grain length, grain width, length: breadth ratio, biological yield per plant, and harvest index. The mean data were subjected to the analysis of variance (Panse and Sukhatme, 1967) and the mean sum of squares, obtained from the analysis of variance, was subjected to

estimation of genetic parameters of variation (Singh and Choudhary, 1985). Estimates of variability parameters, heritability and genetic advance were calculated using standard methods (Burton and Devane, 1953; Johnson *et al.*, 1955). The same data set were subjected to analysis of covariance and genotypic and phenotypic correlation coefficients (Singh and Choudhary, 1985).

The analysis of variance for 13 traits revealed highly significant differences among the genotypes for all the observed characters indicating the existence of high variability among the varieties. Thus, there is an ample scope for selection of different quantitative characters for rice improvement. The appearance of a large extent of variability might be due to the diverse type of cultivars under different agro-ecological condition in the zone. Earlier several workers, who worked on rice, have reported the presence of variability amongst the genotypes of rice for different quantitative traits. (Singh *et al.*, 2011; Dhurai *et al.*, 2014; Das *et al.*, 2014; Lingaiah *et al.*, 2020; Ahmed *et al.*, 2021). The estimated genetic parameters of variation are presented in **Table 1**. There was good agreement of the values of genotypic and phenotypic variance, indicating relatively less influence of environment in expression of these traits. Genotypic and phenotypic variance was observed highest for biological yield followed by filled grains per panicle and plant height. However, highest genotypic coefficient of variation (GCV) along with phenotypic coefficient of variation (PCV) was observed for biological yield followed by harvest index and grain yield. Mere presence of variability does not indicate the effectiveness of selection unless the heritable fraction of the variation is known (Burton 1952). Heritability in broad sense was estimated and found highest in days to 50% flowering (98.7%), followed by days to maturity, and filled grains per panicle. More than 80% heritability in broad sense was observed for all the traits except effective tillers per plant, grain yield and biological yield. Thus, the traits, harvest index, biological yield, filled grains per panicle and grain yield having high GCV and considerably higher magnitude of heritability could be considered for further genetic improvement of a trait. In order to quantify the genetic gain obtained from selection, along with heritability, estimation of genetic advance is important. High heritability with high genetic advance is very effective in predicting the resultant effect for selecting the best suitable cultivar (Sharma and Richaria, 1995). Again, it has been reported from previous work that heritability along with genetic advance serve as the definitive criteria to arrive at a reliable conclusion about selection (Dhurai *et al.*, 2014). Genetic advance as *per cent* of mean was highest for biological yield (94.33%), followed by harvest index (78.96%), grain yield (80.16%) and filled grains per panicle (66.28%). Thus, the traits, *viz.*, biological yield, harvest Index, filled grains per panicle and grain yield were found promising for obtaining further genetic gain on selection. (Bhadru *et al.*, 2012)

**Table 1. Genetic parameter of variations for 13 quantitative traits in 64 rice cultivars**

Genetic Parameters	DF	DM	PH (cm)	PL (cm)	ET	FG per panicle	100 GW (g)	GY per plant (g)	GL (mm)	GB (mm)	Grain L:B	BY	HI
Mean	117.97	149.67	145.38	25.93	10.01	124.9	2.172	23.64	8.23	2.93	2.88	98.80	28.47
Range	72-154	103-188	91.76-202.3	18.3-33.1	4.8-14.2	44.9-257.44	1.3-3.19	7.88-51.5	7.1-9.67	1.96-4.38	2.09-4.51	19.049-250.73	7.234-54.67
Genetic variation	333.7	312.95	614.5	7.65	2.28	1667.9	0.113	86.23	0.20	0.17	0.18	2068.5	125.8
Env variation	4.29	5.58	56.07	1.26	1.45	565.81	0.016	1.5	0.45	0.016	0.021	22.33	4.34
Phenotypic variation	338.008	318.53	671.6	8.92	3.74	1724.7	0.129	87.83	0.65	0.19	0.20	2090.9	130.19
GCV	15.48	11.81	18.14	10.64	15.11	32.69	15.49	39.28	6.01	14.3	14.92	45.75	39.40
PCV	15.58	11.92	20.11	11.49	19.33	33.25	16.56	39.64	10.2	14.94	15.78	48.28	40.07
Heritability (%)	98.7	98	81.36	85	61	96	90	75	87.5	91	89	78	96
Genetic Advance	37.39	36.12	48.83	5.28	2.43	82.79	0.79	18.95	0.64	0.82	0.82	93.19	22.72
GA as percent of Mean	31.71	24.14	33.71	20.36	24.27	66.28	36.40	80.16	7.78	28.27	29.28	94.33	79.83
CV	1.76	1.57	8.68	4.34	12.0	6.03	0.13	5.35	0.127	0.12	0.14	13.5	7.32

Grain yield being the function of several component traits, direct selection is not effective for this. Therefore, it is required to estimate the correlation of different components traits amongst themselves and with grain yield. This indicates the selection criteria for obtaining improvement in yield and better understanding of the shared biological pathway (Rheenen *et al.*, 2019). In the present investigation correlation matrix for the 13 traits were prepared at both phenotypic and genotypic levels, which are presented in **Table 2 and Table 3**. The analysis revealed good agreement between genotypic and phenotypic correlation coefficients indicating less influence of environmental fluctuation in the experimental material. Grain yield was found to be positively and significantly correlated with 100 - grain weight, grain length, grain breadth, biological yield and harvest index at both genotypic and phenotypic level. This finding finds co- linearity with the observations made by other workers (Akinwale *et al.*, 2011; Ratna *et al.*, 2015). However, negative significant correlation of grain yield was observed with days to 50% flowering and days to maturity. This observation of the late maturing genotypes being low yielder might be due to the traditional photosensitive genotypes with poor yield traits. Similar results were also observed by other workers (Zahid *et al.*, 2006; Pradhan *et al.*, 2021) which implies an increase in flowering time and maturity increases the time period for harvest which causes loss in yield. Thus, it indicated that direct selection for grain weight, grain breadth, grain length, biological yield and harvest index will bring simultaneous improvement in grain yield. Negative correlation of traits provides important clue as to what kind of character combinations will have to be considered

while selecting indirectly to improve the grain yield. The traits with positive significance with yield also showed positive correlation amongst them such as grain weight with harvest index and biological yield; harvest index with biological yield. Grain length and grain breadth, although showed positive association with grain yield, did not show positive correlation with other traits having positive association with grain yield. Grain length and grain width were negatively correlated, indicating selection for longer grain will yield long slender types of grains. Also, it came to light that both genotypic and phenotypic level, days to 50% flowering is positively and significantly correlated with days to maturity and filled grains per panicle which were in agreement with the findings of Verma *et al.*, 2021. It can also be concluded that since medium to long duration varieties synthesize more carbohydrate, they could produce more filled grains per panicle (Verma *et al.*, 2021).

Negative and significant correlations were observed between biological yield with days to flowering and maturity. Grain weight was also negatively associated with panicle length and effective tillers per plant. Undesirable negative association observed in grain yield with days to 50% flowering and days to maturity needs to be broken in order to further improve grain yield. Recombination breeding with recurrent selection may be suggested for breaking such undesirable linkage. Panicle length, one of the important yield attributing traits, showed non-significant association with grain yield. This may be due to its negative association with other yield traits like 100-grainweight. Another important yield trait, effective tillers per plant also showed negative association with

**Table 2. Genotypic correlation matrix for grain yield and other traits in 64 rice genotypes.**

	DF	DM	PL HT	PL	ET	FG	100GW	GY	GL	GW	L:B	BY	HI
DF	1												
DM	0.992**	1											
PL HT	-0.049 <sup>NS</sup>	-0.064 <sup>NS</sup>	1										
P L	-0.067 <sup>NS</sup>	-0.030 <sup>NS</sup>	0.386**	1									
ET	-0.026 <sup>NS</sup>	0.007 <sup>NS</sup>	-0.114 <sup>NS</sup>	0.080 <sup>NS</sup>	1								
FG	0.186*	0.178*	-0.072 <sup>NS</sup>	0.037 <sup>NS</sup>	-0.110 <sup>NS</sup>	1							
100 GW	-0.093 <sup>NS</sup>	-0.074 <sup>NS</sup>	0.087 <sup>NS</sup>	-0.202*	-0.320**	-0.05 <sup>NS</sup>	1						
GY	-0.233**	-0.212*	-0.011 <sup>NS</sup>	0.048 <sup>NS</sup>	0.071 <sup>NS</sup>	0.050 <sup>NS</sup>	0.300**	1					
GL	0.003 <sup>NS</sup>	0.008 <sup>NS</sup>	0.163 <sup>NS</sup>	0.087 <sup>NS</sup>	-0.187*	0.198*	0.13 <sup>NS</sup>	0.205*	1				
GW	-0.133 <sup>NS</sup>	-0.123 <sup>NS</sup>	-0.159 <sup>NS</sup>	-0.065 <sup>NS</sup>	0.163 <sup>NS</sup>	-0.17 <sup>NS</sup>	0.00 <sup>NS</sup>	0.295**	-0.857**	1			
L:W	0.325**	0.296**	-0.053 <sup>NS</sup>	-0.091 <sup>NS</sup>	-0.059 <sup>NS</sup>	0.293**	-0.02 <sup>NS</sup>	-0.10 <sup>NS</sup>	0.009 <sup>NS</sup>	-0.093 <sup>NS</sup>	1		
BY	-0.238**	-0.197*	0.071 <sup>NS</sup>	0.204*	0.085 <sup>NS</sup>	0.295**	0.232**	0.205*	0.109 <sup>NS</sup>	-0.012 <sup>NS</sup>	-0.50**	1	
HI	0.075 <sup>NS</sup>	0.088 <sup>NS</sup>	-0.006 <sup>NS</sup>	0.059 <sup>NS</sup>	0.277**	0.733**	0.224*	0.182*	0.080 <sup>NS</sup>	-0.018 <sup>NS</sup>	0.274**	0.313**	1

NB: \* Significant at 0.05 probability level, \*\* Significant at 0.01 level of probability, NS= Non significant

**Table 3. Phenotypic correlation matrix for grain yield and other traits in 64 rice genotypes**

	DF	DM	PH	PL	ET	FG	100Gw	GY	GL	GB	L:B	BY	HI
DF	1												
DM	0.977**	1											
PH	-0.049 <sup>NS</sup>	-0.061 <sup>NS</sup>	1										
PL	-0.058 <sup>NS</sup>	-0.032 <sup>NS</sup>	0.328**	1									
ET	-0.014 <sup>NS</sup>	-0.014 <sup>NS</sup>	-0.102 <sup>NS</sup>	0.071 <sup>NS</sup>	1								
FG	0.174*	0.172 <sup>NS</sup>	-0.058 <sup>NS</sup>	0.034 <sup>NS</sup>	-0.090 <sup>NS</sup>	1							
100Gw	-0.089 <sup>NS</sup>	-0.069 <sup>NS</sup>	0.047 <sup>NS</sup>	-0.166 <sup>NS</sup>	-0.261**	-0.060 <sup>NS</sup>	1						
GY	-0.217*	-0.194*	0.001 <sup>NS</sup>	0.054 <sup>NS</sup>	0.066 <sup>NS</sup>	0.032 <sup>NS</sup>	0.296**	1					
GL	0.009 <sup>NS</sup>	0.003 <sup>NS</sup>	0.151 <sup>NS</sup>	0.077 <sup>NS</sup>	-0.125 <sup>NS</sup>	0.171 <sup>NS</sup>	0.126 <sup>NS</sup>	0.189*	1				
GB	-0.127 <sup>NS</sup>	-0.108 <sup>NS</sup>	-0.143 <sup>NS</sup>	-0.050 <sup>NS</sup>	0.116 <sup>NS</sup>	-0.152 <sup>NS</sup>	0.013 <sup>NS</sup>	0.306**	-0.858**	1			
L:B	0.319**	0.291**	-0.048 <sup>NS</sup>	-0.084 <sup>NS</sup>	-0.043 <sup>NS</sup>	0.294**	-0.023 <sup>NS</sup>	-0.101 <sup>NS</sup>	0.003 <sup>NS</sup>	-0.083 <sup>NS</sup>	1		
BY	-0.232**	-0.192*	0.072 <sup>NS</sup>	0.194*	0.080 <sup>NS</sup>	0.287**	0.237**	0.205*	0.112 <sup>NS</sup>	-0.019 <sup>NS</sup>	-0.484**	1	
HI	0.074 <sup>NS</sup>	0.083 <sup>NS</sup>	-0.010 <sup>NS</sup>	0.063 <sup>NS</sup>	0.231**	0.711**	0.214*	0.174*	0.077 <sup>NS</sup>	-0.016 <sup>NS</sup>	0.270**	0.307**	1

NB: \* Significant at 0.05 probability level, \*\* Significant at 0.01 level of probability, NS= Non-significant.

Abbreviations for table 1, 2 and 3: DF-days to 50% flowering, DM-days to maturity, PH-plant height, PL-panicle length, EF-effective tillers, FG-filled grains, GW-grain weight, GY-grain yield, GL-grain length, GB-grain breadth, BY-biological yield, HI-harvest index. GCV- genetic coefficient of variation, PCV- Phenotypic coefficient of variation. CV-coefficient of variation

100-grain weight and grain length, which made it to be non-significantly associated with grain yield. Filled grains per panicle exhibited non-significant association with grain yield. However, it exhibited positive association with biological yield, harvest index, grain length. In spite of having associated positively with them, its non-significant association with grain yield might be due to its positive association with days to flowering and maturity, which in turn exhibited negative association with grain yield. Such negative association, if broken by recombination breeding,

would pave the way for further yield improvement in these genotypes

In the present investigation, it appeared that the set of indigenous rice genotypes were diverse with respect to 13 quantitative traits under study showing potentiality for further improvement. Character association studies indicated that direct selection of 100-grain weight, grain breadth, biological yield, harvest index and grain length would bring about improvement in yield. Recombination

breeding may be suggested to break undesirable negative association or to induce positive association of important yield components with grain yield.

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