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Studies on Variability and Interrelationship of Panicle Components and Their Association with Grain Yield in Traditional Rice

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Abstract: *Forty four lowland traditional rice genotypes were evaluated during kharif season of 2009-10 at Zonal Adaptive Research Station, Krishnagar, Nadia, West Bengal for 23 panicle yield and its attributing traits. Significant varietal differences were observed for all the characters. The GCV was less than PCV for all the characters indicating considerable influence of the environment on their expression. High GCV and PCV were observed for number of grains on secondary branches panicle^{-1}, number of spikelets on secondary branches panicle^{-1}, 100 grain weight, 100 kernel weight, panicle yield, number of secondary branches panicle^{-1} and number of spikelets panicle^{-1} whereas, the remaining characters expressed low to medium GCV. High heritability along with high genetic advance as percentage of mean were exhibited by number of spikelets on secondary branches panicle^{-1}, number of grains on secondary branches panicle^{-1}, 100 grain weight, 100 kernel weight and panicle yield indicating their control by additive gene action and chances of further improvement by selection. Among the panicle yield attributing traits, number of primary branches per panicle, number of grains on primary branches panicle^{-1}, number of spikelets on primary branches panicle^{-1}, grain length, grain breadth, grain thickness, kernel breadth, kernel thickness, 100 grain weight, 100 kernel weight correlated significantly and positively with panicle yield both at the genotypic and phenotypic levels whereas, high significant and positive genotypic and phenotypic association revealed between number of secondary branches panicle^{-1} and number of spikelet panicle^{-1}, number of spikelets on secondary branches panicle^{-1} and number of grains on secondary branches panicle^{-1}.*

Key words*: Traditional rice, genetic advance, heritability, correlation coefficients*

I. Introduction

Rice (*Oryza sative* L.) is one of the most important cereals and is the main food crop to the lives of billions of people around the world as world rice consumption increased 40 percent in the last 30 years, from 61.5kg per capita to about 85.9kg per capita in terms of milled rice.(Source: www.unctad.org). It is considered as one of the oldest domesticated grain.

The genus Oryza probably originated in the humid regions of the Gondowana land supercontinents by Chang (1976). In order to feed the growing population ventures are being made in all the rice growing areas to augment the yield per hectare but the success of hybridization and thereafter selection of desirable segregants depends largely on the selection of parents with high genetic variability for different characters. The diversity in crop varieties is considered as a significant parameter for increasing food production, in mitigating poverty and promoting economic growth overall contributing to the development of Agriculture. It serves as an insurance against unknown future needs and conditions thereby contributing to the stability of forming systems at local, national and global levels (Singh *et al*. 2000). For a rational approach to the improvement of yield, it is essential to have some information on the nature of inheritance and association between different yield components and their relative contributions to yield. The correlation analysis measures the existence of relationship between various plant characters and determines the components on which selection can be based for improvement in seed yield. Hence, the present study was conducted to evaluate the extent of genetic variation and trait relationship for various panicle characters in the rice cultivars that all contributed to the yield, so accordingly after harvest, 23 such panicle component characters were examined for each variety to evaluate their contribution to the yield value.

II. Materials And Methods

The present investigation was carried out using 44 traditional lowland rice cultivars, collected from the gene bank of rice Research Station, Chinsurah, Hoogly during kharif season of 2009 at the Instructional Farm of Zonal Adaptive Research Station, Krishnagar, Nadia, West Bengal (23˚24´N latitude and 88˚31´E longitude with an altitude of 9.75 meters above mean sea level). The soil reaction gives a slightly acidic pH of 6.0, with low soluble salts (EC of 0.15 dS m^{-1}**),** medium organic carbon content (0.57%), Total N (0.056%), medium in available P (25.28 kg ha^{-1}) and K (148.77 kg ha^{-1}).

The materials were grown using completely randomized block design with three replications. Each entry was transplanted (45 days old seedling) in a plot of $6m^2$ with a spacing of 20cm. between rows and 15cm. between plants in a row. A random sample of five competitive plants was used for observations on different traits under study. Nutrients ($N:P_2O_5:K_2O$) @ 40:20:20 kg ha^{-1} were applied. During the crop period the water depth of the field was 40-50cm.

Among the 44 lowland landraces of rice, out of West Bengal, nine cultivars were collected from 24 Parganas (N), eight from Midnapore (W), two from each Midnapore(N) , Midnapore(E), West Dinajpur and Jalpaiguri, four cultivars from Assam, three cultivars each from Uttar Pradesh and Orissa, and one from Bangladesh. The panicle characters observed in undergoing the experiment were panicle length, number of nodes panicle^{-1}, number of primary branches panicle^{-1},number of secondary branches panicle^{-1},number of spikelets on primary branches panicle^{-1},number of spikelets on secondary branches panicle^{-1},number of spikelets panicle^{-1},number of grains on primary branches panicle^{-1},number of grains on secondary branches panicle^{-1}, fertility% of spikelets on primary branches panicle^{-1}, fertility% of spikelets on secondary branches panicle^{-1}, fertility% of spikelets panicle^{-1}, grain length, grain breadth, grain length/breadth ratio, grain thickness, kernel length, kernel breadth, kernel length/breadth ratio, kernel thickness, 100 grain weight, 100 kernel weight and panicle yield. Various statistical calculation procedures were undertaken for evaluation of the characters. Variance and covariance analysis was in the usual way suggested by Singh and Chaudhury (1985). Genotypic and phenotypic coefficient of variation (GCV and PCV) were calculated using the formula suggested by Al-Jibouri *et al.* (1958). For calculating the genotypic and phenotypic correlation co-efficient for all possible combination, the formula suggested by Singh and Chaudhury (1985) was adopted. Genotypic correlation co-efficient is estimated according to the following formula.

$$r_{X1X2} = \frac{C_{ov}(X1X2)}{\sqrt{V(X1) \times V(X2)}}$$

r_{X1X2} = correlation between two characters

$C_{ov}(X1X2)$ = covariance of X1 & X2

$V(X1)$ = variance for the variable X1

$V(X2)$ = variance for the variable X2

The calculation of phenotypic correlation (r_p) and genotypic correlation (r_g) have been calculated from the corresponding variance and covariance.

III. Results And Discussion

The analysis of variance revealed highly significant mean squares due to genotypes for all the 23 characters of the panicle, including the presence of significant difference among genotypes. The considerable range of variation expressed for the traits indicated good scope for genetic improvement. The estimates of phenotypic coefficient of variation(PCV) revealed higher values than genotypic coefficient of variation (GCV) as for panicle length (8.34 and 7.0 respectively), number of nodes panicle^{-1}, (14 and 9.82 respectively), number of primary branches panicle^{-1} (15.30 and 12.80), number of secondary branches panicle^{-1} (29.90 and 25.0) and number of spikelets on primary branch panicle^{-1}(17.11 and 13.68). Characters like kernel thickness (11.98 and 11.55), 1000 grain weight(32.68 and 32.68), 100 kernel weight(33.16 and 33.12), The PCV and GCV resulted in almost equal values, indicating that environment does not have much effect on these traits, therefore selection can be effected on the basis of phenotypic values with equal probability of success. GCV was higher for number of spikelets on secondary branches panicle^{-1} (35.51), 100 kernel weight (33.12), 100 grain weight(32.68), panicle yield (32.08), number of secondary branches panicle^{-1} (25.01) and number of spikelets panicle^{-1} (24.03) (table 1). Ghosh *et al*.(1981) and Hussain et *al*.(1987) also reported high GCV for 100 grain weight; Singh *et al*.(2000), Shibani and Sree Ram Reddy(2000) and Singh *et al*. (2005) for grain yield and Ahmed *et al*. (2000) for 100 grain weight and grain yield. Phenotypic coefficient of variation (PCV) followed almost a similar trend. The high values of GCV for these traits suggested the possibility of yield improvement through selection on these traits. Similar findings were also reported by Kaul and Kumar (1982), Maurya *et al*. (1976) and Chakraborty and Hazarika (1994).

Highest heritability was observed for 100 grain weight (99.99%) followed by 100 kernel weight (99.80%), grain breadth(97.77%), kernel breadth (97.48%), kernel length (96.24%), kernel length/breadth ratio (95.14%), grain length/breadth ratio (93.22%), kernel thickness (92.96%), grain thickness (92.70%), grain length (92.41%), panicle yield (88.80%), and number of grains on secondary branches panicle^{-1} (80.31%) (table 1). High heritability enables the breeder to select plants on the basis of phenotypic expression (Johnson *et al*., 1955).However high heritability alone did not necessarily lead to increase genetic advance unless sufficient genetic variability existed in the population.

Burton (1952) suggested that GCV together with heritability estimates would give the best picture of the amount of advance to be expected from selection. Characters like number of spikelets on secondary branches panicle^{-1}, 100 grain weight, 100 kernel weight, and panicle yield showed high amount of GCV along with high heritability. These characters could be improved directly through selection. This indicated predominance of additive gene action in expression of these traits as suggested by Panse (1957) and Gandhi *et al.* (1964). Some additive portion of genetic variance is fixable in nature, so selection of these traits (on the basis of phenotypic performance) is expected to be effective. For effective selection, genetic advance was computed because high heritability does not necessarily mean an increased genetic response to signify the selective advantage accruing in an additive character (Johnson, 1955). Hence, one has to consider high heritability estimates and high genetic advance together to select better potent with desirable additive effect (Panse, 1957). In the present study, number of spikelets on secondary branches panicle^{-1}, number of grains on secondary branches panicle^{-1},100 grain weight, 100 kernel weight, and panicle yield itself showed high heritability together with high genetic advance. This indicated that these characters were mostly governed by the additive gene action. Therefore, selection based on phenotypic performance of these traits would be effective.

Regarding correlation study, interrelationships of major yield contributing characters on yield is essential to the plant breeder in order to ensure effective selection. In rice, number of findings based on common yield contributing traits has been reported (Rajagopalan, 1967; Shivani and Sree Rama Reddy, 2000) but these lacking for panicle components have also been reported (Jauoria *et al.*, 1991). Of the two types of correlations, the genotypic correlation is chiefly accounted for linkage, pleiotropic action of genes and effect of selection. The phenotypic correlation is genotypic and environmental in origin and provides information about association between two observable characters.

In this study, genotypic correlation coefficients were in general higher than corresponding phenotypic ones demonstrating that the observed relationships among various characters were due to genetic causes. Panicle yield was significantly and positively correlated with number of primary branches panicle^{-1}, number of spikelets on secondary branches panicle^{-1}, number of grains on primary branches panicle^{-1}, grain length, grain breadth, grain thickness, kernel length, kernel breadth, kernel thickness, 100 grain weight and 100 kernel weight at both genotypic and phenotypic level (table 2). This was in agreement with the earlier reports of Sinha *et al* (1999). Reddy (1991), Acharya *et al*. (1995) and Prashnath *et al*. (1999) also observed significant positive correlation at both genotypic and phenotypic level for 100 grain weight. With regard to component characters, panicle length exhibited significant positive association only with number of nodes panicle^{-1}at phenotypic level. Number of primary branches panicle^{-1} showed highest significant positive association with number of spikelets on primary branches panicle^{-1}, number of grains on primary branches panicle^{-1}, and number of spikelets panicle^{-1} at both phenotypic and genotypic level (table 2).

High significant and positive genotypic and phenotypic association revealed between number of secondary branches panicle^{-1}, number of spikelets panicle^{-1}, number of spikelets on secondary branches panicle^{-1}, number of grains on secondary branches panicle^{-1}.This is in agreement with earlier works of Sinha *et al*.(1999) for number of grains on secondary branches panicle^{-1}. For number of spikelets on secondary branches panicle^{-1}, results revealed a significant and negative relationship with most of the traits except number of grains on secondary branches panicle^{-1}. Importance of secondary branches for improvement of grain number was also reported by Prasad and Sharma (1973).

IV. Conclusion

It has been observed that yield of rice per unit area is primarily determined by the mean panicle yield and the number of effective tillers (i.e. number of panicles). But beyond a certain limit, accommodating more tillers per unit area through choice of cultivar and for agronomic management cannot be expected to enhance yield; further, increase in yield per unit area would necessarily come from increase in mean panicle yield. Thus, information on panicle yield determination should be of considerable value in the development of heavy panicle type rice varieties having high yield potential and productivity.

Thus, in overall, it can be concluded that the grain characters in particular, as, grain length, grain breadth, grain thickness, kernel length, kernel breadth, kernel thickness, 100 grain weight and 100 kernel weight show a direct impact on the yield character of the panicle as a whole while the rest of the panicle component characters, as, panicle length, number of primary branches panicle^{-1},number of secondary branches panicle^{-1},number of spikelets panicle^{-1} ,number of spikelets on primary branches panicle^{-1} ,number of spikelets on secondary branches panicle^{-1} ,number of grains on primary branches panicle^{-1} , number of grains on secondary branches panicle^{-1} ,fertility % of spikelets panicle^{-1}, fertility % of spikelets on primary branches panicle^{-1} and fertility % of spikelets on primary branches panicle^{-1} contribute indirectly, i.e., via the grain components, to the yield character of the panicle.

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Table 1: Estimation of statistical and genetical parameters of agromorphological traits for different landraces of rice

Sl. No.	Traits	Mean±S.E.	Range	GCV	PCV	h^2 (Heritability)	Genetic advance in percent of mean(%)	CV %
1	Panicle length	26.86±0.99	23.20-30.8#	7.00	8.33	70.53	12.11	4.52
2	No. of nodes panicle^{-1}	8.51±0.69	6.33-11	9.81	13.99	49.21	14.19	9.97
3	No. of pri. branches panicle^{-1}	12.09±0.82	8.66-14.88	12.79	15.30	69.91	22.04	8.39
4	No. of sec. branches panicle^{-1}	39.42±5.27	20.22-65.44	25.00	29.90	69.95	43.09	16.39
5	No. of spikelets on pri. br. panicle^{-1}	72.03±6.03	51.44-98.33	13.68	17.10	63.98	22.55	10.26
6	No. of spikelets on sec br. panicle^{-1}	136.24±20.50	47.55-282.33	35.51	40.01	78.77	64.93	18.43
7	No. of spikelets panicle^{-1}	208.07±22.83	108.22-346.88	24.03	27.53	76.17	43.21	13.44
8	No. of grains on pri. br. panicle^{-1}	64.61±6.22	42-85.66	13.84	18.19	57.90	21.70	11.80

9	No. of grains on sec. br. panicle^{-1}	104.54±16.15	39.99-223.11	38.23	42.66	80.31	70.59	18.92
10	Fertility % of spikelets on pri. br. panicle^{-1}	89.76±4.28	79.30-95.82	2.73	7.13	14.68	2.16	6.58
11	Fertility % of spikelets on sec. br. panicle^{-1}	77.22±6.24	41.55-95.05	13.67	16.88	65.63	22.82	9.89
12	Fertility % of spikelets panicle^{-1}	81.98±4.15	55.70-93.80	9.71	11.53	70.98	16.87	6.21
13	Grain length	8.15±0.28	6.04-11.05$^{@}$	14.90	15.50	92.41	29.52	4.27
14	Grain breadth	2.83±0.06	1.89-3.72$^{@}$	17.85	18.05	97.77	36.37	2.69
15	Grain length/breadth	2.93±0.11	2.18-4.16$^{@}$	18.49	19.16	93.22	36.80	4.98
16	Grain thickness	2.00±0.05	1.6-2.43	11.24	11.68	92.70	22.31	3.15
17	Kernel length	5.71±0.14	4.08-7.97$^{@}$	15.56	15.87	96.24	31.46	3.07
18	Kernel breadth	2.41±0.05	1.7-3.24$^{@}$	17.73	17.95	97.48	36.06	2.85
19	Kernel length/breadth	2.41±0.08	1.77-3.42$^{@}$	19.63	20.13	95.14	39.45	4.43
20	Kernel thickness	1.78±0.04	1.46-2.27	11.54	11.97	92.96	22.94	3.17
21	100 grain weight	2.37±0.007	1.08-3.65$^{\$}$	32.68	32.68	99.99	67.32	0.37
22	100 kernel weight	1.84±0.02	0.84-2.84$^{\$}$	33.12	33.15	99.80	68.17	1.50
23	Panicle yield	3.915±0.36	1.81-7.16	32.07	34.04	88.80	62.27	11.39

Note: # - cm, @ - mm, $ - g

Table 2. Genotypic and Phenotypic correlation coefficients among twenty thee quantitative traits of 44 traditional rice cultivars

Traits	Ch1	Ch2	Ch3	Ch4	Ch5	Ch6	Ch7	Ch8	Ch9	Ch10	Ch11	Ch12	Ch13	Ch14	Ch15	Ch16	Ch17	Ch18	Ch19	Ch20	Ch21	Ch22	Ch23
Ch1		0.400**	-0.350**	-0.155	-0.120	-0.041	-0.119	-0.022	-0.009	0.260*	0.149	0.287**	-0.539**	-0.218*	-0.224*	-0.205	-0.573**	-0.190	-0.283**	-0.156	-0.442**	-0.415**	-0.510**
Ch2	0.287**		0.355**	0.554**	0.630**	0.396**	0.571**	0.405**	0.662**	0.224*	0.819**	0.284**	-0.458**	-0.412**	0.021	-0.426**	-0.413**	-0.380**	0.003	-0.338**	-0.492**	-0.461**	-0.058
Ch3	-0.166*	0.251*		0.298**	0.379**	0.857**	0.219*	0.853**	0.183	-0.072	0.049	-0.131	0.221*	0.158	0.001	0.107	0.256*	0.149	0.050	0.143	0.251*	0.237*	0.588**
Ch4	0.007	0.405**	0.397**		0.965**	0.102	0.980**	0.011	0.926**	-0.195	-0.447**	-0.106	-0.381**	-0.526**	0.157	-0.630**	-0.244*	-0.482**	0.189	-0.613**	-0.495**	-0.485**	0.097
Ch5	0.018	0.430**	0.446**	0.947**		0.266*	0.980**	0.161	0.905**	-0.226*	-0.501**	-0.122	-0.406**	-0.414**	0.031	-0.534**	-0.293**	-0.367**	0.059	-0.503**	-0.421**	-0.444**	0.172
Ch6	0.062	0.248*	0.809**	0.192	0.325**		0.074	0.984**	0.033	-0.029	0.016	-0.086	0.082	0.246*	-0.170	0.222*	0.114	0.253*	-0.127	0.275**	0.285**	0.208*	0.539**
Ch7	0.001	0.392**	0.287**	0.953**	0.977**	0.118		-0.031	0.930**	-0.224*	-0.519**	-0.109	-0.440**	-0.479**	0.073	-0.594**	-0.318**	-0.432**	0.093	-0.575**	-0.490**	-0.497**	0.076

Ch 8	0.086	0.233*	0.736**	0.123	0.239*	0.908**	0.046		-0.001	0.152	0.193	0.082	0.104	0.313**	-0.208*	0.276**	0.137	0.323**	-0.169	0.327**	0.291**	0.253**	0.539**
Ch 9	0.069	0.433**	0.243*	0.880**	0.887**	0.061	0.918**	0.049		0.139	-0.155	0.253*	-0.495**	-0.522**	0.071	-0.620**	-0.397**	-0.470**	0.061	-0.605**	-0.584**	-0.519**	0.019
Ch 10	0.184	0.072	-0.087	-0.199	-0.230*	-0.070	-0.224*	0.153	0.152		0.968**	0.978**	-0.105	-0.047	-0.029	0.009	-0.170	-0.020	-0.117	0.007	-0.172	-0.023	-0.060
Ch 11	0.090	0.003	-0.043	-0.140	-0.166	-0.053	-0.166	0.363**	-0.027	0.547**		0.892**	0.106	0.303**	-0.157	0.261*	0.101	0.319**	-0.181	0.266*	0.042	0.213*	0.044
Ch 12	0.215*	0.127	-0.080	-0.088	-0.108	-0.075	-0.098	0.052	0.279**	0.934**	0.317**		0.236*	-0.152	-0.038	-0.100	-0.300**	-0.113	-0.140	-0.096	-0.290**	-0.148	-0.138
Ch 13	-0.422**	-0.316**	0.211*	-0.299**	-0.341**	0.088	-0.372**	0.091	-0.423**	-0.084	0.030	-0.170		0.369**	0.472**	0.490**	0.981**	0.313**	0.528**	0.445**	0.741**	0.749**	0.554**
Ch 14	-0.189	-0.298**	0.132	-0.425**	-0.354**	0.196	-0.411**	0.209*	-0.454**	-0.038	0.109	-0.116	0.358**		-0.633**	0.948**	0.352**	0.994**	-0.576**	0.931**	0.821**	0.794**	0.583**
Ch 15	-0.162	0.014	0.022	0.122	0.031	-0.086	0.056	-0.112	0.053	-0.024	-0.056	-0.023	0.496**	-0.619**		-0.484**	0.479**	-0.668**	0.992**	-0.497**	-0.160	-0.132	-0.095
Ch 16	-0.177	-0.259*	0.082	-0.514**	-0.459**	0.153	-0.516**	0.195	-0.541**	0.019	0.123	-0.064	0.460**	0.903**	-0.442**		0.468**	0.947**	-0.432**	0.998**	0.895**	0.861**	0.584**
Ch 17	-0.476**	-0.298**	0.216*	-0.214*	-0.259*	0.098	-0.288**	0.111	-0.367**	-0.149	0.042	-0.252*	0.934**	0.340**	0.464**	0.445**		0.304**	0.555**	0.429**	0.736**	0.751**	0.620**
Ch 18	-0.171	-0.245*	0.118	-0.407**	0.326**	-0.191	-0.387**	0.223*	-0.423**	-0.023	0.093	-0.092	0.292**	0.974**	-0.643**	0.900	0.294**		-0.612**	0.934**	0.803**	0.764**	0.587**
Ch 19	-0.221*	-0.031	0.047	0.150	0.049	-0.091	0.078	-0.100	0.048	-0.085	-0.024	-0.112	0.505**	-0.559**	0.946**	-0.404**	0.559**	-0.614**		-0.447**	-0.093	-0.053	-0.016
Ch 20	-0.124	-0.230*	0.137	-0.479**	-0.409**	0.219*	-0.479**	0.254*	-0.515	-0.005	0.106	-0.090	0.413**	0.884**	-0.459**	0.921**	0.416**	0.894**	-0.417**		0.857**	0.832**	0.551**
Ch 21	-0.370**	-0.346**	0.230*	-0.415**	-0.368**	0.228*	-0.434**	0.221*	-0.523**	-0.145	0.159	-0.234*	0.712**	0.811**	-0.154	0.862**	0.727**	0.793**	-0.091	0.826**		0.923**	0.751**
Ch 22	-0.344**	-0.318**	0.201	-0.402**	-0.383**	0.168	-0.437**	-0.193	0.461**	-0.021	0.077	-0.120	-0.720**	0.784**	-0.128	0.826**	0.735**	-0.755**	0.053	0.804**	0.922**		0.715**
Ch 23	-0.346**	-0.315**	0.540**	0.193	0.257*	0.468**	0.168	0.475**	0.129	-0.019	0.086	-0.066	0.511**	0.543**	-0.080	0.519**	0.561**	0.536**	-0.012	0.501**	0.708**	0.676**	

*and**indicate significance at 5% and 1% levels, respectively. Upper diagonal correlations are genotypic correlations and lower diagonal correlations are phenotypic correlation. Correlation coefficient r=0.206-0.266 and r>0.266 are significant at at 5% and 1% level respectively.