

Genetic Variability and Association of Yield Attributing Characters with Grain Yield in Deepwater Rice

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ABSTRACT: A study on genetic variability and association of yield attributing characters with grain yield was carried out using 35 deepwater rice genotypes. High genotypic co-efficient of variation (GCV) was observed for plot yield, EBT/m², plant height and days to 50% flowering (DFF). For all the traits, estimates of the phenotypic co-efficient of variation (PCV) were higher than GCV, indicating presence of environmental influence. High heritability and genetic advance was observed for plot yield, EBT/m² and plant height. Plot yield had significant positive association with test weight, EBT/m² and DFF. However, test weight had the maximum direct effect on grain yield

Keywords: Genetic variability, correlation, deepwater rice, path analysis

Eastern India comprising of the states of Assam, Bihar, Orissa, West Bengal and eastern parts of Madhya Pradesh is largest rice growing region of the country. For more than one half of the country's population, rice is the source of energy and livelihood. Accounting for approximately 58% of the total rice area, share of eastern region to the National rice production is less than 48%. Stagnant yield level that is lower than the National average is the concern of the planners and researchers. Yield revolution was witnessed in irrigated areas following the introduction of plant type based high yielding varieties in mid sixties bypassed the eastern region, as the varietal technology hardly suited its highly diverse rainfed environment. Impressive yield growth was achieved successively in the northern and southern regions during last three decades enabled the country to achieve and sustain self-sufficiency in rice and food so far. With productivity growth tapering off in these regions and area under rice shrinking all over, sustenance of the present trend of productivity growth, inevitable for sustaining self-sufficiency, is not possible without stepping up the yield level in the eastern India. Although it is widely recognised that key to India's sustained food security lies in eastern India, our understanding of the problems constraining the yield levels and research and development efforts to remedy

them are still inadequate.

The success of any breeding program depends on understanding the genetic nature of the character of interest, creation and prediction of genetic variability in subsequent generations and their inter relationship with other characters. Yield is a complex character and is influenced by various other characters, therefore it is essential to understand the association of other characters with yield in addition to the information on genetic variability. Breeding for semi-deep / deepwater rice is a challenging task because all these information is meagre under stress situations. However, there are several reports on genetic variability and correlation studies on different characters in rice under normal conditions. Keeping in view this urgent need, this investigation was undertaken to understand the genetic variability and correlation between yield and other yield attributing characters under this dynamic and fragile ecology.

MATERIALS AND METHODS

The materials for the present investigation consisted of 35 deepwater rice genotypes collected from different parts of the country. These were grown in a randomized complete block design with three replications during wet season 2004 at the Central Rice Research Institute (CRRRI) farm, Cuttack. The water depth varied from 50 - 100 cm during the growth period of crop. The entries were direct seeded with six rows per entry having 30 hills per row with 20 × 15 cm spacing and care was taken to maintain 1 - 2 seedlings per hill. Observations on quantitative traits like plant height, panicle length, EBT/m² and seed test weight were recorded on five randomly selected plants excluding the border rows from each entry while days to 50% flowering (DFF) and plot yield were recorded on plot basis. The genotypic and phenotypic co-efficient of variations were computed through Burton's method (1952). Heritability and genetic advance were worked out as the method of Hanson *et al.* (1955). Phenotypic correlation co-efficient was calculated according to the procedure suggested by Aljibouni *et al* (1958) and path analysis was worked out following Dewey & Lu (1959).

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RESULTS AND DISCUSSIONS

Analysis of variance (ANOVA) brought out significant differences for the characters under study allowing the path coefficient analysis to be used (Table 1). The Estimates of mean, range, co-efficient of variation (CV), genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), heritability (G^2) and genetic advance (GA) of six characters are presented in Table 2. There was wide variation for all the characters under study. It is observed that the PCV was higher than the GCV indicating environmental effect on the expression of the characters.

It is observed that all the genotypes exhibited considerable variation for all the traits (Table 1). The maximum variation was observed for plot yield followed by EBT/m², plant height and DFF. This indicates that there is scope for further

improvement of these characters through selection. Higher genetic coefficient of variation was observed for plot yield, EBT/m² and plant height while lower values were observed for other traits. High GCV values for plot yield, EBT/m² and plant height indicate that these characters can be manipulated for breeding high yielding varieties through hybridization and selection in subsequent generations in rice improvement programme under deepwater situation.

The heritability estimates for all the characters ranged from 95.3% (for panicle length) to 99.9% (for plot yield) (Table 2). The genetic advance recorded very high variability ranging from 11.70% (panicle length) to 160.58% (plot yield). Moderate to high degree of heritability estimates associated with moderate to high genetic advance for plot yield, EBT/m² and plant height indicate the presence of additive gene effects hence selection based on phenotypic

Table 1. Analysis of variance for six characters of 35 deepwater rice genotypes (mean sum of squares).

Characters	Sources of variation		
	Replication (2)	Genotypes (34)	Errors (68)
Days to 50% flowering	0.924	375.477**	1.139
Plant height	82.638**	996.360**	6.158
Panicle length	0.410	6.813**	0.625
EBT/ m ²	0.867	1511.575**	9.298
Seed test weight	0.106	8.982**	0.136
Yield	0.003	2.949**	0.006

**Significant at 1% level of probability.

Table 2. Estimates of mean, range, CV, GCV, PCV, heritability (G^2) and genetic advance (GA) of six characters

Characters	Mean	Range	CV(%)	GCV(%)	PCV(%)	G^2 (%)	GA (%)
Days to 50% flowering	151.15	121.33 - 168.67	35.59	7.39	7.40	99.70	15.03
Plant height (cm)	124.5	89.00 - 157.00	1.99	14.59	14.64	99.38	29.97
Panicle length (cm)	25.28	22.67 - 28.33	3.13	5.68	5.96	95.30	11.70
EBT/m ²	135.75	84.67 - 178.00	2.25	16.48	16.53	99.38	33.85
Seed test weight (g)	24.12	20.03 - 27.53	1.53	7.12	7.18	99.16	14.68
Yield (kg/ha)	1270	213.3 - 3557	6.1	77.95	78.03	99.90	160.58

Table 3. Phenotypic correlation coefficients among six traits in rice.

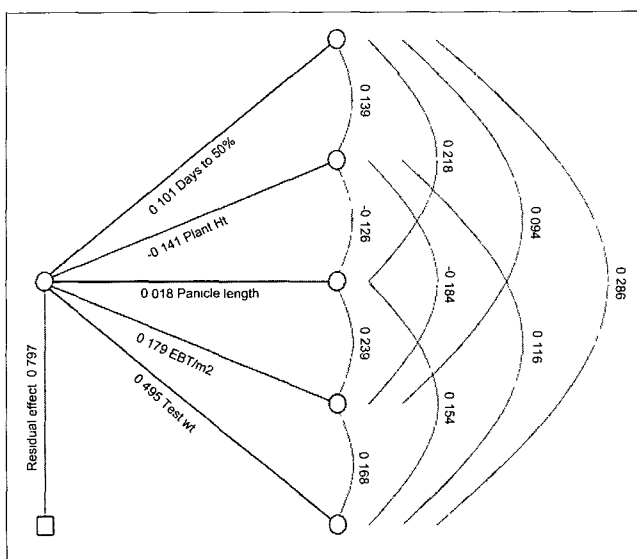
Characters	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	EBT/m ²	Seed test weight (g)	Yield (kg/ha)
Days to 50% flowering	1.00	0.14	0.22*	0.09	0.29**	0.24**
Plant height (cm)		1.00	-0.13	-0.18	0.12	-0.10
Panicle length (cm)			1.00	0.24*	0.15	0.18
EBT/ m ²				1.00	0.17	0.30**
Seed test weight (g)					1.00	0.54**
Yield (kg/ha)						1.00

*and **significant at 1% and 5% level of probability, respectively.

Table 4. Direct and indirect effects of different characters on yield.

Characters	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	EBT/m ²	Seed test weight (g)	Phenotypic correlation with yield
Days to 50% flowering	0.10	0.01	0.02	0.01	0.03	0.24**
Plant height (cm)	-0.02	-0.14	0.02	0.03	-0.02	-0.10
Panicle length (cm)	0.01	-0.01	0.02	0.01	0.01	0.18
EBT/ m ²	0.02	-0.03	0.04	0.18	0.03	0.30**
Seed test weight (g)	0.14	0.06	0.08	0.08	0.50	0.54**
Residual effect	0.78					

** Significant at 1% level of probability.

**Fig. 1.** Phenotypal path diagram for yield.

performance of these character will be effective (Panse, 1957). The characters like DFF, panicle length and test weight exhibited high heritability values in conjunction with low genetic advance indicate that these characters might be under the control of non-additive gene effects. A similar finding was reported by Singh *et al* (1990) for panicle length; Shukla *et al* (1972) and Chaudhary *et al* (1973) for grain yield and Bhattacharya & Mishra (1981) for plant height. The phenotypic correlations between six characters are presented in Table 3. Test weight, EBT/ m² and DFF exhibited positive significant association with grain yield. Correlation co-efficient between test weight and grain yield was maximum (0.54). This suggested that test weight is an important trait for improvement of grain yield.

From Fig. 1 and Table 4, it is clear that test weight had the maximum direct effect on grain yield and the next highest

direct effect on yield is through EBT / m². This suggests that these characters can be maneuvered successfully for breeding high yielding varieties for this dynamic and fragile ecology.

ACKNOWLEDGEMENT

The financial help by the Council of Scientific and Industrial Research (CSIR), New Delhi in the form of SRA (Scientists' Pool Scheme of Government of India) to Dr. Lotan Kumar Bose for this study is gratefully acknowledged.

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