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Genetic Variability and Character Association in Upland Rice Genotypes Developed through Anther Culture for Mid-altitude Areas of Meghalaya

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ABSTRACT

Genetic variability, correlation and genetic divergence studies were conducted in nine rice genotypes developed through F2-derived anther culture. Estimates of genetic parameters showed that percentage of phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for most of the characters indicating influence of environment on the characters. GCV was higher for yield/plant. Heritability estimates for days to flowering, maturity, plant height, yield/plant and grain yield were high. Genetic advance as percentage of mean was highest for yield/plant followed by grain yield which indicated that meaningful genetic gain can be obtained through F2-derived anther culture. Analysis of divergence among double haploid (DH) lines showed that, F2 system could lead to higher frequency of desirable genotypes.

INTRODUCTION

Double haploid (DH) breeding has been successfully used in rice improvement programmes and new varieties have been developed through this breeding method (Ni, 1989). In general, anthers from F_1 hybrids are used for double haploid production. However, this system allows limited opportunities for recombination and so the DH population may be in linkage disequilibrium. Moreover, when anthers from F_1s are used for double haploid production, random samples of gametes are fixed and genetic drift results in high rejection frequency during selection. Thus, production of a large population of double haploids from individual crosses becomes necessary to obtain meaningful genetic advance (Snape, 1989). The above problems can be overcome largely if anthers from F_2 or F_3 generations are used for production of double haploids. This will allow more cycles of recombination and selection can be practiced among F_2 or F_3 individuals. Anthers from selected individuals, thus, can be used for double haploid production.

In any genetic improvement programme study of the nature and extent of genetic variations involved in the inheritance of quantitative characters like yield and yield components is essential and it holds true for DH breeding also. Since only the genetic portion of variability contributes to gain under selection information about parameters of genotype-environment complex is of immense importance to breeders (Allard, 1960). Burton (1952) suggested that estimate of genetic coefficient of variations and heritability can give a clear picture of the extent of gain expected from selection. The present study was undertaken to estimate genetic parameters and correlation coefficients between grain yield and other yield contributing characters in upland rice genotypes developed through anther culture. Genetic divergence among the genotypes was studied to assess interrelationship among genotypes.

MATERIALS AND METHODS

The study was conducted in wet season (June-October) of 1998 with 14 medium duration genotypes 9 of which were developed through culture of anthers from selected F_2 individuals of a cross PSN6131. Three exotic genotypes (IET 13459, IET 13783 and IET 15046) were selected from All India Co-ordinated Trials and two local genotypes (Bali and Take) were collections from Meghalaya and Nagaland, respectively.

All the genotypes were grown at the research farm of ICAR Research Complex for NEH Region, Umiam, Meghalaya under direct seeded upland condition following a randomized complete block design with 5.6 m^2 plots and 5 replications. Standard fertiliser doses recommended for the state (60 : 60 : 40 - N : P : K) was applied. No plant protection measure was taken. However, one spray of pre-emergence weedicide at the time of seeding and two hand weeding were done to control weeds. Observation on days to flowering was recorded when more than 50% plants in a plot showed complete flowering. Yield and other yield contributing characters were recorded from five randomly selected plants from the middle row of each plot. Grain yield/ha and grain yield/plant yield was recorded from grains with 140 gm/Kg or less water content. Yield in tonnes/hectare was calculated from plot yield.

The genotypic and phenotypic coefficients of variations were computed as per the procedure of Burton (1952). Heritability and genetic advances were worked out as per the method outlined by Hanson *et al.* (1955). Simple correlation coefficients were calculated following the method proposed by Robinson *et al.* (1951). Analysis of divergence was calculated using Mahalanobis D^2 method (Mahalanobis, 1936)

RESULTS AND DISCUSSION

Highly significant differences were observed among the DH genotypes for all the characters studied. Mean sum of square (MS) values for genotypes were significant for all characters. Estimates of genetic parameters are presented in Table 1. Genotypic coefficient of variation (GCV) was high for grain yield/plant (22.574) and grain yield/ha (13.777) and were close to corresponding phenotypic coefficient of variation (PCV). In general, PCV was higher than GCV for all characters. Broad sense heritability estimates for days to flowering (95.1%), maturity (94%), plant height (85.9%), yield/plant (86.2%) and grain yield (74.8%) were high. Heritability estimates for number of spikelet/panicle and per cent spikelet fertility were low. Genetic advance as percentage of mean was highest for yield/plant (43.18%) followed by grain yield (24.54%).

Estimation of genetic parameters of DH lines showed higher level of phenotypic coefficient of variation compared to genotypic coefficient of variation indicating predominant influence of

Table 1. Estimates of genetic parameters of DH genotypes

Characters	Range of mean	GCV %	PCV %	h^2 %	GA as % of mean
Days to flowering		4.551	4.668	95.1	9.142
Days to maturity	92.8-99.7	3.370	3.476	94.0	6.730
Plant height (cm)	123-127.5	5.919	6.386	85.9	11.30
No. of Panicle bearing tillers	106.86-113.8	9.039	12.738	50.3	13.212
Panicle length (cm)	3.08 - 4.33	3.737	5.222	51.2	5.509
spikelet/panicle	21.29-23.82	4.464	7.784	32.9	5.275
Spikelet fertility %	112.91-134.73	2.484	5.163	23.2	2.462
Yield/plant (cm)	71.31-83.77	22.574	24.309	86.2	43.185
100 grain weight (gm)	6.39-9.18	6.597	11.732	31.6	7.642
Grain yield (q/ha)	28.73-32.15	13.777	15.933	74.8	24.540

environment on the expression of characters. Bhatacharyya and Mishra (1981) and Rema Bai *et al.* (1992) made similar observations. Burton (1952) suggested that a character having high value for GCV coupled with high heritability would be more valuable for selection. According to Johnson et al. (1955) high heritability coupled with high genetic advance would be more useful in predicting the effect of selection. High heritability and moderate genetic advance was shown by yield/plant and grain yield (Table 2) which also showed high GCV indicating preponderance of additive gene action (Panse, 1957). High heritability with high genetic gain for yield/plant has been reported by Rema Bai *et al.* (1992) and the same for grain yield has been reported by Shukla *et al.* (1972) and Jalwar *et al.* (1972). High heritability for days to flowering, maturity duration, plant height, yield/plant and grain yield and meaningful genetic gain for characters like yield/plant and grain yield indicated the relative advantages of F_2 system of double haploid breeding over the F_1 system.

Computation of simple correlation coefficients of 10 agronomic characters including yield (Table 2) showed that plant height, number of panicle bearing tillers and 1000 grain weight were positively and significantly correlated with yield. Days to flowering and days to maturity were negatively correlated with yield but they were not significant. Number of panicle bearing tillers per plant showed significant negative correlation with days to flowering and days to maturity but significant positive correlation with yield/plant and grain yield. Panicle length was positively and significantly correlated with per cent spikelet fertility and yield/plant.

Agronomic characters *viz.* number of panicle bearing tillers, panicle length, spikelet/panicle, seed fertility percentage, yield /plant and 100 grain weight showed positive correlation with yield. However, among these, correlation of panicle bearing tillers and yield/plant were signifi-

Table 2 Simple correlation coefficients (r) of different yield and yield contributing characters of DH lines.

	M	PH	PBT	PL	SPN	F%	Y/P	GW	Grain yield (q/ha)
Days to flowering	0.958**	-0.409	-0.615*	0.181	0.354	0.138	-0.011	-0.034	-0.395
Days to maturity (M)		-0.391	-0.598*	-0.207	0.334	0.170	0.006	0.011	0.368
Plant height (PH)			0.449	0.252	0.430	0.550	0.346	0.229	0.592*
No. of panicle bearing tillers (PBT)				0.151	-0.099	0.122	0.582*	0.216	0.699*
Panicle length (PL)					0.332	0.576*	0.750*	0.298	0.435
No. of spikelets/panicle (SPN)						0.552	0.281	0.268	0.219
Spikelet fertility % (F %)							0.511	0.306	0.439
Yield / plant (Y/P)								0.428	0.770**
100 grain weight (GW)									0.383

cant. Samonte *et al.* (1998) in a study of yield and yield related traits cf rice concluded that number of spikelet/panicle, spikelet fertility percentage and number of panicle bearing tillers contributes positively to yield and 100 grain weight has a negative correlation with number of spikelet/panicle and spikelet fertility percentage. In this study though 100-grain weight was positively correlated with all characters except days to 50% flowering none of the correlation was significant.

Mahalanobis D^2 was used for estimating divergence among DH lines, exotic and local genotypes. Based on D^2 values the genotypes were grouped into 3 clusters. All DH lines were grouped in cluster I, the exotic genotypes were included in cluster II; whereas the local genotypes formed cluster III. Intercluster distance was highest between cluster II and I (15.19) followed by cluster II - III (13.35). Intracluster distances in cluster I and III were low (4.33 and 4.98, respectively). Percent contribution of different characters to total divergence indicated that maximum contribution to total divergence was from yield/plant (51.52%) followed by days to flowering (16.67%) and panicle length (12.12%). Low intracluster distance in the cluster that included DH lines showed that these lines were genetically closer. This was presumably because of their origin from the same cross.

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