Evaluation of Rice (*Oryza sativa* L.) Accessions for Growth and Yield Attributes in Aerobic Condition

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ABSTRACT

The objective of this study was to evaluate 300 rice accessions and four check varieties for growth and yield component traits under aerobic condition. The analysis of variance for the ten characters studies revealed high significant difference among the genotypes both at five and one per cent level of significance except for test weight, seed length and single panicle weight thus, wide range of variability was observed for all the characters. In general, the phenotypic co-efficient of variation (PCV) was greater than genotypic coefficient of variation (GCV) for all the traits studied, indicating significant influence of environment on expression of the traits. The estimate of broad sense heritability (h^2) was highest for biomass, genetic advance as per cent mean was high for total seed weight, single panicle weight and number of tiller per plant. High values of PCV, GCV, h^2 and genetic advance as per cent mean were observed for grain yield per plant. Total seed weight was positively associated with above ground biomass, single panicle weight and number of tillers. A significant negative correlation between plant heights at 45 DAS with number of tillers was observed. The genotypes viz., MAS-IL858, MAS-IL869, MAS-IL748, MAS-IL835 and MAS-IL707 were found high yielders among introgression lines as compared with checks.

INTRODUCTION

Rice is food, culture and life of many Asians. The food requirement of the developing world is increasing at an alarming rate as the population rate shows an increasing trend. Thus 350 million tons more rice will have to be produced by 2020 AD (Khush 1995). Improvement of the rice grain yield per unit area is the only potential way to achieve increased rice production because of the reduction in area devoted to rice production (Cassman 2003). Thus, to increase the yield potential of rice, many strategies have been developed including new plant type and exploiting hybrid vigour through hybrid rice varieties. Identification of genes contributing to higher yield, disease and pest resistance, salinity, temperature and drought tolerance from wild weedy and land races in rice are possible if the selection strategy of the parental lines shifts from looking for the phenotype to looking for the genes with the aid of genetic linkage maps and molecular markers. Rice grain yield is a quantitative polygenic trait and highly influenced by environment (Ashfaq *et al*. 2012). The availability of genetic variability as well as gathering information of traits having agronomic importance are prerequisites to initiate breeding programme in any crop (Dubley and Moll 1969). The improvement of an economically important and complex traits like grain yield depends on many other component characters such as number of tillers/plant, panicle weight, number of grains/panicle (Akinwale *et al*. 2011) and the amount of variability present in the breeding material. Even the significance and extent of association of grain yield and yield components should be considered to determine the selection of germplasm on the basis of genetic variation prevailing (Habib *et al*. 2005). Hence, the study of variability provides an opportunity for selecting the superior genotypes while the knowledge of associations among various quantitative characters contributing to yield helps the breeder in the simultaneous improvement of several characters in the selection programme. In the present study, an attempt has been made to determine the genetic variability and associations between yield and its related components.

MATERIALS AND METHODS

The material for the present study comprised of three hundred rice accession and four check varieties 'IR64', 'Budda', 'Antasa1i' and 'Moroberekan'. The experiment was carried out at Main Research station (MRS), Hebba1, University of Agricultural Sciences (UAS), Banga1ore, using Randomized Block Design replicating twice, with a spacing of 20 cm between rows and 15 cm between plants. Observations were recorded on five randomly selected plants per genotype per replication for the traits such as plant height (cm), number of panicles/plant, panicle length (cm), test weight (g), grain yield/plant (g), seed length (cm), biomass (g), single panicle weight (g), number of tillers/plant and plant height at 45 days after sowing (DAS).

Statistical analysis of the data on individual characters was performed using SAS V6.12 statistical package (SAS Institute, Inc., 1996). The Genotypic coefficient of variation (GCV) and Phenotypic coefficient of variation(PCV) were computed as suggested by Burton and Devane (1953) and for heritability (h^2) and genetic advance (GA) the method outlined by Hanson *et al.* (1956) and Johnson *et al*. (1955), respectively, was employed. The correlation coefficients was estimated using the formula by Sunderraj *et al.* (1972) and were then compared with 'r' values at n-2 degrees of freedom at 1% and 5% significance level.

RESULTS AND DISCUSSION

The analysis of variance revealed significant difference among genotypes for all the characters except test weight, seed length and single panicle weight, which were not significant **Table 1**.

High GCV and PCV values indicate presence of considerable amount of variability for total seed weight, biomass, single panicle weight and number of tillers/plant. Lower differences between PCV and GCV values were ob-

Short Communication

Table 1 Analysis of variance for ten traits of introgression lines.

Source of variance	df	Mean sum of squares									
		Xl	X2	X3	X4	X5	X6	X7	X8	X9	Xl0
Genotypes	304	106.02*	6.17* *	7.25**	0.41	64.9**	0.04	321.2**	0.83	9.407**	100.4**
Replication	1	101	25.86	8.78	1.04	69.28	0.01	970	7.33	0.269	810.5
Error	303	32.08	2.33	1.74	0.19	6.05	0.039	27.98	0.12	2.12	26.4
CD at 5%		11.09	2.98	2.57	0.84	4.8	0.39	10.35	0.67	2.84	10.05
CD at 1%		14.58	3.92	3.37	1.11	6.31	0.51	13.6	0.88	3.74	13.21
CV		9.22%	9.45%	16.93%	19.60%	20.99%	25.69%	18.15%	18.80%	17.10%	10.50%

X1	Plant height (cm)	X6	Seed Length (cm)
X2	Number of productive tillers	X7	Biomass (g)
X3	Panicle length (cm)	X8	Single panicle weight (g)
X4	Test weight (g)	X9	Number of tillers per plant
X5	Total seed weight (g)	X10	Plant height at 45 DAS (cm)

Table 2 Estimation of genetic parameters in introgression lines of rice.

Character	Mean	Range		PCV	GCV	h^2	GA%
		Min	Max				
Plant height (cm)	61.41	43.7	110.5	13.91	9.52	46.87	13.43
Number of productive tillers	16.14	10.9	23.32	42.56	18.1	18.08	15.85
Panicle length (cm)	7.8	3.00	14.09	51.9	11.57	4.97	5.32
Test weight (g)	2.26	1.05	5.13	107.1	5.33	0.25	0.55
Total seed weight (g)	11.71	1.03	40.47	172	51.63	9.01	31.93
Seed length (cm)	0.77	0.56	1.21	182	8.86	0.1	0.57
Biomass (g)	29.13	6.48	128.7	49.42	38.9	61.93	63.65
Single panicle weight (g)	1.87	0.40	4.50	133.9	36.2	7.3	20.15
Number of tillers per plant	8.47	3.50	16.5	29.75	21.05	50.03	30.67
Plant height at 45 DAS (cm)	48.75	32.4	78.10	16.8	11.76	49.02	16.96

Table 3 Phenotypic correlation coefficient among ten characters studied in introgression lines of rice.

Traits	X2	X3	X4	X5	X6	X7	X8	X9	X10
Xl	0.494**	0.214**	0.074	0.382**	0.032	0.618**	0.387**	0.214**	0.394**
X2		0.362**	0.233**	0.467**	0.194**	0.458**	0.535**	0.279**	0.138*
X3			0.15**	0.578**	0.076**	0.632**	0.213**	0.684**	-0.154
X4				0.319**	0.137**	0.169**	0.426**	0.12*	0.016
X5					0.066	0.714**	0.632**	0.492**	0.024
X6						0.033	0.14*	0.069	0.043
X7							0.463**	0.523**	0.058
X8								0.178**	0.108
X9									-0.128

served for plant height, number of tillers/plant and plant height at 45 DAS as presented in **Table 2**. This indicates high genetic influence in the expression of these traits, Difference between GCV and PCV was also observed by Das *et al.* (2005); Keshava Murthy *et al.* (2011), studied 10 traits in rice under aerobic conditions and observed that all the characters showed low GCV than PCV indicating the influence of environment on these traits. Akinwale *et al.* (2011) in their study on rice observed that number of grains per panicle exhibited the highest genotypic variance and also the highest environmental variance among all the traits studied. However, they observed that panicle weight had the lowest magnitude of genotypic, environmental and phenotypic variance and there was small difference between GCV and PCV for days to heading, days to maturity, plant height and panicle length indicating that these traits are genetically controlled.

Heritability estimates ranged from 61.93% in biomass to 0.1% in seed length. Genetic advance as per cent mean ranged from 63.65 to 0.55% for biomass and test weight, respectively. High heritability with high GA was observed for biomass. Since h^2 is an estimate of the heritable portion of the variation, a higher h^2 value in quantitative characters are useful as they provide the base of selection on the phenotypic performance. Similar results in rice (*Oryza sativa* L.) were reported by others (Nandarajan and Rajeshwari 1993; Sarma and Borgihain 1998; Kuldeep *et al.* 2004; Das *et al.* 2005; Mall *et al.* 2005; Girish *et al.* 2006; Ganapathy *et al.* 2007; Kishor *et al.* 2008; Krishna and Hittalmani 2009; Keshava Murthy *et al.* 2011) who found a higher

value of h^2 and GA for various traits under study indicating the importance of these traits for efficient selection based on phenotypic performance for further improvement. This indicates that the expression of this character is mainly due to the additive gene effect (Panse 1957). This trait could be improved by mass selection and other methods based on progeny testing.

Moderate estimates of h^2 and higher GA was observed for number of tillers/plant. The same trend was reported by Kumar *et al.* (2001) and Kishor *et al.* (2008) who found variation for h^2 and GA for various traits under study. Panse (1957) suggested that if the expression of a particular character in a specific environment is mainly due to non-additive gene effect such as dominance and epistasis then GA would be low, heterosis breeding could be used to improve such trait. In general, all the characters provide good base for selection as they had moderate to high values of h^2 and GA. Thus information regarding the genetic co-efficient of variation, heritability and genetic advance will be useful in developing reliable selection indices. The genotypes viz., MAS-IL858, MAS-IL869, MAS-IL748, MAS-IL835 and MAS-IL707 were found to be high yielders among introgression lines as compared with checks.

The phenotypic correlations among traits were evaluated by regressing phenotypic values of one trait on those of another trait. Grain yield is the primary trait for selection in breeding program; secondary traits that are associated with yield can provide additional information for breeders during selection. Grain yield or total seed weight showed significant positive association with all the traits observed

except for seed length and plant height at 45 DAS. A significant positive correlation between number of productive tillers with panicle length, test weight, total seed weight, seed length biomass, single panicle length, number of tillers and plant height at 45 DAS. Hence the selection for panicle length would be effective for indirect selection of all these traits. Highest significant correlation coefficient of 0.714 was observed between total seed weight and biomass. Highest negative correlation coefficient of -0.128 was observed between number of tillers/plant and plant height at 45 DAS but it was not significant (**Table 3**). Rao and Shrivastava (1999) reported positive correlation of grain yield with days to 50% flowering, days to maturity, fertile spikelets/panicle and number of grains/spikelet. Zhuang *et al.* (2002) and Thompson *et al.* (2003) reported a significant and high positive association of grain yield with number of panicles, number of fertile spikelets/panicle and test weight. Yogameenakshi *et al.* (2004) observed a significant and high association of grain yield with plant height, panicle/plant, panicle length, number of fertile grains/panicle and harvest index.

The results obtained on genetic variability parameters indicate considerable variation in the plant material observed. High heritability and high genetic advance revealed ample scope for improvement by selection process. Genotypes MAS-IL858, MAS-IL869, MAS-IL748, MAS-IL835 and MAS-IL707 that performed superior for grain yield will be promoted towards development of new varieties.

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