

Genetic Parameters for Yield Components and Dormancy Related Traits in Rice (*Oryza sativa* L.)

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ABSTRACT

The present investigation was under taken to study the extent of variability and genetic parameters for ten yield components and dormancy related traits using 119 recombinant inbred lines along with parents (BPT 2231 and MTU1001). High phenotypic and genotypic coefficient of variation, heritability and genetic advance as per cent of mean were recorded for germination percentage at 5 days and 10 days after harvesting, free amino acids and total soluble sugars. The results revealed that number of ear bearing tillers, grain yield per plant, germination (%) at 5 days and 10 days after harvesting, free amino acids and total soluble sugars exhibited high heritability and genetic advance as per cent of mean suggesting the role of additive gene action in the inheritance of this traits and simple selection will be highly rewarding for improving this character. While all other characters manifested moderate to high heritability estimates and low to moderate values for genetic advance as per cent of mean indicating the role of both additive and non-additive gene action.

Key words: Heritability and genetic advance, Rice, Variability.

Long spell of rainy weather particularly during cyclones in coastal areas causes pre-harvest sprouting which results in great loss of yield and poor quality of produce resulting in very low market price and thereby losses to the rice farmers. Pre-harvest sprouting (PHS) in rice is caused due to lack of seed dormancy. Seed dormancy (SD) is an important agronomic trait affecting grain yield and seed quality (Hu *et al.*, 2003). In crop production, cultivars with moderate dormancy are needed to protect the grains from germinating before harvesting and to ensure good grain quality. Therefore, understanding of the genetic basis of seed dormancy is of major concern for both geneticists and plant breeders to solve the problem of pre-harvest sprouting (Guo *et al.*, 2004). Further, knowledge on available variability for various traits is necessary for an effective crop improvement programme. Presence of wider spectrum of variability highly dependent on enhance the chances of selecting a desired genotype. Besides genetic variability, knowledge on heritability and genetic advance measures the relative degree to which a character is transmitted to progeny, thereby helps the breeder to employ a suitable breeding method to achieve the objective. Keeping the above points in view, the present investigation was carried out with the objective to estimate the extent of genetic variability, heritability and genetic advance.

MATERIAL AND METHODS

The present investigation was carried out using recombinant inbred lines (RILs SD1-SD119) population

developed by crossing strongly dormant (MTU 1001) and weakly dormant (BPT 2231) parents during *khariif*, 2018-19 at Agricultural College Farm, Bapatla. The trial was laid out in a simple lattice design. Each genotype was grown in four rows of 3 m length with a spacing of 20 cm between the rows and 15cm between the plants. Data was collected on five randomly selected plants per genotype per replication for four quantitative traits namely plant height, panicle length, number of ear bearing tillers per plant and grain yield per plant. However data on days to 50% flowering test weight, germination (%) at 5 days and 10 days after harvesting, free amino acids, and total soluble sugars were recorded on plot basis. The germination (%) at 5 days and 10 days after harvesting was assessed by following the procedure delineated by Wan *et al.* (1997). The physiological parameters *viz.*, free amino acids and total soluble sugars were estimated by following the prescribed protocol of Moore and Stein (1948) and Hedge and Hofreiter (1962), respectively. The mean data was utilized for calculating the phenotypic and genotypic variations as per Burton and Devane (1953). The PCV, GCV values were classified as described by Subramanian and Menon (1973). Heritability (h^2) in the broad sense was computed as suggested by Allard (1960) and heritability in the broad sense was categorized as per the classification given by Johnson *et al.* (1955). The range of genetic advance as per cent of mean was classified and calculated based on the formula given by Johnson *et al.* (1955).

Table 1. Analysis of variance for grain yield, yield components and dormancy related traits in rice (*Oryza sativa* L.)

	Source	Replication	Treatments	Error
S. No.	Degrees of freedom	1	120	100
Mean sum of squares				
1	Days to 50% flowering	0.26	27.72**	0.09
2	Ear bearing tillers	0.68	6.32**	0.17
3	Plant height	5.18	83.40**	1.479
4	Panicle length	0.37	3.61**	1.19
5	Test weight	0.02	3.83**	0.022
6	Grain yield per plant	12.99	59.66**	10.62
7	Germination (%) at 5 days after harvesting	25.79	1200.66**	18.247
8	Germination (%) at 10 days after harvesting	20.83	1044.71**	10.591
9	Free amino acids	0.002	1.44**	0.004
10	Total soluble sugars	0.71	59.77**	0.357

** Significant at 1% level

Table 2. Mean, variability, heritability and genetic advance as per cent of mean for yield, yield components and dormancy related traits in rice (*Oryza sativa* L.).

S. No	Character	Mean	Range		Coefficient of Variation		Heritability % (Broad sense)	Genetic advance as per cent of mean (5% level)
			MIN	MAX	PCV	GCV		
1	Days to 50% of flowering	108.40	96.00	120.50	3.44	3.43	99.32	8.00
2	Ear bearing tillers	11.19	7.00	17.78	16.11	15.67	94.64	41.63
3	Plant height (cm)	111.89	89.67	136.30	5.82	5.72	96.52	12.86
4	Panicle length (cm)	25.29	19.30	29.80	6.13	4.35	50.40	14.61
5	Test weight (g)	21.50	15.78	24.00	6.46	6.42	98.87	17.90
6	Grain yield per plant (g)	32.26	19.38	42.58	18.38	15.35	69.76	40.02
7	Germination (%) 5 days after harvesting	44.73	0.00	95.00	55.18	54.35	97.01	115.85
8	Germination (%) 10 days after harvesting	65.71	10.00	98.00	34.96	34.60	97.99	73.50
9	Free amino acids (mg/100g)	1.89	0.85	4.08	44.92	44.79	99.41	145.14
10	Total soluble sugars (mg/100g)	20.06	10.47	31.85	27.32	27.16	98.81	61.2

RESULTS AND DISCUSSION

The analysis of variance for 119 RILs population of rice for 10 characters is presented in Table 1. The analysis of variance showed that the mean sum of squares for the genotypes were highly significant for all the traits measured, suggesting the presence of sufficient variability among the materials under study. The estimates of phenotypic coefficient of variation for all characters under study were higher than the estimates of genotypic coefficient of variation less amount of variation between these indicated the

meager influence of environment on the expression of these traits. High PCV and GCV were recorded for germination at 5 days (55.18 and 54.35) after harvesting followed by free amino acids (44.92 and 44.79), germination at 10 days after harvesting (34.96 and 34.60), and total soluble sugars (27.32 and 27.16) (Table 2). Moderate PCV and GCV were recorded for number of ear bearing tillers per plant (16.11 and 15.67) and grain yield per plant (18.38 and 15.35), while all other characters exhibited low estimates. Moderate PCV and GCV for number of ear

bearing tillers per plant and grain yield per plant were also reported by Sandeep *et al.* (2018) and Girma *et al.* (2018), respectively.

Heritability is the measure of transmission of characters from generation to generation and estimates of heritability are helpful to the breeder in selecting superior individuals for effective utilization in breeding programmes. The estimates for heritability ranged from 50.4 (panicle length) to 99.32 (days to 50% flowering) while the genetic advance as per cent of mean varied from 8.0 (days to 50% flowering) to 145.14 (free amino acids). Except panicle length all other characters namely days to 50% flowering, number of ear bearing panicles, plant height, test weight, grain yield per plant, germination (%) at 5 days and 10 days after harvesting, free amino acids, total soluble sugars had manifested high heritability. The characters namely number of ear bearing tillers per plant, grain yield per plant, germination at 5 days and 10 days after harvesting, free amino acids and total soluble sugar had recorded high genetic advance as per cent of mean, while the remaining traits under study manifested low to moderate values for genetic advance.

CONCLUSION

Based on the results of variability parameters, it was concluded that germination (%) at 5 days and 10 days after harvesting, free amino acids and total soluble sugars exhibited high genotypic and phenotypic coefficient of variation along with high heritability and genetic advance as per cent of mean indicating that predominance of additive gene action in the inheritance of these traits. Hence simple selection will be highly rewarding for improving these characters. These findings are in agreement with the Krishnakumar and Kumaravadivel (2018) and Kalyan *et al.* (2017). Gu *et al.* (2005a) who reported moderate to high heritability for dormancy. The remaining characters under study namely days to 50% flowering, number of ear bearing tillers, plant height, panicle length, test weight and grain yield per plant exhibited low to moderate PCV and GCV, moderate to high heritability coupled with low to high genetic advance estimates suggesting that both additive and non-additive gene action effects in the expression of these traits. Similar findings were reported by Kishore *et al.* (2015), Singh *et al.* (2018) and Krishnakumar and Kumaravadivel (2018).

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