



## Membrane Processing of Sugarcane juice

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### ABSTRACT

The experiment was conducted with an objective to estimate the variability, heritability and genetic advance of 31 rice genotypes (twenty hybrids, nine parents and two checks) for 17 morphological and physiological traits. The results revealed that high heritability coupled with high genetic advance was observed for number of effective tillers per plant, number of filled grains per panicle, number of ill filled grains per panicle, 1000 grain weight, LAD at 60-80 DAT, root dry weight, shoot dry weight, root shoot ratio and grain yield per plant suggesting the role of additive gene effect while the traits *viz.*, days to 50 per cent flowering, days to maturity, plant height, panicle length, SCMR at 80 DAT and harvest index are governed by both additive and non additive gene effect. Low estimates for both heritability and genetic advance were shown by SLA at 80 DAT and SLW at 80 DAT indicating the role of non additive gene action.

Key words: *Heritability, Genetic advance, Rice, Variability.*

Rice is a staple food for half of the world's population and more than 60% of Indian population. In India rice is cultivated in an area of 43.95 mha with a production of 104.80 mt and with an average productivity of 2392 kg ha<sup>-1</sup>. Andhra Pradesh has an area, production and productivity of 3.80 mha, 11.57 mt and 2856 kg ha<sup>-1</sup>, respectively (Indiastat, 2014-15). Knowledge on the nature and magnitude of the genetic variation governing the inheritance of quantitative characters like yield and its components is essential for effective genetic improvement. A critical analysis of the genetic variability parameters *viz.*, Genotypic Coefficient of Variability (GCV), Phenotypic Coefficient of Variability (PCV), heritability and genetic advance for different traits of economic importance is a major pre-requisite for any plant breeder to work with crop improvement programmes. Thus the present study was conducted to know the variability parameters for yield, yield contributing and physiological traits in rice.

### MATERIAL AND METHODS

Evaluation of 20 hybrids generated from crossing five lines and four testers in line x tester fashion along with nine parents and two checks (NLR40024 and NLR30491) following Randomized Block Design with two replications was carried out at Agricultural Research Station,

Nellore during *kharif* and *rabi* 2015-16. All the 31 genotypes were grown in three rows of 3.15 m length with 20 x 15 cm spacing. Standard agronomic practices were followed to maintain optimum plant population. Data was recorded on ten plants for each replication on nine morphological traits *viz.*, days to 50 % flowering, days to maturity, plant height, number of effective tillers per plant, panicle length, number of filled grains per panicle, number of ill-filled grains per panicle, 1000 grain weight and grain yield per plant along with eight physiological traits *viz.*, leaf area duration at 60-80 DAT, SPAD chlorophyll meter reading at 80 DAT, specific leaf area at 80 DAT, specific leaf weight at 80 DAT, harvest index, root dry weight, shoot dry weight and root shoot ratio and the mean data was subjected to statistical analysis for genetic parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) using the formulae given by Burton (1952). Heritability in broad sense was calculated using the formula given by Hanson *et al.* (1956) and genetic advance as per cent of mean was estimated by formula suggested by Johnson *et al.* (1955).

### RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for majority of the characters studied indicating a high degree of variability in the material (Table 1). The genotypic

coefficient of variation (GCV) values were close to phenotypic coefficient of variation (PCV) which indicated less influence of environment on expression of these traits (Table 2).

The estimates of PCV and GCV were high for characters *viz.*, Number of ill-filled grains per panicle, root dry weight, shoot dry weight and root shoot ratio, indicating the minimal influence of environment and presence of high genetic variability for these traits in the experimental material. Hence, selection on the basis of phenotype for these traits can be effective. These findings were in accordance with the results of Shrivastava *et al.* (2014), Shajedur *et al.* (2015) and Sathya and Jebaraj (2015). High PCV and moderate GCV were observed for number of effective tillers per plant (19.28 and 23.28, respectively), grain yield per plant (19.35 and 23.94) and harvest index (16.16 and 21.34). These findings are in accordance with Ramanjaneyulu *et al.* (2014). Moderate PCV and GCV were observed for number of filled grains per panicle, 1000 grain weight and LAD at 60-80 DAT. These observations were in conformity with the results of Khare *et al.* (2014) for filled grains per panicle and 1000 grain weight. Moderate PCV and low GCV were observed for panicle length and SLA at 80 DAT. Similar result for panicle length was also reported by Hossain *et al.* (2015). While low PCV and GCV were observed for days to 50% flowering, days to maturity, plant height, SCMR at 80 DAT and SLW at 80 DAT indicating low variability for these characters in the present experimental material and therefore little scope for improvement of these traits. Similar trend was observed by Khare *et al.* (2014) for days to 50% flowering and days to maturity, Hossain *et al.* (2015) for plant height and Khatun *et al.* (2015) for SCMR.

Heritability estimates along with genetic advance are more helpful in predicting the genetic gain under selection than heritability estimates alone. Heritability and genetic advance as per cent of mean were high for the characters *viz.*, Number of effective tillers per plant, number of filled grains per panicle, number of ill-filled grains per panicle, 1000 grain weight, LAD at 60-80 DAT, root dry weight, shoot dry weight, root shoot ratio and grain yield per plant indicating that these characters were less influenced by environment and governed by additive gene action which may be exploited through

breeding methods involving simple selection. Similar results of high heritability and genetic advance as per cent of mean were observed by Khatun *et al.* (2015) for the traits number of effective tillers per plant, number of filled grains per panicle, number of ill-filled grains per panicle, 1000 grain weight and grain yield per plant, Sathya and Jebaraj (2015) for root dry weight and root shoot ratio and Ukaoma *et al.* (2013) for shoot dry weight.

High heritability coupled with moderate genetic advance as per cent of mean was observed for days to 50% flowering (91.0 and 14.27, respectively). Khatun *et al.* (2015) reported similar results for days to 50% flowering. High heritability coupled with low genetic advance as per cent of mean was observed for days to maturity (89.0 and 9.62), plant height (61.0 and 8.6) and SCMR at 80 DAT (64.0 and 8.26), Verma *et al.* (2011) obtained similar results for plant height and days to maturity. Moderate heritability (57.0) coupled with high genetic advance as per cent of mean (25.2) was observed for harvest index. While moderate heritability (44.0) coupled with low genetic advance as per cent of mean (9.71) were observed for panicle length, Sathya and Jebaraj (2015) reported similar results for panicle length. These results indicate the role of both additive and non-additive gene actions in the inheritance of these traits thus these traits can be improved by population improvement methods.

Low heritability coupled with low genetic advance as per cent of mean were observed for SLA at 80 DAT (4.0 and 1.0, respectively) and SLW at 80 DAT (9.0 and 1.92) indicating the role of non-additive gene actions in the inheritance of these traits and can be improved by heterosis breeding. Similar results for SLA at 80 DAT and SLW at 80 DAT were obtained by Abarshahr *et al.* (2011).

In conclusion this study helps the breeder to decide breeding programme i.e. simple selection for number of effective tillers per plant, number of filled grains per panicle, number of ill-filled grains per panicle, 1000 grain weight, LAD at 60-80 DAT, root dry weight, shoot dry weight, root shoot ratio and grain yield per plant, population improvement for days to 50% flowering, days to maturity, plant height, panicle length, SCMR at 80 DAT and harvest index, and heterosis breeding for SLA at 80 DAT and SLW at 80 DAT.

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

Source of variations	d.f.	DFF	DM	PH (cm)	NETP	PL (cm)	NFGP	NIFGP	1000 GW (g)	LAD at 60-80 DAT
Mean sum of squares										
Replications	1	8.5323	19.7581	9.6577	1.1138	0.1310	0.7458	20.2123	0.1756	3510.035
Entries	30	93.2452**	80.0183**	38.3000**	13.645**	7.4032**	1600.299**	444.267**	16.9903**	13305.53**
Error	30	4.2989	4.7581	9.4006	2.0235	2.9126	203.1161	15.3109	0.2261	1701.7217
Mean sum of squares										
Source of variations	d.f.	SCMR at 80 DAT	SLA at 80 DAT (cm <sup>2</sup> /g)	SLW at 80 DAT (g/cm <sup>2</sup> )	HI	RDW (g)	SDW (g)	RSR	GYP (g)	
Mean sum of squares										
Replications	1	2.2458	80.3929	0.0000043	12.9907	0.2633	78.6489	0.0000	2.3265	
Entries	30	12.982**	46.4510	0.0000027	141.03**	8.0001**	483.89**	0.0015**	87.2264**	
Error	30	2.8435	42.6933	0.0000023	38.2423	0.9610	51.7144	0.0001	18.2795	

\*\* Significant at 1% level

DFF- days to 50% flowering, DM- days to maturity, PH- plant height, NEPT- number of effective tillers per plant, PL- panicle length, NFGP- number of filled grains per panicle, NIFGP- number of ill-filled grains per panicle, 1000 GW- 1000 grain weight, LAD- leaf area duration, SCMR- spad chlorophyll meter reading, SLA- specific leaf area, SLW- specific leaf weight, HI- harvest index, RDW- root dry weight, SDW- shoot dry weight, RSR- root shoot ratio, GYP- grain yield per plant

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

S. No.	Character	Mean	Range		Coefficient of variation		Heritability %(broad sense)	Genetic advance as per cent of mean
			Minimum	Maximum	GCV% (%)	PCV% (%)		
1.	DFF	91.95	82.50	109.00	7.25	7.59	91	14.27
2.	DM	123.82	115.50	139.50	4.95	5.26	89	9.62
3.	PH (cm)	74.37	66.88	83.50	5.11	6.57	61	8.26
4.	NETP	12.51	8.09	19.83	19.28	22.38	74	34.29
5.	PL (cm)	20.97	17.20	25.20	7.14	10.83	44	9.71
6.	NFGP	159.29	105.05	218.30	16.59	18.85	77	30.10
7.	NIFGP	27.48	9.00	82.70	53.30	55.17	93	106.10
8.	1000 GW (g)	16.08	11.33	23.05	18.00	18.24	97	36.59
9.	LAD at 60-80 DAT	657.69	480.50	871.93	11.58	13.17	77	20.97
10.	SCMR at 80 DAT	44.94	40.70	50.00	5.01	6.26	64	8.26
11.	SLA at 80 DAT (cm <sup>2</sup> /g)	63.19	52.36	75.76	2.17	10.57	04	01
12.	SLW at 80 DAT (g/cm <sup>2</sup> )	0.0160	0.0133	0.0191	3.04	9.89	09	1.92
13.	HI	44.36	25.46	68.03	16.16	21.34	57	25.20
14.	RDW (g)	7.08	3.90	12.69	26.51	29.91	79	48.40
15.	SDW (g)	71.51	45.52	101.04	20.55	22.88	81	38.03
16.	RSR	0.10	0.054	0.18	26.27	28.56	85	49.75
17.	GYP (g)	30.34	17.33	42.00	19.35	23.94	65	32.23

DFF- days to 50% flowering, DM- days to maturity, PH- plant height, NEPT- number of effective tillers per plant, PL- panicle length, NFGP- number of filled grains per panicle, NIFGP- number of ill-filled grains per panicle, 1000 GW- 1000 grain weight, LAD- leaf area duration, SCMR- spad chlorophyll meter reading, SLA- specific leaf area, SLW- specific leaf weight, HI- harvest index, RDW- root dry weight, SDW- shoot dry weight, RSR- root shoot ratio, GYP- grain yield per plant

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