

Genetic Variability Studies on Agronmic and Physiological Traits Suitable for Direct Seeding in Rice (*Oryza sativa* L.)

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ABSTRACT

The present study conducted in the year 2014, aims to reveal the importance of some agronomic, physiological traits related to direct seeding in rice and genetic variability existing in the 48 rice genotypes. The coefficient of variation at phenotypic (PCV) and genotypic (GCV) levels were high for plant height, number of filled grains per panicle, number of total grains per panicle, test weight and moderate for the trait leaf area index, number of productive tillers per plant, total number of tillers m⁻², grain yield plant⁻¹, biological yield plant⁻¹, harvest index, anaerobic germination, seedling root length, seedling shoot length, seedling vigour index and basal culm diameter. Low PCV and GCV were observed for days to 50% flowering, panicle length, spikelet fertility and rate of germination. From the results, high heritability coupled with high genetic advance was observed for the traits plant height, leaf area index, number of productive tillers plant⁻¹, total number of tillers m⁻², number of filled grains panicle⁻¹, number of total grains panicle⁻¹, test weight, biological yield plant⁻¹, harvest index and other physiological traits which indicated the predominance of additive gene effects in controlling these traits. Early and simple selection could be exploited due to fixable additive gene effects of these traits.

KEY WORDS: Direct seeding, genetic advance, heritability, rice, variability,

Rice (*Oryza sativa* L.) is the most important staple food of all over world population and ranks 3rd after wheat and maize in terms of production and consumption (Akinbile *et al.*, 2011). Asia accounts for over 95% of global rice production with China (194.3 mt) and India (148.3 mt), ranked first and second respectively (*ricestat.irri.org*).

Rice is commonly grown by transplanting seedlings into puddled soil. Puddling and transplanting require large amount of water and labor, both of which are becoming increasingly scarce and expensive, making rice production less profitable. Under the situation of water and labour scarcity, farmers are changing either their rice establishment methods from transplanting to direct seeding. Direct seeded rice requires specially bred cultivars having good mechanical strength in the coleoptiles to facilitate early emergence of the seedlings, early seedling vigour for weed competitiveness, efficient root system for anchorage and to tap soil moisture from lower layers (Zhao *et al.*, 2006). Ability to germinate under anaerobic conditions and tolerance of early submergence are important for establishing a good DSR crop (Ismail *et al.*, 2009).

The genetic improvement of plant population depends on the presence of genetic variability and the extent to which the desirable traits are transmissible. Besides genetic variability, knowledge on heritability and genetic advance plays a predictive role in breeding, expressing the reliability of phenotype as a guide to its breeding value (Burton, 1952). Since many quantitative characters are highly influenced by environment, there is a need to partition the overall variability into its heritable and non-heritable components with the help of suitable genetic parameters such as genetic coefficient of variation, heritability estimates and genetic advance.

MATERIALS AND METHODS

In the present investigation 48 rice genotypes, were grown in randomized block design with two replications at Andhra Pradesh Rice Research Institute (APRRI) and Regional Agricultural Research Station (RARS), Maruteru, West Godavari District, Andhra Pradesh. The field was prepared after puddling, into 96 plots of six square meter size and leveled properly. The seed of individual entry was soaked in water one day ahead of sowing in cloth bags. The pre germinated seed was broadcasted on to the prepared plots. Recommended crop husbandry activities were followed to raise a healthy crop stand. The data was recorded on five randomly selected plants for 13 agronomic traits viz., days to 50% flowering, plant height (cm), leaf area index, number of productive tillers per plant, total number of tillers per m⁻², panicle length (cm), number of filled grains per panicle, number of total grains per panicle, spikelet fertility (%), test weight (g), grain yield per plant (g), biological yield per plant (g), harvest index and six physiological traits viz., seedling root length (mm), seedling root length (mm), rate of germination (%), seedling vigour index and anaerobic germination (%).

Standard statistical procedures were used for the analysis of variance, genotypic and phenotypic coefficients of variation (GCV and PCV) (Burton, 1952), heritability (Lush, 1940) and genetic advance (Johnson *et al.*, 1955).

RESULTS AND DISCUSSION

The analysis of variance showed a wide range of variation and significant differences for all the 19 characters under study (Table 1), indicating the presence of adequate variability. The recordings of the means, co-efficient of variation, heritability and genetic advance as per cent of means are presented in Table:2. Phenotypic coefficient of variation ranged from 5.03 to 25.45%. The highest PCV was recorded by number of total grains panicle⁻¹, whereas the lowest was recorded by spikelet fertility (%). Genotypic co-efficient of variation (GCV) followed the similar trend as that of PCV and the variation between PCV and GCV was very less indicating nominal interference of environment the expression of the traits, except grain yield per plant and germination. The co-efficient of variation at phenotypic (PCV) and Genotypic (GCV) levels were high for the traits plant height, number of filled grains panicle-1, number of total grains panicle⁻¹, test weight, anaerobic germination and moderate for the traits leaf area index, number of productive tillers plant⁻¹, total number of tillers m⁻², biological yield plant⁻¹, seedling root length (mm), seedling shoot length (mm), vigour index and basal culm diameter. Low PCV and GCV were observed for the traits days to 50% flowering, panicle length, spikelet fertility and rate of germination (Table 2). The similar results of high PCV and GCV were reported by Saidaiah *et al.* (2010), Gangashetty *et al.* (2013) and Lingaiah *et al.* (2014) for plant height, number of grains panicle⁻¹ and test weight. The differences in magnitude of PCV and GCV were more for quantitative characters indicating more influence of environment in their governance, where it was less for plant height, test weight and vigour index indicating the considering in the expression of these traits, irrespective of growing conditions.

In the present study, heritability was high for all the characters days to 50% flowering, plant height (cm), leaf area index, number of productive tillers per plant, total number of tillers per m⁻², panicle length (cm), number of filled grains per panicle, number of total grains per panicle, spikelet fertility (%), test weight (g), grain yield per plant (g), biological yield per plant (g), harvest index, seedling root length (mm), seedling root length (mm), rate of germination (%), seedling vigour index and anaerobic germination (%). The maximum value was recorded by test weight (g) (99.73%) and the minimum was recorded by the anaerobic germination (%) (59.68%). Heritability is the heritable portion of phenotypic variance and is a good index of the transmission of characters from parents to their offspring (Folconar, 1981). The estimates of heritability help the plant breeder in selection of elite genotypes from divergent population. But heritability itself does not provide any indication towards the amount of genetic progress that would result in selecting best individual; rather it depends upon the amount of genetic advance.

In the present set of materials, all the characters except days to 50% flowering, panicle length (cm), spikelet fertility (%) and rate of germination (%) expressed high genetic advance as per cent of mean. Similar trend was obtained by Venkata Subbaiah *et al.* (2011), Ravindra Babu *et al.* (2012) and Aditya *et al.* (2013) for days to 50% flowering, panicle length (cm) and spikelet fertility (%). The highest genetic advance as per cent of mean was expressed by the trait number of total grains panicle⁻¹ (50.42 %) and the lowest (8.44 %) was expressed by the trait spikelet fertility (%).

Relationship of heritability and genetic advance also give an idea about the type of gene action. From the results, high heritability coupled with high genetic advance was observed for the

S. No.	Character	Replications (df:2)	Treatments (df : 54)	Error (df : 108)
1	Days to 50% flowering	4.594	52.392	6.913
2	Plant height (cm)	0.076	974.515	1.976
3	Leaf area index	0.010	0.282	0.017
4	Number of productive tillers plant-1	0.454	2.810	0.240
5	Total number of tillers m ⁻²	64.682	136.826	47.592
6	Panicle length (cm)	1.233	6.757	0.362
7	Number of filled grains per panicle	1.397	2684.749	149.036
8	Number of total grains per panicle	1.955	5654.729	109.685
9	Spikelet fertility (%)	2.175	27.203	2.786
10	Test weight (g)	0.003	41.940	0.058
11	Grain yield per plant (g)	30.263	76.111	16.459
12	Biological yield per plant (g)	34.500	350.223	54.750
13	Harvest index (%)	0.167	69.989	4.188
14	Anaerobic germination (%)	84.375	342.531	86.503
15	Seedling root length (mm) @ 14 DAS	0.032	4.649	0.527
16	Seedling shoot length (mm) @ 14 DAS	2.109	9.047	0.536
17	Rate of germination	4.824	36.324	8.249
18	Seedling vigour index	9554.049	182809.859	9678.282
19	Basal culm diameter (mm)	0.000	0.910	0.021

Table -1: Analysis of variance for 19 characters in 48 rice genotypes

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2. ive tillers plant ⁻¹ 7. ers m ⁻² 201. 22. ains per panicle 159. ains per panicle 210.	51 11 25	21.55	486.27	488.25	09.60	45.33	44.21
ive tillers plant ⁻¹ 7. ers m ⁻² 201. 22. ains per panicle 159. ains per panicle 210.		15.24	0.13	0.15	88.72	0.71	27.85
ers m ⁻² 201. 22. ains per panicle 159. ains per panicle 210.	36 15.40	16.78	1.28	1.53	84.25	2.14	29.12
ains per panicle 22. ains per panicle 210.	44 11.59	12.08	544.62	592.21	91.96	46.10	22.89
ains per panicle 159. ains per panicle 210.	58 7.92	8.36	3.20	3.56	89.82	3.49	15.46
ains per panicle 210.	40 22.34	23.61	1267.86	1416.89	89.48	69.39	43.53
	98 24.96	25.45	2772.52	2882.21	96.19	106.38	50.42
.) 76.	98 4.54	5.03	12.21	14.99	81.42	6.49	8.44
21.	75 21.04	21.07	20.94	21.00	99.73	9.41	43.28
r plant (g) 75.	73 16.05	18.79	147.74	202.49	72.96	21.39	28.24
nt (g) 30.	08 18.15	22.61	29.83	46.29	64.44	9.03	30.02
40.	13 14.30	15.18	32.90	37.09	88.71	11.13	27.74
tion (%) 67.	40 16.79	21.73	128.01	214.52	59.68	18.01	26.72
h (mm) 10.	14.04	15.74	2.06	2.59	79.64	2.64	25.82
gth (mm) 11.	93 17.28	18.34	4.26	4.79	88.81	4.00	33.55
n (%) 83.	60 4.48	5.65	14.04	22.29	62.99	6.13	7.33
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triats days to plant height (cm), leaf area index, number of productive tillers per plant, total number of tillers per m⁻², number of filled grains per panicle, number of total grains per panicle, test weight (g), grain yield per plant (g), biological yield per plant (g), harvest index, seedling root length (mm), seedling root length (mm), seedling vigour index and anaerobic germination (%) which indicates the predominance of additive gene effects, in controlling these traits. Early and simple selection could be exercised due to fixable additive gene effects. Similar results regarding heritability and genetic advance for plant height (cm), number of productive tillers plant-1, number of filled grains per panicle, test weight (g), grain yield per plant (g) and harvest index were obtained by Venkata Subbaiah et al. (2011), Ravindra Babu et al. (2012) and Aditya et al. (2013). The traits days to 50% flowering and panicle length expressed high heritability coupled with moderate genetic advance there would be greater role of additive and nonadditive gene effects and selection might be postponed to later generations to harness the nonadditive gene action for these traits. High level of heritability provides a good promise to plant breeders for the direct selection of quantitative traits based on the phenotypic performance. Therefore, these characters can be improved very easily and a high genetic gain from phenotypic selection will be effective for future breeding programmes.

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