

ASSESSMENT OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR YIELD AND QUALITY TRAITS IN INDIGENOUS LANDRACES OF RICE (*Oryza sativa* L.)

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ABSTRACT

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In this investigation genetic variability, heritability and genetic advance was studied in 39 indigenous landraces of rice along with two checks for evaluation of yield and quality traits during kharif, 2021. Variance studies showed significant variations among all the indigenous landraces of rice for all the yield and quality traits, suggesting presence of significant amount of variance. Total grain panicle⁻¹, number of filled grains panicles⁻¹, number of chaffy grains plant⁻¹ grain yield plant⁻¹, test weight, grain size, alkali spreading value and gel consistency showed high values of GCV and PCV. This indicates that considering these traits for direct selection will result in genetic improvement. The yield and quality traits which showed high estimates for genetic advance as % of mean along with high heritability were gel consistency, chaffy grain panicle⁻¹, total grain panicle⁻¹, filled grain size (mm), grain length (mm), alkali spreading value, protein (ppm), kernel breadth after cooking (mm), grain size (mm), grain length (mm), amylose content, grain breadth (mm), plant height (cm), grain yield plant⁻¹ and test weight (g). This implied that additive gene activity influenced the inheritance of these traits, thus providing scope for further improvement through selection.

KEYWORDS: Genetic variability, heritability, genetic advance, indigenous landraces.

INTRODUCTION

Rice landraces, local varieties, indigenous lines play a pivotal role for food nutritional and health security besides resistance to diseases and pests. Rice is a food grain crop of global importance with special preference in all Asian countries. Grain yield improvement is the prime objective for plant breeders from several decades but demand for good quality rice also increased in current decade as living standards of people got gradually improved. Therefore, improvement of grain quality features of rice becomes utmost objective next to vield enhancement and has become major concern in the rice breeding programs to meet the consumer preference and market demand. Rice varieties having good milling parameters, good appearance quality, good cooking and eating parameters, can be considered as a superior grain quality rice variety which increases the total economic value of rice. Fine or short slender grain varieties with intermediate amylose and alkali spreading value, intermediate gel consistency and high-volume expansion of cooked rice is preferred by consumers.

Several studies on genetic variability parameters and descriptive statistics for grain quality traits have been previously conducted. In spite of that, unexploited genetic variability still exist in rice landraces which are of equally important in selecting the superior parents. These superior parents can give extreme heterosis and superior recombinants for better grain quality components. Genetic parameters such as genotypic coefficient of variation and phenotypic coefficient of variation are the important for mining the amount of variability present in the germplasm. Role of environmental attributes on the expression of any genotype and reliability of characters can be determined precisely by high broad sense heritability in conjunction with high genetic advance.

MATERIAL AND METHODS

The investigations were conducted at ARS, Nellore Acharya N.G. Ranga Agricultural University, Andhra Pradesh, India. The experimental material consisted of 41 indigenous landraces of rice (Oryza sativa L.) genotypes carried out during Kharif, 2021 in a Randomized Block Design with three replications for yield and quality traits and its attributes (days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), number of panicle plant⁻¹, number of filled grain panicle⁻¹, number of chaffy grain panicle⁻¹, number of total gain panicle⁻¹, spikelet fertility (%), harvest index, 1000 grain weight (g), grain length (mm), grain breadth (mm), grain size (L/B ratio), kernel length (mm), kernel breadth (mm), kernel length after cooking (mm), kernel breadth after cooking (mm), alkali spreading value, gel consistency (mm), amylose content, protein (ppm) and zinc (ppm). Analysis of

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variance was carried out as suggested by Panse and Sukhatme (1967), GCV and PCV were carried out as per the methods suggested by Burton (1952). Heritability (BS) and Genetic Advance were estimated by using the formula suggested by Allard (1960) and Johnson *et al.* (1955) respectively.

RESULTS AND DISCUSSION

Analysis of variance

Analysis of variance was used to determine the degree of variation of observed characters among indigenous landrace of rice and the results are presented in tables 1 and 2. For all the characters, the study of variance showed extremely significant variations among the 41 indigenous landraces of rice, suggesting that significant genetic variation present in the material.

Genotypic and phenotypic coefficient of variance

For all the characters, the genotypic variance was smaller than phenotypic variance, which indicates that environment had masking effect on the expression of genetic variability (Table 3 and 4). The characters like number of total grain panicle⁻¹ (GCV: 29.16%; PCV: 29.41%), number of filled grains panicles⁻¹ (GCV: 29.52%; PCV: 29.83%), number of chaffy grains plant¹ (GCV: 29.52%; PCV: 29.83%) grain yield plant⁻¹ (GCV: 36.73%; PCV: 40.18%) test weight (GCV: 21.94%; PCV: 24.82%), grain size (GCV: 24.14 %; PCV: 25.11%), alkali spreading value (GCV: 28.53%; PCV: 28,99%) and gel consistency (GCV: 46.97%; PCV: 47.04%) exhibited higher estimates of GCV and PCV indicating the ample amount of variation among the genotypes studied. Therefore, direct selection would be effective for the improvement of these characters. This was in conformity with the findings of Priyanka et al. (2020) and Thakure and pandey (2020) for number of total grain panicle⁻¹, Farooq et al. (2019) for number of filled grain panicle⁻¹, Babu et al. (2012) and Dhanwani et al. (2013) for number of chaffy grain panicle⁻¹, Singh et al. (2019) and Sharma et al. (2020) for grain yield panicle⁻¹.

Heritability and Genetic Advance

Estimating heritability helps breeders manage the resources needed to successfully select for desirable characteristics and achieve maximum genetic gain with minimal effort and resources. Broad sense heritability (h^2_b) is an estimate of the total contribution of the genetic variance to the total phenotypic variance of trait. It measures the relative amount of heritable portion of total variability and provides information on the extent to which a particular morphogenetic trait can be transmitted

to successive generation.

All characters show high heritability viz., gel consistency (99.70), chaffy grain panicle⁻¹ (99.60), days to 50% flowering (99.30), total grain panicle⁻¹ (98.30), filled grain panicle⁻¹ (97.90), days to maturity (97.80), kernel length after cooking (mm) (97.70), alkali spreading value (96.80), protein (ppm) (94.90), kernel breadth after cooking (mm) (93.00), grain size (mm) (92.40), grain length (mm) (92.20), amylose content (91.90), grain breadth (mm)(85.90), plant height (cm) (85.40), grain yield plant⁻¹ (83.60), test weight (g) (78.10), spikelet fertility (%) (78.10), kernel breadth (mm) (77.30), kernel length (mm) (68.40), panicle length (cm) (67.80), harvest index (%) (67.30), zinc (ppm) (66.70) and number of panicles plant⁻¹ (45.80) indicating that these were less influenced by environment. These results are in line with the findings of Kurmanchali et al. (2019) and Jan and Kashyap (2020) for gel consistency, Dhanwani et al. (2013) for number of chaffy grain panicle⁻¹, Jan and Kashyap (2020) and Priyanka et al. (2020) for kernel length after cooking, Mithilesh et al. (2017) for alkali spreading value, Jan and Kashyap (2020) and Kumar et al. (2020) for kernel breadth after cooking, Kumar et al. (2018) and Priyanka et al. (2020) for grian yield plant⁻¹, Amegan et al. (2020) and Kumar and Kar (2020) and Thakur and Pandey (2020) for spikelet fertility, Kumar and Kar (2020) and Thakur and Pandey (2020) for panicle length, Chowdhury et al. (2016) for zinc and Pandey *et al.* (2018) number of panicle plant⁻¹.

Higher values of heritability indicated that it may be due to higher contribution of genetic component and these traits were expected to remain stable under varied environmental conditions. Therefore, for improving these traits the selection will be more effective in early generation on the basis of *per se* performance of these traits.

In the present investigation, high heritability coupled with high genetic advance as per cent of mean was observed for gel consistency ($h_{b}^{2} = 99.70\%$, GAM = 96.63%), chaffy grain panicle⁻¹ ($h_{b}^{2} = 99.60\%$, GAM = 56.28%), total grain panicle⁻¹ ($h_{b}^{2} = 98.30\%$, GAM = 59.55%), filled grain panicle⁻¹ ($h_{b}^{2} = 97.90\%$, GAM = 60.19%), Kernel length after cooking (mm) ($h_{b}^{2} =$ 97.70%, GAM = 20.31%), alkali spreading value ($h_{b}^{2} =$ 96.80%, GAM = 57.82%), protein (ppm) ($h_{b}^{2} = 94.90\%$, GAM = 32.35%), kernel breadth after cooking (mm) ($h_{b}^{2} = 93.00\%$, GAM = 24.65%), grain size (mm) ($h_{b}^{2} =$ 92.20%, GAM=33.77%), amylose content ($h_{b}^{2} = 91.90\%$, GAM = 33.71%), grain breadth (mm) ($h_{b}^{2} = 85.90\%$, GAM = 23.55%), plant height (cm) ($h_{b}^{2} = 85.40\%$, GAM

		Μ	ean sum of squar	28
S. No.	Character	Replications (df : 2)	Genotypes (df : 40)	Error (df : 80)
1.	Days to 50% flowering	0.40	217.06**	0.52
2.	Days to maturity	2.09	210.52**	2.49
3.	Plant height (cm)	22.44	917.85**	49.65
4.	Panicle length (cm)	1.20	12.53**	1.71
5.	No. of panicles plant ⁻¹	3.61	6.52**	4.86
6.	No. of filled grains panicle ⁻¹	33.06	6173.95**	42.94
7.	No. of chaffy grains panicle ⁻¹	0.40	124.49**	0.91
8.	Total grains panicle ⁻¹	14.79	8031.23**	46.07
9.	Spikelet fertility (%)	0.31	21.62**	1.84
10.	Test weight (g)	1.17	59.27**	5.07
11.	Harvest index (%)	0.07	109.54**	15.25
12.	Grain yield plant -1	53.72	430.43**	68.26
13.	Grain length (mm)	0.07	5.33**	0.15
14.	Grain breadth (mm)	0.01	0.34**	0.02
15.	Grain size	0.04	1.50**	0.04
16.	Kernel length (mm)	0.15	1.07**	0.19
17.	Kernel breadth (mm)	0.01	0.20**	0.02
18.	Kernel length after cooking (mm)	0.01	1.54**	0.15
19.	Kernel breadth after cooking (mm)	0.03	0.45**	0.92
20.	Alkali Spreading value	0.01	1.72**	0.02
21.	Gel consistency	0.74	1115.45**	1.03
22.	Amylose Content	1.19	51.41**	1.46
23.	Protein (ppm)	0.26	4.82**	0.46
24.	Zinc (ppm)	1.38	6.73**	2.67

Table 1. Analysis of variance for 22 characters in 41 genotypes of rice

** : Significant at 5% level
* : Significant at 1% level
DAT : Days After Transplanting

			Ra	Range	Vari	Variance	Coefficient	Coefficient of Variation	Heritability		Genetic
S. No	Character	Mean	Min	Max	Genotypic	Genotypic Phenotypic	Genotypic (%)	Phenotypic (%)	(Broad Sense) (%)	Genetic advance	advance as per cent of mean (%)
1.	Days To 50% Flowering	108.22	90.33	127.5	72.18	72.70	7.85	7.88	99.30	17.44	16.11
2.	Days to maturity	138.79	123.33	160.00	69.64	71.24	6.01	6.08	97.80	17.00	12.25
э.	Plant height (cm)	140.81	69.27	158.87	289.40	339.05	12.08	13.08	85.40	32.38	22.99
4	Panicle length (cm)	26.07	21.67	29.8	3.61	5.32	7.28	8.85	67.80	3.22	12.35
5.	Number of panicles plant ⁻¹	10.73	8.00	15.47	1.56	3.40	11.62	17.18	45.80	1.74	16.20
6.	Filled grain panicle ⁻¹	153.12	85.6	320.53	2043.67	2086.61	29.52	29.83	97.90	92.16	60.19
7.	Chaffy grain panicle ⁻¹	23.51	13.62	49.47	41.43	41.62	27.38	27.44	09.66	13.23	56.28
%	Total grain panicle ⁻¹	176.94	104.00	369.99	2661.72	2707.79	29.16	29.41	98.30	105.37	59.55
9.	Spikelet fertility (%)	86.5	80.92	91.22	6.59	8.44	2.97	3.36	78.10	4.68	5.41
10.	Grain yield plant ⁻¹	31.59	15.69	63.45	134.66	161.12	36.73	40.18	83.60	21.85	69.17
11.	Test weight (g)	19.38	11.67	30.67	18.07	23.14	21.94	24.82	78.10	7.74	39.93
12.	Harvest index (%)	50.25	42.86	64.96	31.43	46.68	11.16	13.60	67.30	9.48	18.86
13.	Grain length (mm)	7.69	5.31	11.47	1.72	1.87	17.07	17.78	92.20	2.60	33.77
14.	Grain breadth (mm)	2.66	1.84	3.41	0.11	0.13	12.34	13.31	85.90	0.63	23.55
15.	Grain size (mm)	2.89	1.33	4.67	0.49	0.53	24.14	25.11	92.40	1.38	47.81
16.	Kernel length (mm)	5.38	4.30	7.67	0.31	0.45	10.34	12.50	68.40	0.95	17.62
17.	Kernel breadth (mm)	2.63	2.22	3.45	0.06	0.08	9.29	10.57	77.30	0.44	16.82
18.	Kernel length after cooking (mm)	7.14	5.24	8.87	0.51	0.52	9.97	10.09	97.70	1.45	20.31
19.	Kernel breadth after cooking (mm)	3.09	2.01	3.93	0.15	0.16	12.41	12.87	93.00	0.76	24.65
20.	Alkali spreading value	2.64	1.33	4.33	0.57	0.59	28.53	28.99	96.80	1.53	57.82
21.	Gel consistency	41.03	16.00	91.00	371.47	372.50	46.97	47.04	99.70	39.65	96.63
22.	Amylose content	23.91	16.73	33.57	16.65	18.11	17.07	17.80	91.90	8.06	33.71
23.	Protein (ppm)	7.79	6.53	14.63	1.58	1.66	16.12	16.55	94.90	2.52	32.35
24.	Zinc (nom)	16.48	14.34	20.72	1.92	2.88	8.42	10.30	66.70	2.33	14.16

Table 2. Genetic variability and genetic parameters for yield and grain quality traits in rice

= 22.99%), grain yield plant⁻¹ ($h_b^2 = 83.60\%$, GAM = 69.17%) and test weight (g) ($h_b^2 = 78.10\%$, GAM = 39.93%) indicating the predominance of additive gene action. Therefore, phenotypic selection would be more effective for improvement of these characters. These results were in confirmation with the findings of Jan and Kashyap *et al.* (2020) for gel consistency, Dhanwani *et al.* (2013) for number of chaffy grain panicle⁻¹, Lingaiah *et al.* (2019) and Thakur and Pandey (2020) for number of filled grain panicle⁻¹, Devi *et al.* (2019) for number of filled grain panicle⁻¹, Devi *et al.* (2019) and Thakur and Pandey (2020) for kernel breadth after cooking, Radha *et al.* (2019) and Thakur and Pandey (2020) for grain size,

From the foregoing discussion, high heritability coupled with high genetic advance as per cent of mean was observed for gel consistency, number of chaffy grain panicle⁻¹, number of total grain panicle⁻¹, number of filled grain panicle⁻¹, kernel length after cooking, alkali spreading value, protein, kernel breadth after cooking, grain size, grain length, amylose content, grain breadth, plant height, grain yield plant⁻¹ and 1000 grain weight the predominance of additive gene action and thus, direct selection for these traits would be effective.

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