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## Estimates of genetic variability, heritability and genetic advance for yield and its component traits in advanced breeding lines of rice (*Oryza sativa* L.)

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### Abstract

Forty four rice genotypes which includes 40 advanced breeding lines and four check varieties were evaluated in randomized block design for 15 quantitative characters to estimate the extent of genetic variability, heritability (broad sense) and genetic advance as per cent of mean. The analysis of variance revealed significant variability for all the characters studied. Among the 15 characters studied, high phenotypic and genotypic coefficients of variation were recorded for the traits viz., number of chaffy grains panicle<sup>-1</sup>, grain yield plant<sup>-1</sup>, number of filled grains plant<sup>-1</sup>, harvest index, 100 grain weight and biological yield plant<sup>-1</sup> indicating the presence of large amount of variation among the genotypes. High heritability coupled with high genetic advance as per cent of mean was recorded for number of chaffy grains panicle<sup>-1</sup>, grain yield plant<sup>-1</sup>, number of filled grains panicle<sup>-1</sup>, 100 grain weight, harvest index, biological yield plant<sup>-1</sup>, plant height, number of panicles plant<sup>-1</sup> days to maturity and days to 50% flowering indicating that these traits were governed by additive gene effects and may be chosen as selection criteria for formulating breeding strategies in rice.

**Keywords:** Rice, advanced breeding lines, genetic advance, heritability, variability

### Introduction

Rice (*Oryza sativa* L.) is one of the oldest domesticated grass crops that is cultivated around the world due to uptake of it as staple food by majority of the people. Globally rice is cultivated in 162.05 million hectares of area with production of 755 million tonnes (Food and Agriculture Organization, 2020) [5]. In India, rice is grown around in 43.78 million hectares with a production of 177.64 million tonnes (Food and Agriculture Organization, 2020) [5]. India ranks first in terms of area and second in terms of production following China, the largest producer of rice

Assessment of genetic variability in any crop species is highly essential for the selection of a suitable breeding programme. The efficiency of selection depends upon magnitude of genetic variability present in plant population. Grain yield and its component traits are quantitative in nature, the breeder has to pick out superior genotypes from the knowledge of components of variation. The fundamental component is splitting of total variation into phenotypic and genotypic components and magnitude of these components for several characters is measure of type of gene action, which helps in determining a suitable breeding procedure for improving a trait. Usually, estimation of genetic variability alone will be unable to provide a clear cut indication of the improvement that can be achieved by means of simple selection. Hence, it should be used in combination with heritability and genetic advance. Therefore, the objective of this study was to evaluate the genetic variability, heritability and genetic advance of grain yield and its component traits in rice genotypes to aid the future breeding programs for yield improvement.

### Material and Methods

The present investigation was carried out using 44 rice genotypes grown in randomized block design with three replications during *kharif*, 2020 at Wetland farm, S.V. Agricultural College, Tirupati. Each genotype was grown in a two rows of 3 m length with a spacing of 20 cm between rows and 15 cm between plants within the row. In all, 44 genotypes observations were recorded on five randomly selected plants per genotype per replication for traits plant height (cm), panicle length (cm), number of panicles plant<sup>-1</sup>, biological yield plant<sup>-1</sup> (g),

harvest index (%), 100 grain weight (g), grain length (L)(mm), grain breadth (B)(mm), grain size (LB ratio), number of filled grains panicle<sup>-1</sup>, number of unfilled grains panicle<sup>-1</sup>, spikelet fertility (%) and grain yield per plant (g). However, days to 50% flowering and days to maturity were recorded on plot basis.

### Statistical Analysis

The variation among 44 genotypes for different characters was tested for significance by using analysis of variance technique as suggested by Panse and Sukhatme, (1961) [15]. Genotypic and phenotypic coefficient of variations were computed by the method suggested by Burton (1952) [5] and heritability was estimated by formula given by Lush (1940). The procedure of Johnson *et al.* (1955) [8] was followed for calculating the genetic advance and genetic advance as per cent of mean. The data analysis was carried out with INDOSTAT software.

The PCV and GCV are categorized as low (< 10%), moderate (10-20%) and high (> 20%) as suggested by Sivasubramanian and Madhavamenon (1973) [20]. Heritability was classified as low (below 30%), moderate (30-60%) and high (above 60%) as given by Johnson *et al.* (1955) [8]. The range of genetic advance as per cent of mean was classified as low (< 10%), moderate (10-20%) and high (> 20%) as suggested by Johnson *et al.* (1955) [8].

### Results and Discussion

Analysis of variance (ANOVA) revealed significant differences for all the 15 traits under study. Significant differences among the genotypes in the present investigation justified the presence of sufficient variability. Selection of the above material for further breeding activities is encouraged by the presence of variability. The details pertaining to analysis of variance are furnished in Table 1.

The estimates of PCV were slightly higher than the corresponding GCV estimates for all the characters studied (Table 2) indicating that the influence of environment is less on these characters. Therefore, phenotypic selection would be effective for the improving these traits. The traits, number of chaffy grains panicle<sup>-1</sup>, grain yield plant<sup>-1</sup>, number of filled grains plant<sup>-1</sup>, harvest index, 100 grain weight and biological yield plant<sup>-1</sup> registered higher GCV and PCV values indicating that presence large amount of variation among the genotypes. Similar results were obtained by Saha *et al.* (2019) [18] and Gupta *et al.* (2020) [21] for number of chaffy grains panicle<sup>-1</sup>; Sharma *et al.* (2020) [11] for grain yield plant<sup>-1</sup>; Dhavaleshvar *et al.* (2019) [12] for number of filled grain panicle<sup>-1</sup>; Gour *et al.* (2017) [6] and Bisne *et al.* (2009) [17] for harvest index; Saha *et al.* (2019) [18] and Panigrahi *et al.* (2017) for 100 grain weight; Gour *et al.* (2017) [6] and Yadav *et al.* (2017) [27] for biological yield plant<sup>-1</sup>.

Moderate GCV and PCV values were observed for the traits *viz.*, plant height, days to 50% flowering and days to maturity while number of panicles plant<sup>-1</sup> had moderate GCV and high PCV. These observations were in agreement with the earlier reports of Sri Lakshmi *et al.* (2020) [22] for days to 50%

flowering; Dhavaleshvar *et al.* (2019) [12] for plant height; Abilash *et al.* (2018) [1] and Bisne *et al.* (2009) [17] for number of panicles plant<sup>-1</sup>. Panicle length exhibited low GCV and moderate PCV values which was supported by findings of Bhor *et al.* (2020) [3] and Bhargavi *et al.* (2021) [2]. Low estimates of GCV and PCV values were recorded for the characters *viz.*, grain size, grain length, grain breadth and spikelet fertility indicating that the variability for these characters among the genotypes was meagre. Similar findings were reported by Dhavaleshvar *et al.* (2019) [12] and Swapnil *et al.* (2020a) [24] for grain size (LB ratio); Islam *et al.* (2019) [7] and Swapnil *et al.* (2020a) [24] for grain length; Sharma *et al.* (2020) [11] and Swapnil *et al.* (2020b) [25] for spikelet fertility; Islam *et al.* (2019) [7] and Swapnil *et al.* (2020a) [24] for grain breadth.

High heritability coupled with high genetic advance as per cent of mean (Table 2) was recorded in number of chaffy grains panicle<sup>-1</sup>, grain yield plant<sup>-1</sup>, number of filled grains panicle<sup>-1</sup>, 100 grain weight, harvest index, biological yield plant<sup>-1</sup>, plant height, number of panicles plant<sup>-1</sup>, days to maturity and days to 50% flowering. It indicates the presence of additive gene action in inheritance of these characters and less influence of environment on expression of these characters. Early and simple selection could be exercised due to fixable additive gene effects. A similar kind of results for high heritability coupled with high genetic advance was earlier reported by Saha *et al.* (2019) [18] for number of chaffy grains panicle<sup>-1</sup>; Bhor *et al.* (2020) [3] and Bhargavi *et al.* (2021) [2] for grain yield plant<sup>-1</sup>; Prasad *et al.* (2017) [16] and Sri Lakshmi *et al.* (2020) [22] for number of filled grains panicle<sup>-1</sup>; Sri Lakshmi *et al.* (2020) [22] and Saha *et al.* (2019) [18] for 100 grain weight; Gour *et al.* (2017) [6] and Bisne *et al.* (2009) [17] for harvest index; Gour *et al.* (2017) [6] and Osman *et al.* (2020) [9] for biological yield plant<sup>-1</sup>; Bhor *et al.* (2020) [3], Swapnil *et al.* (2020a) [24] and Singh *et al.* (2018) for Plant height; Prasad *et al.* (2017) [16] for number of panicles plant<sup>-1</sup>; Singh *et al.* (2013) [19] and Sri Lakshmi *et al.* (2020) [22] for days to 50% flowering.

Grain size, grain length, and grain breadth had high heritability but moderate genetic advance as per cent of mean. Whereas, spikelet fertility showed high heritability and low genetic advance as per cent of mean. The high heritability is exhibited due to favourable environment effect rather than the genotype and selection for such traits may not be rewarding. Similar results were published by Gour *et al.* (2017) [6] and Osman *et al.* (2020) [9] for days to maturity; Swapnil *et al.* (2020a) [24] and Panigrahi *et al.* (2017) for grain size *et al.* (LB ratio); Bhargavi *et al.* (2021) [2] and Vinod *et al.* (2018) [26] for grain length; Islam *et al.* (2019) [7] for grain breadth; Padmaja *et al.* (2008) [13] and Kumar *et al.* (2017) [23] for spikelet fertility.

Panicle length showed moderate heritability and genetic advance as per cent of mean which was supported by findings of Sri Lakshmi *et al.* (2020) [22] and Prasad *et al.* (2017) [16]. It shows the presence of non-additive gene action. Hence, it could be suggested that the improvement of these characters might be difficult through simple selection.

**Table 1:** Analysis of variance for yield and its component traits in 44 rice genotypes

S. No.	Trait	Mean sum of squares		
		Replication	Genotypes	Error
		2 (d.f.)	43 (d.f.)	86 (d.f.)
1	Days to 50% flowering	9.21	501.76**	3.89
2	Days to maturity	4.57	545.39**	9.40

3	Plant height (cm)	28.32	830.88**	29.27
4	Panicle length (cm)	6.61	14.36**	3.79
5	Number of panicles plant <sup>-1</sup>	1.86	10.76**	1.47
6	Biological yield plant <sup>-1</sup> (g)	27.34	543.29**	69.22
7	Harvest index (%)	44.95	327.25**	32.97
8	100 grain weight (g)	0.02	0.52**	0.01
9	Number of filled grains panicle <sup>-1</sup>	16.69	5778.47**	205.11
10	Number of chaffy grains panicle <sup>-1</sup>	33.86	223.45**	11.25
11	Spikelet fertility (%)	5.98	46.83**	2.03
12	Grain length (mm)	0.01	1.05**	0.01
13	Grain breadth (mm)	0.00	0.10**	0.00
14	Grain size (LB ratio)	0.00	0.20**	0.01
15	Grain yield plant <sup>-1</sup> (g)	14.88	237.81**	7.95

\*\* Significant at 1 per cent level

**Table 2:** Variability and genetic parameters for yield and its component traits in 44 rice varieties

S. No.	Character	Mean	Range		Variance		Coefficient of variation		Heritability (Broad sense) (%)	Genetic advance (GA)	GA as percent of mean (%)
			Min	Max	Genotypic	Phenotypic	Genotypic (%)	Phenotypic (%)			
1	Days to 50% flowering	101.17	82.67	145.67	165.96	169.84	12.73	12.88	97.71	26.23	25.93
2	Days to maturity	129.23	109.33	173.67	178.66	188.06	10.34	10.61	95.00	26.84	20.77
3	Plant height (cm)	111.84	86.07	154.93	267.20	296.47	14.62	15.40	90.13	31.97	28.58
4	Panicle length (cm)	24.61	20.74	29.66	3.52	7.32	7.63	10.99	48.15	2.68	10.90
5	Number of panicles plant <sup>-1</sup>	9.56	6.33	14.00	3.10	4.57	18.41	22.36	67.80	2.99	31.23
6	Biological yield plant <sup>-1</sup> (g)	61.08	34.80	96.47	158.02	227.25	20.58	24.68	69.54	21.59	35.36
7	Harvest index (%)	45.71	25.24	76.00	98.09	131.06	21.67	25.05	74.85	17.65	38.62
8	100 grain weight (g)	1.85	1.17	2.55	0.17	0.18	22.25	22.88	94.56	0.83	44.57
9	Number of filled grains panicle <sup>-1</sup>	159.43	91.93	320.53	1857.79	2062.90	27.03	28.49	90.06	84.26	52.85
10	Number of chaffy grains panicle <sup>-1</sup>	17.43	5.70	49.60	70.73	81.99	48.25	51.95	86.28	16.09	92.33
11	Spikelet fertility (%)	90.22	72.74	95.30	14.93	16.97	4.28	4.57	88.02	7.47	8.28
12	Grain length (mm)	7.74	6.87	9.29	0.35	0.36	7.59	7.73	96.51	1.19	15.36
13	Grain breadth (mm)	2.47	2.15	2.81	0.03	0.04	7.31	7.68	90.61	0.35	14.33
14	Grain size (LB ratio)	3.14	2.51	3.72	0.07	0.07	8.15	8.52	91.51	0.51	16.06
15	Grain yield plant <sup>-1</sup> (g)	27.68	14.40	61.60	76.62	84.57	31.62	33.22	90.60	17.16	62.01

## Conclusion

The analysis of variance revealed the presence of significant differences among 44 genotypes for all the traits studied. High PCV and GCV were recorded for the traits *viz.*, number of chaffy grains panicle<sup>-1</sup>, grain yield plant<sup>-1</sup>, number of filled grains plant<sup>-1</sup>, harvest index, 100 grain weight and biological yield plant<sup>-1</sup> indicating that large amount of variation is present among the genotypes. High heritability coupled with high genetic advance as per cent of mean was recorded for number of chaffy grains panicle<sup>-1</sup>, grain yield plant<sup>-1</sup>, number of filled grains panicle<sup>-1</sup>, 100 grain weight, harvest index, biological yield plant<sup>-1</sup>, plant height, number of panicles plant<sup>-1</sup> days to maturity and days to 50% flowering indicating that these traits were mostly under the control of additive gene action and direct selection of these traits would be effective for crop improvement.

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## References

- Abilash R, Thirumurugan T, Sasikumar D, Chitra S. Genetic studies in F<sub>2</sub> for biometrical traits in Rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*. 2018;9(3):1067-1076.
- Bhargavi M, Shanthi P, Reddy VLN, Mohan Reddy D, Ravindra Reddy B. Estimates of genetic variability, heritability and genetic advance for grain yield and other yield attributing traits in rice (*Oryza sativa* L.). *The Pharma Innovation Journal* 2021;10(5):507-511.
- Bhor TJ, Kashid NV, Kadam SM. Genetic variability, character association and path analysis studies for yield components traits in promising rice (*Oryza sativa* L.) genotypes. *Journal of Pharmacognosy and Phytochemistry* 2020;9(4):1953-1956.
- Burton GW. Quantitative inheritance in grasses. *Proceedings of Sixth International Grassland Congress*. 1952;1:277-283.
- FAO (Food and Agriculture Organization), FAOSTAT Database. FAO, Rome 2020.
- Gour L, Koutu GK, Singh SK, Patel DD, Shrivastava A, Singh Y. Genetic variability, correlation and path analyses for selection in elite breeding materials of rice (*Oryza sativa* L.) genotypes in Madhya Pradesh, *The Pharma Innovation Journal* 2017;6(11):693-696.
- Islam MZ, Mian MAK, Ivy NA, Akther N, Rahman MM. Genetic variability, correlation and path analysis for yield and its components in restorer lines of rice. *Bangladesh Journal of Agricultural Research*. 2019;44(2):291-301.
- Johnson HW, Robinson HF, Comstock RE. Estimation of genetic and environmental variability in soybean. *Agronomy Journal* 1955;47(3):314-318.
- Khalid A Osman, Kyung-HO Kang, Ahmed A El-Siddg, Yassir M Ahmed, Sara M Abdalla. Assessment of genetic variability for yield and attributed traits among rice doubled haploid (DH) lines in semi-arid zone Sudan. *African Journal of Agricultural Research* 2020;16(7):939-946.
- Lush JL. Intra-sire correlation and regression of offspring in ramsasa method of estimating heritability of characters. *Proceedings of American Society of Animal Production* 1940;33:292-301.
- Madhvi Sharma, Anil Kumar Singh, Romesh Kumar

- Salgotra, Bupesh Kumar Sharma, Sunil Shivaji Gangurde, Parshant Bakshi *et al.* Study of genetic variability and heritability for various morphological and yield attributed traits in RIL population of basmati rice (*Oryza sativa* L.). International Journal of Chemical Studies. 2020;8(2):2699-2702.
12. Mutturaj Dhavaleshvar, Malleshappa C, Dushyanth Kumar BM. Variability, correlation and path analysis studies of yield and yield attributing traits in advanced breeding lines of rice (*Oryza sativa* L.). International Journal of Pure and Applied Biosciences 2019;7(1):267-273.
  13. Padmaja D, Radhika K, Subba Rao LV, Padma V. Studies on variability, heritability and genetic advance for quantitative characters in rice (*Oryza sativa* L.). Journal of Plant Genetic Resources. 2008;21(3):196-198.
  14. Panigrahi AK, Bharathi M, Kumaravadivel N. Genetic variability and character association studies in advanced backcross generation of rice (*Oryza sativa* L.). Journal of Pharmacognosy and Phytochemistry 2018;7(1):2397-2400.
  15. Panse VG, Sukhatme PV. *Statistical methods for agricultural workers*, 2<sup>nd</sup> edition, ICAR, New Delhi 1961.
  16. Prasad KR, Krishna KVR, Bhave MHV, Rao LVS. Genetic variability, heritability and genetic advance in boro rice (*Oryza sativa* L.)germplasm. International Journal of Current Microbiology and Applied Sciences. 2017;6(4):1261-1266.
  17. Rita Bisne, Sravgi AK, Verulkar SB. Study of heritability, genetic advance and variability for yield contributing characters in rice. Bangladesh Journal of Agricultural Research 2009;34(2):175-179.
  18. Setu Rani Saha, Lutful Hassan, Ashraful Haque Md., Mirza Mofazzal Islam, Rasel Md. Genetic variability, heritability, correlation and path analyses of yield components in traditional rice (*Oryza sativa* L.) landraces. Journal of Bangladesh Agricultural University 2019;17(1):26-32.
  19. Singh AK, Sharma P, Singh PK. Studies on Genetic Characteristic of Upland Rice (*Oryza sativa* L.). International Journal of Agriculture, Environment & Biotechnology 2013;6(4):515-520.
  20. Sivasubramanian S, Madhavamenon P. Combining ability in rice. Madras Agricultural Journal 1973;60:419-421.
  21. Sneha Gupta, Sameer Upadhyay, Ganesh Kumar Koli, Sanket Rajendra Rathi, Prashant Bisen, Bapsila Loitonbam *et al.* Trait association and path analysis studies of yield attributing traits in rice (*Oryza sativa* L.) Germplasm. International Journal of Bio-resource and Stress Management 2020;11(6):508-517.
  22. Sri Lakshmi M, Suneetha Y, Srinivas T. Genetic variability, correlation and path analysis for grain yield and yield components in rice genotypes. Journal of Pharmacognosy and Phytochemistry. 2020;10(1):1369-1372.
  23. Sudhir Kumar, Bhuvaneshwari S, Lamalakshmidivi E, Sharma SK, Ansari MA, Meghachandra Singh I *et al.* Estimation of genetic variability, correlation and path analysis in short duration rice genotypes of Manipur. Journal of Agricultural Research 2017;4(2):112-118.
  24. Swapnil, Krishna Prasad, Manigopa Chakraborty, Singh DN, Priyanka Kumari, Jenny Priya Ekka. Genetic variability, correlation and path coefficient studies in F<sub>2</sub> generation of rice (*Oryza sativa* L.). International Journal of Chemical Studies 2020a;8(4):3116-3120.
  25. Swapnil, Krishna Prasad, Manigopa Chakraborty, Singh DN, Jenny Priya Ekka, Priyanka Kumari. Genetic variability, correlation and path coefficient studies in F<sub>3</sub> generation of rice (*Oryza sativa* L.). International Journal of Current Microbiology and Applied Sciences 2020b;9(9): 1304-1312
  26. Vinod Kumar, Dharendra Singh, Ritika Singh. Assessment of genetic variability, heritability and genetic advance for yield and quality traits in basmati (*Oryza sativa* L.) genotypes of Himachal Pradesh. Journal of Pharmacognosy and Phytochemistry 2018;7(2):1323-1326.
  27. Yadav R, Rajpoot P, Verma OP, Singh PK, Singh P, Pathak V. Genetic variability, heritability and genetic advance in Rice (*Oryza sativa* L.) for grain yield and its contributing attributes under sodic soil. Journal of Pharmacognosy and Phytochemistry 2017;6(5):1294-1296.