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Study of Genetic Variability in Rice (Oryza sativa L.) Genotypes for Yield and its Component Traits

Sudhanshu Pandey[1], S.K. Payasi[1], Yogendra Singh[2], S.K. Tripathi[1]
[1]*JNKVV, College of Agriculture, Rewa. E-mail: sudhanshu.pandey@jnkvv.org*
[2]*JNKVV, College of Agriculture, Jabalpur*

Abstract: The experiment was conducted at the instructional farm of the College of Agriculture, Rewa (M.P.). The crosses were made in a diallel manner using 10 parents in on-way, excluding reciprocal, during Kharif 2018. During Kharif 2019, 45 F1's and their parents were evaluated to study the "genetic parameters of variation in rice (Oryza sativa L.)" in a randomized block design (RBD) with three replications. The cross-combination IR64 X NPT14-10 was found to be best for yield and most of the yield-attributing traits. Moderate estimates of phenotypic and genotypic coefficients of variation were recoded for grain yield per plant (15.83 and 14.15), number of effective tillers per plant, number of tillers per plant, weight of panicle, and test weight. High heritability was recorded for days to maturity (92.27), followed by test weight (89.93), plant height (83.96), grain yield per plant (79.92), days to 50% flowering (79.38), weight of panicle (77.76), number of grains per panicle (77.63), and biological yield per plant (74.44). The high genetic advance was recorded for grain yield per plant (26.06), followed by test weight (20.49). High heritability coupled with high genetic advance was recorded for test weight, followed by grain yield, indicating that these traits were governed by additive gene action. Heritability estimates indicated that these traits were heritable and less influenced by the environment. Hence, these traits were more suitable for direct selection for higher seed yield in rice.

Keywords: GCV, PCV, Heritability, Genetic advance, Additive gene action

INTRODUCTION

Rice (Oryza sativa L.) is a globally essential cereal food crop for over half the world's population (Muthayya *et al.*, 2014; EI Sayed *et al.*, 2021). It has valuable nutritional benefits with high contents of carbohydrates, minerals, calories, protein, and vitamins (Kun *et al.* 2013), and its grain comprises carbohydrates (71.1 g), protein (7.3 g), crude fat (2.2 g), and is low in fiber. Its fat content is primarily omega-6 fatty acids, which are considered pro-inflammatory. Globally, its cultivated area is almost 162 million hectares, with a production of 756 million tons (FAOSTAT, 2021). This production should be increased to cope with continuing population growth and the threat of environmental pressures (Chang *et al.*, 2016).

In India, the major rice-growing states are Uttar Pradesh, West Bengal, Odisha, Bihar, Chhattisgarh, Andhra Pradesh, and Madhya Pradesh. West Bengal is the largest producer of rice, followed by Uttar Pradesh. Rice is one of the most important food grains in production and consumption; it occupies 23.3 percent of the gross cropped area of the country and contributes 43 percent of total food grain production. In India, there are 45.07 mha with a production of 122.27 mt and a productivity of 2713 kg/ha (Agricultural Statistics at a Glance 2021, Government of India, Ministry of Agriculture and Farmers Welfare, Directorate of Economics and Statistics). In M.P., rice is grown in an area of about 1.98 mha with a production of 4.52 mt and a productivity of 2270 kg/ha (Annual Report, 2018-19, Directorate of Economics and Statistics, Department of Agriculture and Farmers Welfare, Ministry of Agriculture and Farmers Welfare, Govt. of India).

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MATERIALS AND METHODS

The experiment was conducted at the instructional farm of the College of Agriculture, Rewa (M.P.), situated in the northeastern part of Madhya Pradesh at 24º 30′ North latitude, 81º 15′ East longitude, and 365.7 meters above mean sea level. Rewa traditionally falls under the rice-wheat crop zone and belongs to the "Kymore Plateau and Satpura Hills Agro-Climatic Zone" of Madhya Pradesh. The climate of Rewa is subtropical, i.e., hot and dry summers and cold winters, with an average annual rainfall of 1140 mm. The crosses were made in a diallel manner using 10 parents in on-way, excluding reciprocal, during Kharif 2018. The experiment was laid out in a randomized block design (RBD) with three replications to evaluate 55 genotypes (45 F1's and 10 parents) during Kharif 2019. Each genotype was transplanted in two rows of 2 meters with 20 cm spacing between row to row and 15 cm between plant to plant. The recommended dose of fertilizer for the transplanted condition was applied. The observations of quantitative traits were recorded based on five plants taken from each cross and parent.

RESULTS AND DISCUSSION

Data from the analysis of variance and genetic parameters of variations influenced by various genotypes are presented in Tables 1, 2, and 3.

The analysis of variance was carried out to partition the total variance into variances due to genotype and other sources for all traits. The mean sum of squares due to treatment was found to be highly significant for all the morphological traits under study, indicating the presence of an adequate amount of variability among the treatments. The magnitude of the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters. Moderate GCV and PCV were recorded for grain yield per plant (14.15, 15.83), respectively, which suggested less environmental influence and a greater role of genetic factors in the expression of the traits. Similar findings were also reported by Babu *et al.* (2012), Adhikari *et al.* (2018), and Divya *et al.* (2018) for grain yield per plant.

Similarly, moderate genotypic and phenotypic coefficients of variation were also observed for the number of effective tillers per plant (11.67, 15.62), number of tillers per plant (10.21, 14.49), weight of panicle (10.43, 11.83), and test weight (10.49, 11.06). Whereas, the number of filled grains per panicle (7.67, 10.94), biological yield per plant (9.43, 10.93), and number of grains per panicle (9.08, 10.31) recorded a moderate phenotypic coefficient of variation and a low genotypic coefficient of variation. Similar findings were also reported by Savitha and Usha (2015), and Dey *et al.* (2019) for the number of effective tillers per plant and the number of filled grains per panicle. Low estimates of genotypic and phenotypic coefficients of variation were recorded in plant height, panicle length, days to maturity, and days to 50% flowering. Sala and Shanthi (2016) reported similar results for plant height and panicle length, and for days to 50% flowering similar findings were illustrated by Gautam *et al.* (2016), and Singh *et al.* (2018).

The heritability estimates for twelve quantitative characters ranged from 49.11 to 92.27 for the number of filled grains per panicle and days to maturity, respectively. The heritability (broad sense) was high for days to maturity (92.27), followed by test weight (89.93), plant height (83.96), grain yield per plant (79.92), days to 50% flowering (79.38), weight of panicle (77.76), number of grains per panicle (77.63), biological yield per plant (74.44), and it was observed to be moderate for the number of effective tillers per plant (55.80), panicle length (54.43), number of tillers per plant (49.57), and number of filled grains per panicle (49.11). Similar results have also been illustrated for these traits by Islam *et al.* (2015), Sameera *et al.* (2016), Gour *et al.* (2017), Neupane *et al.* (2018), Singh *et al.* (2018), Sandeep *et al.* (2018), Lipi *et al.* (2020), Ganapati *et al.* (2020), and Fentie *et al.* (2021).

The genetic advance is commonly predicted as a product of the heritability ratio and the selection differential. The high heritability, accompanied by a high genetic gain over the percent of the mean, shows that there is an additive gene effect for the trait. If high heritability is accompanied by low genetic gain, the over-percentage of the mean shows non-additive gene action. Therefore, the estimates of genetic gain over percent of the mean are important to get an idea of the effectiveness of selection. A high genetic advance was pointed for grain yield per plant (26.06), followed by test weight (20.49). Whereas, it was found to be moderate for the weight of the panicle (18.95), followed by the number of effective tillers per plant (17.96), biological yield per plant (16.76), number of grains per panicle (16.48), plant height (15.31), number of tillers per plant (14.79), and number of filled grains per panicle (11.07). While panicle length (6.83), days to maturity (6.01), and days to 50% flowering (4.87) had exhibited a low genetic gain over the percent of the mean, Similar findings were suggested by Fentie *et al.* (2021), Ghirmire *et al.* (2019), Divya *et al.* (2018), Singh *et al.* (2018), Devi *et al.* (2017), Edukondalu *et al.* (2017), Acharya *et al.* (2018), Singh *et al.* (2015), and Ketan and Sarkar (2014) for grain yield per plant, test weight and most of the traits under study. Days to maturity observed low genetic gain over percent of the mean. It indicated that there was little influence of environmental effects on the inheritance of these traits, and these traits were governed by non-additive genes, so direct selection is not beneficial. Further improvements in yield potentiality and yield traits for these genotypes are suggested by creating variation and selection.

The high heritability coupled with high genetic gain over the percent of mean was observed for test weight, followed by grain yield. It indicated that these traits were governed by additive gene action, and selection for these traits in segregating populations is more effective. Hence, it indicated the predominance of additive gene action in controlling these characters. By this, Immanuel *et al.* (2011), Devi *et al.* (2017), Prasad *et al.* (2017), Singh *et al.* (2018), and Sandeep *et al.* (2018) for test weight, and Singh *et al.* (2015), Edukandalu *et al.* (2017), Acharya *et al.* (2018), Singh *et al.* (2018), Dey *et al.* (2019), Ghimire *et al.* (2019), and Fentie *et al.* (2021) for grain yield per plant. Plant height, weight of panicle, number of grains per panicle, and biological yield per plant exhibited high heritability and moderate genetic gain over the percent of the mean. This

Table 1: Analysis of Variance For Yield and its Component Traits

Source of Variation	*Df*	Mean sum of squares											
		DF	*DM*	*PH (cm)*	*NT*	*NET*	*PL (cm)*	*WP*	*NG*	*NFG*	*BY*	*TW (g)*	*GY (g)*
Replication	2	20.169***	6.406**	10.155	0.233	0.118	6.723**	4.419	832.49***	436.66***	15.197	1.484	1.897
Treatments	54	7.628***	40.391***	164.582***	5.217***	4.182***	4.311***	24.151***	329.84***	217.18***	58.646***	17.117***	25.757***
Error	108	0.061	1.097	9.855	1.321	0.874	0.941	2.102	28.91	55.77	6.023	0.616	1.991

*** Significant at 0.1% level of probability. ** Significant at 1% level of probability. * Significant at a 5% level of probability.

DF- Days to 50% flowering, DM – Days to maturity, PH – Plant height, NTP -Number of tillers per plant, NET- Number of effective tillers per plant, PL- Panicle length, WP-Weight of panicle, NGP- Number of grains per panicle, NFG- Number of filled grains per panicle, BY- Biological yield per plant, TW- Test weight, GY- Grain yield per plant

Table 2: Mean, range, and coefficient of variance (CV) of parents and crosses for twelve quantitative traits.

Traits	*Parents*			*Crosses*			*CV*
	Mean	*Range*		*Mean*	*Range*		
		Min	*Max*		*Min*	*Max*	
DF	57.80	54.67	61.33	57.61	54.67	60.67	1.353
DM	117.87	110.67	124.00	119.37	112.33	125.33	0.880
PH (cm)	86.76	82.47	93.67	88.96	72.53	108.33	3.545
NT	10.31	9.60	12.60	11.36	9.67	16.07	10.291
NET	8.02	7.33	9.80	9.21	7.60	13.07	10.388
PL (cm)	22.47	21.07	24.47	23.84	20.93	25.60	4.111
WP	22.87	17.99	27.51	26.67	20.86	31.58	5.581
NG	106.23	94.67	123.00	112.77	92.33	135.00	4.876
NFG	90.50	83.67	108.67	95.59	74.67	115.33	7.805
BY (gm)	39.86	37.03	46.50	45.42	35.61	52.07	5.527
TW weight (gm)	23.73	19.50	27.70	22.06	18.60	27.63	3.509
GY (gm)	16.58	15.07	21.77	20.63	14.97	25.33	7.093

Table 3: Estimates of Genetic Variability

S. No.	*Character*	*Range*		*PCV*	*GCV*	*H2 (bs) %*	*GA over percent mean*
		Min.	*Max.*				
1	DF	53.00	62.00	2.98	2.65	79.38	4.87
2	DM	110.00	126.00	3.16	3.04	92.27	6.01
3	PH (cm)	71.00	113.4	8.85	8.11	83.96	15.31
4	NT	9.00	17.80	14.49	10.21	49.57	14.79
5	NET	7.00	14.40	15.62	11.67	55.80	17.96
6	PL (cm)	19.00	26.60	6.09	4.49	54.43	6.83
7	WP	15.12	34.75	11.83	10.43	77.76	18.95
8	NG	81.00	138.00	10.31	9.08	77.63	16.48
9	NFG	64.00	125.00	10.94	7.67	49.11	11.07
10	BY (g)	34.40	54.21	10.93	9.43	74.44	16.76
11	TW (g)	18.00	28.60	11.06	10.49	89.93	20.49
12	GY (g)	14.00	26.67	15.83	14.15	79.92	26.06

PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, H2= Heritability (broad sense), GA over percent mean = Genetic advance

also indicates the greater role of non-additive gene action in their inheritance, suggesting heterosis breeding could be used to improve these traits. Similar findings were also reported by Acharya *et al.* (2018) and Singh *et al.* (2015) for plant height and biological yield. Whereas high heritability coupled with low genetic gain over percent of mean were exhibited for days to maturity and days to 50% flowering, it indicates that the selection is not effective for these traits. Similar findings were supported by Sameera *et al.* (2016). Moderate heritability coupled with moderate genetic gain over percent of the mean was observed for the number of tillers per plant, the number of effective tillers per plant, and the number of filled grains per panicle. Moderate heritability coupled with low genetic advance over percent of the mean was observed for panicle length. In this regard, Singh *et al.* (2015) reported a similar finding for the number of tillers per plant.

CONCLUSION

From the present investigation findings, it may be concluded that significant genetic variability was observed for all the traits studied. The cross IR64 X NPT 14-10 was found to be the best for yield and most of the yield attributes. The high heritability was observed for days to maturity, test weight, plant height, grain yield per plant, days to 50% flowering, weight of panicle, number of grains per panicle, and biological yield per plant. It indicated that these traits were heritable and less influenced by the environment. The genetic advance was recorded as high for grain yield per plant and test weight. High heritability coupled with high genetic gain over the mean were observed in test weight, followed by grain yield. It concluded that these traits were governed by additive gene action and that the selection of these traits would be effective, as genetic advances are high due to additive gene action.

REFERENCE

Acharya S, Shrestha A, Acharya N, Poudel A and Acharya S. 2018. Genetic variability, heritability and correlation analysis in quantitative traits of irrigated rice (Oryza sativa L.). Biosciences Biotechnology Research Asia 15(3): 729.

Adhikari BN, Joshi BP, Shrestha J and Bhatta NR. 2018. Genetic variability, heritability, genetic advance, and correlation among yield and yield components of rice (Oryza sativa L.). *Journal of Agriculture and Natural Resources* 1(1):149-160.

Agricultural Statistics at a Glance 2021, Government of India, Ministry of Agriculture and Farmers Welfare, Directorate of Economics and Statistics.

Annual Report, 2018-19, Directorate of Economics and Statistics, Department of Agriculture and Farmers Welfare, Ministry of Agriculture and Farmers Welfare, Govt. of India

Babu VR, Shreya K, Dangi KS, Usharani G and Nagesh P.2012. Genetic variability studies for qualitative and quantitative traits in popular rice (Oryza sativa L.) hybrids of India. *International Journal Scientific and Research Publication* 2(6): 1-5.

Chang, Z., Chen, Z., Wang, N.A., Xie, G., Lu, J., Yan, W., Zhou, J., Tang, X., and Deng, X.W. (2016) Construction of a male sterility system for hybrid rice breeding and seed production using a nuclear male sterility gene Proc. Natl. Acad. Sci., 113 (49) (2016), pp. 14145-14150

Dey P, Sahu S and Kar RK. 2019. Estimation of Phenotypic Coefficients of Variation (PCV), Genotypic Coefficients of Variation (GCV), Heritability and Genetic Gain for Yield and its Components in Rice Landraces of Odisha. *International Journal of Agriculture, Environment and Biotechnology* 12(3): 181-185.

Devi A, Kumari P, Dwivedi S, Verma OP, Singh PK, and Dwivedi DK. 2017. Estimation of Heterosis for seed yield and yield attributing traits in rice under Salinity condition. *Journal of Pharmacognosy and Phytochemistry* 6(4): 1345-1354.

Divya J, Raju CD, Rao LS and Aparna K. 2018. Genetic Variability Studies in genetically diverse rice genotypes. *International Journal of Current Microbiology and Applied Sciences* 7(4): 1169-1172.

Edukondalu B, Ram Reddy V, Shobha Rani T, Aruna Kumari Ch and Soundharya B. 2017. Studies on variability, heritability, correlation, and path analysis for yield, yield attributes in rice (Oryza sativa L.). *International Journal of Current Microbiology and Applied Sciences* 6(10): 2369-2376.

El Sayed MAA, Kheir AMS, Hussein FA, Ali EF, Selim ME, Majrashi A, El Shamey

EAZ. (2021). Developing new lines of Japonica rice for higher quality and yield under arid conditions. PeerJ 9: e11592 https://doi.org/10.7717/peerj.11592

Faostat, 2021. Food and Agriculture Organization of the United Nations. Statistical Database. <http://www.fao.org/faostat/en/#data> (Accessed on 2 August 2021).

Fentie, B. D., Bayuh Belay Abera, B.B. and Ali H. M. 2021. Association of Agronomic Traits with Grain Yield of Lowland Rice (Oryza Sativa L.) Genotypes. *International Journal of Research in Agricultural Science* 8 (3): 2348 – 3997

Ganapati RK, Rasul MG, Sarker U, Singha A and Faruquee M. 2020. Gene action of yield and yield contributing traits of submergence tolerant rice (Oryza sativa L.) in Bangladesh. Bulletin of the National Research Centre 44(1): 1-7.

Gautam A, Suresh J and Madhav MS. 2016. Study of genetic variability in genotypes of rice (Oryza sativa L.). *Research Journal of Agricultural Sciences* 7 (1): 235-236.

Ghimire NH and Mahat PM. 2019. Genetic variability and correlation coefficients of major traits in cold tolerance rice (Oryza sativa L.) under mountain environment of Nepal. *International Journal of Applied Sciences and Biotechnology* 7(4): 445-452.

Gour L, Koutu GK, Singh SK, Patel DD, Shrivastava A and Singh Y.2017. 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 6(11): 693-696.

Immanuel SC, Pothiraj N, Thiyagarajan K, Bharathi M and Rabindran R. 2011. Genetic parameters of variability, correlation and path coefficient studies for grain yield and other yield attributes among rice blast disease resistant genotypes of rice (Oryza sativa L.). *African Journal of Biotechnology* 10(17): 3322-3334.

Islam MA, Raffi SA, Hossain MA and Hasan AK. 2015. Analysis of genetic variability, heritability, and genetic advance for yield and yield-associated traits in some promising advanced lines of rice. Progressive Agriculture 26(1): 26-31.

Ketan R and Sarkar G. 2014. Studies on variability, heritability, genetic advance and path analysis in some indigenous Aman rice (Oryza sativa L.). *Journal of Crop and Weed* 10(2): 308-315.

Lipi LF, Hasan MJ, Akter A, Quddus MR, Biswas PL, Ansari A and Akter S. 2020. Genetic variation, heritability, and genetic advance in some promising rice hybrids. *SAARC Journal of Agriculture* 18(2): 39-49.

Muthayya,S.,Sugimoto,J.D.,Montgomery,S.,&Maberly, G. F. (2014). An overview of global rice production, supply, trade, and consumption. Annals of the New York Academy of Sciences, 1324, 7–14.

N. Neupane, A Poudel, P Gaire. 2018. Correlation and Variability among Yield and Yield Attributes of Advance Rice Genotypes in Rain Fed Condition. Research & Reviews: *Journal of Crop Science and Technology* 7(1): 27–34.

Prasad KR, Radha-Krishna KV, Bhave MHV and Subba-Rao LV. 2017. Genetic

variability, heritability and genetic advance in boro rice (Oryza sativa L.) germplasm. *International Journal of Current Microbiology and Applied Sciences* 6(4): 1261-1266.

Sameera SK, Srinivas T, Rajesh AP, Jayalakshmi V and Nirmala PJ. 2016. Variability and path co-efficient for yield and yield components in rice. *Bangladesh Journal of Agricultural Research* 41(2): 259-271.

Sandeep S, Sujatha M, Subbarao LV, and Neeraja CN. 2018. Genetic variability, heritability, and genetic advance studies in rice (Oryza sativa L.). *International Journal of Current Microbiology and Applied Sciences* 7: 3719-3727.

Savitha P and Usha KR. 2015. Assessment of genetic variability and correlation studies among traditional land races and improved cultivars for segregating generation of rice (Oryza sativa L.). *International Journal of applied and Natural science* 6(2): 135-140.

Singh A, Singh AP, Singh A, Maurya MK, Yadav V, Singh H, Singh A and Avasthi S. 2018. Study of simple correlation coefficients for yield and its component traits in rice (Oryza sativa L.). *Journal of Entomology and Zoology Studies* 6(4): 1774-1777.

Singh M, Singh HP, Saha R, Samal P, Hussain ME, Sharma S, Nitesh SD and Koutu GK. 2018. Genetic Analysis of Green Super Rice (Oryza sativa L.) for Yield and Quality Traits. *International Journal of Current microbiology and applied sciences* 7 (2): 3166-3173.

Singh S, Sahu H and Sahu PK .2015. Variability and genetic parameters for grain yield in CMS based rice hybrid (Oryza sativa L.). *Journal of Plant Development Sciences* 7(3): 247-250.