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Genetic variability and heritability studies for yield and quality traits in rice (*Oryza sativa* L.)

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Abstract

The research work was executed Research cum Instructional Farm, Genetics and Plant Breeding department of IGKV Raipur (C.G.) during kharif 2022. The research material under research comprised of 28 rice germplasm lines including four checks namely Swarna, MTU 1318, Pooja and, Jaldubi which were tested in RCBD with two replications. The observation of research investigation were recorded for total twenty characters.

The analysis of variance showed that there was a highly significant variation in genotypes for all of the studied characters. A small difference between PCV and GCV suggests that the environment has little impact on the concerning traits. The characters for which highest and lowest heritability obtained were grain yield per plant (95.92) and days to maturity (41.58), respectively and medium estimates of heritability obtained for 1000 seed weight (g) (51.68%). For quality trait, grain elongation ratio medium heritability estimates were obtained and all other quality characters showed high estimates of heritability which were head rice recovery (%) (99.37%). The advance breeding lines showed genetic advance as% of mean from low to high value. While, noting for genetic advance as percent of mean, the yield characters observed with highest value was number of effective tillers per plant (48.99%) and least value was obtained for traits, days to maturity (5.87%) along with high genetic advance as a percent of mean indicates that the heritability is most likely caused by additive gene action and selection in batter generations may be effective.

Keywords: Rice, variability, heritability, genetic advance

Introduction

Rice belongs to family Poaceae and it is believed to be originated in South East Asia. "Rice is Life", the famous motto of the International Rice Year 2004, emphasized the importance of rice as a food and commerce commodity. India has the largest rice-growing area in the world, ranks second in production, with about 130 million metric tones in 2022-2023, after China. In rice breeding programmes, yield increase is the primary breeding goal and recognizing of the type and degree of genetic variation influencing the inheritance of quantitative features like yield and yield components is critical for successful genetic improvement. Plant breeders frequently choose yield components that tangentially increase yield. A trait's heritability is crucial in determining how it will react to selection. It has been established that in order to plan a successful breeding programme and genetic improvement of plants for quantitative traits requires accurate estimates of heritability.

Materials and Methods

The experimental material included 28 rice genotypes including 24 advance breeding line and four checks namely Swarna, MTU 1318, Pooja and, Jaldubi. Genotypes rice of were evaluated at the Research cum Instructional Farm, Department Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur. The genotype were evaluated is Randomised Block Design with replications. All the observation were recorded from randomly selected plants. The details of experimental are given in Table No. 1

Table 1: List of experimental material

Entry No.	Designation	Entry No.	Designation
1.	R 2404-144-1-61-1	15.	R 2451-327-1-302-1
2.	R 2404-144-2-62-1	16.	R 2374-115-1-31-1
3.	R 2418 299-2-252-1	17.	R 2289-123-1-39-1
4.	R 2548-C7-4-487-1	18.	R 2554-C13-6-531-1
5.	R 2443-C2-2-450-1	19.	R 2430-405-1-383-1
6.	R 2372-105-2-17-1	20.	R 2451-350-1-347-1
7.	R 2404-133-1-50-1	21.	R 2374-115-3-33-1
8.	R 2419-318-1-276-1	22.	R 2554-C13-7-532-1
9.	R 2451-333-2-326-1	23.	R 2553-C12-1-519-1
10.	R 2451-327-3-304-1	24.	R 2553-C12-2-520-1
11.	R 2445-458-2-431-1	25.	Swarna (check)
12.	R 2445-454-1-429-1	26.	MTU 1318 (check)
13.	R 2554-C13-5-530-1	27.	Pooja (check)
14.	R 2419-322-2-289-1	28.	Jaldubi (check)

Results and Discussion

Heritability (%)

The estimates of heritability for yield and quality characters ranged from medium to high heritability. The quantitative characters for which highest and lowest heritability obtained were grain yield per plant (95.92) and days to maturity (41.58), respectively. Quantitative characters for which high heritability obtained were grain yield per plant (95.92%), biological yield per plant (94.02%), number of effective tillers per plant (91.09%), number of filled grains per panicle (89.48%), panicle length (88.30%), number of spikelet per panicle (87.47%), flag leaf length (80.73%), harvest index (%) (76.94%). Medium estimates of heritability obtained for yield characters were 1000 seed weight (g) (51.68%), plant height (42.80%), spikelet fertility (%) (42.80%), days to 50% flowering (42.00%), days to maturity (41.58%). The highest and lowest value of heritability obtained for quality characters were grain yield per plant (95.92%) and days to maturity (41.58%), respectively. According to Babu *et al.*, (2012) [11] and Ashok *et al.*, (2013) [12], the magnitude of heritability is classified as low (<50%), medium (50-60%) and high (>60%). High broad sense heritability for plant height was reported by Ketan and Sarkar (2014) [13] and Tuhina *et al.* (2015) [14]. Higher broad sense heritability for panicle length and grain yield was reported by Ammar *et al.* (2014) [15], and Seyoum *et al.* (2012) [9] and revealed higher heritability for days to flowering, plant height, grain yield and panicle length. For quality trait elongation ratio medium heritability estimates were obtained and all other quality characters showed high estimates of heritability which were head rice recovery (%) (99.37%), kernel length (mm) (96.75%), paddy grain length (mm) (95.97%), paddy grain breadth (mm) 84.81%, paddy L/B ratio (88.18%), amylose content (%) (79.38%), kernel breadth (mm) (71.39%). Similar results were obtained by Saha *et al.*, (2019) [16] Parimala and Devi (2019) [17], Paikra *et al.* (2021) [18] for Hulling (%) and amylase content.

Estimates of heritability observed by different yield and quality characters presented in table 2 and 3.

Genetic advance as% of mean

The advance breeding lines showed genetic advance as% of mean from low to high value. While noting for genetic advance as percent of mean, the yield characters observed with highest value was number of effective tillers per plant (48.99%) and least value was obtained for trait days to maturity (5.87%). High estimates of genetic advance as % of mean obtained from characters were number of effective tillers per plant (48.99%), number of spikelet per panicle

(41.74%), number of filled spikelet (44.79%), flag leaf length (30.31%), grain yield per weight (68.24%), biological yield per plant (47.61%), harvest Index (%) (34.09%), plant height (27.68%). Moderate value of genetic advance as % of mean were obtained from 1000 seed weight (14.59%). Low estimates of genetic advance as % of mean was noted for spikelet fertility % (8.67%), panicle length (cm) (8.52%) days to 50% flowering (6.23%), days to maturity (5.87%). In the same manner observations for quality characters were taken which showed that trait with highest value of genetic advance as % of mean was head rice recovery (33.25%) and lowest value was for amylose (6.54%). Quality characters for which high estimates of genetic advance as% of mean obtained were head rice recovery % (33.25%). Similar findings were obtained by Rathi *et al.*, (2019) [8], Ganpati *et al.*, (2020) [2] and Behera *et al.*, (2018) [19]. The table 2 and 3 presents the varying level of genetic advance as% of mean obtained in different characters i.e. low (<10%), moderate (10-20%) and high (>20%): Table 2 and 3 Level of genetic advance as% of mean observed in different yield and quality characters. High genetic advance for grains per panicle was reported by Chandra *et al.* (2009) [11] and Pankaj *et al.* (2011) [20], for effective tillers per m² and grain per panicle by Nandan *et al.* (2010) [6] and for plant height by Bharadwaj *et al.* (2007) [21]. Similarly, lower magnitude of genetic advance for panicle length was reported by Padmaja *et al.* (2011) [7].

The heritability (%) is a rough estimate of a character's expression. Heritability is defined by Falconer and Mackay (1996) [22] as the measure of the relationship between breeding values and phenotypic values. Estimating heritability helps breeders manage the resources needed to successfully select for desirable characteristics and achieve maximum genetic gain with minimal effort and resources. The degree of gain achieved in a character under a certain selection pressure is referred to as genetic advance. The best conditions for selection are high genetic advance combined with high heritability estimates (Larik *et al.*, 2000) [23]. It also shows the existence of additive genes in the trait, implying that crop improvement can be achieved by selecting such characters. Individual assessment of the parameters is less trustworthy and useful than heritability estimates with genetic advance. Therefore, estimates of heritability with genetic advance are used for selecting characters for improvement.

The quantitative characters in which high heritability and high genetic advance as% of mean was obtained were panicle length, number of effective tillers per plant, number of spikelet per plant, number of filled spikelet, flag leaf length, grain yield per plant, biological yield per plant, harvest index (%).

In quality characters the characters in which high heritability with high genetic advance obtained were head rice recovery. Presence of high heritability and high genetic advance as% of mean shows presence of paramount of additive gene action in these characters thus selection is future generation will be successful for improvement of such characters. Similar results were observed in recent studies by Singh *et al.*, (2020) [10] and Kumar *et al.*, (2020) [5].

However, for quantitative characters plant height and spikelet fertility% and for the quality characters grain length, grain breadth, kernel length, kernel breadth, high heritability with moderate genetic advance as% of mean was obtained. Presence of high heritability and moderate genetic advance suggests presence of non-additive gene action, thus heterosis breeding will be successful for improving these characters. Same findings were obtained by previous studies by Singh *et al.*, (2020) [10] and Kumar *et al.*, (2020) [5].

Table 2: Genetic variability parameters for yield and yield contributing characters

SN	Characters	Mean	Range		CD at 5%	CV %	GCV	PCV	h ² (bs)	GA as % of mean
			Min.	Max.						
1	Days to 50% flowering	97.96	90.5	110.5	11.04	5.49	4.673	7.21	42.006	6.239
2	Days to maturity	126.32	118.5	141.5	13.59	5.24	4.423	6.859	41.584	5.876
3	Plant height (cm)	120.12	77.67	173.64	12.83	5.21	14.302	15.221	88.301	27.686
4	No. of effective tillers per Plant	8.93	4.9	14.7	1.43	7.79	24.917	26.107	91.096	48.991
5	Panicle length (cm)	24.57	21	27.99	3.68	7.31	6.323	9.664	42.806	8.522
6	No. of spikelets per panicle	185.14	86.1	264.9	31.15	8.2	21.667	23.167	87.472	41.744
7	No. of filled spikelets per panicle	155.48	60.6	227	25.14	7.88	22.989	24.302	89.487	44.798
8	Spikelet fertility %	84.07	69.13	94.22	12.83	7.44	6.434	9.834	42.806	8.672
9	Flag leaf length (cm)	43.2	33.6	67.61	7.09	8	16.376	18.225	80.732	30.31
10	Grain yield per plant (g)	18.07	9.08	44.24	2.59	6.98	33.825	34.537	95.92	68.244
11	1000 seed weight (g)	23.43	17.16	28.64	4.58	9.53	9.857	13.711	51.688	14.599
12	Biological yield per plant	45.71	22	73.71	5.63	6.01	23.839	24.584	94.028	47.619
13	Harvest Index (%)	39.79	21.74	60.1	8.43	10.33	18.869	21.512	76.941	34.096

Table 3: Genetic variability parameters for quality characters

SN	Character	Mean	Range		CD at 5%	CV %	GCV	PCV	h ² (bs)	GA as % of mean
			Min.	Max.						
1	Grain length (mm)	8.950	7.480	10.25	0.33	1.78	8.689	8.87	95.97	17.535
2	Grain breadth (mm)	2.860	2.050	3.3	0.2	3.4	8.043	8.733	84.814	15.258
3	Kernel length (mm)	6.500	5.650	7.23	0.15	1.13	6.154	6.257	96.753	12.470
4	Kernel breadth (mm)	2.210	1.940	2.45	0.18	3.91	6.178	7.312	71.397	10.754
5	L: B ratio (of Grain)	3.160	2.470	3.89	0.23	3.51	9.602	10.225	88.184	18.575
6	Head rice recovery %	46.020	34.700	61.98	1.22	1.29	16.193	16.244	99.370	33.252
7	Amylose content %	19.930	18.560	21.03	0.74	1.82	3.567	4.003	79.385	6.546

Conclusion

There is high variability of grain physical properties existed among the rice genotypes studied. The genotypic and phenotypic variances may provide information for future breeding program. The highest heritability with the highest genetic advance value is demonstrated by grain yield per plant and head rice recovery trait that might give useful information. As number of effective tillers per plant, grain length with long and kernel length as the main feature for development of high quality rice for consumer market.

The existing breeding material showed high level of variability heritability and genetic and as% mean for most of the characters. Hence, these can be released in future breeding programs or can be released as superior variety.

References

- Chandra BS, Reddy TD, Ansari NA, Kumar SS. Correlation and path analysis for yield and yield components in rice (*Oryza sativa* L.). *Agric Sci Digest*. 2009;29(1):45-47.
- Ganapati RK, Rasul MG, Sarker U, Singha A, Faruquee M. Gene action of yield and yield contributing traits of submergence tolerant rice (*Oryza sativa* L.) in Bangladesh. *Bull Natl Res Cent*. 2020, 44(8).
- International Year of Rice. Gender and rice. Factsheet. Gramene Reference ID 8371. 2004.
- Kumari BK, Kumar BNVS, Jyothula DPB, Rao NM. Diversity analysis in rice breeding lines for yield and its components using principal component analysis. *J Pharmacogn Phytochem*. 2021;10(1):905-909.
- Kumar A, Kumar S, Singh S, Prasad J, Jeena AS, Upreti MC. Genetic variability, heritability and genetic advance studies for quantitative and quality traits in basmati rice (*Oryza sativa* L.). *J Pharmacogn Phytochem*. 2020;9(4):2065.
- Nandan R, Sweta, Singh SK. Character association and path analysis in rice (*Oryza sativa* L.) genotypes. *World J Agric Sci*. 2010;6(2):201.
- Padmaja D, Radhika K, Rao LVS, Padma V. Studies on genetic divergence in rice germplasm. *Crop Res*. 2011;40(1/3):117-121.
- Rathi SR, Bisen PS, Sinha BS, Upadhyay S. Genetic analysis and trait association for yield related traits in F2:3 biparental population of rice under slightly sodic condition. *Electron J Plant Breed*. 2019;10(3):1105-1112.
- Seyoum M, Alamerew S, Bante K. Genetic variability, heritability, correlation coefficient and path analysis for yield and yield related traits in upland rice (*Oryza sativa* L.). *J Plant Sci*. 2012;7(1):13-22.
- Singh SK, Pandey V, Mounika K, Singh DK, Khaire AR, Habde S, *et al*. Study of genetic divergence in rice (*Oryza sativa* L.) genotypes with high grain zinc using Mahalanobis' D2 analysis. *Electron J Plant Breed*. 2020;11(2):367-372.
- Babu M, Vlasblom J, Pu S, Guo X, Graham C, Bean BD, *et al*. Interaction landscape of membrane-protein complexes in *Saccharomyces cerevisiae*. *Nature*. 2012 Sep 27;489(7417):585-589.
- Ashok PC, Praveen BB, Bellini N, Riches A, Dholakia K, Herrington CS. Multi-modal approach using Raman spectroscopy and optical coherence tomography for the discrimination of colonic adenocarcinoma from normal colon. *Biomedical optics express*. 2013 Oct 1;4(10):2179-2186.
- Ketan R, Sarkar G. Studies on variability, heritability, genetic advance and path analysis in some indigenous Aman rice (*Oryza sativa* L.). *Journal of Crop and Weed*. 2014;10(2):308-315.
- Tuhina-Khatun M, Hanafi MM, Rafii Yusop M, Wong MY, Salleh FM, Ferdous J. Genetic variation, heritability, and diversity analysis of upland rice (*Oryza sativa* L.) genotypes based on quantitative traits. *BioMed research international*. 2015;2015(1):290861.
- Ammar K, El-Metwally M, Almazroui M, Abdel Wahab MM. A climatological analysis of Saharan cyclones. *Climate dynamics*. 2014 Jul;43:483-501.

16. Saha S, Jeon BH, Kurade MB, Govindwar SP, Chatterjee PK, Oh SE, *et al.* Interspecies microbial nexus facilitated methanation of polysaccharidic wastes. *Bioresource technology*. 2019 Oct 1;289:121638.
17. Parimala K, Devi KR. Estimation of variability and genetic parameters in indica and japonica genotypes of rice (*Oryza sativa* L.). *Int. J. Curr. Microbiol. App. Sci.* 2019;8(3):1138-1142.
18. Paikra SK, Mishra M. Role of physicochemical organization of *Rhyothemis variegata* wing in monitoring bactericidal activity. *Surfaces and Interfaces*. 2021 Dec 1;27:101576.
19. Behera SS, Ray RC, Zdolec N. *Lactobacillus plantarum* with functional properties: an approach to increase safety and shelf-life of fermented foods. *BioMed research international*. 2018;2018(1):9361614.
20. Pankaj S, Kumar JS, Nema RK. Comparative analysis of MIT rule and Lyapunov rule in model reference adaptive control scheme. *Innovative Systems Design and Engineering*. 2011 Oct;2(4):154-162.
21. Bharadwaj S, Bharadwaj A, Bendoly E. The performance effects of complementarities between information systems, marketing, manufacturing, and supply chain processes. *Information systems research*. 2007 Dec;18(4):437-453.
22. Falconer DS. *Introduction to quantitative genetics*. Pearson Education India; c1996.
23. Larik AS, Malik SI, Kakar AA, Naz MA. Assessment of heritability and genetic advance for yield and yield components in *Gossypium hirsutum* L. *Scientific Khyber*. 2000;13(1):39-44.