RESEARCH

GENETIC ASSESSMENT AND ASSOCIATION ANALYSIS OF TRADITIONAL RICE (*ORYZA SATIVA* L.) GENOTYPES OF BASTAR REGION

Shivam Sharma*, Indrajeet, Falguni Yadav, Sonali Kar and D.P. Singh

Department of Genetics and Plant Breeding, S.G. College of Agriculture and Research Station, Kumhrawand, Jagdalpur, Bastar 494001 (C.G.)
Department of Genetics and Plant Breeding S.G. College of Agriculture and Research Station Kumhrawand, Jagdalpur, Bastar 494001 (C.G.)
Email: shivamsharmaofficial@gmail.com

Abstract: An experiment titled "Genetic assessment and association analysis of traditional rice (*Oryza sativa* L.) genotypes of Bastar Region" was conducted in *Kharif* 2023 at the Research cum Instructional Farm of S.G. College of Agriculture and Research Stationat Jagdalpur, Bastar, IGKV, Raipur (C.G.). An augmented complete block design was used for genetic evaluation. ANOVA analysis found all the value are significant at 1% level of significance. Genetic variability analysis identified days to 50% flowering with the highest heritability (44.46%), while plant height showed the highest genetic advance as a percentage of the mean (6.19). Correlation studies indicated that grain yield per plant had a positive significant correlation with traits such as number of effective tillers per plant, harvest index, number of filled grains per panicle, biological yield and test weight. Selection for these traits could be beneficial in improving grain yield.

Keywords: Rice, Heritability, Genetic advance, GCV, PCV, Association analysis, Correlation

INTRODUCTION

Rice (*Oryza sativa* L.) is as taple food crop globally, cultivated mainlyin Asia,which accounts for85%oftheworld's riceproduction. In India, rice covers 47.83 million hectares, contributing to 21.5% of global production, with Chhattisgarh growing rice on 3.77 million hectares. In Chhattisgarh, unique landraces cultivated by farmers exhibit high yield potential and disease resistance but remain underutilized. Bastar, in southern Chhattisgarh, displays significant genetic diversity in rice, with many indigenous varieties. Expanding the morphological traits and landraces studied is crucial for comprehensive genetic evaluation. Evaluating the genetic variability of a trait is essential for plant breeders to design effective breeding programs. Heritability serves as an indicator of how traits are passed from parents to offspring and it plays a crucial role in the breeding process. Akshay *et al*. (2022)

MATERIALS AND METHODS

The experiment utilized athirteen-block Augmented Complete Block Design, incorporating 147 genotypes (including 4 checks: Bastar Dhan 1, Samleshwari, Danteshwari and CGl919), with each block containing 15 entries randomly distributed. The research was conducted at Research cum Instructional farm of S.G. College of Agriculture and Research station, Jagdalpur, IGKV, Raipur (C.G.). Each accession comprised two rows measuring three meters in length, spaced 20 cm apart with a 10 cm plant-to-plant distance. The experiment was sown on 5 July, 2023. The following parameters are used to evaluate *viz.* are days to 50% flowering, plant height (cm), flag leaf length (cm), flag leaf width (cm), number of effective tillers per plant, panicle length (cm), number of filled grains per panicle, test weight (cm), paddy length (mm), paddy breadth (mm), paddy L/B ratio, kernel length (mm), kernel breadth (mm), kernel L/B ratio, biological yield per plant (g), harvest index (%), grain yield per plant (g). Genotypic and phenotypic coefficients of variation, heritability (broad sense) and genetic advance as a percentage of the mean were calculated following the procedures of Burton and Devane (1953).

RESULTS

The analysis of variance (ANOVA) indicated substantial differences between the genotypes for all traits,highlighting a significant level of variability and inherent genetic variation among the studied genotypes.
The analysis found that heritability ranged from 44.46% (days to 50% flowering) to 3.34% (panicle length). According to Johnson *et al*. (1955) the

*Corresponding Author

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calculated heritability was divided into three categories. None characters showed high heritability. Moderate heritability (30-60%) was found in character like days to 50% flowering (44.46%), while low heritability (<30%) was found for the characters viz., plant height (29.77%) followed by number of filled grains per panicle (28.35%), paddy breadth (23.57%), kernel breadth (23.57%), harvest index (22.62%), test weight (22.47%), paddy length (19.64%), kernel length (19.0%), paddy L/B ratio (16.34%), flag leaf width (16.14%), kernel L/B ratio (14.52%), grain yield per plant (8.10%), flag leaf length (13.0%), number of effective tilers per plant (5.44%), biological yield per plant (4.63%), panicle length (3.34%).

Genetic advance as percent of mean was varied from 6.19% (plant height) to 0.50% (panicle length). Genetic advance as percent of mean was categorized as per the formula suggested by Johnson *et al.* (1955). None of the traits exhibited high (>20%) or moderate (11-20%) genetic advance as a percentage of the mean. Instead, all 17 characters studied showed low (0-10%) genetic advance as a percentage of the mean. None of the studied characters was observed for high heritability coupled with high genetic advance and high heritability coupled with moderate genetic advance. Moderate heritability coupled with low genetic advance was found for character days to 50% flowering. Low heritability coupled with low genetic advance suggesting non-additive gene action in inheritance of this trait (Nirmaladevi *et al.,* 2015). Low heritability coupled with low genetic advance as percent of mean was observed for the characters viz., plant height, number of effective tillers per plant, panicle length, flag leaf length, flag leaf width, number of filled grains per panicle, test weight, paddy length, paddy breadth, paddy L/B ratio, kernel length, kernel breadth, kernel L/B ratio, biological yield per plant, harvest index and grain yield per plant. The findings were similar to report by Ali *et al.,* 2018 and Pradeep *et al.,* 2018 for number of filled grains per panicle.

PCV values were somewhat greater than GCV values, suggested that environmental factors had an impact on character expression (Sudeepthi *et al.,* 2020 and Verma *et al.,* 2023). High GCV and PCV were not observed in this study. Low GCV with moderate PCV were observed for the characters like grain yield per plant, kernel L/B ratio, flag leaf length and plant height. Low GCV and PCV were found for characters like days to 50% flowering, number of effective characters, panicle length, flag leaf width, number of filled grains per panicle, test weight, paddy length, paddy breadth, paddy L/B ratio, kernel length, kernel breadth, biological yield per plant and harvest index. The findings were similar to report by Saha *et al.,*2019 for days to 50% flowering, Hefena *et al.,* 2016 and Abhilash *et al.,* 2018 for days to 50% flowering, panicle length and test weight, Similar result by Balaji

et al., 2022 and Mahbub *et al.,* 2015 for days to 50% flowering.

Association analysis is a key method in breeding programs as it provides insights into the relationships among different traits and helps identify the key traits for selection in genetic improvement of grain yield. The effectiveness of the selection process is influenced by the degree of association. Grain yield per plant found positive significant correlation with harvest index (0.871**), biological yield per plant (0.807**), number of filled grains per panicle (0.612**), test weight (0.552**) and number of effective tillers per plant (0.196*), while positive nonsignificant correlation with traits like paddy length (0.131), kernel length (0.127), kernel breadth (0.102), paddy breadth (0.101), paddy L/B ratio (0.056), days to 50% flowering (0.050), kernel L/B ratio (0.046), flag leaf width (0.021) and plant height (0.020). Grain yield per plant showed negative nonsignificant correlation with flag leaf length (-0.126) and panicle length (-0.083). Similar result by Sadimantara *et al.,* 2021 for 1000 grain weight, number of filled grains per panicle, Similar reported result by Russinga *et al.,* 2020 paddy length and paddy L/B ratio, paddy breadth and 1000-grain weight). Similar positive correlation observed between grains number and grain yield reported by Thorat *et al.*, 2019 and Swamy *et al.*, 2014.

In the present investigation it was found that grain yield per plant observed strong positive and significant correlation with the traits like harvest index, biological yield per plant, number of filled grain per panicle, test weight and number of effective tillers per plant. It suggests a strong correlation between these traits and grain yield per plant, indicated that selection for these traits could be beneficial in improving grain yield (Manasa *et al.,* 2022).

CONCLUSION

Genetic variability analysis revealed that days to 50% flowering had highest heritability (44.46%), while genetic advance as percentage of mean was found highest for plant height (6.19). Moderate heritability coupled with low genetic advance as percent of mean was identified for days to 50% flowering. Moderate PCV with low GCV was found for grain yield per plant. This trait can be further evaluated as selection parameters. Correlation studies identified that grain yield per plant showed positive significant correlation with the traits such as biological yield per plant, harvest index, test weight, number of filled grains per panicle and number of effective tillers per plant. These traits have positive effect on grain yield. Improvement in this trait can improve overall grain yield in high yielding genotypes.

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Table 1. Mean sum of squares of 17 yield and yield attributing traits

Source of variation	d.f.	Days to 50% flowering	Plant height(cm)	Number of effective tillers	Panicle length (cm)	Flag leaf length (cm)	Flag leaf width(cm)	Number of filled grains per panicle	Test weight (g)	Paddy Length (mm)
Block	12	61.44**	261.26**	2.46**	10.23**	31.33**	0.058**	1000.49**	11.08**	0.516**
Treatment	146	89.14**	409.87**	0.94**	3.31**	11.52**	0.051**	394.05**	19.89**	0.669**
Checks	3	883.49**	44.19	0.79	5.47**	27.25**	0.486**	7.46	4.20	2.008**
Test	142	69.60**	149.38**	0.98**	3.71**	13.00**	0.043**	383.60**	20.17**	0.641**
Check vs Test	1	480.58**	38496.70**	-2.98**	-59.04**	-245.62**	-0.042	3037.03**	27.05**	0.547**
Error	36	8.40	67.35	0.56	2.34	9.69	0.016	68.56	4.44	0.170
Total	194	72.45	337.12	0.97	3.56	12.41	0.045	371.16	16.48	0.567

Source of variation	d.f.	Paddy Breadth (mm)	Paddy L/B ratio	Kernel length (mm)	Kernal breadth (mm)	Kernel L/B ratio	Biological yield per plant (g)	Harvest index (%)	Grain yield per plant (g)
Block	12	0.046**	0.090**	0.429**	0.046**	0.144**	77.55**	34.23**	39.75**
Treatment	146	0.114**	0.145**	0.581**	0.114**	0.227**	43.29**	28.75**	23.31**
Checks	3	0.095**	0.663**	1.584**	0.095**	0.997**	23.86**	54.54**	29.03**
Test	142	0.116**	0.135**	0.552**	0.116**	0.210**	41.28**	27.06**	21.52**
Check vs Test	1	-0.157**	0.003	1.731**	-0.157**	0.291**	386.85**	191.37**	259.96**
Error	36	0.024	0.043	0.152	0.024	0.075	53.66	6.38	11.33
Total	194	0.093	0.123	0.492	0.093	0.193	47.33	24.94	22.11

Table 2. Minimum, Maximum, Mean, Standard error and Standard deviation of 17 character sunder study

Characters	Minimum X_{min}	Maximum X_{max}	Mean X	Standard error (SE)	Standard deviation(σ)
Days to 50% flowering	52.0	93.0	76.81	0.95	8.36
Plant height(cm)	63.40	145.20	97.02	1.34	13.16
Number of effective tillers per plant	5.20	10.60	8.26	0.34	0.98
Panicle length(cm)	16.60	27.62	21.45	0.41	1.90
Flag leaf length(cm)	17.77	39.80	26.24	0.70	3.56
Flag leaf width (cm)	0.93	2.17	1.52	0.17	0.21
Number of filled grains per panicle	60.67	154.00	103.85	1.92	19.56
Test weight(g)	14.60	34.30	26.92	0.86	4.44
Paddy length (mm)	6.20	11.00	7.77	0.29	0.79
Paddy breadth (mm)	2.20	6.00	2.91	0.13	0.22
Grain L/B ratio	1.08	3.64	2.69	0.22	0.36
Kernel length(mm)	4.70	8.30	6.28	0.29	0.74
Kernel breadth(mm)	1.57	5.37	2.28	0.15	0.22
Kernel L/B ratio	1.02	4.22	2.79	0.27	0.45
Biological yield per plant(g)	42.20	72.00	58.67	0.84	6.40
Harvest index	26.34	47.63	38.21	0.84	5.17
Grain yield per plant(g)	12.40	33.00	22.55	0.98	4.63

Table 3. Genetic parameters of variation for 17 yield and yield attributing characters

Characters	var(g)	var(p)	Heritability (%)	GA	GA% mean	GCV (%)	PCV(%)
Days to 50% flowering	6.73	15.13	44.46	3.56	4.64	3.38	5.06
Plant height (cm)	28.54	95.90	29.77	6.00	6.19	5.51	10.09
Number of effective tillers per plant	0.03	0.59	5.44	0.09	1.04	2.17	9.31
Panicle length (cm)	0.08	2.42	3.34	0.11	0.50	1.33	7.26
Flag leaf length (cm)	0.40	7.09	5.68	0.31	1.19	2.42	10.15
Flag leaf width (cm)	0.00	0.02	16.14	0.05	2.98	3.60	8.96
Number of filled grains per panicle	27.12	95.68	28.35	5.71	5.50	5.02	9.42
Test weight (g)	1.29	5.73	22.47	1.11	4.11	4.21	8.89
Paddy length (mm)	0.04	0.21	19.64	0.19	2.40	2.62	5.92
Paddy breadth (mm)	0.01	0.03	23.57	0.09	2.96	2.96	6.10
Paddy L/B ratio	0.01	0.05	16.34	0.08	2.84	3.42	8.45
Kernel length (mm)	0.04	0.19	19.00	0.17	2.70	3.01	6.91
Kernel breadth (mm)	0.01	0.03	23.57	0.09	3.78	3.78	7.78
Kernel L/B ratio	0.01	0.09	14.52	0.09	3.17	4.03	10.59
Biological yield per plant (g)	1.64	35.30	4.63	0.57	0.97	2.18	10.13
Harvest index (%)	1.86	8.24	22.62	1.34	3.50	3.57	7.51
Grain yield per plant (g)	1.00	12.33	8.10	0.59	2.60	4.43	15.57

Table 4. Correlation coefficients analysis of yield and yield attributing characters

Characters	DFF	PH	NET	PL	FLL	FLW	NFGP	TW	PL	PB	PL/B	KL	KB	KL/B	BY/P	HI	GY/P
DFF	1.000	0.079	0.016	0.048	0.051	0.336**	0.071	-0.002	0.002	0.018	-0.016	-0.014	0.012	-0.023	0.009	0.065	0.050
PH		1.000	-0.127	0.243**	0.176*	0.259**	0.006	0.089	-0.075	0.032	-0.086	-0.059	0.028	-0.073	0.017	0.011	0.020
NET			1.000	-0.134	-0.093	0.090	-0.173*	-0.188*	0.000	-0.052	0.042	0.009	-0.051	0.054	0.162*	0.178*	0.196*
PL				1.000	0.297**	0.213**	0.046	-0.090	-0.055	-0.037	-0.049	-0.061	-0.043	-0.049	-0.040	-0.090	-0.083
FLL					1.000	0.130	-0.082	-0.023	-0.039	0.265**	-0.205*	-0.063	0.257**	-0.229**	-0.051	-0.140	-0.126
FLW						1.000	-0.092	0.030	0.064	0.234**	-0.099	0.046	0.227**	-0.121	0.052	0.000	0.021
NFGP							1.000	-0.017	0.036	0.053	0.002	0.016	0.054	-0.013	0.456**	0.559**	0.612**
TW								1.000	0.129	0.173*	0.002	0.142	0.171*	-0.001	0.464**	0.484**	0.552**
PL									1.000	0.023	0.772**	0.965**	0.033	0.714**	0.113	0.103	0.131
PB										1.000	-0.534**	0.012	0.997**	-0.588**	0.039	0.139	0.101
PL/B											1.000	0.745**	-0.502**	0.980**	0.062	0.021	0.056
KL												1.000	0.018	0.736**	0.119	0.090	0.127
KB													1.000	-0.559**	0.038	0.140	0.102
KL/B														1.000	0.061	0.006	0.046
BY/P															1.000	0.421**	0.807**
HI																1.000	0.871**
GY/P																	1.000

*,** significant at 5% and 1% level, respectively

DFF= Days to 50% flowering, PH= Plant height (cm), NET= Number of effective tillers, PL= Panicle length (cm), FLL= Flag leaf length (cm), FLW= Flag leaf width (cm), NFGP= Number of filled grains per panicle, TW= Test weight (g), PL= Paddy length (mm), PB= Paddy breadth (mm), PL/B= Paddy L/B ratio, KL= Kernel length (mm), KB= Kernel breadth (mm), KL/B= Kernel L/B ratio, BY/P= Biological yield per plant (g), HI= Harvest index (%), GY/P= Grain yield per plant (g)
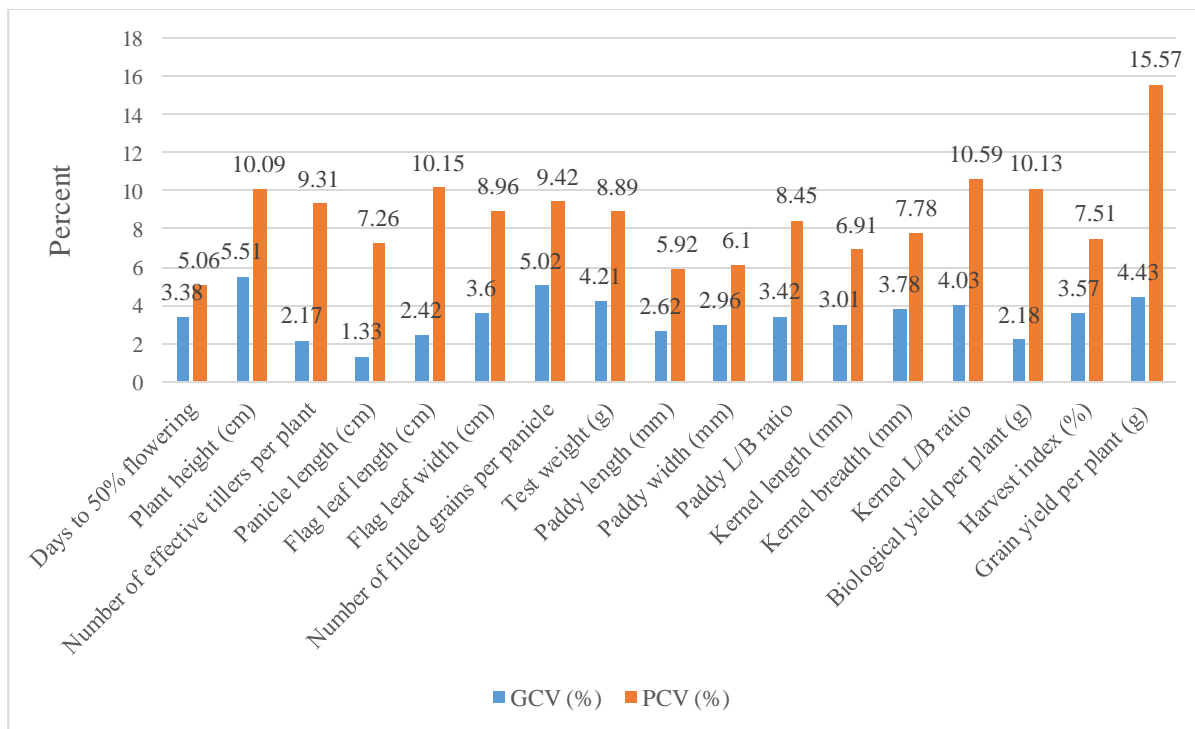

Fig 1: Bar diagram representing phenotypic and genotypic coefficient of variation for 17 yield and yield attributing characters
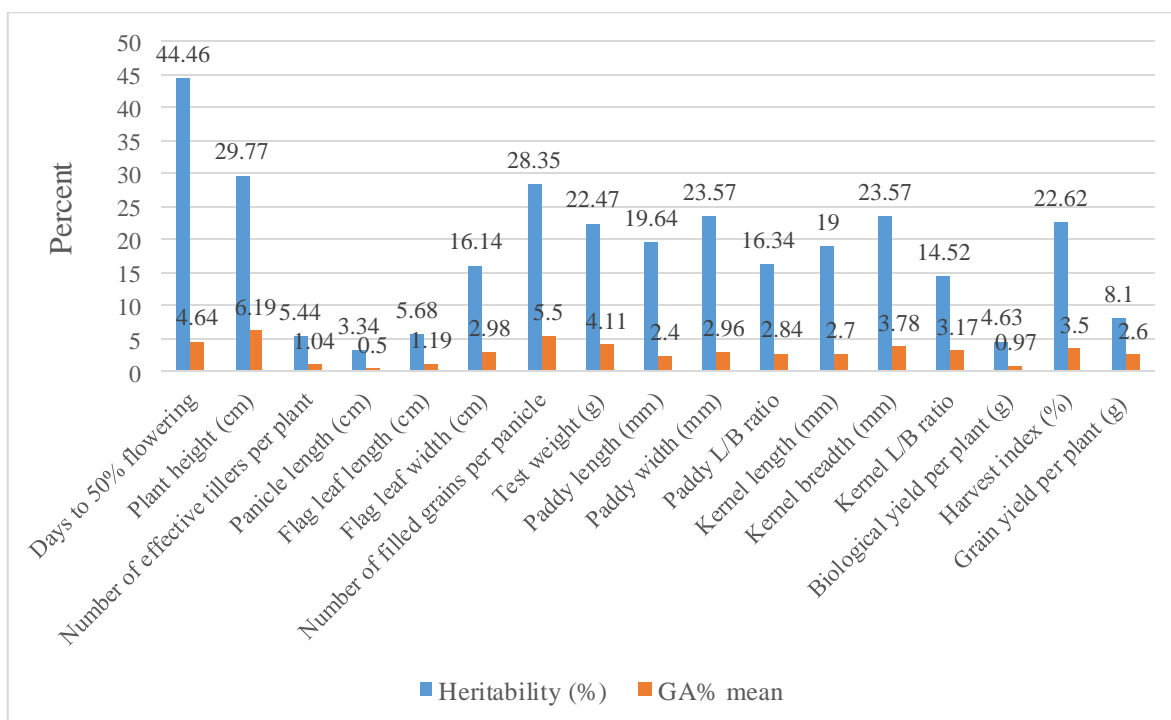

Fig 2: Bar graph representing heritability coupled with genetic advance as percent of mean for 17 yield and yield attributing traits

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