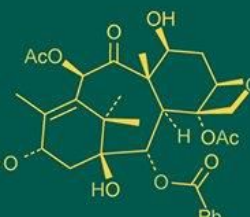
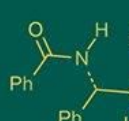


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Assessment of genetic variability parameters and genetic diversity for yield traits in advanced breeding lines of rice (*Oryza sativa* L.)

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Abstract

In this investigation genetic variability, heritability and genetic advance was studied in forty nine advanced breeding lines along with four checks for ten yield are related traits during *kharif* (wet season), 2023. The analysis of variance exhibited highly significant differences among all advanced breeding lines for the entire set of yield parameters, unequivocally indicating the presence of substantial and exploitable genetic variability within the evaluated population. The number of spikelets per panicle (18.11), number of filled spikelets per panicle (17.62) and 1000 seed weight (15.29) harvest index (12.68) showed moderate values of GCV and PCV. This indicates that these traits are suitable for direct selection to achieve genetic improvement. The yield traits which showed high estimates for genetic advance as % of mean along with high heritability were number of spikelets per panicle, number of filled spikelets per panicle, 1000 seed weight and harvest index. This suggests predominant additive gene action, enabling effective improvement through selection. Forty nine entries were grouped into 6 clusters. The highest number of genotypes appeared in Cluster I, which contain 26 genotypes followed by Cluster II, which contain 12 genotypes followed by Cluster III, which contain 8 genotypes followed by Cluster IV, which contain 1 genotypes followed by Cluster VI, and VII had one accession, respectively. The pattern of group constellation proved the existence of significant amount of variability.

Keywords: Rice, genetic variability, heritability and genetic advance and genetic divergence

Introduction

Rice (*Oryza sativa* L.) ($2n = 24$) is a major cereal crop that belongs to the Poaceae family and the Oryzoidea subfamily. It is known as the "Global Grain" because it is a staple food in over 100 countries. It is the world's oldest domesticated grain (10,000 years) and the primary source of nutrition for 2.5 billion people. Rice is globally grown in 161 million ha area with 713 million tons rice production. Rice is the keystone of India's national food security. It holds around 22-23 percent of cropped land and produces around 149.07 million tonnes per year (Anonymous 2024) [4]. It accounts for 24-26 percent of global rice production and 38-40 percent of the country's overall food grain production. China is the world's leading producer of rice. China produced 145.28 million tonnes of rice, paddy in 2024, accounting for 27 percent of global rice, paddy demand. China, India, Bangladesh, Indonesia, and Vietnam are the top five nations respectively, accounting for 77 percent of the total rice production. In India rice is grown on 49 million hectares, yielding 142 million tonnes and yielding 4.39 tonnes per hectare. West Bengal, Punjab and Uttar Pradesh are the top three states in rice production, with total rice production of 15.75 million tonnes, 12.50 million tonnes and 11.82 million tonnes, respectively and contributing 10.43 %, 8.28 %, and 7.82 % to the total rice production share of the country (Anonymous, 2024) [4]. Rice is also an export crop that contributes greatly to the economy.

Chhattisgarh is a state in central India, with a geographical area of 137.90 lakh hectares. It is known for rice cultivation and called "rice bowl of India" and is necessary to examine its absolute and relative changes and have an estimate of likely supply of this crop as well as other cereal crops such as maize and wheat in the state. In Chhattisgarh, rice occupies acreage of 3899.34 ha. with the productivity of 3212 kg/ha (Anonymous, 2023) [1].

“Selection primarily depends on variability among genotypes for yield and its components. Hybridization programs require parents with high variability to combine desirable traits for improved grain quality and yield. Heritability coupled with genetic advance is a more reliable predictor of selection response than heritability alone (Paul *et al.*, 2006) ^[21].

Genetic diversity is essential for crop improvement, enabling the development of superior recombinants (Manonmani and Fazlullah Khan, 2003) ^[13]. Selection of parents in hybridization programs is guided by genetic divergence, using methods like UPGMA clustering and Mahalanobis D^2 analysis to identify genotypes with broader differences for desired traits, even under stress conditions (Patil, 2014) ^[17].

Materials and Methods

The present experiment was carried out at Research cum Instructional field, Department of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur (C.G.) during *kharif* (wet season), 2023.

The experimental material comprises of total 49 advanced breeding lines of rice along with 4 checks namely Swarna, Chhattishgarh Dhan-1919, NDR 8002 and Pooja. During *kharif*, 2023, the experiment was conducted in a Randomized Block Design in three replications maintaining inter and intra row spacing 20 x 15 cm. The observations during the investigation were recorded on the basis of five random plants selected at optimum stage of plant growth from each line in 3 replications for the evaluation of yield.

Results and Discussion

The analysis of variance revealed a significant difference in all of the attributes, such as days to 50 % flowering, plant height, numbers of effective tillers per plant, panicle length, number of spikelets per panicle, number of filled spikelets per panicle, spikelet fertility %, 1000 seed weight, harvest index and grain yield per plant. Similar results were also reported by Bagudam *et al.* (2018) ^[6] and Hasan *et al.* (2020) ^[11], Khan *et al.* (2023) ^[19], Kumar *et al.* (2023) ^[20] and Gupta *et al.* (2021) ^[18]. This clearly illustrates that all genotypes have variability in all aspects. The fact that genotype x environment interaction accounts for such a large and reasonably significant portion of total variation indicates that genotypes react to the environment differently.

Analysis of variance

Analysis of variance was used to determine the degree of variation of observed characters among advanced breeding lines of rice and the results are presented in tables 1 and 2. For all of the characters, the study of variance showed extremely significant variations among the 49 advanced breeding lines, suggesting significant genetic variation in the material. For all yield characters tested, an F-test revealed that the values of mean sum of squares were significant (at 1% level of significance). High genetic variability for different yield traits in rice was also reported by Khan *et al.* (2023) ^[19] and Nikhil *et al.* (2023) ^[14].

Genotypic and phenotypic coefficient of variance

The value for GCV and PCV ranged from low to moderate. For all characters, the genotypic variance was smaller than phenotypic variance, this indicates that environment had masking effect on the expression of genetic variability (Table 2). Trait number of spikelets per panicle (18.11; 19.53) had high GCV and PCV value followed by number of filled spikelets per panicle (17.62; 19.17), 1000 seed weight (15.29; 17.25) and harvest index (12.68; 14.53). This indicates the existence of wide genetic base among the advanced breeding lines taken under study and possibility of genetic improvement through direct selection for these traits. These results are in conformity with the findings of Asante *et al.* (2019) ^[5], Limbongan *et al.* (2021) ^[12] and Nanda *et al.* (2021) ^[15].

Heritability and Genetic Advance

Estimates of heritability for yield characters ranged from low to high heritability. The yield characters for which highest and lowest heritability obtained were number of spikelets per panicle (85.99%) and panicle length (25.97%) respectively. Yield characters for which high heritability obtained were number of spikelets per panicle (85.99%), numbers of filled spikelets per panicle (84.54%), 1000 seed weight (78.63%), harvest index (76.11%), plant height (65.36). Medium estimates of heritability obtained for yield characters were number of effective tillers (58.42%), days to 50% flowering (51.45%), grain yield per plant (49.48%), spikelet fertility (44.11%). The yield characters for which low heritability obtained were panicle length (25.97%). Similar results were obtained by Asante *et al.* (2019) ^[5], Kumar *et al.* (2023) ^[20].

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 spikelets per panicle (34.60%) and least value was obtained for trait panicle length (3.59%). High estimates of genetic advance as % of mean obtained from characters were number of spikelets per panicle (34.60%), numbers of filled spikelets per panicle (33.38%), 1000 seed weight (27.94%), harvest index (22.79%). Moderate value of genetic advance as % of mean were obtained from characters plant height (cm) (15.17%), grain yield per plant (14.36%), number of effective tillers per plant (12.13%). Similar results were obtained by Sahu *et al.* (2020) ^[22].

High heritability does not always indicate high genetic gain, therefore the best conditions for selection are high genetic advance combined with high heritability estimates (Manju *et al.*, 2021) ^[10]. The yield traits which showed high values for genetic advance as % of mean along with high heritability were number of spikelets per panicle, number of filled spikelets per panicle, 1000 seed weight, harvest index. This implied that additive gene activity influenced the inheritance of these features. Following a simple selection method, these traits can be improved. Similar results were observed in recent studies by Nath *et al.* (2021) ^[16], Nikhil *et al.* (2023) ^[14], Chamar *et al.* (2021) ^[8] and Gupta *et al.* (2021) ^[18].

Table 1: Analysis of variance for yield characters in advanced breeding lines of rice

S. No.	Source	Mean Sum of Squares (MSS)		
		Replication	Treatment	Error
	Degrees of freedom	2	48	96
1	Days to 50% flowering	6.7550	130.847**	31.311
2	Plant height (cm)	36.3270	370.337**	55.596
3	Number of effective tillers per plant	0.6120	1.227**	0.235
4	Panicle length (cm)	0.8320	4.233**	2.062
5	No. of spikelets per panicle	8.8320	4110.153**	211.729
6	No. of filled spikelets per panicle	48.7240	2668.008**	153.281
7	Spikelet fertility %	21.5630	109.931**	32.646
8	1000 Seed weight (g)	9.8340	50.069**	4.159
9	Harvest index %	3.340	168.078**	15.917
10	Grain yield per plant (g)	16.9470	23.295**	5.915

Table 2: Genetic variability parameters for yield and yield contributing characters in advanced breeding lines of rice

S. No.	Character	Mean	Range		CD at 5%	CV%	Coefficient of variance		h ² %	GA	GA % mean
			Max.	Min.			PCV	GCV			
1	Days to 50% flowering	108.10	118.67	89.67	9.07	12.01	5.68	7.92	51.45	8.51	8.39
2	Plant height (cm)	7.18	149.67	93.60	12.08	16.00	9.11	11.27	65.36	17.06	15.17
3	Number of effective tillers	24.67	9.53	6.46	0.79	1.04	7.71	10.08	58.42	0.91	12.13
4	Panicle length (cm)	141.51	28.80	21.93	2.33	3.08	3.42	6.70	25.97	0.89	3.59
5	Number of spikelet per panicle	39.33	137.67	137.67	23.58	31.22	18.11	19.53	85.99	68.86	34.60
6	Number of filled grains per panicle	78.79	253.57	126.17	20.07	26.57	17.62	19.17	84.54	54.84	33.38
7	Spikelet fertility (%)	2.35	94.20	68.60	9.26	12.26	6.11	9.20	44.11	6.94	8.36
8	100 seed weight (g)	42.91	34.60	16.67	3.31	4.38	15.29	17.25	78.63	7.15	27.94
9	Harvest index (%)	46.51	74.51	41.26	6.47	8.56	12.68	14.53	76.11	12.80	22.79
10	Grain yield per plant (g)	19.33	29.57	16.73	3.94	5.22	9.91	14.09	49.48	3.49	14.36

Table 3: Mean performance of breeding lines in individual clusters for the character

Clusters/characters	I	II	III	IV	V	VI
Days to 50% flowering	98.24	105.81	104.88	94.33	108.00	104.67
Plant height	114.04	109.34	109.58	96.33	109.90	149.67
No. of effective tillers per plant	7.42	7.25	7.76	7.13	6.80	9.53
Panicle length	25.26	24.13	24.82	25.17	24.57	25.60
No. of spikelets per panicle	176.88	210.18	237.81	234.87	293.60	201.40
No. of filled spikelets per panicle	150.32	157.71	207.24	221.13	201.27	169.63
Spikelet fertility	85.26	75.27	87.95	94.20	68.60	84.03
1000 seed weight	26.96	26.08	21.18	27.83	23.50	18.73
Harvest index (%)	56.22	52.45	59.08	74.51	55.49	58.63
Grain yield per plant	24.32	23.68	25.35	25.50	26.03	19.40

Table 4: Cluster pattern of 49 advanced breeding lines

Cluster number	No. of advanced breeding lines	Advanced breeding lines
I	26	R 2701-1-1, R 2701-26-1, R 2699-8-1, R 2451-225-1-25-1, R1853-105-1-82-1, Swarna(C), R2698-42-1, IR10N134, R 2701-6-1, R 2698-123-1, R 2370-496-1-278-1, CG Dhan 1919 (C), R 2370-277-1-123-1, R 1915-115-1-88-1, R 2406-220-1-188-1, R 2404-346-1-164-1, R 2356-219-1-99-1, R 2370-265-1-116-1, R 2422-777-1-360-1, R2369-475-1-251-1, R 2408-241-1-200-1, R 2419-523-2-315-1, R 2447-1027-1-456-1, R 2370-96-1-8-1, R 2406-220-1-188-1, R 2377-70-2-61-1
II	12	R 2404-144-1-61-1, R 2370-124-1-100-1, R1896-82-1-60-1, R1624-61-3-61-1, R 2698-51-1, R1624-61-1-59-1, R 2348-201-1-91-1, R1624-61-2-60-1, IR14V1020, R 2447-1027-1-456-1, NDR 8002 (C), R 2408-237-1-196-1
III	8	R 2409-105-1-201-2, R 2370-263-1-114-1, R 1138-688-3-533-1, R 2370-120-1-97-1, R 2374-115-2-32-2, R 2358-109-1-86-1, R1921-178-1-117-1, R 2467-RP5568-DRR-SPS-129-1
IV	1	Pooja (C)
V	1	R 2412-338-1-236-1
VI	1	R 2419-1248-1-610-1

Forty nine entries were grouped into 6 clusters. The highest number of genotypes appeared in Cluster I, which contain 26 genotypes followed by Cluster II, which contain 12 genotypes followed by Cluster III, which contain 8 genotypes followed by Cluster IV which contain 3 genotypes followed by Cluster VI, VII and VIII had one accession, respectively. The pattern of group constellation proved the existence of significant amount of variability.

Mean cluster values showed a wide range of variations for all the characters undertaken in the investigation (Table 4.12). Cluster III exhibited highest mean values for characters number of filled spikelets per panicle (207.24). Cluster IV exhibited maximum number of highest means which were for characters spikelet fertility (94.20), 1000 seed weight (27.83), harvest index (74.51). Highest mean values for days to 50% flowering (108.00), number of

spikelets per panicle (293.60), grain yield per plant (26.03) were exhibited by cluster V. Cluster VI exhibited highest mean values for plant height (149.67), number of effective tillers and panicle length (25.60).

Inter and intra cluster distances among the six clusters were computed and presented. The intra cluster distance ranged from 0.00 (cluster IV, V and VI) to 18.52 (cluster III). Maximum inter cluster distance was present between cluster IV and V (213.13) followed by between cluster III and V (132.99), cluster V and VI (123.16), cluster I and V (115.46). Minimum inter cluster distance was present between cluster III and VI (29.56). Parents should be selected from the two clusters which have wider inter cluster distance for higher variability and heterotic effect. Inter-cluster distances exceeded intra-cluster distances, reflecting greater diversity among distant breeding lines. While heterosis is important, quality traits are equally crucial, and rice improvement programs focus on identifying maximum transgressive segregant. These results are similar to the findings of Mandavi *et al.* (2023) ^[24], Thakur *et al.* (2023) ^[26], Lavanya *et al.* (2022) ^[25], consistent with previous findings.

Conclusion

The analysis of variance verified genetic variability in the experimental material by demonstrating significant differences among the rice genotypes all the assessed traits. PCV values were higher than GCV values indicating the influence of environmental factors. Moderate magnitude of PCV coupled with GCV was exhibited by traits number of spikelets per panicle (18.11), number of filled spikelets per panicle (17.62), 1000 seed weight (15.29) and harvest index (12.68). A slightly higher PCV than the GCV indicated that the environment had a lesser impact on the traits under study. Thus, direct selection may be effective in improving these traits. High heritability combined with high genetic advance as a percent of mean was recorded only for spikelets per panicle, number of filled spikelets per panicle, 1000 seed weight, harvest index. Clustering showed that varieties from similar regions fell into distinct groups, indicating that genetic and geographical diversity are largely independent. Thus, genetic resources from different clusters can serve as valuable donors for improving agronomic traits in hybridization programs, contributing to high-yielding, widely adaptable and resilient varieties.

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