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Genetic analysis for yield and quality traits in advanced breeding lines of rice (*Oryza sativa* L.)

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Abstract

In this study, forty-four advanced breeding lines and three checks of rice were evaluated to determine the genetic diversity exhibited by the experimental material during *kharif* 2022. The variance investigations revealed highly substantial differences across the 47 advanced breeding lines, indicating that the material has significant genetic variability. Number of filled grains, number of unfilled grains, grain yield, head rice recovery %, amylose %, gel consistency, and alkali spreading value were shown to have high phenotypic and genotypic coefficients of variation. This implies that genetic advancement will result via direct selection. The number of effective tillers per plant, number of filled grains per plant, weight of 100 seeds (g), biological yield per plant, harvest index, yield of grains per plant, head rice recovery %, gel consistency test, and amylose content were the yield and quality traits that showed high values for genetic advance as % of mean as well as high heritability. This meant that the inheritance of these characteristics was controlled by additive gene activity.

Keywords: Paddy, SIET-3, genetic variation, heritability, genetic advance, yield and yield contributing traits, quality traits

Introduction

Rice belongs to the genus *Oryza*, the family Poaceae, and the tribe *Oryzaceae*. The genus *Oryza* can be observed all through the tropics and subtropics of the world. It consists of 25 different species, 23 of which exist in the wild, and just two are farmed (*Oryza sativa* and *Oryza glaberrima*). *Oryza sativa* is grown largely in Asia, whereas *Oryza glaberrima* is grown in Africa (Roy *et al.*, 2013) [11]. Because starch, a form of carbohydrate, is the predominant nutritious component of rice, it provides instant energy. Rice has an average nitrogenous component composition of only 8%, whereas the amount of fat or lipids is negligible, at only 1%. Despite this, rice is still thought of as a complete food. Rice is the Asia-Pacific region's main crop. The estimated demand by 2025 is mind-boggling, as rice consumption in major Asian countries would rise faster than population growth. In summary, rice consumption in Asia will increase by more than 51 percent by 2025 compared to 1995. Heritability and genetic progress are key selection criteria when traits that contribute to yield are considered. Heritability estimates combined with genetic advancement are often more reliable than estimated heritability alone when forecasting the advantages of selection. The product of multiple elements known as yield components yield is a dynamic quantitative characteristic that is controlled by several gene interactions with the environment. Selecting parents exclusively based on yield may be deceptive. Plant breeders must therefore comprehend the relationship between yield and the traits that contribute to it in order to create a variety that is commercially viable (Paul *et al.*, 2006) [8].

Materials and Methods

During the *kharif* season of 2022, the present test was conducted out at the Research cum Instructional farm Department of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur (C.G.), while the lab work was done at the Quality laboratory, Department of Genetics and Plant Breeding, RRL, IGKV, Raipur (C.G.).

Total of 44 SIET-3 (State Initial Evaluation trials) breeding lines of rice, together with the three checks Narendra 395, Karma Mahsuri, and IGKV R 1244, were used for the experiment. The experiment was set up in a Randomised Block Design with two replications during *kharif* 2022. Throughout the study, five random plants from each line were selected at the ideal stage of developing plants for the assessment of both quality and yield metrics in the two replications.

Results and Discussion

The current study used forty-four advanced breeding lines of rice and three checks. The experimental material was grown in RBD (randomized block design) with two replications at the Research cum Instructional farm, Department of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur (C.G.), and the laboratory work was done at the Quality laboratory, Department of Genetics and Plant Breeding, RRL, IGKV, Raipur (C.G.). To acquire a comprehensive picture of genotype variability, the genetic characteristics of variability were investigated. For the different analyses, eleven yield characters and nineteen quality characters were used. Five plants were chosen at random from each replication for observation, while days to 50% flowering noted on a plot basis.

Analysis of variance

To determine the variances across lines for a given trait, analysis of variance was utilized, which is used for assessing the extent of variability in observable traits across advanced breeding lines of rice. The results are shown in tables 1 and 2 for yield and quality characters, respectively. The variability analysis performed for each character revealed exceptionally large variances between the 44 SIET-3 (State Initial Evaluation trials) advanced breeding lines, revealing that the source material included a tremendous degree of genetic variability. An F-test revealed that the mean sum of squares values for all yield and quality characteristics studied were significant (at the 1% threshold of significance). Devi *et al.*, (2017) [3] and Pravallika *et al.*, (2022) also reported similar results

Table 1: Variance analysis for yield attributing characters in SIET-3 rice breeding lines

S. No.	Sources of variance	Mean sum of squares		
		Replication (df=1)	SIET-3 lines (df=46)	Error (df=46)
1	Days to 50% flowering	6.130	128.660**	1.345
2	Plant height (cm)	11.900	225.380**	42.650
3	Number of effective tillers/plants	0.170	2.960**	1.450
4	Panicle length (cm)	4.550	4.110**	1.090
5	Number of filled grains/panicle	299.540	1216.360**	267.740
6	Number of unfilled grains/panicles	191.000	276.890**	170.100
7	Spikelet fertility %	27.300	84.130**	23.360
8	100 seed weight (g)	0.0049	0.360**	0.022
9	Biological yield per plant (g)	8.160	120.725**	4.740
10	Harvest index %	24.641	76.319**	5.650
11	Grain yield per plant (g)	2.170	15.210**	1.490

Table 2: Variance analysis for quality characters in SIET-3 breeding lines of rice

S. No.	Sources of variance	Mean sum of squares		
		Replication (df=1)	SIET-3 lines (df=46)	Error (df=46)
1	Paddy Length (mm)	0.072	1.164**	0.266
2	Paddy Breadth (mm)	0.013	.091**	0.044
3	Paddy length breadth ratio	0.125	0.353**	0.100
4	Brown Rice Length (mm)	0.031	0.511**	0.069
5	Brown Rice Breadth (mm)	0.056	0.054**	0.010
6	Brown Rice length/breadth ratio	0.079	0.162**	0.031
7	Kernel Length (mm)	0.005	0.402**	0.071
8	Kernel Breadth (mm)	0.001	0.043**	0.009
9	Kernel length/breadth ratio	0.003	0.121**	0.028
10	Hulling%	8.760	20.600**	3.300
11	Milling%	7.190	33.350**	0.860
12	Head Rice Recovery %	3.700	201.800**	24.100
13	Cooked Rice Length (mm)	6.800	0.480**	0.240
14	Cooked Rice Breadth (mm)	0.042	0.046	0.033
15	Cooked Rice length/breadth	0.077	0.078	0.048
16	Elongation ratio	0.016	0.0156**	0.006
17	Gel Consistency Test	49.100	206.440**	10.460
18	Alkali Spread Value	1.530	2.199**	0.810
19	Amylose Content %	0.300	105.490**	9.660

Variation coefficients by genotype and variation coefficients by phenotype

All the features under research exhibited stronger phenotypic coefficient than genotypic coefficients of variation (Table 3 and table 4), which suggests that the environment has a muffling influence on the occurrence of genotypic variation, according to the results of genetic variability. The range of variance found for each of the traits under examination suggested that there was substantial range of variation. Trait number of unfilled grains per panicle (48.83.) had highest

PCV and GCV value followed by effective tiller per plant (23.55; 21.66) and number of filled grains per panicle (22.32; 17.84) lowest value of PCV and GCV was observed for panicle length (6.47; 4.93) followed by days to 50% flowering (7.78, 7.70) and spikelet fertility (8.64, 6.49). For quality characters also range of PCV and GCV was from low to high. Highest PCV and GCV value observed for trait) amylose% (34.35; 31.33) followed by alkali gel consistency (31.05; 29.52) and head rice recovery (23.3; 22.9). Lowest PCV and GCV values obtained for trait hulling% (4.56; 3.88) which

were followed by milling% (6.25; 6.01) and cooked rice length (7.10; 4.03). Characters which showed moderate value of GCV and PCV were number of effective tillers per plant, 100 seed weight (g), paddy L/B ratio, brown rice L/B ratio, kernel L/B ratio, kernel breadth after cooking (mm) and cooked rice L/B ratio. Characters showed high value of GCV

and PCV were number of filled grains per panicle, biological yield per plant (g), number of unfilled grains per panicle, harvest index %, grain yield per plant (g), gel consistency, amylose %, alkali spreading value and head rice recovery %. Similar findings were reported by Islam *et al.* (2015) [6] and Akshay *et al.*, (2022) [1] in their studies.

Table 3: Variation in genetic variables for yield and yield contributing traits in SIET-3 breeding lines of rice

S. No	Source of Variation	Mean	Range		Variance		Heritability	GA	GA % Mean
			Highest	Lowest	GCV	PCV			
1	Days to 50%flowering	103.610	120.500	94.500	7.700	7.780	97.930	16.260	15.690
2	Plant height (cm)	116.360	148.500	90.830	8.210	9.940	68.170	16.250	13.970
3	Number of effective tillers/plants	6.360	10.000	3.500	21.160	23.550	80.780	2.490	39.190
4	Panicle length (cm)	24.880	28.380	21.530	4.930	6.470	57.930	1.920	7.730
5	Number of filled grains/panicle	122.040	183.700	84.500	17.840	22.320	63.920	35.860	29.390
6	Number of unfilled grains/panicles	18.960	67.750	5.580	38.530	48.820	23.890	7.350	38.790
7	Spikelet fertility %	84.880	94.640	71.560	6.420	8.640	56.530	8.530	10.500
8	100 seed weight (g)	2.390	3.280	1.600	17.060	18.160	88.280	0.790	33.030
9	Biological yield per plant (g)	41.650	65.300	30.200	18.270	19.010	92.430	15.080	36.200
10	Harvest index %	34.610	50.660	23.820	17.170	18.490	86.210	11.360	32.840
11	Grain yield per plant (g)	14.230	20.400	8.800	18.390	20.300	82.120	4.890	34.340

Table 4: Variation in genetic variables for quality traits in SIET-3 rice breeding lines

S. No	Source of Variation	Mean	Range		Variance		Heritability	Genetic Advance	GA as % Mean
			Highest	Lowest	GCV	PCV			
1	Paddy Length	8.66	10.20	7.45	7.70	9.70	62.77	1.09	12.6
2	Paddy Breadth	2.40	2.80	1.85	6.33	10.84	34.07	0.18	7.61
3	Paddy length/breadth Ratio	3.60	4.64	2.90	9.70	13.07	55.70	0.54	15.0
4	Brown Rice Length	6.66	7.70	5.75	7.05	8.07	76.28	0.84	12.69
5	Brown Rice Breadth	2.18	2.50	1.75	6.70	8.20	67.49	0.24	11.45
6	Brown Rice L/B Ratio	3.07	3.63	2.52	5.80	8.33	67.35	0.43	14.09
7	Kernel Length	6.35	7.30	5.55	4.21	7.65	69.68	0.69	10.99
8	Kernel Breadth	2.06	2.35	1.75	4.81	7.88	62.78	0.21	10.1
9	Kernel length/breadth ratio	3.08	3.69	2.56	6.90	8.80	62.33	0.35	11.36
10	Hulling %	75.70	79.86	63.83	3.88	4.56	72.34	5.10	6.80
11	Milling %	66.50	74.01	51.65	6.05	6.21	94.97	8.00	12.1
12	Head Rice Recovery %	49.20	64.47	26.98	19.10	21.56	78.63	17.21	34.93
13	Cooked Rice Length	8.50	9.95	7.50	4.03	7.10	32.33	0.40	4.73
14	Cooked rice Breadth	2.88	3.20	2.55	2.77	6.90	16.04	0.06	2.2
15	Cooked Rice length/breadth Ratio	2.90	3.55	2.65	4.13	8.47	23.77	0.12	4.14
16	Elongation Ratio	1.31	1.56	1.15	4.94	7.88	39.29	0.09	6.37
17	Gel Consistency Test	33.50	83.00	27.00	29.52	31.05	90.35	19.38	57.80
18	Alkali Spread Value	5.50	7.00	3.50	14.96	22.03	45.76	1.15	20.77
19	Amylose Content	22.08	47.19	13.84	31.33	34.35	83.21	13.00	58.88

Heritability and GA as % of mean

Estimates of heritability quality and yield contributing traits ranged from medium to high heritability. The yield characters for which highest and lowest heritability obtained were days to 50% flowering (97.93%) and unfilled grains per panicle (23.89%) respectively. Yield characters for which high heritability obtained were 100 seed weight (g) (88.28%), days to 50% flowering (97.93%), plant height (cm), effective tillers (80.78) (68.17%), number of filled grains per panicle (63.92%), grain yield per plant (g) (82.12%), biological yield per plant (g) (92.43%) and harvest index (86.21). Similar findings have been reported by Saha *et al.*, (2019) [12] and Parimala and Devi (2019) [7].

The advance breeding lines showed GA as % of mean from low to high value. While noting for GA as % of mean, the yield characters observed with highest value was number of effective tillers per plant (39.19%) and least value was obtained for spikelet fertility (6.5%). High estimates of genetic advance as % of mean obtained from characters

number of effective tillers per plant (39.19), number of filled grains per panicle (29.39), number of unfilled grains per panicle (38.79) 100 seed weight (g) (33.03) biological yield per plant (g) (36.20), harvest index% (32.84), grain yield per plant (g) (34.34). Rathi *et al.*, (2019) [10] and Ganpati *et al.*, (2020) [5] also obtained similar results.

Individual evaluations of heritability and genetic advance are less reliable and practical than heritability projections based on genetic advancement. In order to choose characteristics for improvement, estimations of heritability with genetic progress are applied.

The yield characters with the highest heritability and GA % of mean were the number of effective tillers per plant, the number of filled grains per panicle, the weight of 100 seeds (g), the biological yield per plant, the harvest index, and the yield of grains per plant. Head rice recovery %, gel consistency test, and amylose content were among the quality features that had strong heritability and high genetic progress as a percentage of mean. Due to the significant additive gene

action present in these characters, which is indicated by their high heritability and strong genetic advance as a percentage of mean, selection (mass selection and progeny selection) will be effective in enhancing these traits. Allam *et al.* (2015) also reported similar results. Similar results were reported by Babu *et al.*, (2012)^[2].

Conclusion

From the above study we can conclude that there was a lot of variances across advance breeding lines for yield attribution and quality attributes. Since genotypic variability was considerably less than variation in phenotype, we can safely say that environment has considerable effect on the expression of characters. Traits with high GA % of mean, as well as high heritability, were the number of effective tillers /plants, the number of filled grains /plant, the weight of 100 seeds (gm), the biological yield /plant, the harvest index, the yield of grains /plant, the head rice recovery%, the gel consistency test, and the amylose content demonstrating presence of gene activity that is additive in nature and thereby making selection viable for these traits.

Conflict of Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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