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Application of genetic parameters for betterment of yield and yield contributing traits in rice (*Oryza sativa* L.)

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Abstract

Genetic variability is crucial for effective selection and breeding in rice improvement programs. This study assesses the genetic variability parameters for yield and its contributing traits in rice hybrids using 25 cross combinations, including parents, and checks. was studied at IGKV Raipur, Chhattisgarh for 13 characteristics. In this analysis depicts higher estimates of GCV and PCV observed for grain yield per plant, biological yield per plant, total tillers per plant, and effective tillers per plant. The high value of Phenotypic coefficient of variance than Genotypic coefficient of variance indicates influence of environment. Moderate values of GCV and PCV were noticed in plant height, harvest index, 1000 seed weight, number of filled spikelets per panicle and the total number of spikelets per panicle. Lower estimates were recorded for spikelet fertility (%), days to 50% flowering, and days to maturity. The PCV was generally higher than the GCV, and showed less influence of environment for the expression of yield traits. High heritability was observed for traits like biological yield per plant, total tillers per plant, total number of spikelets per panicle, grain yield per plant, number of filled spikelets per panicle, 1000 seed weight, effective tillers per plant, spikelet fertility (%), plant height, harvest index, days to 50% flowering, panicle length, and days to maturity. Genetic advance as a percentage of mean was also found higher for grain yield per plant, biological yield per plant, total tillers per plant, effective tillers per plant, plant height, harvest index, 1000 seed weight, number of filled spikelets per panicle, and total number of spikelets per panicle. Moderate genetic advance was observed for panicle length and spikelet fertility (%). Lower genetic advance was observed for days to 50% flowering and days to maturity. Traits with high heritability and high genetic advance as a percentage of mean are likely controlled by additive gene action, making them suitable for selection and genetic improvement. Traits with high heritability but moderate genetic advance may involve both additive and non-additive gene actions. Recommending these potential lines for genetic improvement through selection. The findings provide valuable insights for breeders aiming to enhance crop performance through targeted trait selection and breeding strategies.

Keywords: Variability, GCV, PCV, Heritability (h^2) and genetic advance

1. Introduction

Rice (*Oryza sativa* L.) is one of the most important staple crops globally, serving as a primary food source for over half of the world's population, particularly in Asia and Africa (Khush 2005) [13]. With its origins traced back to Asia, specifically in the regions of China and India, rice cultivation dates back thousands of years, making it deeply intertwined with human civilization and cultural heritage (Civáň *et al.* 2013) [7].

The significance of rice in global food security cannot be overstated, as it provides essential nutrients and calories to billions of people worldwide. Its adaptability to various environmental conditions, coupled with its high yield potential, makes rice a versatile and resilient crop (Farooq *et al.*, 2014) [11].

Furthermore, rice plays a crucial role in agricultural economies, providing livelihoods for millions of farmers and contributing significantly to national economies in rice-growing regions (Barker *et al.*, 2018) [3].

Despite its importance, rice production faces numerous challenges, including biotic and abiotic stresses, under changing climatic scenarios.

Addressing these challenges requires a deeper understanding of rice genetics, physiology, and agronomy, as well as the development of improved varieties through breeding programs and biotechnological advancements (Muthayya *et al.*, 2014) [15].

Genetic improvement mostly relies on the magnitude of genetic variability present in the population. The broad genetic base among the parents is highly significant since it provides a highly heterotic and ideal combination in segregating generations. Heritability, a measure of how well traits are transferred from parents to their offspring, is crucial in the selection of plants for breeding. Information on predicted gains from the selection of superior people is provided by genetic advances. Heritability and genetic advance are the main two selection indices that may be used to forecast the gain under selection. The measurement of genotypic and phenotypic coefficient of variation (GCV & PCV), heritability and genetic advance gives substantial information to the breeder in the selection of desired traits since they are recognized as key selection parameters. When selection is performed relying on yield contributing characteristics, heritability and genetic advance are vital selection parameters. Choosing parents too much based on yield may be deceptive. As a consequence, knowing the link between yield and its contributing characters it is important for plant breeders to develop an economically viable variety. In this context, research efforts focused on enhancing rice productivity, sustainability, and resilience are paramount to ensure food security and alleviate poverty in rice-dependent regions worldwide.

2. Materials and Methods

Elite rice genotypes which comprise five lines and five testers and their cross combinations were studied. Five lines were crossed with the five testers in line \times tester fashion to generate a total of twenty-five F1 hybrid combinations and the experiment was laid out in RCBD with two replications, at the Research cum Instructional Farm, Rice Breeding Unit, Department of Genetics and Plant Breeding, COA, IGKV Raipur, Chhattisgarh located between 17° 14' and 24° 45' N latitude and 79° 16' and 84° 15' E longitudes whereas, Raipur lies at 21° 16' N and 81° 36' E with a height of 289.60 m above the mean sea level., India. The experiment was conducted during *Kharif* 2022.

2.1 Statistical analysis

The data was collected on five randomly selected and tagged plants from each accession. Recommended cultural practices were used for cultivating rice crop throughout the investigation. Average results from the sampled plant with respect to different traits were used for statistical analysis.

A. Phenotypic variance

Phenotypic variance calculating given formula:

$$VP = VG + VE$$

Where,

VP = Phenotypic variance VG = Genotypic variance

VE = Environmental variance.

B. Genotypic variance

Genotypic variance calculating given formula:

$$VG = VP - VE$$

Where,

VG = Genotypic variance

VP = Phenotypic variance

VE = Environmental variance.

C. Genotypic and phenotypic coefficient of variance:

The genotypic and phenotypic coefficient of variation were calculated according to the formula given by Falconer (1981).

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sigma_g}{\text{mean}} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sigma_p}{\text{mean}} \times 100$$

Categories of range of variation as given by Sivasubramanian and Madhavamenon (1973) [19].

< 10%: Low

10-20%: Moderate

>20%: High.

D. Heritability (broad sense)

Heritability in a broad sense was calculated as the ratio of genotypic variance to the phenotypic variance and expressed as a percentage (Falconer, 1981).

$$\text{Heritability (h}^2\text{ (b))} = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

The calculated heritability was classified into three groups as suggested by Johnson *et al.* (1955):

0-40% = Low

40-60% = Moderate

>60% = High.

A. Expected genetic advance (GA)

The genetic advance was calculated by adopting the following formula given by Johnson *et al.* (1955):

$$GA = k \times h \times \sqrt{\sigma^2_p}$$

Where,

h = Heritability in broad sense

k = Selection differential, which is equal to 2.06 at 5% intensity of selection.

\sqrt{p} = Phenotypic standard deviation.

3. Results and Discussion

Table 1: Analysis of variance

S.NO.	Source of variations	df	1	2	3	4	5	6
1	Replication	1	0.03	0.02	0.1	0.02	0.34	0.97
2	Treatments	34	28.70**	6.90**	1346.53**	17.81**	19.82**	17.11**
3	Parents	9	35.81**	4.52**	1962.33**	35.83**	31.89**	24.90**
4	Parents (Lines)	4	6311**	0.58	745.27**	29.29**	52.22**	39.21**
5	Parents (Testers)	4	9.66**	9.42**	423.18**	10.87**	4.01**	5.15**
6	Parents (L vs T)	1	28.80**	0.68	12987.16**	161.88**	62.13**	46.67**
7	Parents vs Crosses	1	487.22**	61.04**	923.52**	6.39	58.17**	58.41**
8	Error	34	1.56	1.11	21.07	1.28	0.16	0.23
	Total	69	14.91	3.95	673.89	9.41	9.85	8.56
S.NO.	Source of variations	7	8	9	10	11	12	13
1	Replication	73.95	116.38	4.5	9.61	5.23	3.86	0.09
2	Treatments	2694.43**	2111.71**	111.54**	28.33**	683.42**	170.13**	193.31**
3	Parents	4270.21**	2985.92**	109.95**	15.93**	1032.51**	198.29**	389.96**
4	Parents (Lines)	6558.43**	5852.87**	129.84**	8.23**	1784.24**	310.09**	764.55**
5	Parents (Testers)	1048.84**	572.47**	35.90**	27.56**	45.98**	130.27**	15.93**
6	Parents (L vs T)	8002.80**	1171.98**	326.59*	0.21	1971.70**	23.16**	387.73**
7	Parents vs Crosses	14242.67**	818.60**	963.71**	134.79**	742.63**	62.10**	42.42**
8	Error	21.48	22.2	1.55	0.34	4.49	5.9	1.56
	Total	1339.35	1053.18	55.79	14.26	339.05	86.79	96.02

3.1 Analysis of variance (ANOVA) for parents and hybrids

Analysis of variance was performed on the replication wise mean data for the thirteen yield and its contributing traits of 25 rice genotypes that include 5 lines and 5 testers. The analysis of variance revealed a significant difference in all of the attributes, such as days to 50% flowering, days to maturity, plant height, panicle length (cm), total number of tiller/plants, total number of effective tillers/plants, total number of spikelets/panicles, number of filled spikelets/panicle, spikelet fertility %, 1000 seed weight, biological yield/plant (g), harvest index and grain yield/plant (g). Table 2. shows the results of the analysis of variance, as well as the significant differences for each of the features studied. This indicates that the materials utilized in this investigation have genetic variability among them.

3.2 Range and mean performance of different characters

Days to 50% flowering varied from 92.75 days (BLM-9) to 104.75 days (R2404-346-164-1) with an overall mean of 97.60 days and in the hybrids, it ranged from 87.50 days (PKV-HMT x MTU1217) to 96.50 days (PKV-HMT x CR3969-24-2-1-1-1) with an overall mean of 91.76 days among five lines and five testers along with their 25 F₁s. The mean of parents for days to maturity ranged from 118.95 days (CR3969-24-2-1-1-1) to 123.85 days (BLM-9) and the mean came out to be 121.70 days, whereas in the hybrids the values ranged from 115.95 days in a cross combination of R1853-105-1-82-1 x CR3969-24-2-1-1-1 to 122.50 days in a cross combination of TCDM-1 x CR3969-24-2-1-1-1 with an overall mean of 119.63 days. The plant height (cm) in parents ranged from 79.12 cm (PKV-HMT) to 167.87 cm (BLM-9) with an overall parental mean of 127.79 cm. The mean value of the hybrids ranged from 52.92 cm (PKV-HMT x Improved Sambha Mahsuri) to 156.92 cm (R1853-105-1-82-1 x MTU1217) with an overall average of 119.75 cm. The mean value for panicle length (cm) in parents ranged from 18.41 cm (PKV-HMT) to 31.58 cm (BLM-9) with an overall parental mean of 25.90 cm. The mean value of the hybrids ranged from 18.92 cm (TCDM-1 x MTU1217) to 29.55 cm (R1853-105-1-82-1 x BLM - 9) with an overall average of 25.23 cm. The mean performance of parents for total tillers per plant ranged from

5.50 (MTU1217) to 18.95 (R2404-346-164-1) with an overall mean of 8.96. In the hybrids, it ranged from 4.16 (PKV-HMT x Improved Sambha Mahsuri) to 15.80 (R2404-346-164-1 x BLM-9) with an overall mean of 10.98. The mean performance of parents for effective tillers per plant ranged from 4.75 (MTU1217) to 16.98 (R2404-346-164-1) with an overall mean of 8.50. In the hybrids, it ranged from 4.12 (PKV-HMT x Improved Sambha Mahsuri) to 15.30 (R2404-346-164-1 x BLM - 9) with an overall mean of 10.53. The total number of spikelets per panicle in parents ranged from 150.42 (R1853-105-1-82-1) to 285.45 (R2404-346-164-1) with an overall parental mean of 212.75. The mean value of the hybrids ranged from 197.90 (TCDM-1 x CR3969-24-2-1-1-1) to 295.70 (R2404-346-164-1 x Improved Sambha Mahsuri) with an overall average of 244.32. The mean value for the number of filled spikelets per panicle in parents ranged from 121.50 (PKV-HMT) to 245.95 (R2404-346-164-1) with an overall parental mean of 178.04. The mean value of the hybrids ranged from 137.30 (PKV-HMT x BLM-9) to 246.80 (R2404-346-164-1 x Improved Sambha Mahsuri) with an overall average of 185.60. The mean performance of parents for spikelet fertility (%) ranged from 76.12% (DRR Dhan 62) to 96.72% (TCDM-1) with an overall mean of 83.96%. In the hybrids, it ranged from 64.67% (TCDM-1x Improved Sambha Mahsuri) to 88.94% (R1853-105-1-82-1x MTU1217) with an overall mean of 75.74%. The 1000 seed weight (g) in parents ranged from 14.93 g (CR3969-24-2-1-1-1) to 24.10 g (MTU1217) with an overall parental mean of 17.54 g. The mean value of the hybrids ranged from 15.31 g (R1853-105-1-82-1 x MTU1217) to 30.09 g (MTU2411 x MTU1217) with an overall average of 20.61 g. The mean of parents for biological yield per plant (g) ranged from 25.92 g (PKV-HMT) to 102.90 g (R2404-346-164-1) and the mean came out to be 46.04 g, whereas in the hybrids the values ranged from 24.23 g in a cross combination of (PKV-HMT x Improved Sambha Mahsuri) to 91.90 g in a cross combination of (R2404-346-164-1 x BLM - 9) to 53.25 g. The mean value for harvest index (%) in parents ranged from 32.8% (TCDM-1) to 58.08% (R2404-346-164-1) with an overall parental mean of 44.56%. The mean value of the hybrids ranged from 20.89% (TCDM-1 x CR3969-24-2-1-1-1) to 57.61% (R1853-105-1-82-1 x CR3969-24-2-1-1-1)

with an overall average of 42.48 . The mean of parents for grain yield per plant (g) ranged from 12.75 g (CR3969-24-2-1-1-1) to 59.75 g (R2404-346-164-1) and the mean came out to be 20.77 g, whereas in the hybrids the values range from 7.40 g in a cross combination of PKV-HMT x Improved Sambha Mahsuri to 43.50 g in a cross combination of R2404-346-164-1 x BLM – 9 with an overall average of 22.49 g.

3.3 Phenotypic and genotypic coefficient of variation

The result showed that the phenotypic coefficient of variation (PCV) was higher in magnitude than the genotypic coefficient of variation (GCV) for all the quantitative characters studied in the investigation. This reveals that observed variation is due to both genotype and influence of environment.

Higher estimates of PCV were recorded as 36.78 percent for grain yield/plant, 29.68 percent for biological yield/plant, 24.90 percent for total tillers/plant and 24.33 percent for effective tillers/plant. Moderate estimates of PCV were recorded as 18.08 percent for harvest index, 17.63 percent for plant height, 15.75 percent for 1000 seed weight, 14.61 percent for number of filled spikelets/panicle, 12.84 percent for total number of spikelets/panicle and 10.25 percent for panicle length. Lower estimates of the phenotypic coefficient of variation were shown by spikelet fertility % (7.92 percent), days to 50% flowering (3.49 percent) and days to maturity (1.45 percent).

Higher estimates of GCV were recorded in 36.34 percent for grain yield per plant, 29.39 percent for biological yield per plant, 24.61 percent for total tillers per plant and 23.84 percent for effective tillers per plant. Characters having moderate values of GCV were 17.22 percent for plant height, 17.18 percent for harvest index, 15.48 percent for 1000 seed weight, 14.39 percent for number of filled spikelets per panicle, 12.69 percent for total number of spikelets per panicle and 9.23 percent for panicle length. Lower estimates of GCV were exhibited by spikelet fertility % (7.75 percent), days to 50% flowering (3.22 percent) and days to maturity (1.16 percent). Similar findings were reported by Barde *et al.* (2021) ^[1] for both characters, Bhargavi *et al.* (2021) ^[5] founded same result for genetic variability in given traits for grain yield and Noatia *et al.* (2021) ^[16] reported similar findings for grain yield. the data is presented in Table 2.

3.4 Heritability (h^2)

The heritability was high in the traits *i.e.*, biological yield/plant (98.05%), total tillers/plant (97.69%), total number of spikelets/panicle (97.64%), grain yield/plant (97.62%), number of filled spikelets/panicle (96.91%), 1000 seed weight in g (96.52%), effective tillers/plant (95.99%), spikelet fertility (95.94%), plant height (95.45%), harvest index (90.27%), days to 50% flowering (85.30%), panicle length (81.15%) and days to maturity (63.58%). Similar findings were reported by Bhargavi *et al.* (2021) ^[5] and Dhidhi *et al.* (2021) for panicle length, Barhate *et al.*, (2021) for days to 50% flowering and days to maturity.

3.5 Genetic advance (%)

A high degree of the genetic advance (GA) as a percent of mean was observed for the characters like grain yield/plant (73.97%), biological yield/plant (59.95%), total tillers/plant (50.11%), effective tillers/plant (48.12%), plant height (34.66%), harvest index (33.62%), 1000 seed weight (31.32%), number of filled spikelet/panicle (29.18%) and total number of spikelet/panicle (25.82%). Characters exhibiting moderate range for genetic advance as a percent of mean reported were panicle length (17.13%) and spikelet fertility % (15.65%). The exhibiting low ranges for genetic advance as a percent of mean reported for the characters such as days to 50% flowering (6.12%) and days to maturity (1.90%). Similar findings were reported by Yashwanth *et al.* (2021) ^[20] founded same result for genetic advance in given traits for grain yield and Chamar *et al.* (2021) ^[6] reported similar findings for effective tillers/plant and grain yield.

High heritability coupled with the high genetic advance as a percent of mean was reported for the traits of grain yield/plant, biological yield/plant, total tillers/plant, effective tillers/plant, plant height, harvest index, 1000 seed weight, number of filled spikelet/panicle and total number of spikelet/panicle indicating that the expression of such characters controlled by the additive gene action and thus simple selection will be effective for the improvement of these characters. High heritability coupled with the moderate genetic advance as a percent of mean was observed in panicle length and spikelet fertility % suggesting that control of expressions by both additive and non-additive gene action suggests that the selection cannot be practiced for improving these traits, thus heterosis breeding could be successful. High heritability with low genetic advance as a percent of mean was shown in days to 50% flowering and days to maturity, as it was controlled by non-additive gene action and influence of environment is high.

The analysis of variance for line x tester showed significance for the characters where sufficient variability is present in hybrids. The variance for parents was significant for all the characters studied in the investigation. The variance due to crosses and line x tester were found to be significant for all the characters studied in the research.

Among the lines, the best general combiner is R1853-105-1-82-1 as it has highly significant GCA effects with the days to maturity, panicle length, number of filled spikelets per panicle, spikelet fertility % and harvest index. Out of the total testers studied, BLM-9 came to be the best general combiner. BLM-9 has highly significant GCA effects with effective tillers per plant, total tillers per plant, spikelet fertility %, grain yield per plant and harvest index %. Similar findings were reported by Dhavaleshvar *et al.* (2019) for plant height and 1000 seed weight, Noatia *et al.* (2021) ^[16] reported similar finding for number of spikelets per panicle, filled spikelet per panicle and 1000 seed weight which are same as my result, Bhargavi *et al.* (2021) ^[5] founded same result for test weight and grain yield per plant.

Table 2: Genetic parameters for yield and its contributing traits

Characters	Mean	Range		GCV (%)	PCV (%)	h ² (bs) (%)	GA% mean
		Min.	Max.				
Days to 50% flowering	93.43	87.50	104.75	3.49	3.22	85.30	6.12
Days to maturity	120.22	115.95	123.85	1.45	1.16	63.58	1.90
Plant height(cm)	122.05	52.92	167.87	17.63	17.22	95.45	34.66
Panicle length (cm)	25.42	18.41	31.58	10.25	9.23	81.15	17.13
Total tillers/plant	10.40	4.16	18.95	24.90	24.61	97.69	50.11
Effective tillers/plant	9.95	4.12	16.98	24.33	23.84	95.99	48.12
Total number of spikelets panicle ⁻¹	235.30	150.42	295.70	12.84	12.69	97.64	25.82
Number of filled spikelets panicle ⁻¹	183.44	121.50	246.80	14.61	14.39	96.91	29.18
Spikelet fertility (%)	78.09	64.67	96.72	7.92	7.75	95.94	15.65
1000 seed weight (g)	19.74	14.93	30.09	15.75	15.48	96.52	31.32
Biological yield/plant (g)	51.19	24.23	102.90	29.68	29.39	98.05	59.95
Harvest Index (%)	43.07	20.89	58.08	18.08	17.18	90.27	33.62
Grain yield plant ⁻¹ (g)	22.00	7.40	59.75	36.78	36.34	97.62	73.97

4. Conclusion

The analysis of variance was found significant for all the yield and yield contributing traits studies, where sufficient variability is present among the genotypes.

High PCV and GCV was recorded for grain yield per plant, biological yield per plant, total tillers per plant and effective tillers per plant indicating presence of sufficient variability in the hybrids and thereby suggesting that selection of these traits will be useful for genetic improvement.

The ranges of PCV and GCV were found to be in close agreement for grain yield/ plant, biological yield/plant, total tillers/plant, total number of spikelets/panicle, number of filled spikelets/panicle, 1000 seed weight and plant height indicating less influence of environment on these traits.

Among the lines, R1853-105-1-82-1 and among the testers, BLM-9 found to be the best general combiners for more yield and its contributing traits.

The best performing crosses i.e., R1853-105-1-82-1 x Improved Sambha Mahsuri, R1853-105-1-82-1 x DRR Dhan 62, R2404-346-164-1 x BLM – 9, R2404-346-164-1 x MTU1217, MTU2411 x DRR Dhan 62 and MTU2411 x CR3969-24-2-1-1-1 were most promising hybrids based on mean grain yield, GCA and SCA.

5. Future Prospect

Focused Breeding Programs: prioritize traits such as grain yield per plant, biological yield per plant, total tillers per plant, effective tillers per plant, total number of spikelets per panicle, number of filled spikelets per panicle, 1000 seed weight, and plant height. These traits have shown significant variability and less influence from environmental factors, indicating their potential for genetic improvement. Utilization of Best General Combiners: Utilize genotypes like R1853-105-1-82-1 and testers like BLM-9, identified as the best general combiners for yield and its contributing traits, in further breeding programs to enhance overall performance.

Hybridization Strategies Focuses on developing hybrids involving the best performing crosses, such as R1853-105-1-82-1 x Improved Sambha Mahsuri, R1853-105-1-82-1 x DRR Dhan 62, R2404-346-164-1 x BLM – 9, R2404-346-164-1 x MTU1217, MTU2411 x DRR Dhan 62, and MTU2411 x CR3969-24-2-1-1-1. These crosses have shown promising results in terms of mean grain yield, general combining ability and specific combining ability.

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