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## Genetic variability, heritability and genetic advance for yield and yield attributing traits in rice (*Oryza sativa* L.)

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### Abstract

Rice (*Oryza sativa* L.) is a significant cereal crop with high agricultural importance. In this study, the genetic variability and heritability of various quantitative traits related to grain yield were investigated in different rice genotypes. The experiment was conducted at Raipur Chhattisgarh, India, using a randomized complete block design with three replications. The analysis of variance revealed significant variations among the rice genotypes for all the traits studied. The genotypic and phenotypic coefficients of variance indicated a higher magnitude of phenotypic variation compared to genotypic variation, suggesting the influence of genotype-environment interaction. The estimation of heritability in broad sense and genetic advance as a percentage of mean provided insights into the inheritance pattern of the traits. The results showed that several traits, such as days to 50% flowering, plant height, effective tillers per plant, filled grains per panicle, spikelet fertility, harvest index, biological yield, seed yield per plant, and 100-seed weight, exhibited high heritability estimates and significant genetic advances. These findings suggest the presence of additive and non-additive gene actions controlling these traits, highlighting their potential for selection and improvement through breeding programs. The study provides valuable information for developing selection criteria to enhance rice yield and its associated characteristics.

**Keywords:** Rice, genetic variability, heritability, genetic advance

### Introduction

Rice (*Oryza sativa* L.) is a self-pollinated cereal crop with the chromosomal number  $2n=24$  and is a member of the Gramineae family. Two domesticated species—Asian rice (*O. sativa*,  $2n=24$ ) and African rice (*O. glaberrima*,  $2n=24$ ) as well as 22 wild species are known to make up the genus *Oryza* the Gondwanaland continents are where the genus *Oryza* originated. After China, India is first in terms of rice output and second in terms of rice area. The state of Chhattisgarh is well-known as the "Rice Bowl of India" since it produces the most. The basic prerequisite for carrying out any crop enhancement plan is the presence of sufficient genetic variability. It is important to pick the genotypes based on heritability and genetic advancement since phenotypic selection based on their performance may occasionally be ineffective because these genotypes may perform poorly in later segregating generations. (Singh *et al.* (2021) [27]) The genotypic coefficient of variation, which indicates the heritable component of genetic variability, quantifies the extent of genetic variability. The amount of genetic gain anticipated as a result of selection would be determined by genetic variability and heritability estimates (Burton, 1952) [3]. To develop selection criteria for the constructive yield augmentation by breeding, it is therefore imperative to examine the diversity for grain yield and its characteristics, quality, and nutritional aspects in rice genotypes.

### Materials and Methods

The current experiment will be conducted at Research cum Instructional farm, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, Department of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur (C.G.) during *kharif* 2022. The experimental material consisted of parents, Rajeshwari, Mahamaya, IGKV R 1244, IC0496940, IC0491194, IC0491254, IC0558317 and their  $F_1$ ,  $F_2$ ,  $F_3$ . For the various analyses, 12 yield characters were taken into consideration. The experiment was conducted in a RCBD with three replications to evaluate seven parents along with six  $F_1$ ,  $F_2$ ,  $F_3$  generations. Each genotype will be raised in plot size of 3.0 x 2.0 m and intra row spacing of 20 cm x 10 cm. five plants were chosen at random from each plot in each replication to record observations on different attributes.

## Result and Discussions

### Analysis of variance

Table 1 displays the findings of the analysis of variance, which was used to assess the degree of variation in the observed traits among rice genotypes. Every attribute that was the subject of the analysis of variance was determined to be highly significant. Analysis of variance for five populations derived from six crosses revealed that existence of considerable amount of genetic variability for yield.

### Genotypic and phenotypic coefficient of variance

The phenotypic and genotypic coefficients of variance of all the observed significantly for quantitative traits of five population which is showed in table 2. This is indicating that PCV is higher than GCV in all traits under investigations. This might be related to genotype-environment association. Similarly, result was found by Lingaiah *et al.* (2015)<sup>[18]</sup>, Iqbal *et al.* (2018)<sup>[14]</sup> and Saha *et al.* (2019)<sup>[25]</sup>.

### Heritability and Genetic advance

Estimate of heritability in broad sense and genetic advance as percentage of mean for yield and its components have been presented in table 2. Most of the crosses showed high heritability estimates with medium genetic advance as percentage of mean for days to 50% flowering. Broad sense heritability ranged from 84.30% (Rajeshwari x IC0496940) to 96.30% (Mahamaya x IC0491254). Genetic advance as percentage of mean ranged from 6.23% (Rajeshwari x IC0496940) to 15.67% (Mahamaya x IC0491254). Result indicates that involvement of additive and non-additive gene action controlling this trait. Result are in agreement with Padmaja *et al.* (2008)<sup>[21]</sup>, Jambhulkar *et al.* (2014)<sup>[15]</sup>, Rashmi *et al.* (2017)<sup>[24]</sup>, Tiwari *et al.* (2019)<sup>[28]</sup>, Singh *et al.* (2020)<sup>[26]</sup> and Faysal *et al.* (2022)<sup>[9]</sup>. Priyanka *et al.* (2020)<sup>[23]</sup> and Dhidhi *et al.* (2021)<sup>[7]</sup>.

Plant height, most of the crosses showed high heritability estimates. Heritability estimates ranged from 45.90% to 97.10 per cent. Highest heritability estimates were observed in cross Rajeshwari x IC0491254 (97.1%) followed by Rajeshwari x IC0496940 (95.0%), Mahamaya x IC0491194 (87.5%), Mahamaya x IC0491254 (80.6%), IGKV R1244 x IC0491194 (80.1%). Cross, IGKV R1244 x IC0558317 (45.9%) showed medium broad sense heritability. Genetic advance as percentage of mean ranged from 5.47% (IGKV R 1244 x IC0558317) to 39.27% (Rajeshwari x IC0491254). Similar result found with Singh *et al.* (2020)<sup>[26]</sup> and Faysal *et al.* (2022)<sup>[9]</sup>, Jambhulkar *et al.* (2014)<sup>[15]</sup>, Rashmi *et al.* (2017)<sup>[24]</sup>. In panicle length most of crosses showed high heritability as well as medium genetic advance as percentage of mean. Like cross, Mahamaya x IC0496940. Similar result found with Jambhulka *et al.* (2014)<sup>[15]</sup>.

Rajeshwari x IC0491254 was observed high heritability (91.27%) and high genetic advance as percentage of mean (84.52%) for effective tillers per plant. Similarly, total tillers per plant showed high heritability and high genetic advance as percentage of mean estimates were reported for crosses, Rajeshwari X IC0491254 (90.90%, 79.07%) followed by Mahamaya x IC0496940 (86.46%, 53.95%), IGKV R 1244 x IC0558317(80.33%, 53.26%) and IGKV R 1244 x IC0491194 (73.16%, 43.39%). Similar result found with Singh *et al.* (2020)<sup>[26]</sup>. Number of filled grains per panicle, most of crosses found highest heritability with high genetic advance as percentage of mean. Heritability ranged from 77.10% (IGKV R 1244 x IC0558317) to 96.10% (Mahamaya x

IC0491254). Genetic advance ranged from 12.48% (IGKV R 1244 x IC0558317) to 48.69% (Rajeshwari x IC0491254). For Number of unfilled grains per panicle, The high broad sense heritability with high genetic advance as percentage of mean observed for cross, Mahamaya x IC0496940 (66.8%, 28.52%). Similar result observed with Lingaiah *et al.* (2020)<sup>[18]</sup>, Singh *et al.* (2020)<sup>[26]</sup>, Kumari and Parmar (2020)<sup>[17]</sup>, Williams *et al.* (2021)<sup>[29]</sup>.

The genetic advance as per percentage of mean was ranged from 4.28% (IGKV R 1244 x IC0558317) to 12.74 (Rajeshwari x IC0491254) for spikelet fertility. Heritability estimates were recorded in all the crosses and highest recorded in Rajeshwari x IC0491254 (83.5%). High heritability were observed for crosses like Mahamaya x IC0496940 (70.5%) followed by IGKV R 1244 x IC0491194 (66.40%) and Mahamaya x IC0491254 (61.00%). Result agreement with Akshay *et al.* (2022)<sup>[2]</sup>, Chavan *et al.* (2022)<sup>[5]</sup>, Faysal *et al.* (2022)<sup>[9]</sup>, Babu *et al.* (2012)<sup>[4]</sup>, Dhanwani *et al.* (2013)<sup>[6]</sup>, Prasad *et al.* (2013)<sup>[22]</sup>, Singh *et al.* (2021)<sup>[27]</sup>.

Harvest index, the highest broad sense heritability observed in cross, IGKV R 1244 x IC0491194 (81.7). High heritability was observed in Mahamaya x IC0491254 (75.8%) followed by Mahamaya x IC0496940 (69.3), Rajeshwari x IC0496940 (65.3), IGKV R 1244 x IC0558317 (64.1%). Highest genetic advance as per percentage of mean was observed 45.64 in Mahamaya x IC0496940 and it ranged from 13.7 (IGKV R 1244 x IC0558317) to 45.6(Mahamaya x IC0496940). Result agreement with Islam *et al.* (2015)<sup>[13]</sup>, Mallimar *et al.* (2015)<sup>[19]</sup>, Hefena *et al.* (2016)<sup>[12]</sup>, Khaire *et al.* (2017)<sup>[16]</sup>, Rashmi *et al.* (2017)<sup>[24]</sup>, Ali *et al.* (2018)<sup>[11]</sup>, Iqbal *et al.* (2018)<sup>[14]</sup>, Girma *et al.* (2018)<sup>[10]</sup>, Maurya *et al.* (2018)<sup>[20]</sup>, Tiwari *et al.* (2019)<sup>[28]</sup>, Lingaiah *et al.* (2020)<sup>[18]</sup>, Singh *et al.* (2020)<sup>[26]</sup>.

For Biological yield, all the crosses reported high heritability estimates. Cross, Rajeshwari x IC0491254 recorded highest heritability estimate i.e. 98.8% followed by IGKV R 1244 x IC0558317 (98.2%), Mahamaya x IC0496940 (95.80%), Rajeshwari x IC0496940 (95.3%). Mahamaya x IC0491254 (84.80%). Genetic advance as percentage over means was ranged from 15.9 (IGKV R1244 x IC0491194) to 81.1 (Rajeshwari x IC0491254). Similar result observed with Prasad *et al.* (2013)<sup>[22]</sup>, Lingaiah *et al.* (2014)<sup>[18]</sup>, Jambhulkar, *et al.* (2014)<sup>[15]</sup>, Ekka *et al.* (2015)<sup>[8]</sup>, Islam *et al.* (2015)<sup>[13]</sup>, Mallimar *et al.* (2015)<sup>[19]</sup>, Hefena *et al.* (2016)<sup>[12]</sup>, Khaire *et al.* (2017)<sup>[16]</sup>, Rashmi *et al.* (2017)<sup>[24]</sup>, Ali *et al.* (2018)<sup>[11]</sup>, Iqbal *et al.* (2018)<sup>[14]</sup>, Girma *et al.* (2018)<sup>[10]</sup>, Maurya *et al.* (2018)<sup>[20]</sup>, Tiwari *et al.* (2019)<sup>[28]</sup>, Lingaiah *et al.* (2020)<sup>[18]</sup>, Singh *et al.* (2020)<sup>[26]</sup>.

Seed yield per plant, All the crosses showed high heritability estimates varied from 84.00% to 98.9% the highest heritability estimates were recorded in cross IGKV R 1244 x IC0491194 (98.9%) followed by Rajeshwari x IC0491254 (94.7%), IGKVR1244 x IC0558317 (93.9%), Mahamaya x IC0496940 (90.0%), Rajeshwari x IC0496940 (86.7%), Mahamaya x IC0491254 (84.0%) High genetic advance as percent over mean was observed in all the crosses ranged from 35.1 to 89.9%. High genetic advance was observed in cross Rajeshwari x IC0491254 (89.9%) followed by Mahamaya x IC0496940 (81.7%), IGKV R 1244 x IC0491194 (66.0%). Result found similar with Williams *et al.* (2021)<sup>[29]</sup>, Akshay *et al.* (2022)<sup>[2]</sup>, Chavan *et al.* (2022)<sup>[5]</sup>, Maurya *et al.* (2018)<sup>[20]</sup>, Tiwari *et al.* (2019)<sup>[28]</sup>, Lingaiah *et al.* (2020)<sup>[18]</sup>, Singh *et al.* (2020)<sup>[26]</sup>, Jambhulkar, *et al.* (2014)<sup>[15]</sup>, Ekka *et al.* (2015)<sup>[8]</sup>, Islam *et al.* (2015)<sup>[13]</sup>, Mallimar *et al.* (2015)<sup>[19]</sup>, Hefena *et al.* (2016)<sup>[12]</sup>, Khaire *et al.*

al. (2017) [16], Rashmi et al. (2017) [24], Ali et al. (2018) [1], Iqbal et al. (2018) [14], Girma et al. (2018) [10].

100 seed weight, Most of the crosses showed very high broad sense heritability estimates and it ranged from 98.5% to 99.8%. Highest heritability was observed in cross IGKV R 1244 x IC0491194 (99.8%) followed by Rajashwari x IC0491254 (99.6%), Mahamaya x IC0496940 (99.6%), Mahamaya x IC0491254 (99.6%). All the crosses showed high genetic advance as percentage of mean it ranged from

14.85% to 43.98. And highest showed by cross 43.98% (Rajashwari x IC0491254). Similar finding agreement with Maurya et al. (2018) [20], Tiwari et al. (2019) [28], Lingaiah et al. (2020) [18], Singh et al. (2020) [26], Kumari and Parmar (2020) [15], Williams et al. (2021) [29], Akshay et al. (2022) [2], Chavan et al. (2022) [5], Khaire et al. (2017) [16], Rashmi et al. (2017) [24], Ali et al. (2018) [1], Iqbal et al. (2018) [14], Girma et al. (2018) [10]. Gupta et al. (2021) [11].

**Table 1:** Analysis of variance (ANOVA) for different quantitative traits

Rajeshwari *IC0496940												
S.V	DF	1	2	3	4	5	6	7	8	9	10	11
Replicates	2	19.27	88.52	5.49	5.34	1.4	36.06	2.64	27.43	5.39	13.3	23.81
Generations	4	28.83**	646.93**	7.86**	7.13*	29.03**	2452.5**	67.12**	81.97**	413.9**	78.51**	120.9*
Error	8	1.683	11.21	0.94	1.34	1.32	87.31	3.51	1.55	6.65	3.81	18.23
Rajeshwari *IC0491254												
Replicates	2	3.26	13.41	6.05	2.46	0.043	169.26	1.62	20.77	7.78	13.33	24.57
Generations	4	73.33**	1977.90**	41.37**	50.13**	14.31*	2725.4**	73.12**	102.19**	1908.74**	495.26**	140.01*
Error	8	3.68	19.65	1.27	1.61	3.7	46.85	2.95	6.33	7.88	9.14	32.89
Mahamaya*IC0491254												
Replicates	2	7.46	16.17	0.2	0.062	4.72	20.86	2.067	10.52	35.9	40.97	67.45
Generations	4	150.23**	154.75**	18.66**	12.91*	20.69**	2236.43**	61.14**	13.61*	234.63**	54.88**	237.54**
Error	8	1.88	11.5	1.36	2	1.51	29.53	2.44	2.39	13.25	3.28	22.83

1. Days to 50% flowering 2. Plant height 3. Effective tillers per plant 4. Total tillers per plant 5. Panicle length (cm) 6. Number of filled grains per panicle 7. Number of unfilled grains per panicle 8. Spikelet fertility (%) 9. Biological yield per plant (g) 10. Seed yield per plant (g) 11. Harvest index (%) 12. 100 seed weight (g) \*\*Significant at P=1% & \*Significant at P=5%

Mahamaya*IC0496940												
Replicates	2	13.86	112.23**	0.48	1.26	1.29	128.6	22.4	12.4	2.097	2.041	37.78
Generations	4	153.1**	238.23**	10.55**	14.20**	22.46**	711.73**	74.26**	36.04**	1096.8**	222.58**	399.15**
Error	8	6.7	10.86	0.93	0.70	0.98	26.68	10.56	4.4	15.75	7.97	51.32
IGKV R 1244*IC0491194												
Replicates	2	0.8	5.2	3.61	5.0521	4.68	379.4	8.637	17.26	7.26	24.93	30.48
Generations	4	162.16**	485.49**	16.46**	14.76**	14.96**	970.23**	61.75**	28.20*	145.11*	269.56**	247.72**
Error	8	8.96	37.17	1.27	1.6091	1.52	81.98	7.753	4.06	25.28	0.98	17.16
IGKV R 1244*IC0558317												
Replicates	2	8.86	11.74	0.98	0.89	0.97	51.8	3.47	4.51	53.95	58.18	43.31
Generations	4	170.4**	95.57	20.35**	17.81**	18.15**	356.94**	79.12**	21.69*	564.13**	171.37**	42.85*
Error	8	8.95	26.98	0.91	1.34	1.14	32.13	1.94	4.38	3.42	3.64	6.75

1. Days to 50% flowering 2. Days to 50% flowering 3. Effective tillers per plant 4. Total tillers per plant 5. Panicle length (cm) 6. Number of filled grains per panicle 7. Number of unfilled grains per panicle 8. Spikelet fertility (%) 9. Biological yield per plant (g) 10. Seed yield per plant (g) 11. Harvest index (%) 12. 100 seed weight (g)

**Table 2:** Genetic parameters for different yield and its related characters

Crosses	GCV	PCV	h <sup>2</sup>	G.A	G.A %
Days to 50% flowering					
Rajeshwari *IC0496940	3.29	3.59	84.30	5.69	6.23
Rajeshwari *IC0491254	5.26	5.66	86.30	9.22	10.06
Mahamaya*IC0491254	7.75	7.90	96.30	14.22	15.67
Mahamaya*IC0496940	7.58	8.09	87.90	13.49	14.65
IGKV R 1244*IC0491194	7.94	8.61	85.10	13.58	15.09
IGKV R 1244*IC0558317	7.87	8.50	85.70	13.99	15.00
Plant height (cm)					
Rajeshwari *IC0496940	11.16	11.45	95.00	29.22	22.39
Rajeshwari *IC0491254	19.35	19.64	97.10	51.86	39.27
Mahamaya*IC0491254	5.30	5.90	80.60	12.78	9.80
Mahamaya*IC0496940	6.81	7.29	87.50	16.77	13.13
IGKV R 1244*IC0491194	8.84	9.88	80.10	22.54	16.30
IGKV R 1244*IC0558317	3.92	5.79	45.90	6.67	5.47
Panicle length (cm)					
Rajeshwari *IC0496940	11.86	12.68	87.49	5.86	22.86
Rajeshwari *IC0491254	7.05	10.09	48.79	2.71	10.14
Mahamaya*IC0491254	10.30	11.45	80.89	4.68	19.09
Mahamaya*IC0496940	11.05	11.79	87.97	5.17	21.36
IGKV R 1244*IC0491194	7.87	9.10	74.66	3.77	14.00
IGKV R 1244*IC0558317	9.56	10.47	83.26	4.48	17.96
Effective tillers per plant					

Rajeshwari *IC0496940	23.67	28.09	70.99	2.64	41.08
Rajeshwari *IC0491254	42.95	44.95	91.27	7.20	84.52
Mahamaya*IC0491254	34.31	38.15	80.84	4.45	63.54
Mahamaya*IC0496940	29.57	33.57	77.59	3.25	53.65
IGKV R 1244*IC0491194	29.42	32.93	79.85	4.14	54.16
IGKV R 1244*IC0558317	36.95	39.45	87.72	4.91	71.29

Crosses	GCV	PCV	h <sup>2</sup>	G.A	G.A %
<b>Total tillers per plant</b>					
Rajeshwari *IC0496940	19.27	25.11	58.85	2.19	30.45
Rajeshwari *IC0491254	40.26	42.23	90.9	7.90	79.07
Mahamaya*IC0491254	22.37	27.85	64.52	3.16	37.01
Mahamaya*IC0496940	28.17	30.29	86.46	4.06	53.95
IGKV R 1244*IC0491194	24.62	28.79	73.16	3.69	43.39
IGKV R 1244*IC0558317	28.84	32.18	80.33	4.33	53.26
<b>Number of filled grains per panicle</b>					
Rajeshwari *IC0496940	19.07	20.10	90.00	54.88	37.27
Rajeshwari *IC0491254	24.24	24.87	95.00	60.00	48.68
Mahamaya*IC0491254	20.78	21.19	96.10	54.78	41.97
Mahamaya*IC0496940	12.64	13.35	89.50	29.46	24.63
IGKV R 1244*IC0491194	11.58	13.09	78.30	31.37	21.11
IGKV R 1244*IC0558317	7.07	8.05	77.10	18.82	12.79
<b>Number of unfilled grains per panicle</b>					
Rajeshwari *IC0496940	5.31	24.24	4.80	0.59	2.40
Rajeshwari *IC0491254	12.66	18.23	48.30	4.12	18.12
Mahamaya*IC0491254	5.15	16.05	10.30	0.76	3.41
Mahamaya*IC0496940	16.94	20.73	66.80	7.76	28.52
IGKV R 1244*IC0491194	16.43	24.01	46.80	4.97	23.15
IGKV R 1244*IC0558317	14.38	24.40	34.80	3.77	17.47
<b>Spikelet fertility (%)</b>					
Rajeshwari *IC0496940	4.96	10.93	20.60	3.79	4.63
Rajeshwari *IC0491254	6.77	7.41	83.50	10.64	12.74
Mahamaya*IC0491254	2.27	2.91	61.00	3.11	3.65
Mahamaya*IC0496940	3.99	4.75	70.50	5.62	6.90
IGKV R 1244*IC0491194	3.25	3.99	66.40	4.76	5.46
IGKV R 1244*IC0558317	2.76	3.66	56.80	3.73	4.28

crosses	GCV	PCV	h <sup>2</sup>	G.A	G.A %
<b>Harvest index</b>					
Rajeshwari *IC0496940	14.02	17.36	65.30	9.74	23.34
Rajeshwari *IC0491254	13.46	18.65	52.00	8.88	20.00
Mahamaya*IC0491254	18.77	21.56	75.80	15.17	33.67
Mahamaya*IC0496940	26.61	31.96	69.30	18.47	45.64
IGKV R 1244*IC0491194	19.34	21.39	81.70	16.33	36.02
IGKV R 1244*IC0558317	8.35	10.43	64.10	5.72	13.77
<b>Biological yield per plant (g)</b>					
Rajeshwari *IC0496940	23.32	23.88	95.30	23.43	46.90
Rajeshwari *IC0491254	39.64	39.88	98.80	51.54	81.15
Mahamaya*IC0491254	17.24	18.73	84.80	16.29	32.70
Mahamaya*IC0496940	37.01	37.81	95.80	38.28	74.63
IGKV R 1244*IC0491194	9.89	12.63	61.20	10.19	15.94
IGKV R 1244*IC0558317	18.99	19.16	98.20	27.91	38.76
<b>Seed yield per plant (g)</b>					
Rajeshwari *IC0496940	24.19	25.98	86.70	9.57	46.41
Rajeshwari *IC0491254	44.88	46.13	94.70	25.51	89.95
Mahamaya*IC0491254	18.64	20.34	84.00	7.83	35.19
Mahamaya*IC0496940	41.85	44.12	90.00	16.53	81.77
IGKV R 1244*IC0491194	32.22	32.40	98.90	19.39	66.01
IGKV R 1244*IC0558317	24.80	25.59	93.90	14.92	49.50
<b>100 SW</b>					
Rajeshwari *IC0496940	11.21	11.29	98.50	0.72	22.91
Rajeshwari *IC0491254	21.39	21.43	99.60	1.37	43.98
Mahamaya*IC0491254	17.02	17.06	99.60	1.08	35.00
Mahamaya*IC0496940	15.59	15.62	99.60	1.04	32.06
IGKV R 1244*IC0491194	17.55	17.57	99.80	1.12	36.10
IGKV R 1244*IC0558317	7.26	7.31	98.70	0.47	14.85

## Conclusions

The present study explored the genetic variability, heritability, and genetic advance for various yield-related traits in different rice genotypes. The analysis revealed significant variations among the genotypes, indicating the existence of sufficient genetic variability. The phenotypic variation was greater than genotypic variation, implying the influence of environmental factors on trait expression. High heritability estimates and substantial genetic advances were observed for several traits, including days to 50% flowering, plant height, effective tillers per plant, filled grains per panicle, spikelet fertility, harvest index, biological yield, seed yield per plant, and 100-seed weight. These traits are likely controlled by both additive and non-additive gene actions, indicating their potential for selection and improvement through breeding efforts. The findings of this study can serve as a valuable resource for future rice breeding programs aimed at enhancing yield and quality characteristics.

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