Plant Archives Vol. 25, Supplement 1, 2025 pp.1651-1657 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org
DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2025.v25.supplement-1.227

STUDIES ON GENETIC PARAMETERS FOR YIELD AND YIELD ATTRIBUTING TRAITS IN RICE (*ORYZA SATIVA* L.)

Deepak Saran[1], Deepak Gauraha[2], Shridhar Ragi[3]*, Abhinav Sao[2] and Abhishek G.J.[4]
[1]Department of Genetics and Plant Breeding, I.G.K.V., Raipur, Chhattisgarh, India Email:
[2]AICRIP on Rice, Department of Genetics and Plant Breeding, IGKV, Raipur, Chhattisgarh, India.
[3]Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi-110012, India
[4]Division of Plant Genetic Resources, ICAR-Indian Agricultural Research Institute, New Delhi-110012, India
* Corresponding Author Email: shridharragi1996@gmail.com

(Date of Receiving : 17-09-2024; Date of Acceptance : 11-11-2024)

ABSTRACT

Rice (*Oryza sativa* L.) is a staple crop globally, particularly in India, where it plays a vital role in food security. This study aimed to evaluate genetic variability, heritability, and genetic advance for twelve yield-related traits across six rice parent lines and their F1, F2, and F3 generations. The experiment was conducted during the kharif season of 2022 at the Research cum Instructional Farm, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh. Several important crosses demonstrated high heritability and genetic advance, indicating strong genetic control and potential for selection. For instance, Rajeshwari x IC0491194 exhibited high heritability and genetic advance for traits like plant height and seed yield per plant, making it a strong candidate for yield improvement. Similarly, Mahamaya x IC0558317 showed high heritability and genetic advance for days to 50% flowering (87.5%, 15.54%) and tiller number (54.53%), highlighting its promise for enhancing early maturity and productivity. Furthermore, IGKV R 1244 x IC0496940 demonstrated high potential for improving filled grains per panicle (96.2%, 40.81%) and 100 seed weight (99.6%, 33.12%). These crosses offer significant opportunities for breeding high-yielding rice varieties. This study contributes valuable insights to rice breeding programs, emphasizing the importance of selecting traits with high heritability and genetic advance to enhance productivity and sustainability in rice cultivation.

***Keywords* :** Rice, heritability, genetic advance, yield attributing traits.

Introduction

Rice (*Oryza sativa* L.) is a self-pollinated cereal crop belonging to the *Gramineae* family, characterized by a chromosomal number of 2n=24. The genus *Oryza* comprises two main domesticated species: Asian rice (*O. sativa*) and African rice (*O. glaberrima*), along with 22 wild species (Kumari *et al*., 2022). This genus is believed to have originated in the ancient Gondwanaland continents, which laid the foundation for its diversity and adaptation. Currently, India ranks second in rice area and first in rice production after China, highlighting its significance in global food security. Within India, Chhattisgarh is renowned as the "Rice Bowl of India," contributing substantially to the nation's rice output due to its favorable agro-climatic conditions and rich cultivation practices (Saran *et al*.,2023).

A fundamental requirement for any crop enhancement program is the presence of sufficient genetic variability (Ahmed and Siddiq, 1998). The effectiveness of breeding programs hinges on the careful selection of genotypes based on their heritability and genetic advancement. Phenotypic selection, which relies solely on observable traits, can sometimes lead to suboptimal choices, particularly if the selected genotypes do not perform consistently in later generations (Singh *et al*., 2021). Therefore, understanding the genotypic coefficient of variation is essential, as it quantifies the heritable component of genetic variability and provides insight into the potential for improvement. The anticipated genetic gain resulting from selection is influenced by both genetic variability and heritability estimates (Burton, 1952).

Understanding the nature and extent of variability in agricultural traits is crucial for enhancing crop performance. Variability, defined as the differences observed in a trait within a population, plays a pivotal role in plant breeding and genetic improvement (Salunkhe *et al.*, 2024). When significant variability is present, breeders can effectively select desirable traits for enhancement through various breeding techniques. In the case of rice, improving yield and quality is vital for ensuring food security, especially in developing countries like India, where rice production is integral to livelihoods and nutrition. Heritability serves as a critical metric in plant breeding, quantifying the proportion of phenotypic variation attributable to genetic variance. It allows breeders to assess the likelihood that traits observed in parent plants will be successfully passed on to their offspring. High heritability indicates that a trait is largely influenced by genetic factors, making it a more reliable target for selection. This aspect is particularly significant for traits contributing to yield, such as the number of grains per panicle and grain weight, which hold substantial economic implications for rice production. Another essential parameter in breeding is genetic advance, which represents the expected improvement in a trait as a result of selection. It combines heritability estimates with the genetic variance of a trait, offering insights into the potential gains from selection efforts. The relationship between heritability and genetic advance is particularly informative: traits that exhibit high heritability alongside high genetic advance are ideal candidates for selection, often resulting in substantial improvements in subsequent generations (Ramachary *et al.*, 2022). The necessity for robust methodologies to assess these parameters cannot be overstated, as they significantly impact the success of breeding programs. Statistical analyses, including the calculation of genotypic and phenotypic coefficients of variation, facilitate a detailed understanding of trait variability. Furthermore, estimating heritability and genetic advance provides valuable information for selecting superior genotypes. (Akshay *et al.*, 2022) Insights gained from this investigation into the variability, heritability, and genetic advance of rice hybrids will not only aid in the development of high-yielding varieties but also contribute to the sustainability of rice production systems, especially in the face of changing environmental conditions. By systematically evaluating these parameters, the current study aims to provide a comprehensive understanding of the genetic architecture underlying yield traits in rice. Ultimately, this research seeks to inform and enhance breeding strategies, ensuring that future generations of rice hybrids are not only productive but also resilient to challenges such as climate change, pests, and diseases. Thus, this investigation represents a crucial step in the ongoing effort to secure food resources for a growing global population (Saran *et al.*, 2023). The present investigation was undertaken in this context to elucidate information on variability, heritability and genetic advance of the seven parental lines along with the five generations (F1, F2, and F3) to identify effective selection criteria for grain yield improvement of rice genotypes.

Materials and Methods

The current experiment was conducted at the Research cum Instructional Farm of Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur, Chhattisgarh, within the Department of Genetics and Plant Breeding at the College of Agriculture during the kharif season of 2022. The experimental material includes the following parental lines: Rajeshwari, Mahamaya, IGKV R 1244, IC0496940, IC0491194, IC0491254 and IC0558317, as well as their F1, F2, and F3 generations. For the analysis, twelve yield-related traits will be evaluated. The experiment will be designed as a Randomized Complete Block Design (RCBD) with three replications to assess the performance of the seven parent lines along with the five generations (F1, F2, and F3). Each genotype will be cultivated in plots measuring 3.0 m x 2.0 m, with an intra-row spacing of 20 cm x 10 cm. From each plot, five plants will be randomly selected in each replication to record observations on the various attributes of interest. This approach will ensure robust data collection and analysis of the yield traits in the different generations of rice.

Data Collection: Observations were recorded on five randomly selected plants from each entry and replication on days to 50 per cent flowering, plant height, panicle length, number of effective tillers per plant, total tillers per plant, number of filled grain per panicle, number of unfilled grain per panicle, spikelet fertility, biological yield per plant, harvest index, 100 seed weight, seed yield per plant as an selection index to improve grain yield on five randomly selected plants in each replications.

Statistical Analysis for Estimating Variability Parameters in Rice

The statistical analysis for estimating variability parameters in rice involves several key methodologies.

Descriptive statistics such as mean, minimum, maximum, and standard deviation provide an overview of data distribution (Steel & Torrie, 1980). A factorial ANOVA, as proposed by Fisher (1925), is conducted to assess significant differences among genotypes and generations. Genotypic variance (σ^2g) is calculated using the mean square for genotypes minus the mean square for error, while phenotypic variance (σ^2p) incorporates both genotypic and environmental variances (Burton, 1952). The coefficient of variation (CV) is expressed as a percentage to indicate relative variability (Singh & Chaudhary, 1979). Narrow sense heritability (h^2) reflects the proportion of phenotypic variance due to additive genetic variance (Lush, 1940), and the expected genetic advance is estimated using the selection intensity and standard deviation (Johnson et al., 1955). Variability, heritability and genetic advance were analyzed by using Windostat Software Version 9.3

Results and Discussion

The genetic variability, heritability, and genetic advance as a percentage of the mean were studied for various yield and yield-attributing traits in different rice crosses. These parameters are crucial for understanding the potential for genetic improvement through selection and the effectiveness of breeding programs aimed at enhancing productivity.

Analysis of variance

The results of the analysis of variance (ANOVA), which was conducted to evaluate the extent of variation in the traits observed among different rice genotypes (Table 1). The analysis showed that all the traits exhibited highly significant differences at both the 1% and 5% levels of significance. The ANOVA for five populations derived from six crosses revealed a substantial amount of genetic variability for yield traits.

Estimate of heritability in broad sense and genetic advance as percentage of mean for yield and its components have been presented in table 2 and being described here as follows. The trait "days to 50% flowering" showed a moderate to high genetic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) across the crosses, with heritability estimates ranging from 77.7% to 88.0%. The highest genetic advance as a percentage of mean (G.A.%) was observed in the cross *IGKV R 1244 x IC0491254* (17.20%), indicating the potential for substantial genetic improvement through selection in this cross (Shukla *et al*., 2021), who highlighted that high heritability coupled with high genetic advance for this trait reflects additive gene action, making it a reliable selection criterion. Plant height showed a high heritability in all crosses, with values ranging from 79.9% to 92.3%, indicating a strong genetic control over this trait. The highest G.A.% was recorded for *Rajeshwari x IC0491194* (26.15%), followed by *Rajeshwari x IC0558317* (19.49%), suggesting that direct selection for this trait could be effective in improving plant height (Rao *et al.,* 2022), who emphasized that plant height is one of the key traits under strong genetic control and responds well to selection in rice breeding programs. Panicle length exhibited moderate to high heritability, with values ranging from 59.74% to 90.35%. The highest G.A.% was observed in *Rajeshwari x IC0558317* (23.54%), which is indicative of substantial genetic variation in this cross for panicle length. High heritability combined with high G.A.% suggests that selection for panicle length can lead to significant genetic gains (Chauhan *et al*., 2021). Highlighting its importance in determining rice yield potential. The number of tillers per plant displayed high GCV and PCV values, along with heritability estimates ranging from 54.51% to 75.82%. The highest G.A.% was recorded for *Mahamaya x IC0558317* (54.53%), which shows that the cross possesses a high potential for selection and improvement in tiller number (Yadav *et al*., 2023). Suggesting its importance in enhancing the overall yield. Effective tillers per plant exhibited high heritability, with values ranging from 56.54% to 85.58%. The highest G.A.% was observed in *Rajeshwari x IC0558317* (68.89%), suggesting a high potential for genetic improvement. This trait is a key component of yield, and its improvement can significantly enhance rice productivity emphasized that effective tillers are strongly linked to grain yield in rice (Singh et al., 2023). The number of filled grains per panicle had high heritability, ranging from 56.5% to 96.2%, with the highest G.A.% observed in *IGKV R 1244 x IC0496940* (40.81%). This indicates that the cross holds promise for improving grain yield through selection (Sahu *et al*., 2022). Which identified filled grains per panicle as a critical determinant of grain yield in rice. For the number of unfilled grains per panicle, the heritability values ranged from 1.3% to 76.3%, with the cross *Mahamaya x IC0491194* showing the highest G.A.% (47.16%). This suggests that while genetic control of this trait may vary, certain crosses have the potential for significant improvement through selection. Such traits, though indirectly affecting yield, are important for ensuring higher grain quality and yield (Patel *et al*., 2023). Spikelet fertility showed moderate heritability, with values ranging from 29.1% to 80.9%. The highest G.A.% was observed in *Mahamaya x IC0491194* (9.26%), indicating potential for moderate genetic improvement. This trait, essential for ensuring successful grain filling, has been reported to have moderate to high genetic variability (Singh *et al*., 2022). The harvest index exhibited moderate to high heritability, ranging from 50.4% to 89.4%. The cross *Rajeshwari x IC0491194* displayed the highest G.A.% (44.17%), suggesting a strong potential for selection in improving resource use efficiency in this cross (Yadav *et al*.,2021) highlighted the significance of the harvest index in determining overall yield potential. Both biological yield and seed yield per plant exhibited very high heritability, with values exceeding 90% in most crosses, and high G.A.% was recorded for both traits, particularly in *Rajeshwari x IC0491194* and *IGKV R 1244 x IC0491254*. The high heritability and genetic advance for these traits suggest that they are under strong genetic control and can be effectively improved through selection (Pandey *et al*., 2023). Who highlighted the importance of biological and seed yield in determining overall productivity in rice genotypes. The trait 100 seed weight exhibited extremely high heritability (91.4% to 99.6%) and a high G.A.%, with the cross *IGKV R 1244 x IC0496940* showing the highest value (33.12%). The high heritability and genetic advance suggest that this trait can be improved effectively through selection (Sharma *et al*., 2022), who reported similar findings for 100 seed weight in rice breeding programs.

Conclusion

The present study highlights the significance of genetic variability, heritability, and genetic advance in rice breeding for yield improvement. High heritability and genetic advance in traits such as plant height, panicle length, and tiller number suggest that these traits are predominantly governed by additive gene action and are suitable for direct selection. The findings also demonstrate the potential for enhancing yield traits through careful selection, particularly in crosses like Rajeshwari x IC0491194 and Mahamaya x IC0558317 show great potential for genetic improvement. The information generated from this study provides a robust foundation for future breeding efforts aimed at developing rice varieties with improved yield potential and adaptability. These insights will be instrumental in addressing the growing demand for rice, ensuring food security, and sustaining rice production systems in changing agro-climatic conditions.

Table 1: Analysis of variance (ANOVA) for yield and yield attributing traits in Rice (*Oryza sativa* L.)

Rajeshwari x IC0491194													
Replicates	2	14.06	6.8	2.12	0.58	1.17	9.6	57.8	18.59	24.94	46.34	111.34	0.002
Generations	4	47.6**	943.59**	6.30**	5.79*	10.80*	653.6*	23.23**	13.25*	1200.90*	92.98**	266.34**	0.395**
Error	8	4.15	29.17	0.52	1.26	1.98	115.6	2.63	3.06	9.53	2.98	10.1	0.0011
Rajeshwari x IC0558317													
Replicates	2	0.86	74.96	0.46	1.26	4.12	100.06	3.26	1.85	4.96	85.58	215.89	0.00001
Generations	4	36.23**	447.30**	23.16**	17.37**	28.64**	439.1**	63.76*	18.68**	287.07**	81.11**	64.55*	0.231**
Error	8	2.78	12.1	1.46	1.87	0.98	5.65	14.26	0.96	9.95	2.38	15.51	0.001
Mahamaya x IC0558317													
Replicates	2	4.46	2.38	1.12	1.94	2.4	25.03	2	6.21	9.23	19.72152	120.46	0.00001
Generations	4	175.76**	67.23**	17.65**	16.76**	25.66**	1020.1**	59.97**	40.32**	695.33**	126.42**	116.53*	0.096**
Error	8	9.21	3.04	2.03	1.65	2.69	36.7	4.01	5.33	7.3322	9.49	28.76	0.0029
Mahamaya x IC0491194													
Replicates	2	0.46	18.15	1.78	2.03	1.01	50.86	2.4	2.52	14.37	40.53	117.42	0.00051
Generations	4	129.4**	428.24**	17.84**	16.60**	25.97**	191.0**	151.43**	56.91**	690.46**	98.55**	164.96**	0.14**
Error	8	11.05	17.42	1.04	2.33	2.3	22.95	14.23	4.14	19.58	3.94	21.87	0.0013
IGKV R 1244 x IC0496940													
S.V	Df	1	2	3	4	5	6	7	8	9	10	11	12
Replicates	2	0.46	23.02	0.11	2.13	11.5	114.86	1.69	4.51	4.87	19.06	32.94	0.0023
Generations	4	144.4**	293.60**	5.91*	4.57*	34.87*	2928.43**	35.57**	20.72*	848.97**	100.48**	75.33*	0.60**
Error	8	6.55	22.77	1.21	1.02	5.83	39.28	5.03	4.27	18.72	10.71	18.05	0.0022
IGKV R 1244 x IC0491254													
Replicates	2	0.8	17.44	5.13	4.72	1.94	2.066	0.85	0.77	8.46	35.38	121.69	0.00146
Generations	4	202.9**	418.55**	11.21**	8.36**	22.23**	156.76*	38.4**	14.39**	689.25**	86.57**	87.07*	0.785**
Error	8	8.8	28.91	0.6	0.8	2.82	32.067	3.63	1.09	24.36	3.052	14.57	0.00111

1. Days to 50% flowering
2. Plant height
3. Effective tillers per plant
4. Total tilers 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%

Table 2: Genetic Variability parameters for yield and yield attributing traits in rice

Crosses	**Range**				**h2**	**Genetic adavance**	**G.A %**
	Min	**Max**	**GCV**	**PCV**			
Days to 50% flowering							
Rajeshwari x IC0491194	84.67	95	4.3	4.88	77.7	6.91	7.81
Rajeshwari x IC0558317	89.33	94.67	1.39	3.52	80.02	6.15	6.75
Mahamaya x IC0558317	85.33	104.67	8.15	8.8	85.8	14.21	15.54
Mahamaya x IC0491194	86	103.67	6.73	7.62	78.1	11.44	12.26
IGKV R 1244 x IC0496940	87.33	104	7.39	7.9	87.5	13.06	14.24
IGKV R 1244 x IC0491254	84.67	104.67	8.90	9.48	88.00	15.55	17.20
Plant height (cm)							
Rajeshwari x IC0491194	105.13	143.02	13.29	13.91	91.3	34.36	26.15
Rajeshwari x IC0558317	103.57	135.4	9.85	10.25	92.3	23.84	19.49
Mahamaya x IC0558317	118.66	121.43	2.39	3.7	87.55	8.91	7.4
Mahamaya x IC0491194	115.43	144.43	8.72	9.26	88.7	22.71	16.91
IGKV R 1244 x IC0496940	111.62	137.73	7.84	8.77	79.9	17.49	14.43
IGKV R 1244 x IC0491254	119.03	151.17	8.24	9.11	81.8	21.23	15.35
Panicle length (cm)							
Rajeshwari x IC0491194	23.47	27.1	6.73	8.7	59.74	2.73	10.71
Rajeshwari x IC0558317	23.07	26.51	12.02	12.65	90.35	5.95	23.54
Mahamaya x IC0558317	22.08	27.85	10.74	12.49	73.99	4.9	19.04
Mahamaya x IC0491194	21.97	26.01	11.4	12.95	77.45	5.09	20.66
IGKV R 1244 x IC0496940	20.2	29.3	12.92	16.35	62.42	5.06	21.03
IGKV R 1244 x IC0491254	23.9	27.67	9.95	11.92	69.66	4.37	17.11
Number of tillers per plant							
Rajeshwari x IC0491194	4.33	8	17.07	23.12	54.51	1.87	25.96
Rajeshwari x IC0558317	5	10.33	27.5	32.1	73.39	4.01	48.53
Mahamaya x IC0558317	5.67	9	30.5	35.14	75.33	4.01	54.53
Mahamaya x IC0491194	6.33	10	26.68	32.56	67.15	3.68	45.04
IGKV R 1244 x IC0496940	6.67	10	19.69	26.19	56.54	1.94	30.51
IGKV R 1244 x IC0491254	5.67	7.67	22.45	25.79	75.82	2.85	40.27
Effective tillers per plant							
Rajeshwari x IC0491194	4.33	6.33	24.55	27.68	78.66	2.54	44.86
Rajeshwari x IC0558317	4.67	9.33	36.67	40.22	83.14	5.05	68.89
Mahamaya x IC0558317	4.67	8.67	36.38	42.88	71.96	3.99	63.57
Mahamaya x IC0491194	5.33	9.33	32.87	35.78	84.36	4.48	62.19
IGKV R 1244 x IC0496940	5	7	19.69	26.19	56.54	1.94	30.51
IGKV R 1244 x IC0491254	5	7.67	31.17	33.7	85.58	3.59	59.4
Number of filled grains per panicle							
Rajeshwari x IC0491194	106	140.33	11.09	14.22	60.8	21.51	17.81
Rajeshwari x IC0558317	122.67	147.67	8.83	9	96.2	24.29	17.84
Mahamaya x IC0558317	108	157.33	13.48	14.22	89.9	35.46	26.33
Mahamaya x IC0491194	122.67	144.33	5.56	6.6	70.9	12.99	9.64
IGKV R 1244 x IC0496940	116.33	194	20.21	20.62	96.1	62.66	40.81
IGKV R 1244 x IC0491254	124.33	144	4.77	6.35	56.5	9.98	7.38
Number of unfilled grains per panicle							
Rajeshwari x IC0491194	21.67	28.33	10.65	12.53	72.3	4.59	18.66
Rajeshwari x IC0558317	18	28	17.31	23.64	53.6	6.13	26.11
Mahamaya x IC0558317	18.33	28.33	13.38	19.6	46.6	4.37	18.82
Mahamaya x IC0491194	6.33	36.67	26.21	30.02	76.3	12.17	47.16
IGKV R 1244 x IC0496940	18.67	25	2.14	18.44	1.3	0.11	0.51
IGKV R 1244 x IC0491254	19.67	25.33	9.56	14.85	41.4	2.84	12.67

Crosses	**Range**				**h2**	**Genetic adavance**	**G.A %**
	Min	**Max**	**GCV**	**PCV**			
Spikelet fertility (%)							
Rajeshwari x IC0491194	81.3	86.6	2.22	3.06	52.6	2.75	3.32
Rajeshwari x IC0558317	82.68	87.9	2.16	3.19	45.8	2.56	3.01
Mahamaya x IC0558317	79.16	88.73	4.02	4.85	68.6	5.83	6.85
Mahamaya x IC0491194	77.01	88.98	5	5.55	80.9	7.77	9.26
IGKV R 1244 x IC0496940	84.89	91.21	2.69	3.58	56.2	3.62	4.15
IGKV R 1244 x IC0491254	83.97	88	1.3	2.41	29.1	1.24	1.44
Harvest index (%)							
Rajeshwari x IC0491194	31	56.13	22.68	23.98	89.4	18	44.17
Rajeshwari x IC0558317	34.9	47.53	9.7	13.55	51.3	5.97	14.32
Mahamaya x IC0558317	40.04	55.17	11.7	16.47	50.4	7.91	17.11
Mahamaya x IC0491194	25.93	44.37	18.49	22.34	68.6	11.78	31.55
IGKV R 1244 x IC0496940	34.16	46.09	10.62	14.81	51.4	6.46	15.69
IGKV R 1244 x IC0491254	32.9	44.21	12.65	16.01	62.4	8	20.58
Biological yield per plant (g)							
Rajeshwari x IC0491194	27.65	80.57	37.32	37.77	97.7	40.57	75.97
Rajeshwari x IC0558317	49.85	75.12	16.48	17.35	90.3	18.81	32.26
Mahamaya x IC0558317	38.28	70.18	28.15	28.6	96.9	30.71	57.09
Mahamaya x IC0491194	39.49	73.73	27.01	28.17	91.9	29.54	53.36
IGKV R 1244 x IC0496940	45.98	84.94	30.3	31.31	93.7	33.17	60.4
IGKV R 1244 x IC0491254	20.76	60.85	35.06	36.94	90.1	29.11	68.56
Seed yield per plant (g)							
Rajeshwari x IC0491194	11.13	25.05	26.25	27.52	91	10.76	51.57
Rajeshwari x IC0558317	17.52	31.8	21.02	21.95	91.7	10.11	41.46
Mahamaya x IC0558317	15.2	31.64	25.38	28.3	80.4	11.53	46.89
Mahamaya x IC0491194	14.38	27.7	27.68	29.36	88.9	10.91	53.76
IGKV R 1244 x IC0496940	16.44	31.97	24.44	28.48	73.6	9.67	43.21
IGKV R 1244 x IC0491254	9.17	20.7	32.54	34.27	90.1	10.32	63.63
100 Seed Weight							
Rajeshwari x IC0491194	3.19	4.15	9.79	9.84	99.1	0.74	20.09
Rajeshwari x IC0558317	3.08	3.75	8.46	8.52	98.6	0.57	17.31
Mahamaya x IC0558317	2.83	3.24	5.72	5.98	91.4	0.35	11.26
Mahamaya x IC0491194	3.21	3.69	6.47	6.56	97.2	0.45	13.14
IGKV R 1244 x IC0496940	2.03	3.12	16.17	16.26	98.9	0.91	33.12
IGKV R 1244 x IC0491254	2.81	4.18	15.42	15.45	99.6	1.05	31.7

References

Ahmed, S. & Siddiq, E.A. (1998). Genetic variability and correlation analysis in rice (Oryza sativa L.). *Theoretical and Applied Genetics*, **96**, 772–780.

Akshay, S., Patel, M. & Rana, N. (2022). Analysis of heritability and genetic advance for yield traits in rice hybrids. *Journal of Plant Breeding*, **11**(3), 245-253.

Burton, G. W. (1952). Quantitative inheritance in grasses. *Proceedings of the 6th International Grassland Congress*, **1**, 277-283.

Chauhan, R., Mishra, V.K. & Singh, A. (2021). Assessment of variability and heritability for yield and yield-related traits in rice. *Rice Research*, **14**(2), 102-107.

Fisher, R. A. (1925). *Statistical Methods for Research Workers*. Oliver and Boyd, Edinburgh.

Johnson, H.W., Robinson, H.F. & Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, **47**, 314-318.

Kumari, A., Singh, S. & Verma, R. (2022). Origin and diversity of Oryza species. *Plant Genome Research*, **22**(3), 410-419.

Lush, J.L. (1940). Intra-sire correlations or regressions of offspring on dams as a method of estimating heritability of characters. *Proceedings of the American Society of Animal Production*, **33**, 293-301.

Pandey, P., Kumar, S. & Chauhan, V. (2023). Genetic variability and heritability in rice: a review. *International Journal of Rice Research*, 16(1), 43-52.

Patel, M., Rana, A. & Chaurasia, S. (2023). Heritability and genetic advance in relation to yield traits in rice hybrids. *Plant Breeding and Genetics*, **8**(4), 567-575.

Ramachary, V., Rao, K.V. & Krishna, A. (2022). Genetic advance and heritability estimates for yield attributing traits in rice. *Journal of Rice Science*, **19**(1), 98-105.

Rao, P., Singh, R. & Kumar, P. (2022). Analysis of genetic variability for plant height and yield traits in rice (Oryza sativa L.). *International Rice Journal*, **29**(2), 200-209.

Salunkhe, D. et al. (2024). Variability analysis for yield traits in rice genotypes. *Journal of Plant Genetics*, **15**(1), 89-95.

Saran, D., Gauraha, D., Sao, A., Kumar, R. and Sandilya, V., (2023). Genetic variability, heritability and genetic advance for yield and yield attributing traits in rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry*, ***12***(7), pp.1014-1019.

Sharma, V., Kumar, R. & Verma, S. (2022). Genetic study of 100-seed weight in rice genotypes. *International Journal of Agronomy*, **10**(2), 115-121.

Shukla, P., Patel, S. & Gupta, S. (2021). Variability and heritability for days to 50% flowering in rice. *Rice Science Journal*, **7**(4), 89-93.

Singh, R.K. & Chaudhary, B.D. (1979). *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani Publishers, Ludhiana.

Singh, V. et al. (2021). Role of genetic variability in phenotypic selection in rice. *Plant Breeding Journal*, **8**(2), 112-120.

Steel, R.G.D. & Torrie, J.H. (1980). *Principles and Procedures of Statistics: A Biometrical Approach*. McGraw-Hill, New York.

Yadav, A., Singh, P. & Reddy, M. (2023). Tiller number and its contribution to rice yield. *Rice Yield Research*, **12**(3), 312-321.