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TRAIT-PRIORITIZED SELECTION USING GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE ESTIMATES IN AROMATIC RICE LANDRACES OF CENTRAL INDIA

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ABSTRACT

This study aimed to quantify genetic variability, broad-sense heritability, and expected selection response for yield, its components, and quality traits to inform breeding strategies. During *Kharif* 2024 at IGKV, Raipur, Chhattisgarh, 78 rice genotypes (with checks Badshahbhog Selection 1, Chhattisgarh Sugandhit bhog, and Tarunbhog Selection 1) were evaluated in an augmented block design with six blocks and observation recorded for Fifteen traits. Analysis of variance revealed significant genotypic differences for all 15 traits. Phenotypic coefficient of variation generally exceeded Genotypic coefficient of variation, indicating environmental influence on trait expression, yet several economically important traits showed high heritability coupled with high genetic advance as percent of mean, these included days to 50% flowering, plant height, effective tillers, panicle length, days to maturity, 100-seed weight, grain length, grain breadth, length/breadth ratio, head rice recovery, gel consistency, and amylose content. Several entries outperformed checks, with Tendsy and Sham jeera repeatedly identified as promising ideotypes.

Key words: Genetic variability, Heritability, Genetic advance, Aromatic rice, Additive gene action, Phenotypic selection

Introduction

Oryza sativa (2n=24), a member of the Graminae family and Oryzoidea subfamily, serves as the primary food crop for one-third of the global population and occupies nearly 20% of all cultivated land. It is cultivated over a vast geographical range under diverse cultural conditions. Asia, which houses more than half of the world's population, is the largest producer and consumer of rice. Annually, rice is sown on approximately 11% of the world's arable land, making it the second most cultivated crop after wheat. In the last 25 years, rice production has seen a twofold increase, largely due to advancements in technology, including high-yielding varieties and improved agricultural practices Byerlee (1996). Around 90% of the world's rice is grown in Asia and since Asian countries consume over 75% of the global rice supply, rice is vital for the region's food security. With the expected rise in population, the demand for rice is projected to increase further. For about 40% of the world's population, rice is the primary staple food. Most individuals who rely on rice as their main food source live in developing countries Dunna and Roy (2013). For 40% of the global population, it is the main source of calories. Given that over 90% of the world's rice is produced and consumed in Asia, its cultivation is crucial for food security in the region.

India contributes 51.26 million hectares to the global total area and 122.77 million tonnes to the overall production Anonymous (2025). In the 2024-25 period, Chhattisgarh contributes 3.89 million hectares and reported a yield of 3.00 Matric tonns Anonymous (2025). ranks as Uttar Pradesh the top rice-producing state, with

Telangana, West Bengal, and Punjab following.

In recent years, the demand for aromatic rice has surged rapidly in countries that both traditionally and non-traditionally cultivate rice. The taste and aroma of aromatic rice make it highly preferred. Its popularity has soared globally due to culinary innovations, health benefits, and its widespread availability.

To satisfy the rising demand, rice varieties with high yields must possess enhanced agronomic traits and be adaptable to various conditions. The task of selecting for yield is challenging for plant breeders because it is a complex polygenic trait with inherent characteristics Debsharma *et al.*, (2020). Genetic diversity, heritability and the capacity to incorporate preferred traits into new strains are crucial for enhancing rice. The success of breeding programs is significantly boosted by the high genetic variability present in current germplasm, facilitating the rapid development of new varieties Yared and Misteru (2016). Grain yield, a notably intricate trait, is affected by various factors, including the weight of 100 grains, panicle length, the count of grains per panicle, and the number of effective tillers per plant Asante *et al.*, (2019). For breeding programs, it is important to choose parents that exhibit a wide genetic diversity in the morphological and developmental traits previously mentioned, as these traits are influenced by various related morphological and developmental characteristics. The process of selecting suitable candidates and formulating a breeding strategy is significantly enhanced by having access to the previously mentioned information.

Variation serves as the cornerstone for selection, making lines essential to the base population of any crop, thereby ensuring a wide range of variation. Understanding the genetic variation that influences the inheritance of quantitative traits, such as yield and its components, is crucial for effective genetic enhancement. Before initiating any crop development project, it is necessary to conduct a comprehensive analysis of genetic variation and implement appropriate selection methods. Genetic parameters, including the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), are valuable for identifying the level of variability within a genotype. The calculated GCV was found to be less than the corresponding PCV, suggesting that environmental factors affect the expression of the traits examined Miller *et al.*, (1958). According to Falconer (1981), heritability serves as an effective measure for assessing how traits are passed from parents to their children. Heritability estimates offer valuable insights into the likelihood of a genetic trait being inherited by future generations. These estimates are instrumental for breeders in selecting parent organisms for agricultural development programs Rafi and Nath (2004). Despite the potential for high heritability, phenotypic selection may be compromised by environmental influences. Ogunbayo *et al.*, (2014) suggest that a more accurate prediction of selection gain can be achieved by combining heritability estimates with genetic advance, rather than relying solely on heritability. This investigation focuses on evaluating the genetic variation, heritability, and improvements in traits linked to rice yield. The outcomes could contribute to the development of rice genotypes that are tolerant to salt, which would be beneficial for future breeding programs Rashid *et al.*, (2017).

Material and Methods

The study was conducted during the *Kharif* season of 2024 at the Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur, Chhattisgarh. The research site is situated at a latitude of 21.1°N and a longitude of 81.3°E, with an altitude of 289.60 meters above the average sea level. The study involved 78 rice genotypes inclusive of three standard check varieties: Badshahbhog Selection 1, Chhattisgarh Sugandhit bhog, and Tarunbhog Selection 1. The experiment was organized using an Augmented block design across 6 blocks. Measurements of plant height, panicle length, effective tiller per plant, grain yield per plant, and the weight of 100 seeds were taken from five plants randomly selected in each replication. In contrast, the number of days required to reach 50 per cent flowering and maturity was recorded based on the plot at the relevant growth stages. Data were gathered for fifteen traits related to the growth and yield of rice.

The statistical analysis was conducted using the mean values calculated from the six blocks. The analysis of variance (ANOVA) was conducted on the obtained data appropriate for the Augmented randomized block design. This analysis was performed using Windostat 9.50

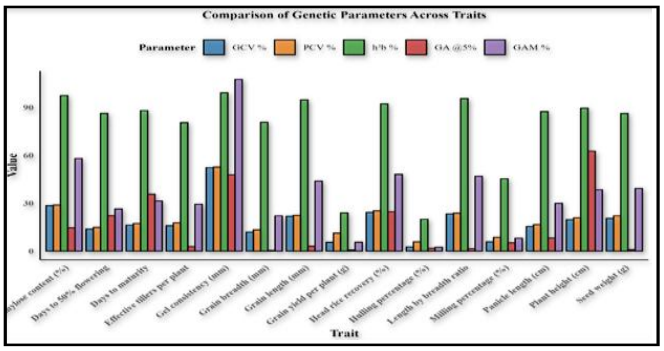


Fig. 1: Graphical representation of phenotypic and genotypic coefficient of variation for yield and its contributing traits.

Table 1: List of experimental material.

S.N.	Accession Name	S.N.	Accession Name	S.N.	Accession Name
1	Shukla phool	27	Antar ved	53	Dubraj
2	Kera ghul	28	Baas patri	54	Muni bhog
3	Ganga baru	29	Kundari	55	Amrit bhog
4	Samudra fen	30	Kher gul	56	Raja bhog
5	Tulsi prasad	31	Kadam phool	57	Sri kamal selection 1
6	Nawab bhog	32	Tulsi manjri	58	Khuddi selection 1
7	Katarni bhog	33	Chini kapur	59	Kankadiya selection 1
8	Jeera dhan	34	Chatri	60	Luchai
9	Kari gilas	35	Aatma sheetal	61	Dhaniya dhan
10	Elaichi	36	Sham jeera	62	Chirai nakkhi
11	Shital bhog	37	Shyam jeera	63	Ambikapur vishnu bhog
12	Samund chini	38	Kubri mohar	64	Chinour balaghat
13	Bhata phool	39	Jata shankar	65	Ambe mohar
14	Tendsy	40	Sri kamal	66	Jawa phool mutant 1
15	Lohandi	41	Til kasturi	67	Nagari dubraj mutant 1
16	Durjayi	42	Bang mooch	68	Trombay C.G. Dubraj mutant 1
17	Kali kamod	43	Lahsun bhog	69	Fundari
18	Kapur sar	44	Mai dubraj	70	Chaattisgarh Sugandhit bhog
19	Dubraj selection 1	45	Dhawra sawa	71	Chhattisgarh devbhog
20	Badshah bhog selection. 1	46	Lokti machi	72	RKM 1
21	Tarun bhog selection 1	47	Bhaisa puchi	73	Layacha
22	Vishnu bhog selection 1	48	Kasturi	74	Gathuwan
23	Bhata phool	49	Thakur bhog	75	Umari
24	Maharaji	50	Jauphool	76	Mokodo (m:550)
25	Chinouri	51	Ganga prasad	77	Mo:8 (aruna)
26	Jai gundi	52	Badshah bhog	78	Mo:19 (krishna jan)

software, as detailed by Indostat Services (2004). For each characteristic, parameters associated with variability, including range, mean, standard deviation, variance, and coefficient of variation, were assessed. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated using the method recommended by Burton (1953). According to the criteria set by Sivasubramanian and Madhavamenon (1973), the extent of variability was categorized as low at 20%. Heritability in the broad sense (h^2) was calculated as the ratio of genotypic variance to phenotypic variance, following the methodology proposed by Hanson *et al.*, (1956). This heritability was classified as low (60%) in accordance with the criteria established by Johnson *et al.*, (1955). Additionally, genetic advance and genetic advance as a percentage of the mean were assessed to determine the anticipated enhancement in traits through selection.

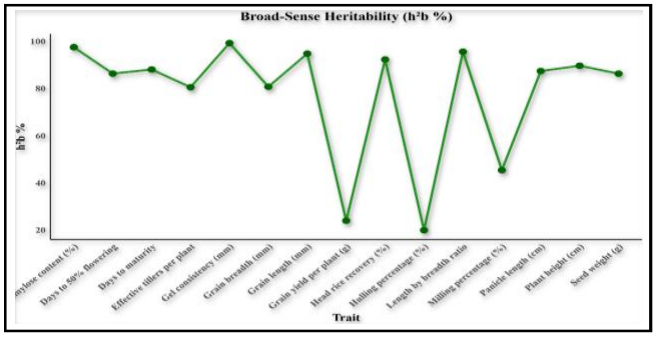


Fig. 2: Graphical representation of Broad sense heritability for yield and its contributing traits.

Results and Discussion

The augmented randomized block design (ARBD) experiment underwent a detailed assessment, which effectively captured both phenotypic and genotypic variability across 15 parameters. Through a thorough

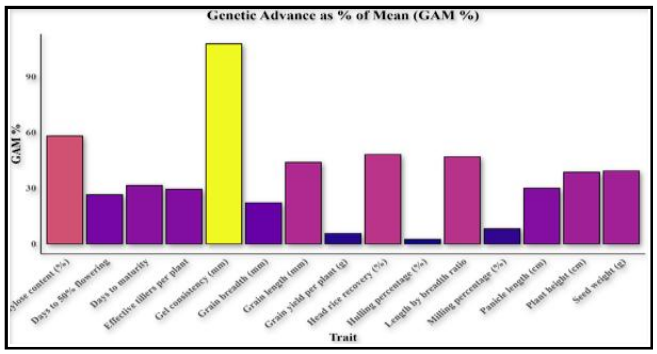


Fig. 3: Graphical representation of Genetic advance as mean for yield and its contributing traits.

Table 2: Analysis of variance of ten yield and yield attributing traits in rice.

Trait	Blocks	Checks	Genotypes	Error
Degree of freedom	5	2	77	10
Days to 50% flowering	136.42	176.72	156.12**	21.34
Plant height (cm)	648.42	666.97	1152.20**	119.37
Effective tillers per plant	1.32	2.38	2.99**	0.58
Panicle length (cm)	2.20	13.95	20.87**	2.62
Days to maturity	86.57	135.34	386.01**	46.11
Seed weight (g)	0.03	0.20	0.23**	0.03
Grain yield per plant(g)	4.70	3.91	2.43**	1.84
Grain length (mm)	0.83	0.57	2.56**	0.13
Grain breadth (mm)	0.01	0.06	0.07**	0.01
Length by breadth ratio	0.16	0.004	0.64**	0.02
Hulling percentage (%)	5.42	4.11	18.09**	14.48
Milling percentage (%)	12.75	9.54	31.59**	17.25
Head rice recovery (%)	25.64	104.23	168.68**	12.95
Gel consistency (mm)	1411.83	140.22	547.42**	4.05
Amylose content (%)	0.71	8.86	53.15**	1.31

variance analysis, significant genotypic differences were identified in all 15 traits, highlighting the diverse genetic backgrounds present in the germplasm. The experiment demonstrated strong precision, as indicated by the coefficient of variation (CV) values, which consistently ranged from 4.53% to 9.89%. Moreover, the careful separation of total variance allowed for a clear and statistically reliable distinction between inherent genetic effects and temporary environmental influences.

In the evaluation of various traits, several test entries consistently outperformed the standard check varieties in terms of average performance. By comparing individual genotypic results with the desired trait directions, we were able to clearly identify promising ideotypes. Among these, genotypes such as Tendsy and Sham jeera frequently stood out as top performers across multiple key parameters in this study. The broad range between the lowest and highest phenotypic expressions underscores the significant potential for selecting lines that meet specific agronomic requirements.

A detailed comparative study of genetic parameters demonstrates a range of heritability and potential genetic improvement across the evaluated spectrum. Traits that demonstrated both high broad-sense heritability (exceeding 60%) and significant genetic advance as a percentage of the mean (GAM over 20%)—including Days to 50% flowering, Plant height (cm), Effective tillers per plant, Panicle length (cm), Days to maturity, Seed weight (g), Grain length (mm), Grain breadth (mm), Length by breadth ratio, Head rice recovery (%), Gel consistency (mm), and Amylose content (%)—are mainly influenced by additive gene action. These findings align with previous studies by Kujur *et al.,* (2023) Due to their genetic makeup, genotypes exhibit a high level of sensitivity to direct phenotypic selection, which opens up significant possibilities for quick genetic advancements. The strong correlation typically found between phenotypic (PCV) and genotypic (GCV) variation coefficients in these important economic traits underscores the reliability of the phenotypic data collected and diminishes the influence of environmental factors.

Broad-sense heritability (h^2) was determined by dividing the genotypic variance by the phenotypic variance, following the formula outlined by Allard (1960). The categorization was based on Robinson *et al.,* (1949) criteria: low (0–30%), moderate (31–60%), and high (>60%). Genetic advance was assessed according to

Table 3: Assessment of genetic variability parameter for yield and yield components in rice (*Oryza sativa* L.).

Trait	Mean	Range		CV	PCV	GCV %	h^2b	GAM
		Min	Max	(%)	%	%	%	%
Days to 50% flowering	84.081	80.00	115.16	5.495	14.861	13.808	86.328	26.428
Plant height (cm)	162.715	94.000	230.00	6.715	20.861	19.751	89.640	38.522
Effective tillers per plant	9.758	6	13	7.824	17.741	15.922	80.550	29.438
Panicle length (cm)	27.490	19.22	34.2	5.898	16.618	15.537	87.405	29.922
Days to maturity	113.344	144.5	150	5.991	17.334	16.266	88.055	31.443
100 Seed weight (g)	2.210	1.14	3.85	8.175	22.086	20.517	86.298	39.263
Grain yield per plant (g)	13.739	10.8	17.10	9.895	11.348	5.556	23.971	5.604
Grain length (mm)	7.132	5.18	11.00	5.125	22.455	21.862	94.791	43.847
Grain breadth (mm)	2.117	1.78	2.90	5.823	13.274	11.929	80.756	22.083
Length by breadth ratio	3.383	2.2	4.70	4.995	23.799	23.269	95.595	46.866
Hulling percentage (%)	72.918	62.80	79.8	5.220	5.834	2.607	19.961	2.399
Milling percentage (%)	64.955	54.1	74.6	6.395	8.654	5.830	45.388	8.091
Head rice recovery (%)	51.364	34	72	7.006	25.286	24.296	92.322	48.090
Gel consistency (mm)	44.454	22	65	4.528	52.632	52.437	99.260	107.619
Amylose content (%)	25.226	19.48	26.32	4.551	28.900	28.540	97.520	58.058

Table 4: PCV and PCV for different traits under study.

Range	Low (<10%)	Moderate (10-20%)
Yield characters for PCV	-	Days to 50%, Plant height (cm), Effective tillers per, Panicle length (cm), Days to maturity, 100 Seed weight (g), Grain yield per plant, Grain length (mm), Grain breadth (mm), Length by breadth.
Yield characters for GCV	-	Days to 50%, Plant height (cm), Effective tillers per, Panicle length (cm), Days to maturity, 100 Seed weight (g), Grain yield per plant, Grain length (mm), Grain breadth (mm), Length by breadth.

Burton (1952). The highest heritability was found for Days to 50% (86.32%), Plant height (cm) (89.64%), Effective tillers per (80.55%), Panicle length (cm) (87.40%), Days to maturity (88.05%), 100 Seed weight (g) (86.29%), Grain length (mm) (94.79%), Grain breadth (mm) (80.75%), Length by breadth (95.59%), gel consistency (99.26 %) followed by amylose content (97.52 %). whereas the lowest heritability was found for grain yield per plant (23.37 %), hulling % (19.96 %), followed by grain yield per plant (23.37 %), milling % (45.38 %). These findings align with previous studies by Nath *et al.*, (2021) and Akshay *et al.*, (2022) for plant height as well as Pravallika *et al.*, (2023) and Gupta *et al.*, (2023) for panicle length and plant height and for effective tillers per plant.

The aromatic rice landraces and varieties showed a spectrum of genetic advances, expressed as a percentage of the mean, with values ranging from low to high according to the classification by Johnson *et al.*, (1955), which considers a genetic advance of 20% as low. This measure is vital for assessing the success of selection in improving traits within breeding programs. Among the yield-related traits studied, Plant height (cm) (38.522), Days to maturity (31.443), 100 Seed weight (g) (39.263), Grain length (mm) (43.847), and Length by breadth (46.866) exhibited significant potential for enhancement through direct selection due to their additive gene action. Moderate genetic advance (10-20%) was observed for several key agronomic traits, including Days to 50% (26.428), Effective tillers per (29.438), Panicle length (cm) (29.922), and Grain breadth (mm) (22.083). These findings align with previous studies by Noatia *et al.*, (2021). In contrast, traits with low genetic advance (<10%), such as Grain yield per plant (5.604), suggest a predominance of non-additive gene action, making them less responsive to traditional selection methods and more suitable for alternative breeding strategies like heterosis breeding to achieve genetic improvement. These findings are crucial for developing targeted breeding strategies based on the genetic architecture of different traits.

Conclusion

The analysis conducted in this study has successfully identified traits with high heritability and landraces that are particularly well-suited for focused crop enhancement. The performance of the genotypes such as Tendsy, kankadiya selection 1, Kali kamod, Chirai nakkhi, Nawab bhog, Chinouri and vishnubhog selection 1variety for various traits such as high yielding, shortest plant height, panicle length, 100 seed weight and number of effective tillers per plant, underscores its considerable potential for advancement into extensive, multi-environment stability trials or its direct application as a superior parental line in future hybridization programs. The results suggest that improving rice productivity can be effectively achieved by selecting traits that significantly contribute to yield and have favorable genetic parameters. Achieving consistent genetic gains in grain yield may require alternative breeding approaches, such as heterosis breeding and performance evaluation across various environments. Strategically applying these analytical insights will significantly accelerate the development and release of superior commercial cultivars.

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