



Study of Variability and Correlation for Yield Attributing and Grain Quality Characters in Aromatic Short Grain Rice

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

This study was conducted in kharif, 2023 at the Indian Institute of Rice Research, Hyderabad, it involved 42 breeding lines and 3 checks in an Augmented Randomized Block Design. This study evaluates genetic variability, heritability, and genetic advance as percent of mean were recorded for all the traits, that revealed high PCV (22.16%) and GCV (20.96%) were recorded by grain yield per plant. Significant variability was observed in traits such as plant height, grain yield per plant, and kernel length, while high heritability coupled with genetic advance as percent of mean were noted

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for traits like plant height (96.20%;25.44%) and grain yield (89.48%;40.91%), indicating these characters could be improved through selection. Correlation analysis revealed that grain yield per plant shows a positive association with days to 50% flowering, plant height, panicle length, number of productive tillers, 1000 grain weight, hulling percentage, head rice recovery, kernel L/B ratio and amylose content suggesting importance should be given to these characters, during selection for improving yield and quality traits of aromatic short grain rice.

Keywords: Aromatic short grain rice; grain quality; yield attributing; genetic variability.

1. INTRODUCTION

“Aromatic rice, known scientifically as *Oryza sativa* L., is a distinct group, prized for its aroma and flavor, making it highly esteemed for quality” [1]. While long-grain aromatic varieties dominate the global market and exports, most indigenous aromatic rice in India are of small to medium grain types, primarily grown for local consumption. Some of these smaller grain types exhibit exceptional aroma and desirable qualities such as elongation upon cooking and taste. These traits make them valuable candidates for enhancing the quality of high-yielding rice varieties.

Plant breeding involves managing and utilizing genetic variability. In crop improvement programs, selecting appropriate parents hinges on the extent of genetic variability within the crop. Assessing variability involves measuring genotypic and phenotypic coefficients of variation for specific traits. Heritability indicates the contribution of genetic factors to phenotype expression. Calculating genetic advance predicts expected genetic gains from selection within a population. Genetic variability is fundamental to any crop improvement program, as the extent of variability directly influences improvements in traits. Understanding the mode of inheritance, variability, and association studies is crucial for implementing effective selection programs aimed at identifying superior genotypes.

This study was conducted to investigate variability, genetic advance and character associations, in aromatic short grain rice genotypes. The aim was to identify effective selection criteria for enhancing both grain yield and quality in aromatic short grain rice varieties.

2. MATERIALS AND METHODS

The experiment was conducted during kharif season in the year 2023, at the Indian Institute of Rice Research, Hyderabad (T.G), India. Experimental material comprised of forty two

breeding lines and three standard check varieties (Shobhini, Sugandha samba and Dubraj) evaluated in Augmented Randomized Block Design with replications of checks in randomised manner in each block. The experimental field was divided into 7 blocks and each block was divided into 9 plots among these 9 plots 6 were used to accommodate test genotypes and 3 plots used to accommodate replicating checks (6 test genotypes along with 3 checks). “All the recommended package of practices was adopted throughout the crop growth period and need based plant protection measures were taken up to raise a healthy crop. Observations were recorded on five randomly selected plants for grain yield per plant; yield component traits, namely, days to 50 percent flowering, plant height, Number of productive tillers per plant, panicle length, grain yield per plant and test weight; and quality characters, namely, kernel length, kernel breadth, length/breadth ratio, hulling percent, milling percent, head rice recovery per cent, amylose content, volume expansion ratio, water uptake and grain type were recorded. However, days to 50 percent flowering were recorded on sample basis. Observations for test weight and all the quality traits studied were obtained from grain samples drawn from each plot in each genotype and check varieties using standard procedures” [2].

The methods employed included ANOVA as described by Panse and Sukhatme [3], PCV (Phenotypic Coefficient of Variation) and GCV (Genotypic Coefficient of Variation) following Burton [4], simple correlation analysis based on Johnson et al. [5], and statistical analysis conducted using R Studio and KAU grapes software for correlation studies.

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance

In the present investigation analysis of variance for yield and its contributing characteristics and quality traits revealed that sufficient variation was

present among the genotypes. The result of the analysis of variance for augmented design with respect to all 15 characters is presented in Table 1. The variation due to blocks was significant or highly significant for most of the characters under study except for days to 50 % flowering, hulling percentage and volume expansion ratio. The differences among the check varieties were also found to be significant or highly significant for all the characters under study except for grain yield per plant, kernel breadth, water uptake, volume expansion ratio and amylose content which showed non-significant. The analysis of variance for different characters in augmented design was done by the method given by Panse and Sukhatme [3].

3.2 Mean Performance

A wider range of variability was revealed for the traits of water uptake (201.67-355.00) followed by milling recovery (78.09-22.64), plant height (125.00-71.29), head rice recovery (70.79%-32.12%) and days to 50 % flowering (116.29-90.43). The results showed that these traits should be used as selection prospects to improve performance through a breeding procedure like selection and hybridization.

3.3 Genetic Variability

“The extent of variability for any character is very important for the improvement of a population through breeding. The estimates of genotypic variation, phenotypic variation, heritability and genetic advance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) for various characters have been presented in Table 2. The extent of influence of environment on any character indicates the magnitude of the difference between the genotypic and phenotypic coefficient of variation. Large difference reflects higher environmental influence while small difference reveals high genetic influence” [6]. “The magnitude of σ^2_p and σ^2_g was highest for the character water uptake (2079.04 and 1736.77) and lowest for the volume expansion ratio (0.08 and 0.02). The relative value of genotypic and phenotypic coefficient of variation provides important information on the magnitude of variation. Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) in all the studied characters it indicates that presence of environmental influence to some degree on the phenotypic expression of the character, but most of the phenotypic coefficient of variation was

contributed by the genotypic component, also good correspondence was observed between PCV and GCV for all the characters. The difference between PCV and GCV was less for the characters day to 50% flowering, plant height, milling percentage, head rice recovery percentage and amylose content” [2]. Phenotypic coefficient of variation ranged from 2.91 (days to 50% flowering) to 22.16 (Grain yield plant-1), while GCV ranges from 2.07 (days to 50% flowering) to 20.96 (Grain yield plant-1).

High PCV and GCV values (>20) were recorded by grain yield plant-1 (22.16 and 20.96). Similar findings of high GCV by Hossain et al. [7], Nirmaladevi et al. [8], Devi et al. [9] for grain yield per plant and Hemalatha et al. [10], Gayathridevi et al. [11] and Pradhan et al. [12] for grain yield per plant.

Moderate PCV and GCV values (>10% <20%) were recorded for a number of productive tillers (14.08 and 10.39), head rice recovery (14.96 and 14.85) and PCV for kernel length (10.05). These findings align with Nirmaladevi et al. [8] for kernel length, Devi et al. [9] for a number of productive tillers and Krishna et al. [13] for head rice recovery percent. This suggests moderate variability for these traits, which can be exploited for improvement through selection in advanced generations. The close correspondence between GCV and PCV values for most traits indicates minimal environmental influence, reflected in their high heritability values.

Low values of PCV and GCV (<10%) were observed for traits such as hulling percentage (3.04% and 2.32), panicle length (8% and 6.90%), volume expansion ratio (6.04% and 2.81%), kernel breadth (7.28 and 6.78), days to 50% flowering (2.91 and 2.07), and GCV for kernel length (9.04). Studies by Kole et al. [14], and Bhartiya et al. [15] also reported low PCV and GCV for days to 50% flowering and panicle length. Similarly, Nirmaladevi et al. [8] found low values for hulling percentage, Vanaja and Babu et al. [16] and Uma Devi et al. [17] observed low values for days to 50% flowering, Krishna et al. [13] found lower values for kernel length, kernel breadth and kernel L/B ratio, Hemalatha et al. [10] for days to 50% flowering and Kumar et al. [6] for panicle length and days to 50% flowering. Lower GCV and PCV suggest a narrow genetic base for these traits. Enhancing these traits may require hybridization or induced mutagenesis to broaden the genetic base, followed by pedigree selection in later generations.

Table 1. Analysis variance and mean sum of squares for different yield and quality traits

S. No	Characters	Mean sum of squares				
		Blocks (d.f=6)	Entries (d.f=44)	Genotypes(d.f=41)	Checks (d.f=2)	Error (d.f=12)
1	DFF	11.66	48.95**	8.90	321.48**	4.37
2	PH	214.57**	179.38**	136.40**	2485.90**	5.18
3	PL	3.63*	2.99**	2.99**	4.23*	0.77
4	NPT	2.66*	3.25**	1.79	15.27**	0.82
5	SPY	24.66**	19.55**	13.64**	3.40	1.43
6	TW	5.82**	8.60**	5.79**	7.69**	0.52
7	HULL	5.73	18.23**	5.77	282.73**	2.41
8	MILL	127.27**	421.41**	64.28**	1711.09**	1.32
9	HRR	48.33**	94.03**	67.66**	516.97**	0.98
10	KL	0.21*	1.12**	0.30**	12.31**	.06
11	KB	0.03**	0.02**	0.02**	0.00	0.00
12	LB	0.03**	0.38**	0.05**	3.84**	0.00
13	WU	2408.20**	3742.88**	2079.04**	846.43	342.26
14	VER	0.07	0.08	0.08	0.04	0.06
15	AC	6.55**	3.82**	3.86**	1.19	0.80

DFF: Days to 50% flowering, PH: Plant height, PL: Panicle length, NPT: no. of productive tillers, GYP: Grain yield per plant, TW: Test weight (1000 seed weight), HULL: Hulling recovery%, MILL: Milling recovery%, HRR: Head rice recovery%, KL: Kernel length, KB: Kernel breadth, L/B: Kernel length and breadth ratio, WU: Water uptake, VER: Volume expansion ratio, AC: Amylosecontent

Table 2. Variability studies for different yield attributing and grain quality traits in aromatic short grain rice cultivars

Parameters	Phenotypic Variance	Genotypic Variance	Environmental variance	GCV (%)	PCV (%)	ECV (%)	Heritability in broad sense (%)	Genetic Advance as % mean
DFF	8.90	4.54	4.37	2.07	2.91	2.04	50.95	3.06
PH	136.40	131.21	5.18	12.58	12.82	2.50	96.20	25.44
PL	2.99	2.22	0.77	6.90	8.00	4.06	74.28	12.26
NPT	1.79	0.98	0.82	10.39	14.08	9.50	54.47	15.82
GYP	13.64	12.20	1.43	20.96	22.16	7.19	89.48	40.91
TW	5.79	5.27	0.52	14.44	15.14	4.53	91.03	28.43
HULL	5.77	3.36	2.41	2.32	3.04	1.97	58.22	3.66
MILL	64.28	62.96	1.32	12.81	12.94	1.85	97.95	26.15
HRR	67.66	66.68	0.98	14.85	14.96	1.80	98.55	30.41
KL	0.30	0.24	0.06	9.04	10.05	4.39	80.92	16.77
KB	0.02	0.02	0.00	6.78	7.28	2.63	86.96	13.05
L / B	0.05	0.05	0.00	7.79	8.16	2.41	91.26	15.36
WU	2079.04	1736.77	342.26	15.41	16.86	6.84	83.54	29.06
VER	0.08	0.02	0.06	2.81	6.04	5.34	21.68	2.70
AC	3.86	3.06	0.80	7.10	7.98	3.63	79.33	13.05

DFF: Days to 50% flowering, PH: Plant height, PL: Panicle length, NPT: no. of productive tillers, GYP: Grain yield per plant, TW: Test weight (1000 seed weight), HULL: Hulling recovery%, MILL: Milling recovery%, HRR: Head rice recovery%, KL: Kernel length, KB: Kernel breadth, L/B: Kernel length and breadth ratio, WU: Water uptake, VER: Volume expansion ratio, AC: Amylose content

Table 3. Correlation coefficient for different yield attributing and quality traits in aromatic short grain rice cultivars

	DFF	PH	PL	NPT	GY	TW	Hull	Mill	HRR	KL	KB	L/B	WU	VER	AC
DFF	1	0.249	-0.338*	0.075	0.205	0.207	-0.205	-0.475***	-0.01	0.346*	-0.136	0.509***	0.113	-0.249	0.049
PH	0.249	1	0.4**	-0.161	0.079	0.251	-0.168	-0.288	-0.05	0.342*	0.248	0.202	0.032	0.088	-0.139
PL	-0.338*	0.4**	1	-0.19	0.173	-0.025	-0.137	-0.033	-0.08	-0.112	0.191	-0.176	0.099	0.13	0.086
NPT	0.075	-0.161	-0.19	1	0.011	0.001	0.323*	-0.088	-0.13	-0.064	-0.119	-0.028	-0.113	-0.128	0.174
GY	0.205	0.079	0.173	0.011	1	0.315*	0.091	-0.253	0.214	-0.021	-0.103	0.152	0.084	-0.099	0.191
TW	0.207	0.251	-0.025	0.001	0.315*	1	0.238	0.067	0.022	0.201	0.545***	-0.046	-0.023	0.243	-0.062
Hull	-0.205	-0.168	-0.137	0.323*	0.091	0.238	1	0.411**	0.154	-0.279	0.177	-0.41**	0.004	0.025	0.03
Mill	-0.475***	-0.288	-0.033	-0.088	-0.253	0.067	0.411**	1	0.155	-0.126	0.421**	-0.474***	-0.312*	0.3*	-0.116
HRR	-0.005	-0.053	-0.079	-0.134	0.214	0.022	0.154	0.155	1	0.203	-0.072	0.142	0.277	0.289	-0.223
KL	0.346*	0.342*	-0.112	-0.064	-0.021	0.201	-0.279	-0.126	0.203	1	0.095	0.564***	-0.004	0.229	0.008
KB	-0.136	0.248	0.191	-0.119	-0.103	0.545***	0.177	0.421**	-0.07	0.095	1	-0.516***	-0.216	0.345*	-0.114
L/B	0.509***	0.202	-0.176	-0.028	0.152	-0.046	-0.41**	-0.47***	0.142	0.564***	-0.516***	1	0.202	0.009	-0.02
WU	0.113	0.032	0.099	-0.113	0.084	-0.023	0.004	-0.312*	0.277	-0.004	-0.216	0.202	1	0.278	-0.159
VER	-0.249	0.088	0.13	-0.128	-0.099	0.243	0.025	0.3*	0.289	0.229	0.345*	0.009	0.278	1	-0.459**
AC	0.049	-0.139	0.086	0.174	0.191	-0.062	0.03	-0.116	-0.22	0.008	-0.114	-0.02	-0.159	-0.459**	1

DFF: Days to 50% flowering, PH: Plant height, PL: Panicle length, NPT: no. of productive tillers, GYP: Grain yield per plant, TW: Test weight (1000 seed weight), HULL: Hulling recovery%, MILL: Milling recovery%, HRR: Head rice recovery%, KL: Kernel length, KB: Kernel breadth, L/B: Kernel length and breadth ratio, WU: Water uptake, VER: Volume expansion ratio, AC: Amylose content

3.4 Heritability

Broad-sense heritability is valuable for selecting elite genotypes from homozygous lines, while narrow-sense heritability is more useful for segregating populations. Broad-sense heritability accounts for both fixable (additive) and non-fixable (dominant and epistatic) variances, offering insights into trait repeatability and aiding breeders in selecting elite genotypes from diverse populations. Heritability estimates for different traits ranged from 21.68% (volume expansion ratio) to 98.55% (head rice recovery%). High heritability suggests effective phenotypic selection but does not indicate the potential genetic progress, which is better assessed with genetic advance estimates, estimates above 70% are more useful for predicting genetic gain.

Heritability estimates were high for traits such as head rice recovery (98.55%), plant height (96.20%), test weight (91.03%), kernel length (80.92%), water uptake (83.54), panicle length (74.28%), grain yield per plant (89.48%), milling recovery (97.95%), kernel breadth and kernel L/B ratio. Conversely, traits like days to 50% flowering, number of productive tillers, hulling percentage and volume expansion ratio showed moderate to low heritability, suggesting the predominance of additive gene action and potential for improvement through selection. These findings are consistent with previous studies on head rice recovery, water uptake, test weight, kernel length, number of effective tillers and hulling recovery as reported by Hussain et al. [18], Nirmaladevi et al. [8], Singh et al. [19], Babu et al. [20], Srivastava et al. [21], Gupta et al. [22], Devi et al. [9] and Manjunatha et al. [2].

3.5 Genetic Advance

Genetic advance as percent of mean was high (>20) for 6 characters, plant height (25.44), grain yield plant-1 (40.91), test weight (28.43) head rice recovery (30.41), milling% (26.15) and water uptake (29.06), while moderate (10-20%) for number of productive tillers per plant (15.82), panicle length, kernel length, breadth, kernel L/B ratio and amylose content and low genetic advance as percent of mean was observed for days to 50% flowering, hulling% and volume expansion ratio.

Generally, traits with high heritability and high genetic advance are controlled by additive gene action [3] and can be improved through simple or

progeny selection methods. Selecting traits with high heritability and genetic advance will likely enhance the accumulation of additive genes and leads to further improvement in performance. The estimate of genetic advance provides a measure of the potential genetic progress achievable by selecting the best individuals.

Heritability estimates (above 70%) along with genetic advance (above 20%) would be helpful in predicting gain under selection than heritability estimates alone. In this study plant height (96.20 and 25.44), grain yield per plant (89.48 and 40.91), test weight (91.03 and 28.43) and water uptake (83.54 and 29.06) which indicate the preponderance of additive gene action such character could be improved through selection. These observations align well with those Nirmaladevi et al. [8] for test weight, Babu et al. [20] and Devi et al. [23] water uptake and plant height by Hossain et al. [7], plant height and a number of productive tillers by Sabesan et al. [24], high genetic advance and heritability for plant height was reported by Akinwale et al. [25] Gayathridevi et al. [11], Pradhan et al. [12] for grain yield per plant. Those characters panicle length, kernel length, kernel breadth, kernel L/B ratio and amylose content with high heritability with moderate or low genetic advance can be improved by intermating superior genotypes of segregating populations developed from combination breeding [26], similar findings were observed with Pratap et al. [27] for panicle length, kernel length, breadth, kernel L/B ratio and amylose content and Kumar et al. [6] for panicle length.

3.6 Correlation Studies

Correlations among yield, yield-contributing traits, and quality traits for 45 aromatic rice genotypes in are shown in Table 3. Grain yield per plant revealed a significant and positive association with 1000 seed weight (test weight) indicating 1000 grain weight has an important role in improving yield potential in rice, similar findings were given by Vanisree et al. [28] and Basavaraja et al. [29]. Positive correlations were observed between grain yield per plant and traits such as days to 50% flowering, plant height, number of productive tillers, test weight and hulling percentage. In contrast, head rice recovery, kernel length and length-to-breadth ratio negatively correlated with panicle length while head rice recovery, kernel L/B ratio and water uptake negatively correlated with kernel width as supported by Devi et al. [30] and Veni et

al. [31]. Positive significant results were obtained among kernel length and kernel L/B ratio; milling recovery with hulling recovery and plant height with panicle length, similar results were obtained by Singh et al. [32] and Russinga et al. [33] for panicle length.

4. CONCLUSION

This study reveals substantial genetic variability among rice genotypes, particularly in traits like grain yield per plant and water uptake, which show high heritability and genetic advance. These findings highlight significant opportunities for enhancing rice performance through targeted breeding. Conversely, traits with lower variability and heritability may require advanced breeding techniques. Overall, the results offer a solid foundation for strategic improvements, promising increased yield and quality in future rice cultivation efforts.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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