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Estimation of genetic variability, heritability and genetic advance in aromatic rice (O*ryza sativa* L.)

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ABSTRACT

The present investigation was conducted at Research Farm, VKSCoA, Dumraon, Buxar, Bihar, during the *kharif* 2022 - 23 to evaluate the gnetic variability, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), heritability and genetic advance in popular aromatic rice (*Oryza sativa* L.). Ten lines and five testers were crossed in a line x tester mating design to produce F_1 hybrids. Results revealed highly significant variations within parents and hybrids. All 16 characters showed high estimates of heritability coupled with high genetic advance as well as less than one average degree of dominance and a predictability ratio of less than one in F_1's. This indicated that the inheritance of maximum characters was governed by additive gene action and the direct selection for these characters would be rewarding

Keywords:*Aromatic Rice (Oryza sativa L.), ANOVA and Heritability*

Rice (*Oryza sativa* L., 2n=24) is a self-pollinated plant that is a member of the grass family Gramineae (Poaceae). There are 25 recognized species in the genus *Oryza*, of which 23 are wild and two are domesticated. *Oryza sativa*, also known as Asian rice, or *Oryza glaberrima*, sometimes known as African rice, is a type of grass. Rice (*Oryza sativa* L.) is the most important staple food crop of the world. Asia is the leader in rice production, accounting for about 90% of the world's production. India has become the world's largest producer of rice, surpassing China. India has the world's largest rice-growing area (51.4 million hectares), and production (150.18 million tonnes) (Anonymous-2025-26).

Aromatic rice is very popular in Asian countries and has recently gained wide acceptance in the USA, Europe, China, and South Africa. Aromatic rice occupies a prime position in Indian culture due to its high quality. The aroma in the rice is due to the presence of 2 acetyl 1 pyroline. India has nearly 300 indigenous collections of aromatic rice varieties (Singh 2016). These varieties fall under different types based on kernel length: small-grained (≤51 mm); medium-grained (5.51–6.60 mm); long-grained (6.61–7.51 mm); and very long-grained (>7.51 mm). In general, there are two types of aromatic rice: basmati and non-basmati types. Basmati is a premium-quality aromatic rice that is mainly cultivated for export purposes due to its huge demand in the international market.

The success of any breeding programme mainly depends on the quantum of genetic variability and the extent to which the desirable characters are heritable (Tiwari *et al*., 2011). Heritability and genetic advance are the direct selection parameters, so correct knowledge of heritability and genetic advance is much more essential in the formulation of a selection strategy.

MATERIAL AND METHODS

This experiment was carried out at the main experimental field of Veer Kunwar Singh College of Agriculture, Dumraon, Buxar, Bihar India. The experimental material was based on a line x tester set of 50 hybrids (F_1's) developed by crossing ten lines (females) with five testers (males). An attempt was made to make fifty cross-combinations during the *Kharif* season in 2022 to generate F_1's. The fifty F_1's along with parents and two checks, Rajendra Kasturi (12-15q/acre) and Badshah Bhog (15-20 q/acre) were evaluated to work out the correlation and path coefficient of Sixteen plant characters *viz*., days to 50% flowering, days to maturity, flag leaf area (cm), number of productive tillers/plant, plant height (cm),

Table 1. Analysis of variance for 16 characters of line × tester set of crosses (F_1s) and their parents in popular aromatic rice (*Oryza sativa* L.)

Characters	Sources of variation											
	Replications	Treatments	Parents	Parents (Line)	Parents (testers)	Line vs testers	Parents *vs* Crosses	Crosses	Lines Effect	Testers Effect	Lines × testers Effect	Error
d.f.	2	64	14	9	4	1	1	49	9	4	36	128
Days to 50% flowering	5.57	421.99**	521.15**	631.29**	168.40**	940.90**	4336.99**	313.75**	332.33**	1467.86**	180.88**	0.92
Days to maturity	1.24	403.99**	523.71**	600.65**	214.57**	1067.78**	4495.11**	286.29**	321.80**	1346.76**	159.59**	0.58
Flag leaf area (cm2)	6.29	47.95**	44.40**	39.34**	59.23**	30.61**	671.94**	36.23**	96.11**	73.93**	17.07**	1.36
No. Productive Tillers /plant	0.16	2.22**	2.11**	2.21**	0.43**	7.86**	28.10**	1.72**	0.98**	2.42**	1.83**	0.18
Plant height (cm)	33.61	674.29**	1350.93**	678.45**	293.04**	11634.69**	14465.45**	199.51**	574.68**	840.70**	34.47**	3.7
Panicle length (cm)	0.04	4.08**	8.91**	9.86**	1.32**	30.75**	22.78**	2.32**	4.55**	5.41**	1.42**	0.36
No of grains/panicle	1.2	1288.88**	482.01**	497.44**	499.90**	271.51**	8.42	1545.55**	1941.62**	9005.70**	617.62**	10.48
Test weight (g)	0.36	18.30**	22.77**	18.23**	19.95**	74.97**	77.86**	15.81**	55.91**	45.19**	2.52**	0.1
Kernel length (mm)	0.003	1.512**	2.524**	1.967**	2.655**	7.022**	0.004	1.253**	3.863**	4.521**	0.238**	0.005
Kernel breadth (mm)	0.003	0.132**	0.090**	0.047**	0.180**	0.122**	0.563**	0.135**	0.141**	0.434**	0.100**	0.001
L:B ratio	0.005	0.902**	1.535**	1.443**	1.879**	0.980**	2.622**	0.686**	1.410**	1.667**	0.396**	0.007
Aroma	0.03	3.01**	5.17**	2.62**	0.0002	48.81**	34.83**	1.74**	5.79**	1.98**	0.70**	0.01
Disease severity	1.41	5.05**	7.85**	8.35**	5.46**	12.85**	0.11	4.35**	18.01**	9.12**	0.41**	0.16
Biological yield /plant (g)	0.22	241.70**	185.52**	155.80**	77.53**	884.98**	1160.43**	239.00**	626.85**	493.48**	113.77**	7.59
Harvest index (%)	1.15	41.96**	25.60**	36.72**	6.33**	2.65	261.26**	42.15**	92.00***	103.99**	22.82**	1.03
Grain yield/plant (g)	1.2	75.38**	36.61**	33.73**	14.48**	151.09**	488.49**	78.03**	197.38**	206.03**	33.96**	1.27

** Significant at 1%

panicle length(cm), number of grains/panicle, test weight (g), kernel length (mm), kernel breadth (mm), l:b ratio, aroma, disease severity, biological yield/ plant (g), harvest-index (%) and grain yield/plant (g), in Randomized Complete Block Design with three replications during *kharif* 2023 to find out the genetic variability, heritability and genetic advance effects of their various attributes on grain yield. Phenotypic (PCV), genotypic (GCV) and environmental (ECV) coefficients of variation for different characters were estimated by formulaes suggested by Burton and de Vane (1953). The estimates of heritability (h_2 (ns)) have been classified by Robinson (1966) into three categories *viz.,* high (> 30%), medium (10-30%) and low (<10%).

RESULTS AND DISCUSSION

Analysis of Variance

The analysis of variance for different characters. The characters under study are presented in Table 1. Highly significant variability was found for all the characters in the present study. The analysis of variance revealed that the mean squares due to treatments and parents, were highly significant for all the characters in F_1s. The analysis of variance revealed that mean squares due to parents (tester) were highly significant for all the characters except non-significant variances for aroma in F_1s. Similar findings has also been reported by earlier researchers (Jayasudha *et al.,* 2009; Rahimi *et al.,* 2010; Sanghera and Hussain 2012; Latha *et al.,* 2013; Kargbo *et al.,* 2019; Sarker *et al.,* 2020 and Kulsum *et al.,* 2022). The analysis of variance revealed that mean squares due to parents *vs* crosses were highly significant for all the characters except non-significant variances for the number of grains/panicle, disease severity, and kernel length in F_1s. The results were supported by understudy (Rahimi *et al*., 2010; Sanghera *et al*., 2012; Bassuony *et al*., 2021; Mazal *et al*., 2021; Shrivastav *et al*., 2023; and Tewachew *et al*., 2024).

Estimation of PCV, GCV, Heritability and Genetic advance

The phenotypic (PCV) and genotypic (GCV) coefficients of variation for the 18 characters have been presented in Table 2. The magnitude of the phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all the traits. The high estimates of phenotypic and genotypic coefficient of variation (> 20%) were estimated for disease severity (PCV = 69.89%, GCV = 66.75%), aroma (PCV = 58.46 %, GCV = 58.16 %) and grain yield/ plant (PCV = 26.15 %, GCV = 25.51%) in F_1s. Similar results have also been reported by (Khedikar *et al.,* 2003; Saxena *et al.,* 2005; Singh and Singh, 2005; Dhanwani *et al.,* 2013;

Table 2. Estimates of general mean, phenotypic (PCV) and genotypic (GCV) coefficient of variation for 16 characters in aromatic rice(Oryza sativa L.)

S.No.	Characters	General Mean ± SE	Coefficient of Variation %	
			PCV	GCV
1	**Days to 50% flowering**	107.50 ± **SE** 0.799	10.95	10.91
2	**Days to maturity**	135.26 ± **SE** 0.65	8.51	8.49
3	**Flag leaf area (cm2)**	28.84 ± **SE** 0.96	14.19	13.59
4	**No. Productive Tillers /plant**	7.64 ± **SE** 0.36	12.08	10.63
5	**Plant height (cm)**	105.51 ± **SE** 1.57	14.65	14.53
6	**Panicle length (cm)**	23.58 ± **SE** 0.52	5.59	4.89
7	**No of grains/panicle**	135.45 ± **SE** 2.70	15.22	15.02
8	**Test weight (g)**	18.68 ± **SE** 0.26	13.36	13.26
9	**Kernel length (mm)**	5.38 ± **SE** 0.06	13.66	13.59
10	**Kernel breadth (mm)**	1.66 ± **SE** 0.03	12.59	12.44
11	**L:B ratio**	3.29 ± **SE** 0.07	17.2	17.03
12	**Aroma**	1.76 ± **SE** 0.09	58.46	58.16
13	**Disease severity**	1.91 ± **SE** 0.32	69.89	66.75
14	**Biological yield /plant (g)**	46.44 ± **SE** 2.22	19.84	18.96
15	**Harvest index (%)**	41.30 ± **SE** 0.82	9.19	8.86
16	**Grain yield/plant (g)**	19.39 ± **SE** 0.91	26.15	25.51

Table 3. Heritability and genetic advance in percent of mean, average degree of dominance and predictability ratio for 16 characters in aromatic rice (Oryza sativa L.)

characters	Heritability ($h^2_{(ns)}$ %)	Genetic advance in percent of mean	Average degree of dominance	Predictability ratio
			$\sqrt{\sigma^2 s/2\sigma^2 g}$	$2\sigma^2 g/(2\sigma^2 g+\sigma^2 s)$
Days to 50% flowering	3.13	22.4	3.91	0.061
Days to maturity	3.39	17.45	3.76	0.07
Flag leaf area (cm2)	4.35	26.82	3.09	0.09
No. Productive Tillers /plant	0.21	19.29	13.03	0.005
Plant height (cm)	14.8	29.71	1.45	0.32
Panicle length (cm)	2.14	8.81	3.92	0.06
No of grains/panicle	6.16	30.54	2.73	0.12
Test weight (g)	17.82	27.09	1.44	0.33
Kernel length (mm)	15.44	27.86	1.61	0.28
Kernel breadth (mm)	1.46	25.32	5.75	0.029
L:B ratio	3.09	34.71	3.94	0.06
Aroma	6.02	119.21	2.73	0.12
Disease severity	19.32	131.33	0.841	0.585
Biological yield /plant (g)	4.06	37.31	3.07	0.095
Harvest index (%)	3.48	17.61	3.61	0.071
Grain yield/plant (g)	5.08	51.28	2.89	0.1

Gyawali *et al.,* 2018; Hasan *et al.,* 2020; Chavan *et al.,* 2022).

The estimates of heritability and genetic advance in percent of mean have been presented in Table 3. High estimates of heritability were recorded for all sixteen characters in F_1s. The genetic advance in percent of mean was found to be very high (>30%) for disease severity (131.33%), aroma (119.21%), grain yield/plant (51.28%), biological yield/plant (37.31%), L:B ratio (34.71%) and number of grains/panicle (30.54%) in F_1s. Similar results were reported by earlier researchers (Kargbo *et al.*, 2019, Prasad *et al.,* 2017, Jaiswal *et al.,* 2020, Shrivastav *et al.* 2023 and Tewachew *et al* 2024).

The values of average degree of dominance were more than unity (>1) revealing over-dominance for fifteen characters except disease severity. The predictability ratio was less than one for all the characters studied in F_1s. The importance of additive gene effects of fixable nature for grain yield and most of the other yield components in the present study suggested that these traits are amenable to improvement through selection even in early generations. This indicated that considerable improvement in the status of grain yield and important yield attributes in rice can still be achieved by following conventional breeding procedures normally used in autogamous crops leading to the development of pure line varieties. The same finding have also been reported by earlier reporters (Awad-Allah *et al.,* 2016; Bassuony and Zsembeli 2021; Abo-Yousef *et al.,* 2022 Shrivastav *et al.* (2023) and Tewachew *et al* 2024).

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