

Genetic Variability, Heritability and Genetic Advance of Aromatic Rice for Yield and its Components

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ABSTRACT: The improvement of yield in aromatic rice is crucial not only to meet the growing demand for its flavorful nature but also to ensure an adequate supply for a population that appreciates its unique qualities. Enhancing both the yield and quality of aromatic rice will not only contribute to food security but also cater to the preferences of consumers seeking a delightful culinary experience. In this regard present investigation consists of 94 aromatic rice genotypes and the experiment was conducted during Sali2019 in Randomized Block Design with three replications. The data were recorded for 17 morphological characters to study genetic variability, heritability, genetic advance and varieties performance. On the basis of mean performance, high grain yield per plant were exhibited by the varieties IRRI 52 followed by Boga Maniki Modhuri Joha, Balum, Chakhow Poreton and Kon Joha-1, accordingly and the genotype Chakhow Poreton was resulted with high performance of grain yield per plant with early flowering followed by Chakhow Sempak, Krishna Joha, Kon Joha-2 and Bor Joha, correspondingly. The highest GCV and PCV were observed for no. of unfilled grain, grain yield per plant, and leaf aroma, indicating these characters could be used for crop improvement. High heritability and genetic advance were also observed for these traits, suggesting that additive gene effects are dominant and effective selection is possible. Our study would make a remarkable contribution towards the understanding of the extent of genetic diversity in indigenous aromatic rice along, along with identification of suitable genotypes to use in future breeding programs.

Keywords: Aromatic rice, Genetic variability, Heritability, Genetic advance, GCV and PCV.

INTRODUCTION

Rice (*Oryza sativa* L.) is an important cereal crop, providing sustenance for at least half of the world's population. About 70% of the world's population is fed by rice (FAO, 2009), and additional food is expected to be produced so that more than nine billion people can live on Earth by 2050. Globally, 755 million tonnes of rice are harvested annually, and this number is expected to increase (FAO, 2020). Earlier aromatic rice is considered as a special group of rice as group V by Glaszmann, (1987), but later Civan *et al.* (2015) found that fragrant rice was a result of a cross between *japonica* and *aus*, and they reasoned that the *tropical* and *temperate japonica* varieties were just later changes of the same crop suggesting that rice farming has a long history in many places aromatic rice has taken a special place because of their unique fragrance from ancient time. Aromatic rices were once called Basmati (bas = aroma), which is a well established fragrant rice variety with long, slender grains. Besides this, there are lots of small and medium grained non basmati locally adapted unique favored varieties which take extraordinary position in aromatic rice race. India, including North eastern region is considered as a home for locally adapted aromatic rice varieties. *Joha* is locally known non basmati aromatic rice type from Assam. Plant

breeding efforts will benefit greatly from better understanding the agro-morphology of aromatic rice germplasm. Numerous agro-morphological markers are used to characterize and study the variety of aromatic rice germplasm. Assam produces a wide variety of aromatic rice (*joha*), but not more is known about the agro morphological worth of any kind. Estimates of heritability combined with genetic improvement are typically more useful than heritability estimates alone for forecasting the gain under selection (Ghosh and Sharma, 2012). Therefore, utilizing future research estimations of rice improvement will depend heavily on estimates of GCV, PCV, heritability, and genetic progress. Keeping this in mind, we studied and examined total of seventeen yield-related agro-morphological parameters examined for ninety four aromatic rice genotypes here.

MATERIALS AND METHODS

The experimental material for the present study consisted of 94 aromatic rice varieties which studies were conducted during Sali Season 2019 at department of Plant Breeding and Genetics, Assam Agricultural University, Jorhat, Assam. The experimental material for the present investigation consisted of ninety four aromatic rice varieties which were obtained from Regional Agricultural Research Station, Titabar, Jorhat,

Assam and department of Plant Breeding and Genetics, Assam Agricultural University, Jorhat, Assam. The varieties are sown in a randomized block design with three replications with spacing of 30 × 20 cm. The nursery was raised on first week of June and transplanted after 30 days. Data were recorded on five randomly selected plants in each entry in each replications for the traits days to 50% flowering, Plant height (cm), effective tiller no., Panicle length (cm), number of filled grain, number of unfilled grain, total spikelet no., fertility percentage, grain length (mm), grain breadth (mm), LB ratio, grain length without husk (mm), grain breadth without husk (mm), dehusked LB ratio, thousand grain weight and grain yield per plant (g). The qualitative test for leaf aroma was done by using Sood and Siddiq (1978) technique of KOH sensory test. The data subjected to R software package to estimate Genetic coefficient of variation (%), phenotypic coefficient of variation (%), heritability (%) (broad sense) and genetic advance as percent of mean. The estimates for variability treated as per the categorization proposed by Sivasubramanian and Madhavamenon (1973), heritability and genetic advance as percent of mean estimates according to criteria proposed by Johnson *et al.* (1955).

RESULTS AND DISCUSSIONS

On the basis of mean performance, the genotype *IRRI 52* was recorded with high performance of grain yield per plant followed by *Boga ManikiModhuriJoha*, *Balum*, *ChakhowPoreton* and *Kon Joha-1*, accordingly. The genotype *ChakhowPoreton* was resulted with high performance of grain yield per plant with early flowering followed by *ChakhowSempak*, *Krishna Joha*, *Kon Joha-2* and *BorJoha*, correspondingly. These genotypes could be used in breeding program for development of high yielding varieties with early flowering.

A. Mean performance of yield attributing traits

In the present study, the analysis of variance showed that there were significant changes between varieties for all traits under study presented in Table 2. Mean performance of all the traits were presented at Table 3. Days to 50% flowering among the ninety four genotypes was ranged from 72 days to 114 days in with grand mean of 86.06. The genotype *Goal Poria Joha-2* showed least number of days (72 days) while *Chefa Sail* showed maximum number of days (114 days) to 50% flowering. Plant height was recorded at a range from 82.04 to 157.89 with a mean of 125.67. The genotype with highest plant height was *Monipuri Joha-3* (157.89 cm) and the genotype *KDM-105* (82.04) was recorded with lowest plant height. Effective tiller number was investigated at a range from 3.80 to 33.37 with a mean value of 7.88. The highest effective tiller number was observed for *Rampal Joha* (33.37) and the genotype *Rn-410* (3.80) was reported with lowest number of tillers. Genotypes were distinguished from each other in respect of panicle length with a mean value of 24.94 cm at a range from 20.1 to 28.74. The highest panicle length was recorded in *Monipuri Joha-3* (28.74) and lowest panicle length was found in *Joha-4 Borah et al.*, *Biological Forum – An International Journal* 15(5): 1516-1522(2023)

(20.91). Genotypes were differentiated from each other in respect of number of filled grain with a mean value of 127.47 at a range from 36.67 to 209.33. The highest number of filled grain was observed in *Maniki Modhuri Joha* (209.33) and the lowest number of filled grain was observed in *Chakhaw* (36.67). Genotypes were differentiated from each other in respect of number of unfilled grain at a range from 5 to 71 with a mean value of 19.90. The highest number of unfilled grain was observed in *Aki Sail* (71) and the lowest number of unfilled grain was observed in *LPK-119-1-1* (5). Total spikelet was reported at a range from 65.33 to 266.00 with a mean value of 147.38. The highest total spikelet number was observed in the genotype *Aki Sail* (266.00) and *Sali Joha* (65.33) was resulted with lowest in total spikelet number. The difference among the genotypes for fertility percentage was reported at a range from 54.44 to 96.88 with a mean percentage value of 85.77. The genotype with highest fertility percentage was observed in *LPK-119-1-1* (96.88) and *Bomma Dema* (54.44) was showed lowest fertility percentage. A significant difference among the genotypes for grain length was resulted at range of 4.00 to 10.00 with a mean value of 6.9 mm among the genotypes. The highest grain length (10.00) was reported in *Lakshmi Joha* and nine more genotypes and the lowest grain length (4.00) was observed in *Chini Sail* and one more genotype. The genotypes were distinguished for grain breadth at a range of 2.00 to 4.00 with a mean value of 2.8 mm among the genotypes. Highest grain breadth was noticed in *Goal Poria Joha-2* (4.00) and eighteen more genotypes and lowest grain breadth (2.00) was observed in *Kon Joha-4* and thirty five additional genotypes. Genotypes were distinguished from each other in terms of grain length to breadth ratio was observed at a range from 2.5 to with a mean value of 4.5. The maximum grain length to breadth ratio was found *Indrabhog*(4.5) and minimum (1.5) was observed *Chefa Sail* and three extra genotypes. A notable difference among the genotypes for grain length without husk was recorded at a range from 3.00 to 8.00 with a mean of 5.3. The highest grain length without husk was noticed in *Goal Poria Joha-2* (8.00) and fourteen supplementary genotypes and lowest in *Kon Joha-4* (3.00) including five more genotypes. Genotypes were distinguished from each other in terms of grain breadth without husk was observed at a range from 1.00 to 3.00 with a mean value of 1.9. The utmost grain breadth without husk was recorded for genotype *Kunkuni Joha-1* (3.00) with fourteen more genotypes and least was observed in *Goal PoriaJoha* (1.00) including twenty eight additional genotypes. A significant variation among the genotypes for dehusked length to breadth ratio was reported a range from 1.3 to 8.00 with a mean value of 3.1. The maximum dehusked length to breadth ratio was recorded for *Indrabhog* (8.00) and minimum was for *Barai Sail* (1.3). Aroma was detected by 1.7 per cent KOH as a sensory test. For aroma, among the 94 germplasm, 19 genotypes were detected for strong aroma including *KetekiJoha* and scored as 4; 31 for moderate aroma and scored as 3; 37 genotypes for low aroma which were scored as 2. The

remaining 7 genotypes were detected for no aroma or very low aroma and hence scored as 1. Sensory analysis of aroma revealed variation of in aroma profile on aromatic rice Genotypes were distinguished from each other in terms of thousand seed weight with mean value of 16.44 at a range from 6.60 to 30.23. The highest thousand seed weight was observed in *Monipuri Joha-3* (30.23) and lowest was in *Barai Sail* (6.60). A significant variation among the genotypes for grain yield per plant was reported at range from 1.96 to 22.91 with a mean value of 9.35. The maximum grain yield per plant was observed in *IRRI 52* (22.91) and minimum was observed in *Goal Poria Joha* (1.96).

B. Coefficient of variation

The mean, estimates of variation (i.e., the genetic coefficient of variation (%), the phenotypic coefficient of variation (%), the heritability (%) (in a broad sense), and the genetic advance (as a percent of the mean) are shown in (Tables 3 and 4). Among the characters, high estimates of GCV and PCV (>20%) were observed for the traits effective tillers number (GCV= 25.41% and PCV= 63.86%), number of filled grain (GCV= 32.83% and PCV= 33.31%), number of unfilled grain (GCV= 41.55% and PCV= 51.26%), total spikelet no. (GCV= 30.13% and PCV= 30.67%), grain length (GCV= 25.05% and PCV= 25.05%), grain breadth (GCV= 28.98% and PCV= 28.98%), length to breadth ratio (GCV= 22.72% and PCV= 22.72%), grain length without husk (GCV= 30.20% and PCV= 30.20%), grain breadth without husk (GCV= 37.95% and PCV= 37.96%), dehusked length to breadth ratio (GCV= 33.54% and PCV= 33.54%), leaf aroma (GCV= 41.10% and PCV= 41.10%), thousand seed weight (GCV= 33.38% and PCV= 33.70%) and grain yield per plant (GCV= 43.89% and PCV= 43.94%). This demonstrates that the sampled genotypes differ from one another genetically. These genotypes may be further enhanced by selective breeding with the purpose of enhancing these features. These results were in conformity with the findings of Aravind *et al.* (2022); Basu *et al.* (2022) for effective tillers number and number of unfilled grain; Saha *et al.* (2019); Ahmed *et al.* (2021); Snehith *et al.* (2022) for number of Filled Grain and number of unfilled grain; Roy *et al.* (2020); Snehith *et al.* (2022); Kumar *et al.* (2022) for effective tiller number and thousand grain weight; Paswan *et al.* (2014) for effective tiller number and length to breadth ratio; Singh *et al.* (2021), Russinga *et al.* (2020) for grain yield per plant, effective tiller number and number of filled grain; Rao *et al.* (2020) for effective tiller number, length to breadth ratio and thousand grain weight, Sudeepthi *et al.* (2020) for effective tiller number; Sabri *et al.* (2020) for grain yield per plant; Srilakshmi *et al.* (2018) for effective tillers number, number of filled grain and number of unfilled grain. Russinga *et al.* (2020); Singh *et al.* (2021); Rambabu *et al.* (2022) concluded with moderate GCV and PCV in grain length and grain breadth and high in length to breadth Ratio.

Moderate estimates of GCV and PCV was observed only in one morphological trait that is plant height (GCV= 11.14% and PCV= 13.41%) that indicates the genetic improvement through selection for this trait may not be always effective. Devicet *et al.* (2012), Srilakshmi *et al.* (2018); Tiwari *et al.* (2019); Sabri *et al.* (2020); Lipi *et al.* (2020); Sudeepthi *et al.* (2020); Rao *et al.* (2020); Pavankumar *et al.* (2022); Rambabu *et al.* (2022); Lingaiah *et al.* (2022); Kumar *et al.* (2022); observed moderate GCV and PCV for this characters.

C. Heritability and genetic advance

The present study found that h^2 broad sense estimates were high (>60%) and that heritability estimates were high for most of the characters, suggesting that phenotypic values would be optimal for selection. However, the selection is most efficient when high estimates of heritability are combined with high levels of genetic progress. High heritability coupled with high genetic advance as per cent of mean was recorded for the characters, number of filled grain ($h^2 = 97.1\%$; G.A.= 66.64%), number of unfilled grain ($h^2 = 93.4\%$; G.A.= 98.66%), total spikelet ($h^2 = 96.5\%$; G.A.= 60.96%), grain length ($h^2 = 99.8\%$; G.A.= 51.60%), grain breadth ($h^2 = 99.2\%$; G.A.= 59.70%), LB ratio ($h^2 = 99.1\%$; G.A.= 46.79%), grain length without husk ($h^2 = 99.3\%$; G.A.= 62.21%), grain breadth without husk ($h^2 = 99.5\%$; G.A.= 78.17%), dehusked LB ratio ($h^2 = 99.6\%$; G.A.= 69.07%), leaf aroma ($h^2 = 99.4\%$; G.A.= 84.66%), thousand grain weight ($h^2 = 98.1\%$; G.A.= 68.10%) and grain yield per ($h^2 = 99.7\%$; G.A.= 90.31%) (Table 4). These characteristics are highly responsive to selection because they are not influenced by environmental factors, demonstrating the prevalence of additive gene effects in their expression. These results were conformity with Kumar *et al.* (2022) for thousand grain weight (g) and grain yield per plant; Saha *et al.* (2019); Ahmed *et al.* (2021) for number of filled grain, number of unfilled grain and total spikelet; Sowjanya *et al.* (2021) for thousand grain weight (g), grain yield per plant, grain length, grain breadth and LB ratio; Islam *et al.* (2015) for number of filled grain, grain length, grain breadth and thousand grain weight (g); Russinga *et al.* (2020) for number of filled grain, total spikelet, grain length, grain breadth and LB ratio; Sowjanya *et al.* (2021) for grain length without husk, grain breadth without husk. High heritability coupled with moderate genetic advance found for the days to 50 % flowering ($h^2 = 99.00\%$; G.A. = 14.73%), plant height ($h^2 = 68.9\%$; G.A. = 19.05%), panicle Length ($h^2 = 98.4\%$; G.A.= 66.64%) and spikelet fertility percentage ($h^2 = 96.4\%$; G.A.= 18.02%). High heritability and moderate genetic advance indicating that both additive and non-additive gene effects were involved in the genetic control. Similar kind of result observed by Saha *et al.* (2019), Kumar *et al.* (2022) for days to 50% flowering; Sumanth *et al.* (2017) for days to 50% flowering, plant height, panicle length; Debsharma *et al.* (2023) for plant height and fertility percentage.

Table 1: List of Aromatic rice genotypes under study.

Sr. No.	Name of the genotype	Sr. No.	Name of the genotype
1.	<i>Joha-1</i>	48.	<i>Kunkuni Joha-2</i>
2.	<i>Joha-2</i>	49.	<i>KonowJoha</i>
3.	<i>MonipuriJoha</i>	50.	<i>KonbogiJoha</i>
4.	<i>Joha-3</i>	51.	<i>Kalijira</i>
5.	<i>Kola Joha-3</i>	52.	<i>KhorikaJoha</i>
6.	<i>SaliJoha</i>	53.	<i>Krishna Joha</i>
7.	<i>Kunkuni Joha-1</i>	54.	<i>KotariBhog</i>
8.	<i>Monipuri Joha-1</i>	55.	<i>Kamini Joha</i>
9.	<i>Monipuri Joha-2</i>	56.	<i>ManikiModhuriJoha</i>
10.	<i>Joha-4</i>	57.	<i>Monipuri Joha-3</i>
11.	<i>Kola Joha-4</i>	58.	<i>Nepali Joha</i>
12.	<i>Tulsi Joha-1</i>	59.	<i>Ronga Joha-1</i>
13.	<i>Kon Joha</i>	60.	<i>Ronga Joha-2</i>
14.	<i>Lakshmi Joha</i>	61.	<i>Rampal Joha</i>
15.	<i>Bengoli Joha-1</i>	62.	<i>Tulsi Joha-2</i>
16.	<i>KetekiJoha</i>	63.	<i>Tulsi Joha-3</i>
17.	<i>Goal PoriaJoha</i>	64.	<i>Joha-6</i>
18.	<i>KarticaJoha</i>	65.	<i>Kdm-105</i>
19.	<i>ChakhowPoreton</i>	66.	<i>Basmati</i>
20.	<i>ChakhowSempak</i>	67.	<i>Joha-7</i>
21.	<i>PhouremMuloi</i>	68.	<i>Iet-23193</i>
22.	<i>Chakhaw</i>	69.	<i>Joha Sail</i>
23.	<i>Konjoha-4</i>	70.	<i>Rn-410</i>
24.	<i>Arab Joha</i>	71.	<i>ProsadBhog</i>
25.	<i>Badsabhog</i>	72.	<i>Lpk-119-1-1</i>
26.	<i>Bengoli Joha-2</i>	73.	<i>Balum</i>
27.	<i>BhaboliJoha</i>	74.	<i>Gua Sail</i>
28.	<i>Boga Joha</i>	75.	<i>Chefa Sail</i>
29.	<i>Bhugri Joha</i>	76.	<i>Soul Pani</i>
30.	<i>BorJoha</i>	77.	<i>Nuon Sail</i>
31.	<i>BogiJoha</i>	78.	<i>BaiganBichi</i>
32.	<i>Boga ManikiModhuriJoha</i>	79.	<i>Bormula Sail</i>
33.	<i>Boga Tulsi</i>	80.	<i>Porbat Jira</i>
34.	<i>Bor Sal Joha</i>	81.	<i>Aki Sail</i>
35.	<i>CheniGuti</i>	82.	<i>Saya Mara</i>
36.	<i>Chubon</i>	83.	<i>Nunga Bain</i>
37.	<i>Goal Poria Joha-1</i>	84.	<i>Kati Sail</i>
38.	<i>Goal Poria Joha-2</i>	85.	<i>Agan Sail</i>
39.	<i>GovindaBhog</i>	86.	<i>Indrabhog</i>
40.	<i>Joha-5</i>	87.	<i>Bomma Dema</i>
41.	<i>Joha Bora</i>	88.	<i>Samudra Feria</i>
42.	<i>KoliJoha</i>	89.	<i>MorichuBhog</i>
43.	<i>Kon Joha-1</i>	90.	<i>Irri 52</i>
44.	<i>Kon Joha-2</i>	91.	<i>Chini Sail</i>
45.	<i>Kon Joha-3</i>	92.	<i>Barai Sail</i>
46.	<i>Kola Joha-1</i>	93.	<i>Bali Sail</i>
47.	<i>Kola Joha-2</i>	94.	<i>Cachar Sail</i>

Table 2: Mean square from analysis of variance for morphological traits in the rice genotypes.

Source of Variance	Degrees of Freedom	DTF	H	T	P	FG	UFG	TS	FP	GL	GB	LBR	GL WH	GBW H	DLB R	Aroma	TSW	GYP
Replication	2	0.057	169.848	12.547	0.235	1419.812	40.014	1900.535	0.533	0	0	0	0	0.0001	0.0002	0	0.994	0.051
Treatments	93	115.125**	675.904**	33.388**	6.942**	5306.290**	298.565**	5986.410**	177.319**	8.836**	1.994**	0.987**	7.650**	1.4819**	3.2598**	3.584**	90.946**	50.519**
Error	186	0.394	88.275	20.813	0.035	52.009	6.842	71.930	2.170	0	0	0	0	0.0001	0.0001	0	0.585	0.040

Table 4: Variability in morphological traits of 94 aromatic rice genotypes.

Sr. No.	Traits	Range		Mean	Coefficients of variation		Heritability % (B. S.)	Genetic advance
		from	to		G.C.V.	P.C.V.		
1.	DTF	72.00	114.00	86.06	7.19	7.22	0.99	14.73
2.	H	82.04	157.89	125.67	11.14	13.41	0.69	19.05
3.	T	3.80	33.37	7.89	25.97	63.43	0.16	21.90
4.	P	20.91	28.74	24.94	6.08	6.13	0.98	12.44
5.	FG	36.67	209.33	127.48	32.83	33.31	0.97	66.65
6.	UFG	5.00	71.00	19.90	49.55	51.27	0.93	98.66
7.	TS	65.33	266.00	147.38	30.13	30.67	0.96	60.96
8.	FP	54.44	96.88	85.77	8.91	9.07	0.96	18.02
9.	GL	4.00	10.00	6.85	25.05	25.05	0.99	51.60
10.	GB	2.00	6.00	2.81	28.98	28.98	0.99	59.70
11.	LBR	1.50	4.50	2.53	22.72	22.72	0.99	46.79
12.	GLWH	3.00	9.00	5.29	30.20	30.20	0.99	62.21
13.	GBWH	1.00	4.00	1.85	37.95	37.96	0.99	78.17
14.	DLBR	1.30	8.00	3.11	33.53	33.53	0.99	69.07
15.	AROMA	1.00	4.00	2.66	41.10	41.10	0.99	84.66
16.	TSW	6.60	30.23	16.44	33.38	33.70	0.98	68.10
17.	GYP	1.96	22.91	9.35	43.89	43.94	0.99	90.31

CONCLUSIONS

The study found that the traits most important for improving rice yield, namely number of filled grains, number of unfilled grains, total spikelet, grain length, grain breadth, LB ratio, grain length without husk, grain breadth without husk, dehusked LB ratio, leaf aroma, thousand grain weight, and grain yield per plant, all have high heritability and genetic advance. This means that these traits are largely determined by the additive effects of genes, and can therefore be improved through hybridization and selection. The high heritability and genetic advance for these traits is good news for rice breeders, as it means that they can make significant progress in improving rice yield through selective breeding. This is important as rice is a staple food for billions of people around the world, and increasing rice yield is essential to ensuring food security. The study also found that the traits leaf aroma and thousand grain weights had the highest heritability and genetic advance.

FUTURE SCOPE

This suggests that these traits may be particularly amenable to improvement through selective breeding. Overall, the study provides valuable insights into the genetic basis of rice yield, and will help rice breeders to develop more effective breeding programs.

Abbreviation used. DTF- Days to 50 % Flowering, H- Height, T- Effective tiller no., P- Panicle length, FG- No. of Filled Grain, UFG- No. of Unfilled Grain, TS- Total Spikelet no., FP- Fertility Percentage, GL- Grain Length, GB- Grain Breadth, LBR- Length Breadth Ratio, GLWH- Grain Length without Husk, GBWH- Grain Breadth without Husk, DLBR- Dehusked Length Breadth Ratio, TSW- Thousand Seed Weight, GYP- Grain Yield per Plant.

Author's Contribution. NB and PPB performed the field experiments and participated in manuscript writing. VVB and RNS analyzed statistical data and manuscript preparation. RNS and VVB corrected and edited the manuscript. RNS coordinated the works. All authors reviewed the manuscript.

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Conflict of Interest. None.

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