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Genetic diversity study in genotypes of aromatic rice (Oryza sativa L.)

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Abstract

The present study on "Genetic Diversity Study in Genotypes of Aromatic Rice" was carried out at the Agricultural Research Farm, Institute of Agricultural and Natural Sciences, Deen Dayal Upadhyaya Gorakhpur University, Gorakhpur, Uttar Pradesh. During the Kharif season of 2024. Twelve genotypes were grown in RBD with three replications and were analysed for morpho-physiological characters. A comprehensive evaluation of 12 aromatic rice genotypes revealed significant genetic variability across all traits studied, as confirmed by ANOVA. The narrow differences between phenotypic and genotypic coefficients of variation (PCV and GCV) suggest minimal environmental influence, particularly for traits such as days to flowering (DFF) and days to maturity (DTM), traits like yield per plant (YPP) showed greater environmental impact High broad-sense heritability coupled with substantial genetic advance as a percent of mean was recorded for several traits, including spikelet fertility% (SPF%), yield per plot(YPP), number of effective tillers(NET), plant height (PH), and kernel breadth (KB), indicating the potential for effective selection. Traits such as SPF%, yield (YP), and KB demonstrated high PCV, GCV, heritability, and genetic advance, underscoring their significance in breeding for yield improvement. Correlation analysis highlighted positive, significant associations of PH, flag leaf width (FLW), number of panicles per plant (NPPP), and several other traits with grain yield. Path coefficients analysis revealed that traits like DTM, flag leaf length (FLL), FLW, SPF%, kernel length (KL), and KB exerted positive and direct effects on grain yield, while traits such as DFF, PH, and PL had negative impacts.

Keywords: Aromatic rice, GCV, PCV, genetic advance, genetic diversity, heritability, correlation, path coefficient analysis

Introduction

Rice ($Oryza\ sativa\ L.$, 2n = 24) is a staple food for more than half of the world's population and plays vital role in global food security. India ranks as the second-largest rice producer, contributing 26% to global rice production after China (USDA, 2023) [14]. In different types of rice, aromatic rice stands out for its unique scent, high cooking quality, and premium market price. Basmati and other traditional short and medium grain aromatic rice varieties, which contain 2-acetyl-1-pyrroline (2AP), are well-known compound is responsible for their distinctive aroma (Kole et al., 2024) [5]. These variants are grown mainly in Uttar Pradesh, West Bengal, Assam, Odisha, and Bihar, where the climate supports their desirable symptoms. Despite High demand, traditional aromatic rice varieties have low yield potential, are vulnerable to market fluctuations, and take longer to grow. This situation encourages many farmers to switch to higher-yielding, non-aromatic types (Azam et al., 2023) [3]. India's aromatic rice, particularly Basmati, is crucial for agricultural exports. In 2022-23, India exported approximately 4.6 million tonnes of Basmati rice, value at over USD \$ 4.7 billion highlighting its significance in the global market. However, to sustain and grow this market, it is essential to develop high-yield, stress-tolerant aromatic rice varieties without Losing their quality. Genetic variability is necessary for any successful reproduction program. Traditional aromatic lenders are valuable sources of genes for grain quality, stress resistance, and adaptability. Nevertheless, many of these lenders are used and not well studied. Therefore, it is important to assess genetic diversity and understand the heredity of important symptoms, which is important for identifying promising genotypes (Anjali et al., 2022) [2].

Materials and Methods

The present study, "Genetic Diversity Study in Genotypes of Aromatic Rice", was conducted at the Agricultural Research Farm, Institute of Agricultural and Natural Sciences, Deen Dayal Upadhyaya Gorakhpur University, Gorakhpur, Uttar Pradesh. During the Kharif season of 2024. Twelve genotypes of aromatic rice from diversed sources were used (Birdpur Kalanamak, Kalanamak Kiran, Rajendra Kasturi, Pusa Sugandha-5, HUR 2.5, Pusa Narendra KN-1, Madhuraj-55, Pusa Basmati-1121, Pusa-1509, Keteki Joha, Gopal Bhog, KN-3). The experiment was conducted using randomized complete block design with three replications and analyzed for morpho-physiological traits. A detailed evaluation of these 12 aromatic rice genotypes revealed significant genetic variability across all traits examined, including days to 50% flowering (DFF), days to maturity (DM), plant height (PH), flag leaf length (FLL), flag leaf width (FLW), No. panicle length (PL), number of effective tillers (NET), number of grains per panicle (NGPP), spikelet fertility% (SPF%), kernel length (KL), kernel breadth (KB), test weight (TW), yield per plot (YPP), yield per plant (YP)Trait association analysis was performed using correlation and path analysis to understand the relationships between different traits and to explore the direct and indirect effects of various traits on yield and component quality components, respectively. Principal analysis was employed to identify similarities between variables, and a cross-breeding program was implemented to develop new varieties.

Results and Discussion

1. Mean performance of genotypes

Yield per plant (YP) was recorded highest in genotype Rajendra Kasturi and lowest in Gopal Bhog. The earliest fifty percent flowering and maturity was exhibited by the genotype Madhuraj-55 indicating the potential of this genotype to be used for developing short duration rice varieties. The highest and lowest mean performance for Number of effective tillers (NET) was shown by Ketki Joha and Pusa Sugandha-5 respectively. Since genotypes Pusa Sugandha-5 is having short stature, this can be exploited to breed for short plant types. Genotype Pusa Basmati-1121 had highest mean for Panicle Length (PL) indicating this can be used as a doner parent for high PL in further crossing programme. Highest Spikelet fertility (SF) was exhibited by Rajendra Kasturi. Genotype Gopal Bhog exhibited highest mean performance for 1000 GW. Kernel length (KL) was found maximum in genotype Pusa-1509. Whereas, highest Kernel breadth (KB) was exhibited by Madhuraj-55. These findings were similar to result obtained by Sharma et al. (2017) [9], Bisne et al. (2009) [4] and Singh et al. (2015) [10].

2. Analysis of Variance

For the 12 genotypes under research, statistical analysis was performed using a Randomized Block Design. The analysis of variance revealed significant genetic differences for all fourteen characteristics evaluated. The results are consistent

with those of Sumanth *et al.* (2017) [11] and Adjah *et al.* (2020) [1], and the analysis of variance across genotypes revealed significant differences for all yield and quality indicators evaluated.

3. Genetic variability, heritability and genetic advance.

From the current study, it is revealed that the traits like spikelet fertility, no. of effective bearing tillers, yield per plant and grains per panicle exhibiting high values of PCV and GCV coupled with high heritability and high genetic advance. Thus, it is highly recommended to select these traits to attain increased yield. Panicle length and test weight showed low values of GCV and PCV, but high heritability with low genetic advance, indicating that these traits are controlled by non-additive gene action and selection for such traits will not be rewarding. This observation aligns with finding by Kumar *et al.* (2020) [6] and Paramanik *et al.* (2024) [8] who also reported that high heritability coupled with high genetic advance indicates additive gene action, facilitating effective selection for yield-related traits in rice.

4. Correlation Coefficient analysis

Panicle length and kernel width showed positive non-significant correlation with grain yield whereas, days to 50% flowering and days to maturity showed negative highly significant correlation with yield. These findings were similar to result obtained by Singh *et al.* (2018) ^[12].

5. Path coefficient analysis

Path coefficient analysis revealed that days to 50% flowering, plant height, number of effective bearing tillers, no. of grains per panicle, spikelet fertility%, kernel length and kernel widths showed direct positive effect on yield. The trait like days to maturity, flag leaf length, flag leaf width, panicle length and test weight had a negative direct effect on yield. Highest positive indirect effect was exerted by days to maturity on grain yield through panicle length followed by flag leaf length via days to maturity, flag leaf width via days to maturity and test weight through days to maturity. Similarly, Mahalakshmi *et al.* (2024) [7] also found that days to 50% flowering, plant height and numbers of grains per panicle had positive direct effect on grain yield, while days to maturity and panicle length exhibited negative direct effects.

6. Genetic divergence using D² analysis

Selecting the best parents with high potential for economically important features is key to the success of any crop development project. This study benefited greatly from research on genetic diversity. This could be useful in recommending potential parents for crossing. Sundaram *et al.* (2000) [13] also endorsed the use of multivariate analysis to pick parents. They proposed that genotypes with a high degree of divergence within a cluster would produce better breeding materials for obtaining the greatest genetic advance in terms of product.

Table 1: Mean performance of genotypes for yield and quality traits.

S. No	Genotypes	DFF	DM	PH	FLL	FLW	PL	NET	NGPP	SPF	KL	KB	TW	YPP	YP
1	Birdpur Kalanamak	129.33	154.33	155.33	46	1.58	26.83	10.5	252.5	60.84	7.34	1.83	12.4	531.67	12.17
2	Kalanamak Kiran	126	150.33	118.55	31.33	1.25	26.83	10.5	222	68.1	7.71	1.79	14.1	748.33	10.14
3	Rajendra Kasturi	108.67	135	143.66	35	1.62	25.5	12	393	75.65	5.87	1.65	10.47	644.33	22.26
4	Pusa Sugandha-5	100.33	130.67	112.6	41.92	1.93	29.25	7	235.5	72.33	10.22	1.95	24.13	617	20.95
5	HUR 2.5	99	125.33	125.55	37.33	1.83	27.17	8	238.5	57.46	10.01	1.87	20.19	582.67	13.5
6	Pusa Narendra KN-1	123.67	148	124.33	29.83	1.55	23.17	11.5	192.5	58.75	8.06	1.75	16.61	429.67	9.47
7	Madhuraj-55	84.67	111.33	114.44	35.25	1.95	28.66	8.5	259	72.38	7.75	1.97	20.92	338.33	16.79
8	Pusa Basmati-1121	97.67	125.67	125.33	27.42	1.48	29.33	7.5	127.5	45.18	12.31	1.93	25.16	434.67	4.53
9	Pusa-1509	95.67	128	113.55	35.83	1.48	28.17	10	129	65.14	12.33	1.9	26.03	435.67	6
10	Keteki Joha	133.33	160.33	159.44	34.83	1.33	27	15	145	54.68	8.47	1.72	14.62	347.33	6.79
11	Gopal Bhog	130.67	161	174.33	33.83	1.25	24.67	14.5	243	42.36	5.78	1.61	28.27	274.33	3.82
12	KN-3	126.67	149.67	118.89	26	1.08	25.83	8.5	285	35.81	7.27	1.64	11.93	301.67	5.7

Table 2: Analysis of variance for Randomized Block Design for yield and quality traits in rice.

Source of	шэн	DFF	DM	PH	FLL	FLW PL	PL	NET	GPP	SPF	KL	KB	TW	YPP	YP
variation				(cm)	(cm)	(cm)	(cm)				(mm)	(mm)	(gm)	(gm)	(g)
Replication	2	89.19	108.03	320.94	0.208	0.016133	0.7105	7.722	1837.9	130.61	0.2685	0.000919	47.86	11186	44.68
Genotypes	11	866.03***	769.79***	1294.87**	96.147***	0.228843*	10.4295**	223.889**	16491.5**	486.75***	14.4284**	0.048247*	114.272**	67689***	118.419***
Error	22	0.38	2.6	161.15	15.335	0.026442	1.2453	32.944	400.3	76.98	0.0693	0.001837	33.042	5322	4.921

^{*, **} significant at 5% and 1% level, respectively

Table 3: Genetic variability parameters study in yield and quality characters

G 4	M	3.41	M	T 7 (-)	X 7 ()	Heritability	C.A.	C A 0/ - C	COV	DOM	
Genotypes	Mean	Min	Max	Var (g)	Var (p)	(%)	GA	GA% of mean	GCV	PCV	
DTF	112.97	84.67	133.33	288.5505	288.9268	99.87	34.97	30.95	15.04	15.046	
DM	139.97	111.33	161	255.7273	258.3308	98.99	32.776	23.42	11.4247	11.4828	
PH (cm)	132.17	112.6	174.33	377.9065	539.0592	70.1	33.53	25.37	14.7083	17.5667	
FLL (cm)	34.55	26	46	26.9372	42.2723	63.72	8.5348	24.71	15.0238	18.8205	
FLW (cm)	1.53	1.08	1.95	0.0675	0.0939	71.88	0.4538	29.74	17.0273	20.0829	
PL (cm)	26.87	23.17	29.33	3.0614	4.3067	71.08	3.0389	11.31	6.5129	7.7248	
NET	10.29	7	15	4.4924	5.6111	80.06	3.9068	44.79	24.3003	27.1579	
GPP	226.88	127.5	393	6.2854	7.7829	80.76	4.6412	44.67	24.1322	26.8535	
SP%	59.05	35.81	75.65	5363.75	5764.005	93.06	145.5371	64.13	32.2712	33.4536	
KL (mm)	8.59	5.78	12.33	136.589	213.5694	63.96	19.2537	32.6	19.7905	24.7468	
KB (mm)	1.8	1.61	1.97	4.7864	4.8557	98.57	4.4746	52.08	25.4653	25.6489	
TW(g)	18.74	10.47	28.27	0.0155	0.0173	89.6	0.2428	13.5	6.9214	7.3123	
YPP(g)	473.81	274.33	473.33	27.0766	60.119	45.04	7.1938	38.4	27.7737	41.385	
YP(g)	11.01	3.82	22.26	20848.78	26171.19	79.66	265.4827	56.03	30.4748	34.1438	

Conclusion

For each of the fourteen traits studied, there was a wide range of variation. ANOVA indicated significant differences between genotypes, indicating a high degree of variability for all parameters investigated; this suggests that there is plenty of room for selecting promising genotypes to further invigorate the breeding effort. For all the traits under study, the values of PCV were more than the GCV, but the differences were small, indicating the role of environment, but with less influence in the expression of these traits. Among the traits, difference between PCV and GCV values high for YPP and low for DFF and DTM. All of the traits in this study were classified as having a very high heritability (BS). Furthermore, for SPF%, YP, KB, EBT, GPP, YPP, DTF, FLW, PH, FLL, DM high heritability combined with high genetic advance as percent of mean of 5% was recorded, indicating effectiveness of selection for the improvement of these traits. According to the findings, traits such as SPF%, YP and KB had the highest PCV, GCV and high heritability and GAM. To increase yield, it is highly recommended that these traits should be chosen. The PH, FLW, NPPP, NET, PL, SPF, KL, NGPP and YPP all demonstrated positive highly significant correlations with grain yield. The DTF and DM were also found to be strongly associated with each other. According to the correlation studies, selecting genotypes with superior performance for the above-mentioned attributes can increase rice grain production. DM, FLL, FLW, NGPP, SPF%, KL, and KB all had a positive direct effect on grain yield. DFF, PH, PL, EBT and TW all had a negative direct effect on grain yield.

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