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Genetic variability and agro-morphological diversity analysis in aromatic rice genotypes of North Eastern India

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Abstract

The research work on variability and genetic diversity was conducted in thirty-two landraces of aromatic rice from various states of north eastern along with two national variety PD-1503 and Basmati 370 in the experimental field of Genetics and Plant Breeding, College of Agriculture, CAU, Imphal, during *Kharif,* 2021. Agro-morphological characters showed significant variations, starch content and crude protein content were non-significant. Phenotypic variance was higher than the corresponding genotypic variance. High genotypic and phenotypic coefficient of variation was observed for the characters such as grain yield per plant, number of grains per panicle, number of panicles per plant and length of leaf blade. Among quality parameters, crude fat content and crude protein content exhibit high genotypic and phenotypic coefficient of variation. High heritability coupled with high genetic advance was observed in number of panicles per plant, number of grains per panicle and crude fat content. The genotypes were grouped into four clusters following Tocher's method of clustering. Maximum genotypes *viz*., 27 genotypes fall in cluster I, while four genotypes fall in cluster II, cluster III has 2 genotypes whereas cluster IV has solitary genotype. Significant amount of variability and genetic diversity observed in the present investigation could be helpful in further improvement of the reported superior genotypes or selection of parents for further hybridization program.

Keywords: Aromatic rice, North east India, Variability. Diversity, Clusters.

INTRODUCTION

Rice is one of the most important cereal crops consumed by more than half of the world's population (Wakte *et al*., 2017). It is even referred to as "Global Grain" since it is being consumed by about 100 countries of the world as a staple food. A vast territorial land of India is inhabited by a great diversity of rice germplasm, among which a short slender aromatic rice cultivars are popular in different traditional rice growing regions (Kumari *et al*., 2018). Almost every region of the country in particular North East states has its own cultivar of aromatic rice that has special quality such as distinct aroma and beautiful colour that attract consumers and offer a great deal in marketing. The Indian aromatic rice, often called Basmati is a nature's gift to the sub-continent and human kind at large (Ahuja *et al*., 1995) and so far, a great emphasis is given only on the improvement of basmati types despite of the growing demand for aromatic rice in international market. The improvement of indigenous aromatic rice, which possess outstanding quality like aroma, cooking quality and taste can assist in supplying global demands. These indigenous aromatic rice genotypes are found to perform very well in its native areas and plays a crucial role in its culture and tradition. However, regarding the yield, the performance of these aromatic rice are not up to the mark as compared to non-aromatic rice due to its tall stature, weak stem that promote lodging and non- responsiveness to higher doses of fertilizers (Panwar *et al*., 1997; Oad *et al*., 2006). In addition to the yield which is utmost importance of rice cultivation, rice breeders of today are also focusing on improving the grain quality which plays an important role in global marketing since improvement in standard of living has increase the purchasing power for good quality rice. In particular, traditional aromatic rice already have promising quality such as pleasing scent, an important role in cultural system and thrive well in their native places and possessed good tolerant towards biotic and abiotic stress. So, incorporating other important agronomical traits will save time and efforts. Hence, development of high yielding good quality aromatic rice possibly fetches a higher income from domestic or international market.

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Broadening the genetic base is an essential requirement for aromatic rice improvement programme for both yield and grain quality. As variation being the basis of plant breeding, the success of any crop improvement programme relies in the extent of variability in the available genetic stock. Knowledge of genetic variability is a prerequisite for making appropriate breeding procedures in crop improvement programmes and the efficiency of selection largely depends on the value of heritability and genetic advance for the character, so high heritability coupled with high genetic advance will ensure the future success of selection (Karthikeyan *et al*., 2010). In addition, the Agro-morphological characterization of germplasm accessions is fundamental step in order to provide information of plants (Lin *et al*., 1991), both qualitative and quantitative traits have been commonly and traditionally used to estimate relationships between genotypes (Goodman, 1972). For the assessment of variation on multivariate scale, Mahalanobis D^2 statistics has been proved to be a powerful technique (Murty and Arunachalam, 1966). It provides a quantitative measure of association between geographic distribution and genetic diversity based on generalized distance (Mahalanobis, 1936). In the present investigation an attempt was made to classify the extent of genotypes for yield and yield attributes including quality traits in Aromatic rice for further use in hybridization programme. Further, the diverse array of our germplasm collection could be an opportunity for selecting parent material that can produce segregants with high genetic variability upon hybridization. So, keeping in mind the important of genetic variability and diversity studies and its application in breeding improved varieties, the knowledge of these genetic parameters value could help in selection of desirable genotypes from the current studies for further improvement.

MATERIALS AND METHODS

The present investigation was carried out with 34 native landraces type aromatic rice cultivars collected from various North east states viz: Manipur, Mizoram, Meghalaya, Tripura, Arunachal Pradesh, Nagaland and Sikkim including two national varieties Basmati 370 and PD-1503 during *kharif,* 2021. The experimental materials were laid down in plot of 42 x 10 m^2 area with 20 x 15 cm spacing using randomized block design with three replications. Observations were recorded on five randomly chosen plants of each genotype per replication for 10 agro-morphological traits and seven quality traits as per National guidelines (Rani *et al*., 2006), for DUS (Distinctiveness, Uniformity and Stability) test and Minimal Descriptors (for characterization and evaluation) of Agri-Horticultural Crops, National Bureau of Plant Genetic Resources (Mahajan and Sapra, 2000). Different grain quality parameters were evaluated by following standard method described by Chopra and Konwar (1976) for starch content, Juliano (1971) for amylose content, AOAC (1970) for crude fat content, Scales and Harrison (1920) for crude protein content and Little *et al*., 1958 for gelatinization temperature. Data analysis was done for each trait to estimate the genetic parameters such as variance, covariance, heritability and genetic advance as per Burton and Devane (1953), Burton (1951), Comstock *et al*., (1949) and Allard (1960). Mahalanobis (1936) D2 statistics was used for assessing genetic divergence among all genotypes. The clustering of D2 values was done by using Tocher's method, as discussed by Rao (1952). While the intra and inter cluster distances were calculated using the formula given by Singh and Choudhary (1985).

RESULTS AND DISCUSSION

From the analysis of variance (**Table 1**), the genotypes were found to express high significant differences for all the traits under study which implied the existence of high variation among the genotypes. This significance differences provides an ample scope for selection of different important yield and quality traits for aromatic rice improvement. The estimate of phenotypic coefficient of variation (PCV) was higher than their respective genotypic coefficient of variation (GCV) for all the traits under study indicating considerable influence of environment on the phenotypic expression of the genotypes (**Table 2**). High PCV and GCV coupled with high heritability and high genetic advance was observed for number of panicles per plant and number of grains per panicle. While moderate PCV and GCV coupled with high heritability and genetic advance was observed for plant height, panicle length, days to 50 % flowering and 1000 grains weight, thus showed the preponderance of additive type of gene action. Among quality traits, crude fat content showed high heritability and high genetic advance while amylose content showed high heritability with moderate genetic advance. It is therefore inferred that these characters can be successfully improved by selection because of the prevalence of additive gene action. Moderate PCV and GCV coupled with high heritability and low genetic advance was estimated for days to 80% maturity, hence improvement for such characters through selection alone would be very limited. However, these characters can be improved through hybridization, followed by selection. Gayathri and Padmalatha, (2018), Lakshmi *et al*. (2017), Osundare *et al*. (2017) and Ravindra Babu *et al*. (2012) also reported similar results in aromatic rice. Higher heritability with high to medium genetic advance were also reported for quality characters of other accession of rice (Karim *et al*., 2007; Karthikeyan *et al*., 2010; Nishant *et al*., 2017; Panwar *et al*., 1997; Ravindra Babu *et al*., 2012; Sarawgi and Bisne, 2007). Sahanab Nath and Kole (2021) reported high heritability for days to flowering, plant height and test weight.

A wide range of variation for all the agro-morphological characters were recorded for thirty-four accessions. The frequency distribution for aroma, gelatinization temperature, grain shape and nine morphological characters is presented in **Table 3**. Out of nine morphological characters, panicle exertion, stigma colour, seed coat colour, awning and hull colour showed four classes of variation while coleoptile colour, leaf blade colour, pubescence of leaf surface, panicle type and grain shape were found to show three different classes. The genotypes were grouped into three groups for aroma intensity and two groups for gelatinization temperature. A majority of genotypes were found to possess green

Table 1. Analysis of variance (ANOVA) for agromorphological and quality traits in aromatic rice

S. No.	Characters	Mean squares
1	Length of leaf blade	374.92**
2	Width of leaf blade	124.00**
3	Plant height	1696.68**
4	Panicle length	62.17**
5	Number of panicles per plant	31.86**
6	Days to 50% flowering	471.24**
7	Days to 80% maturity	530.38**
8	Number of grains per panicle	4776.15**
9	1000 grains weight	62.02**
10	Grain yield per plant	1519.16*
11	Starch content	482.00
12	Amylose content	16.34**
13	Amylopectin content	16.35**
14	Crude fat content	1.58**
15	Crude protein content	13318.71
16	Grain length breadth ratio	1.09**
17	Decorticated grain length breadth ratio	1.03**

** Significant at 1% level ; * Significant at 5% level

Table 2. Estimates of genetic variability parameters for 10 agro-morphological traits and 7 quality traits

S.No.	Characters	Genotypic variance	Phenotypic variance	Heritability (%)	Genetic advance as % of mean	GCV (%)	PCV (%)
1	Length of leaf blade	113.36	124.97	79.37	39.43	23.05	26.29
2	Width of leaf blade	0.035	0.041	67.51	22.71	15.26	18.57
3	Plant height	556.66	565.56	96.40	34.35	17.23	17.27
4	Panicle length	16.78	20.72	89.67	30.60	14.74	15.40
5	Number of panicle**s** per plant	10.23	10.62	89.69	59.20	31.44	33.20
6	Days to 50 % flowering	156.33	157.08	98.60	26.96	19.75	19.89
7	Days to 80 % maturity	169.36	176.79	88.34	19.31	14.24	15.12
8	Number of grains per panicle	1513.56	1749.02	87.59	51.48	43.91	46.91
9	1000 grains weight	18.61	20.67	81.96	30.96	17.53	18.06
10	Grain yield per plant	349.17	506.38	42.54	49.23	46.65	71.52
11	Starch content	121.91	160.66	75.88	25.66	14.30	19.99
12	Amylose content	5.44	5.44	99.99	25.75	12.50	12.51
13	Amylopectin content	5.45	5.45	99.99	5.91	2.87	2.87
14	Crude fat content	0.46	0.52	88.16	68.57	35.76	42.35
15	Crude protein content	0.42	0.70	59.96	8.05	32.17	32.52
16	Grain length breadth ratio	0.33	0.36	53.84	21.19	19.41	26.41
17	Decorticated grain length width ratio	0.30	0.34	85.63	39.26	21.24	23.33

coleoptile colour (70 %), green leaf blade colour (16 %), intermediate pubescence (71 %), just exerted panicle (41%), white colour stigma (50 %), open type panicle (56 %), short and fully awned (18 %), white seed coat colour (50 %), straw hull colour (50 %), mild scented (aroma) (56 %), high gelatinization temperature (76 %) and long bold grain (53 %). Teertha Prasad *et al*. (2021) reported low to high gelatinization temperature in traditional landrace rice.

Thirty-four aromatic rice genotypes were grouped into four clusters by Tocher's method (**Table 4**). Cluster I was

Table 3. Description of morphological and quality traits and frequency distribution of 34 aromatic rice genotypes

S.No.	Traits	Scale/sates	Frequency (%)	Number of genotypes
1	Coleoptile colour	Colourless	12	4
		Green	70	24
		Purple	18	6
2	Leaf blade colour	Light green	7	18
		Green	16	57
		Purple margins	11	25
3	Pubescence of leaf surface	Glabrous	3	1
		Intermediate	71	24
		Pubescent	26	9
4	Panicle exertion	Well exserted	12	4
		Moderate exserted	29	10
		Just exerted	41	14
		Partly exerted	18	6
5	Stigma colour	White	50	17
		Light green	23	8
		Yellow	15	5
		Light purple	12	4
6	Panicle type	Compact	18	6
		Intermediate	26	9
		Open	56	19
7	Awning	Short and partly awned	41	14
		Short and fully awned	32	11
		Long awned	9	3
		Long and fully awned	18	6
8	Seed coat colour	White	50	17
		Light brown	23	8
		Red	6	2
		Variable purple	9	3
		Purple	12	4
9	Hull colour	Straw	50	17
		Golden	17	7
		Golden brown	3	1
		Brown furrows on straw	3	1
		Purple furrows on straw	3	1
		Brown(tawny)	18	6
		Black	3	1
10	Aroma	Mild scented	56	19
		Intermediate	18	5
		Strong scented	26	10
11	Gelatinization temperature	High gelatinization temperature	76	24
		Intermediate gelatinization temperature	24	10
12	Grain shape	Long bold	53	4
		Basmati type	12	18
		Extra long	35	12

Table 4. Distribution of 34 genotypes of aromatic rice into various clusters by Tocher's method

Custer	Number of genotypes	Name of genotypes
I	27	Kom Chakhao Macha, Chakhao Manam Nungsiba2, Wahong Chakhao, Chakhao Kom, Chakhao Angouba , Chakhao Poireiton, ChakhaoTaniang ban, Chakhao nongmei kappi, Chakhao (Moirang) and Basmati (370) x Chakhao Amubi (Dwarf) of Manipur, Kawnglawng, Thatchhe Kawnglawng and America rice of Mizoram, Sitso, Runyule, Ayeng, Vikuho and Tonyu of Nagaland, Mebo, Mopian, Rharile and Mopi anokal of Arunachal Pradesh, KBA Naga, KBA Sorkar and KBA long of Meghalaya, Charke of Tripura and Basmati 370.
II	4	Chakhao Anembi, Chakhao manam nungsibi1, Chakhao (Thoubal) of Manipur Babite rice of Mizoram
III	2	Badiya of Tripura and Ottay of Sikkim
IV	1	PD-1503

Table 5. Average intra and inter-cluster D^2 distance of 34 cultivars of aromatic rice

Clusters	I	II	III	IV
I	715.8			
II	29473.17	1527.77		
III	29214.55	102525.93	1181.83	
IV	92563.80	210169.68	19833.85	-

the largest with 27 genotypes followed by cluster II having four genotypes, cluster III have two genotypes while cluster IV has the solitary genotype. From the average cluster wise mean values (**Table 4**), the genotypes included in the cluster II showed longer and wider length of leaf blade, more amylose content and crude fat content with short maturity duration than genotypes of another clusters. While, genotypes in cluster III showed longer panicle length with a greater number of panicles per plant, taller plants, higher content of starch and crude protein, but they require more days for maturity. Genotypes in cluster IV showed shorter stature of plants with a greater number of grains per panicle, more 1000 grains weight, high grain length breadth ratio with decorticated grain length width ratio and higher grain yield per plant with high content of amylopectin. No single cluster was observed to contain a single genotype with all the desirable traits. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits. The relative contribution of each trait towards divergence would reflect the pattern of divergence among the populations.

Maximum inter cluster distance was observed between cluster IV and cluster II (210169.67) followed by distance between cluster III and cluster II (102525.92); cluster IV and cluster I (92563.79) (**Table 7**). Minimum inter cluster distance was observed between cluster IV and cluster III (19833.85). While maximum intra cluster distance was observed in cluster II (1527.77) followed by cluster III (1181.83). Minimum intra cluster distance was observed in cluster I (715.80). In the present study, different cluster exhibited marked differences in respect of all the character.

From the analysis of contribution of each trait towards divergence (**Table 7**), amylopectin content showed maximum (86.17 %) contribution towards divergence followed by amylose content (11.91%) , days to 50% flowering (0.99 %), plant height (0.20 %), number of grains per plant (0.17 %), width of leaf blade (0.12%), decorticated grain length width ratio (0.11 %), length of leaf blade (0.09%), crude fat content (0.06%), number of panicle per plant (0.04 %), panicle length (0.02 %), days to 80% maturity (0.02), 1000 grains weight (0.01 %), grain yield per plant (0.01%), starch content (0.01%), and crude protein content (0.01 %). These characters which contributed maximum values towards the divergence should form the basis for selection of parents for hybridisation among distantly placed clusters, keeping in view their yielding potential, to obtain a good amount of heterosis and a wider range of segregants in the segregating generations.

While the characters grain length breadth ratio (0.00 %) and crude protein content (0.01 %) contributed minimum towards the genetic divergence in the present study, hence further crop improvement programme based on these characters will not be much useful.

The estimates of genetic parameters using the agro-morphological and quality traits helped in understanding the gene actions of these traits and ensure reliability of selection against these traits. Based on the inter cluster distance, for the improvement of the length of leaf blade crossing of Chakhao manam nungsiba1 of cluster II and Wahong Chakhao of cluster I may produce longer length, while for the improvement of the width of leaf blade crossing of Chakhao manam nungsiba1 and Chakhao

Table 6. Cluster mean for agro-morphic and quality traits

Characters	Cluster I	Cluster II	Cluster III	Cluster IV
Length of leaf blade (cm)	46.13	52.1	42.80	36.50
Width of leaf blade (cm)	1.25	1.30	0.95	1.03
Plant height (cm)	139.66	129.68	141.24	102.60
Panicle length (cm)	27.63	26.16	28.31	27.13
Number of panicles per plant	9.86	9.75	15.13	10.33
Days to 50 % flowering	61.75	59.50	82.33	82.00
Days to 80 % maturity	90.41	88.67	109.33	91.66
Number of grains per panicle	1503.95	1256.20	2000.06	1902.33
1000 grains weight (g)	24.73	22.81	25.76	32.20
Grain length breadth ratio	3.01	3.09	3.09	5.48
Decorticated grain length width ratio	2.58	2.43	2.55	4.50
Starch content (%)	76.99	78.14	78.17	77.14
Amylose content (%)	18.67	14.95	22.33	25.59
Amylopectin content (%)	81.32	85.04	77.66	74.41
Crude fat content (%)	1.90	2.41	1.16	1.50
Crude protein content (%)	12.49	11.37	18.95	15.67
Grain yield (g)	39.77	32.30	48.29	62.13

Table 7. Contribution of individual agromorphological and quality characters towards divergence

S.No.	Characters	Per cent contribution towards divergence
1	Length of leaf blade	0.09
2	Width of leaf blade	0.12
3	Plant height	0.21
4	Panicle length	0.02
5	Number of panicles per plant	0.04
6	Days to 50% flowering	0.99
7	Days to 80% maturity	0.02
8	Number of grains per panicle	0.18
9	1000 grains weight	0.01
10	Grain yield per plant	0.01
11	Starch content	0.01
12	Amylose content	11.92
13	Amylopectin content	86.17
14	Crude fat content	0.07
15	Crude protein content	0.01
16	Grain length breadth ratio	-
17	Decorticated grain length width ratio	0.12

Poireiton of cluster II and I respectively. Crossing of PD-1503 of cluster IV and Chakhao Anembi of cluster II may produce short/dwarf type of plant, for production of longer panicle crossing of Ottay of cluster III and Chakhao nongmei kappi of cluster I may produce desirable longer panicle. From cluster III Ottay has the maximum number of panicles per plant, so crossing of this genotype and PD-1503 of cluster IV might yield genotype with higher number of panicles per plant. There is a high chance of getting grains with higher density by crossing PD-1503 of cluster IV with Badiya of cluster III as both of them are the best genotype on the basis of 1000 grains weight from their respective cluster. For production of short duration plant, crossing of Babite rice of cluster II with Chakhao taniang ban of cluster I may yield segregants with shorter duration for maturity. For increasing the number of grains per panicle crossing of PD-1503 of cluster IV and Runyule of cluster I may give better F1 with higher number of grains per panicle. Crossing of PD-1503 of cluster IV with Ottay of cluster III may produce segregants with higher yield per plant. For improvement of quality traits such as starch content crossing of Badiya of cluster III with Babite rice of cluster II will be beneficial, also crossing of Babite rice with Charke of cluster I may be beneficial for getting segregants with lower content of amylose. For breeding genotypes of higher crude fat content crossing of Chakhao manam nungsiba1 with Chakhao taniang ban may be beneficial. The performance of these cross combinations may further be performed by actual hybridization of the suggested parents. Therefore, a significant amount of variability and genetic diversity observed in the present investigation could be helpful in further improvement of the reported superior genotypes or selection of parents for further hybridization programme.

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