Deciphering the potentiality of some elite aromatic rice landraces of North East India

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ABSTRACT

A field experiment was conducted at the research farm of Sripat Singh college, Jiaganj,West Bengal taking eight rice landraces with two aromatic rice cultivars viz., Biroin and Gandhibiroin of Bagbari village, Karimganj, Assam for the assessment and to study magnitude of genetic variability based on fifteen agro-morphological traits including one biochemical trait. Data on qualitative traits were recorded following DUS test and significant variability was found for the traits like leaf anthocyanin colouration, flag leaf attitude, time of heading and basal leaf sheath coloration. Quantitative traits were analyzed and maximum variability was found for the traits like leaf length, number of grains panicle^{-1}, seedling height and grain yield plant^{-1}. Results showed that high estimates of heritability coupled with high GCV and high genetic advance were found in case of grain yield per plant, number of grains panicle^{-1}, seedling height and crude protein plant^{-1}. The higher genotypic and phenotypic coefficient of variation was found for the traits like grain yield, crude protein number of grains panicle^{-1}, leaf breadth, seedling height and grain breadth. Results also showed that the grain yield plant^{-1} had a highly positive correlation with number of grains panicle (r=0.823)$^{-1}$ followed by 1000 grain weight (r=0.704) and leaf breadth (r = 0.552). Also, leaf breadth (r = 921), flag leaf angle (r = 0.804), grain length (r=0.700), grain L/B ratio (r = 0.625) and grain yield (r = 0.410) had maximum correlation with the leaf length. Hence, these experimental observations would be beneficial for any rice breeding programme to choose the desirable trait for crop improvement programme choosing the appropriate traits of interest from traditional rice having aromatic feature.

Keywords *: Aromatic rice, correlation, heritability, variability*

In India, collected germplasms showed rich source of genetic variability and diversity for its remarkable significant phenotypic variability (Rao *et al.*, 1979). Traditional rice germplasms are the treasure trove of useful beneficial genes which may be used for future crop breeding programme (Chakravorty *et al.,* 2013, Chakravorty and Ghosh, 2014, Chakravorty and Ghosh, 2011). Rice with aromatic features in combination with good yield and early maturity is keenly essential for the crop improvement programme for any research works. Personal interview with the farmers of that locality reflected the different view about the cultivars of these varieties at the village of Bagbari area where these landraces are cultivated using rainwater and river water only without using any ground water. People and farmers depend on the production and yield of these cultivars viz., *Ranjit, Aizong, Biroin, Gandhibiroin, Latma* etc. *Biroin and Gandhibiroin* have aromatic feature. The cultivation of traditional rice is now marginalized due to the rapid cultivation and adaptation of modern high yielding rice having less quality to fight against any environmental stress for last few decades.

However, the farmers of North East India still cultivate these varieties with their higher production to solve the public demand during *kharif* season specially during the social functions and religious activities like Bihu and other Poush parban festival. Also, marketing of scented rice in Chattishgarh area was reported by Marothia *et al.* (2007) where farmers use a small portion of their rice for domestic consumption and sent 87.2per cent for sale. Any crop variety having diversity and variability is highly preferable for crop improvement programme, food production, mitigating poverty and overall solving the economic growth of a nation or country. The diversity ensures to solve and face any future unusual environmental hazards if faces by a country. For developing high yielding superior germplasms the information on GCV, PCV, heritability and genetic advance is needed. The knowledge of association *i.e* genotypic and phenotypic correlation between yield and its component characters is essential for yield improvement through selection programmes (Ismail *et al.*, 2001; Kumar and Sukla, 2002; Chakravorty and Ghosh, 2013). Keeping this in mind, this study was framed to characterize, evaluate those traditional rice landraces with their high yielding ability and few with aromatic feature using different agro-morphological parameters to conserve these beneficial genes which are our true wealth to save our nation from the hunger and to serve the quality food to the people of this earth.

MATERIALS AND METHODS

This experimental work was undertaken in *kharif* season of 2016-17 and 2017-18 in the research farm of Sripat Singh College (23^{0}24′N latitude and 88^{0}31′E

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longitude with an altitude 9.75 meters above sea level) at Murshidabad district, West Bengal following Randomised Complete Block design (RCBD) in two replications with 20 cm row to row and 15cm plant to plant distance. Data were recorded from five randomly selected plants from each replication. Crop was raised following recommended package of practices. Fertilizers (N : P_2O_5 : K_2O) @ 50:25:25 kg ha^{-1} were applied. Analysis of crude protein content from dehusked rice seeds was measured by standard Micro-Kjeldahl (Mossé *et al*., 1988) method. Total eight traditional rice landraces having high yielding potentiality, among which, two cultivars *viz*., Biroin and Gandhibiroin having aromatic feature, collected from Bagbari village of Karimganj district, South Assam were taken for the study. The acidity of the soil was pH of 6.0 with two soluble salts (EC of 0.15dSm^{-1}), medium organic carbon content (0.57%), total N (0.056%), medium in available P (25.28Kg ha^{-1}) and K (148.77Kg ha^{-1}).

Characterization was done on eight qualitative traits following Distinctiveness, Uniformity and Stability (DUS) test guidelines of Protection of Plant Variety and Farmers Right (PPV and FR authority (2001)) and the quantitative traits including one biochemical trait were analyzed following the procedure proposed by Johnson *et al*. (1955). Also, statistical analysis like, mean, standard error of mean, GCV, PCV, heritability, genetic advance and study on association of characters were calculated using SPAR and MSTATC computer software. The quantitative traits were leaf length, leaf breadth, seedling height, flag leaf angle, panicle length, grain length, grain breadth, grain length -breadth ratio, grain weight, no. of grains panicle^{-1}, number of primary branches panicle^{-1}, sterile lemma length, maturity in days, yield plant^{-1} and crude protein plant^{-1}.

RESULTS AND DISCUSSION

For a crop improvement programme, knowledge on extent of variability prevailing for a particular trait for particular cultivar is very much needed through selection process. Selection of diverse lines with diverged genetic features is chosen for hybridization programme. Analysis of variance showed highly significant variation among the genotypes. The magnitude of variability between cultivars showed a good reflection in the mean value and range of genotype traits taken for the study.

Regarding the qualitative traits studied (following the DUS Test), a remarkable variation has been found in significant amount specially among the traits like basal leaf sheath colour, panicle length, ligule colour, time of heading, flag leaf attitude and awn distribution (Table 1).

In respect to fifteen quantitative traits including one biochemical trait taken for the study, genetic advance was found to be the highest (Table 2) in the trait grain yield plant^{-1} (79.97), which is followed by seedling height (48.34), number of grains panicle^{-1} (39.89) and in grain breadth (39.53) (Table 2). High genetic advance for number of grains panicle^{-1} was also recorded by Chaubey and Riccharia (1993). Heritability was maximum for the traits like crude protein plant^{-1} (0.999), grain yield plant^{-1} (0.999), seedling height (0.999) and number of grains panicle^{-1} (0.999) followed by grain length (0.997), grain length : breadth ratio (0.987) and grain weight (0.990). This performance of high heritability and high genetic advance percent of mean were in agreement with the results of Verma and Srivastava (2004). It is known that the traits with high GCV, heritability and genetic advance keeps a prime importance in choosing the trait for efficient plant breeding programme. So, from our analysis, it was revealed that the traits, such as, grain yield, number of grains panicle^{-1}, crude protein plant^{-1}, and leaf length had a combination of these three characters with their high value and can be chosen as a combination of characters for any crop improvement programme (Table 2).

The magnitude of GCV and PCV being same shows that there was least influence of environment in expression of the traits under study. Here the examples of cases have been found perfectly in seedling height (23.45), crude protein plant^{-1} (8.78) and number of grains panicle^{-1} (19.37) (Table 2). It shows that the expression of genes for these characters was also reflected in PCV. The study of GCV and PCV reveals that both types of coefficient of variations were highest for grain yield plant^{-1}, seedling height, grain breadth and number of grains plant^{-1}. Similarly the lowest GCV and PCV were recorded in the characters like flag leaf angle, followed by panicle length and crude protein plant^{-1}. So the expression of gene was same as in phenotypic variation. These findings were in agreement with the findings of Pushpa *et al*. (1999), Venkataramana *et al*. (1999), Kumar *et al*. (1998) and Kaw *et al*. (1999).

Regarding the efficiency estimation study, experimental evidences revealed that grain yield/plant is positively correlated number of grains panicle^{-1} (r = 0.823) followed by 1000 grain weight (r = 0.704), leaf breadth (r = 0.552), and leaf length (r = 0.410) and there is high correlation between the characters which may be taken in to consideration before framing any breeding programme (Table 3). Also, in respect to the intercorrelation among the characters, it has been found that the leaf length is highly correlated with leaf breadth (r = 0.921), flag leaf angle (r = 0.804), grain length (r = 0.700), grain length : breadth ratio(r= 0.625), grain yield plant^{-1} (r = 0.410) and panicle length (r = 0.377) (Table-3). But, panicle length and grain breadth had

Table 1: Frequency distribution for eight qualitative traits in landrace genotypes specially for traditional rice cultivars with aromatic feature of North East India (Using DUS Test in Rice) Total (N) = 08 = 100%

Sl. No.	Code	Trait	No. of accessions	Proportion (%)	Sl. No.	Code	Trait	No. of accessions	Proportion (%)
1		**Basal leaf sheath colour**			**5**		**Leaf anthocyanin colouration**		
	1	Green	5	62.5		1	Absent	2	25.5
	2	Light purple	1	12.5		9	Present	6	75.0
	3	Purple Lines	1	12.5					
	4	Purple	1	12.5					
2		**Ligule colour**			**6**		**Panicle length**		
	1	Green	6	75.0		1	Very short	1	12.5
	2	Light purple	1	12.5		3	Short	1	12.5
	3	Purple	1	12.5		5	Medium	4	50.0
						7	Long	1	12.5
						9	Very long	1	12.5
3		**Auricle colour**			**7**		**Time of heading**		
	1	Colourless	6	75.0		1	Very early	2	25.0
	2	Light purple	1	12.5		3	Early	1	12.5
	3	Purple	1	12.5		5	Medium	4	50.0
	4	Absent	0	00.0		7	Late	1	12.5
						9	Very late	0	00.0
4		**Flag leaf attitude**			**8**		**Anthocyanin colouration of the node**		
	1	Erect	5	62.5		1	Absent	6	75.0
	3	Semierect	3	37.5		9	Present	2	25.0
	5	Horizontal	0	00.0					
	7	Deflexed	0	00.0					

Table-2 Mean, S.E, G. C. V, P.C.V., heritability, GA, CV of fifteen quantitative traits of eight traditional rice cultivars of North East India

Sl	Code	Traits	Mean±S.E	Range	G.C.V	P.C.V	h² (Heritability)	G.A. Value	CV (%)
1	C1	Leaf length	46.13±.32E	54.2-36.1#	14.05	14.06	0.999	28.1	0.70
2	C2	Leaf breadth	1.38±0.05E	1.1-1.6#	12.30	12.89	0.911	24.63	3.85
3	C3	Seedling height	5.15±0.02E	3.1-7.1#	23.45	23.45	0.999	48.34	0.48
4	C4	Flag leaf angle	1.26±0.05E	1.1⁰-1.35⁰	6.14	7.70	0.635	10.31	4.65
5	C5	Panicle length	22.28±0.30E	21.4-25.15#	7.17	7.30	0.964	14.49	1.38
6	C6	Grain length	7.26±0.09E	6.0-9.05$	15.47	15.53	0.992	31.81	1.35
7	C7	Grain breadth	2.58±0.04E	2.0-3.15$	19.30	19.38	0.992	39.53	1.75
8	C8	Grain L : B ratio	2.87±0.58E	1.94-3.55$	18.01	18.12	0.987	36.93	2.03
9	C9	1000 grain weight	22.97±0.38E	29.3-18.15@	16.48	16.56	0.990	33.78	1.66
10	C10	No. of hrains panicle⁻¹	239.1±0.11E	201.5-307.00	19.37	19.38	0.999	39.89	0.49
11	C11	No. of primary branches panicle⁻¹	13.93±0.45E	11.5-16.5	11.34	11.80	0.924	22.40	3.25
12	C12	Sterile lemma length	1.58±0.07E	1.3-2.05$	18.36	18.96	0.937	36.70	4.74
13	C13	Maturity in days	136.8±0.21E	114.0-160.5	13.81	13.90	0.987	28.28	1.58
14	C14	Grain yield	21.12±0.16E	13.26-36.5*	38.82	38.83	0.999	79.97	0.78
15	C15	Crude protein plant⁻¹	182.6±0.18E	151.3-200.15	8.78	8.78	0.999	18.07	0.10

Note #-cm, $- mm, @ -g, *-t ha⁻¹

Table 3 Genotypic and phenotypic correlation coefficients among fifteen quantitative traits of eight traditional rice cultivars

Traits	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13	C14	C15
C1	**1.000**	0.877	-0.163	0.643	0.367	0.693	-0.090	0.617	-0.061	0.093	-0.0208	-0.568	-0.258	0.410	-0.593
C2	0.921**	**1.000**	-0.427	0.332	0.085	0.626	0.127	0.355	0.246	0.109	-0.313	-0.328	-0.180	0.526	-0.628
C3	-0.163	-0.499**	**1.000**	0.280	0.197	-0.060	-0.366	0.260	-0.428	0.220	0.422	-0.279	-0.144	-0.131	0.267
C4	0.804**	0.463**	0.359*	**1.000**	0.458	0.311	-0.276	0.496	-0.205	0.080	0.189	-0.749	-0.005	0.158	-0.086
C5	0.377**	0.052	0.201	0.623**	**1.000**	0.664	0.133	0.408	-0.836	-0.381	-0.229	-0.266	-0.139	-0.547	-0.213
C6	0.700**	0.655**	-0.060	0.402**	0.670**	**1.000**	0.432	0.325	-0.454	-0.226	-0.528	-0.272	-0.417	-0.110	-0.717
C7	-0.090	0.121	-0.367**	-0.386**	0.133	0.433**	**1.000**	-0.704	0.044	-0.551	-0.640	0.039	0.004	-0.398	-0.443
C8	0.625**	0.378**	0.262	0.678**	0.410**	0.322**	-0.705**	**1.000**	-0.424	0.362	0.252	0.189	-0.268	0.288	-0.067
C9	-0.093	0.243	-0.430**	-0.274	-0.857**	-0.452**	0.043	-0.421**	**1.000**	0.419	0.218	0.084	0.188	0.702	0.159
C10	0.093	0.119	0.220	0.106	-0.387**	-0.225	-0.552**	0.365**	-0.421**	**1.000**	0.681	0.253	-0.346	0.823	0.442
C11	-0.213	-0.301	0.439**	0.297*	-0.213	-0.557**	-0.659**	0.252	0.242	0.707**	**1.000**	0.074	0.305	0.396	0.851
C12	-0.588**	-0.406*	-0.291	-0.888**	-0.290*	-0.286*	0.033	-0.194	0.080	0.261	0.070	**1.000**	-0.176	-0.023	0.362
C13	-0.256	-0.194	-0.146	0.039	-0.146	-0.427**	0.006	-0.279*	0.196	-0.348**	0.299*	-0.192	**1.000**	-0.233	0.401
C14	0.410*	0.552**	-0.131	0.190	-0.554**	-0.110	-0.400**	0.292*	0.704**	0.823**	0.411**	-0.024	-0.234	**1.000**	0.059
C15	-0.594**	-0.660**	0.267	-0.111	-0.216	-0.719	-0.445**	-0.067	0.159	0.442**	0.887**	0.373**	0.404**	0.059	**1.000**

Note:

C1=Leaf length, C2=Leaf breadth, C3=Seedling height, C4=Flag leaf angle, C5=Panicle length, C6=Grain length, C7=Grain breadth, C8=Grain length : breadth ratio, C9=1000 grain weight, G10=No. of grains panicle⁻¹, C11=No. of primary branches panicle⁻¹, C12=Sterile lemma length, C13 : Maturity in days, G14=Grain yield, G15=Crude protein Plant⁻¹

*and**indicate significance at 5% and 1% levels, respectively. Upper diagonal correlations are phenotypic correlations and lower diagonal correlations are genotypic correlation. Correlation coefficient r>0.276 and r>0.351 are significant at at 5% and 1% level

maximum negative correlation with the leaf character having values (r = -0.554) and (r = -0.400) respectively. The correlation coefficient showed that number of grains panicle^{-1}serve as most important selection indices of grain yield (Meenakshi *et al.* (1999), Mustafa and Elsheikh (2007)).

Thus it can be safely concluded that we have been able to characterize some promising high yielding rice landraces with aromatic feature. Among the selected germplasms so far studied significant variability has been found in the cultivars along with the aromatic feature both quantitatively and qualitatively. It will help the breeder to select the desirable traits from the varieties for hybridization and crop improvement programme. This study also focus on the need of conservation of such valuable genetic resources of our country which are the reservoir of beneficial gene pool to fight against future environmental hazards to save our people of this globe from hunger and poverty with quality food saving the people from the health risk.

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