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Research Article

GENETIC VARIABILITY STUDIES IN INDIGENOUS PIGMENTED RICE OF NE INDIA FOR THEIR GRAIN QUALITY PARAMETERS

Sangeeta Das[1*] and Ramendra Nath Sharma[2]

[1]Department of Botany, Bahona College, Jorhat, India
[2]Department of Plant Breeding & Genetics, Assam Agricultural University, Jorhat, India

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ABSTRACT

Seventy eight numbers of pigmented rice genotypes collected from different states of NE India were studied at Bahona College, Jorhat, India during kharif season of 2016-17 for genetic parameters, correlation and principal component analysis. Analysis of variance and principal component analysis revealed the presence of high variability among the genotypes for all the traits. High estimates of geneotypic coefficient of variability and heritability coupled with high genetic advance as percent of mean were recorded for iron and manganese content. A positive and significant correlation was observed for Fe content with ash content at genotypic level. The estimates of genotypic variance, heritability and genetic advance as percent of mean indicated that characters iron content, total phenolic content and antioxidant contents are the most important among all the characters studied and selection based on these traits would be very effective in adopting rice improvement programmes enhancing nutritional quality through plant breeding.

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important cereal crops and a major food source for more than half of the global human population including the North Eastern region of India. There is a growing demand for high grain quality rice in both national as well as in the international market. Good quality rice also fetches higher price for the farmers. Pigmented rice has been reported as potent sources of micronutrients, particularly iron, zinc and antioxidant contents and are with nutritional benefits over white rice. The red rice cultivars are having higher antioxidant activity and phenolic content than non-pigmented rice (Zhang et al., 2010). North east (NE) India, the mega biodiversity hot-spot of the world has numerous indigenous pigmented genotypes of rice with tremendous potential of high quality rice (Saikia et al., 2012). These indicate the existence of sufficient genetic variation that can be utilized in a rice breeding programme to address dietary improvement of major crop rice to address malnutrition with enhanced levels of iron, zinc and antioxidants in their seeds.

There are very little or no informations available on mineral as well as phytochemical composition of pigmented rice genotypes of NE India. A systematic evaluation of genetic variability for grain quality parameters of pigmented rice genotypes of NE India will be helpful to select genotypes to be used in further rice improvement programme. Therefore, the present study was undertaken with the objective to study nature and extent of genetic variability for grain phytonutrient quality characters in a set of tradititional pigmented rice genotypes of NE India.

MATERIALS AND METHODS

Seventy eight numbers of pigmented rice genotypes were collected from the farmers of different states of NE India (Table 1) and were purified by two rounds of selfing and selection during July-December, 2016 & 2017. The dehusked rice samples were then ground and stored at 4 °C for further analysis.

Physical properties and colour values

The length (L) and breadth (B) were measured with vernier callipers and L/B ratio was calculated. Colour values of dehusked rice grain were measured using Hunter-Lab (Ultrascan Vis). The color parameters L* (ranges from black = 0 to white = 100), a* (indicates a hue of red-purple) and b* (indicates yellow) were then read (Lamberts et al., 2007). Hue angle and chroma were calculated from a* and b* values.

Physicochemical and biochemical properties

Amylose content was determined by the method described by Juliano (1971). The mineral solution was prepared according to

Corresponding author: **Sangeeta Das**
Department of Botany, Bahona College, Jorhat, India

the method described by AOAC (1970). The results were expressed in mg/100g.

Phytochemicals and antioxidant properties

TPC was determined using a modified version of the Folin–Ciocalteu assay (Slinkard and Singleton, 1977) and the result was expressed in mg GAE/100 g. Total antioxidant capacity of rice extracts was determined using a spectrophotometer following the method described by Choi et al., (2007). The results were expressed as mg TEAC/100g.

Statistical analysis

Analysis of variance was estimated following Panse and Sukhatme, 1985. The phenotypic and genotypic coefficient of variability, heritability in broad sense, genetic advance at 5 per cent selection intensity were computed as suggested by Johnson et al., 1955. The genotypic and phenotypic correlation coefficients among all the traits under study were calculated following Al-Jobouri et al., 1958.

Principal components grouping of the traits were employed to examine the percentage contribution of each trait to total genetic variation. Cluster analysis based on similarity matrices was also employed on agro-botanical data using the un-weighted pair group method with arithmetic mean (UPGMA) to obtain a dendrogram using software R.

RESULTS AND DISCUSSION

Genetic variability analysis

The analysis of variance (Table 2) indicated that sufficient amount of variability is present among the indigenous pigmented rice genotypes for the different phyto-nutritional characters studied and selection would be effective to develop new genotypes with desirable values for Fe, Zn and TEAC contents. The estimates of mean values and different variability parameters studied are presented in Table 3.

Whiteness was more prominent in Manohar sali with the highest L* value whereas lowest L* value was observed for Krishna Bora followed by Chak-Hao-Amubi due to the presence of pigmented external layers of the kernels. The positive a* values for redness were the highest for Tulsi bora and was least for Malaisia and chak-Hao-Amubi. The yellowness (b* value) was highest for Bahbite and lowest for Krishna bora. A more appropriate measure of color can be obtained from the calculation of hue angle and chroma. Hue angle was lowest in Kekoa bau with awn indicating that more redness than others. Chroma, a measure of vividness of colour was highest in Tulsi bora. This colour of the pigmented rice is due to the presence of high amounts of phenolic compounds, especially anthocyanins, a group of reddish or purple flavonoids in pericarp. The phenolic compounds have been found as a major active component for antioxidation. Anthocyanins have been recognized as health-promoting functional food ingredients due to their high antioxidant activity (Zhao et al., 2004).

The genotype Naga-A from Nagaland was found to be with highest value for Fe content and comparative higher values for Zn content and TEAC content. The genotype Kola Konamusori from Jorhat showed highest values for Zn content, but with lower values for Fe and TEAC contents. The genotype Katuk Tara from Karimganj showed highest value for TEAC content but with comparatively lower values for Fe and Zn contents. Thus, these genotypes provided ample scope for their utilization in breeding programme of rice varieties with higher or desirable values for these traits.

The success of any crop improvement programme depends mostly on the amount of genetic variability present for the characters under study. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) provide a measure to compare the variability present among the traits. Among the various characters studied, highest GCV and PCV values were recorded for Fe content, followed by the values for Mn and copper (Cu) content (Table 3) indicating the presence of sufficient genetic variablity for these traits, thereby facilitating selection for these traits to isolate desirable genotypes with good nutrient contents. The lowest GCV and PCV values were recorded for grain length indicationg less scope for selection. The close correspondence observed between GCV and PCV estimates indicated the presence of high genetic variability for the traits which might facilitate selection (Yadav, 2000). Such close values of GCV and PCV may be due to the use of traditional genotype which, because of their selection over long period of time, remains more or less stable across locations (Fukrei et al., 2011).

The broad sense heritability, which gives an idea about the exploitable portion of variation, is regarded as a predictor in the selection procedure. The highest heritability (Table 3) was recorded for TEAC contents followed by Mn and Fe content whereas, lowest heritability was recorded for ash content. The comparatively high heritability values for TEAC and Fe contents indicated that the expression of those characters is less influenced by the environment thus providing scope for their improvement through proper breeding programmes.

High heritability does not always indicate high genetic gain. Therefore, heritability and genetic advance should be considered together. A high heritability estimate associated with high genetic advance was observed for the character Fe content followed by Mn content. This indicates the preponderance of additive gene effects and therefore, simple or progeny selection on the basis of phenotypic performance would be effective (Panse and Sukhatme, 1957). A low heritability coupled with low genetic advance was observed for the character grain length. A high heritability coupled with low genetic advance was observed for the characters TEAC and zinc (Zn) contents, which can be ascribed to the presence of non-additive gene effects. Such characters can be improved by inter mating superior genotypes of segregating population developed from combination breeding (Babu et al., 2012). Thus, the characters Fe, Mn, Cu, TPC and TEAC contents were shown to have high to moderate genotypic variance, high to moderate heritability and greater genetic gain. So, their phenotypic expression would be a good indicator of their genotypic potentiality and simple phenotypic selection based on these characters will be effective to identify superior geneotype containing desired level of phytonutrients and antioxidents. The remaining characters recorded lower scores in the three genetic parameters considered in this study and thereby offering less scope for selection as they were much more under the influence of the environment. Thus, selection with progeny testing will be required.

Correlation studies

The genotypic correlation coefficients in most cases were higher than their phenotypic correlation coefficients indicating the genetic reason of association (Table 4). The colour parameters (L*, a*, b*, chroma and hue angle) showed a

Table 1. List of rice genotypes collected from different parts of NE India.

Sl. No	Name of the genotype	Sl. No.	Name of the genotype	Sl. No	Name of the genotype	Sl. No	Name of the genotype
1	Kekoa Bao (Awn present)	21	Moimonsingia Bao Dhan	41	Banglami	61	Malaisia
2	Manohar Sali	22	Rata Boro	42	Rangai	62	Amona Bao
3	Bora Chokowa	23	Sadakura Bao	43	Basmoti Red	63	Purabenn
4	Bokul Bora	24	Nania Komol	44	Mukta Haar	64	Tulsi Bora
5	Ixojoy Ahu	25	Dud Ratai	45	Guni Ahu	65	Swarnabh
6	Poita Bora	26	Basanta Bahar	46	Bor Mekohi	66	Bahbite
7	Kekoa Bao (Awn absent)	27	Binna Pali	47	Harkona Sali	67	Ronga Bao
8	Bodol Bao	28	Rangoli Bao	48	Wapnah Biong	68	Chimtung
9	Maguri Bao	29	Mantetoi	49	Badal Bao	69	Jhum Mycin
10	Ghew Bora	30	Jangmo	50	Katuk tara	70	Dolmora Bao
11	Bora	31	Balighugor	51	Rongai	71	Kola Konamusori
12	Kola Joha	32	Koimuruli	52	Haru beguni gootia	72	Krishna Bora
13	Bongo Ronga Ahu	33	Inglong Baara	53	Chak-Hao Amubi	73	Teuuru
14	Negheri Bao	34	Kunie	54	Kola Ahu	74	Gobindo Bora
15	Indi Bao	35	Dimrou	55	Jul Bao	75	Naga-A
16	Boga Betha bao	36	Monipur	56	Indranarayan	76	Madel Bao
17	Maju Chokowa	37	Baaraa	57	Ronga Ahu	77	Borjul Bao
18	Miya Bao	38	Lalaus	58	Lohadang	78	Johori Komol
19	Guni Bao	39	Pyjihari	59	Kokua		
20	Ronga Kutha Bao	40	Sosta	60	Agnisail 2		

positive and significant correlation with each other, at genoptypic level. A positive and significant correlation was also observed for Fe content with ash content at genotypic level. The association of TPC is significant but negative with L*. The content of antioxidative substances, i.e., polyphenols in rice grain, is affected by genotype and environment (Goffman and Bergman, 2004). Despites of reports like positive correlation between TPC and antioxidant contents and negative correlations of colour parameters with Fe contents (Yodmanee *et al*., 2011), our study did not show any such correlations, which might be due to the use of different genotypes.

Principal component analysis (PCA)

PCA measures the importance and contribution of each component to total variance. Seven principal components were extracted which cumulatively accounted nearly 85.60% of the total variations present in 78 different indigenous pigmented rice germplasms (Table 5).

The first three components contributed more than 50% of the total variations present. For the first component (PC1), L*, chroma, ash, Mn and Fe content contributed 28.04% of the total variability. For PC2, grain breadth and amylose content has contributed 15.35% of the total variability. For PC3, a*, b* and grain length contributed 12.09% of the total variability. Similarly, for PC4, Cu, Zn and TPC contents contributed 8.51%; for PC5, TEAC content; for PC6, Cu and Fe content and for PC7, grain length contributed to 8.20%, 7.43% and 5.96% of the total genotypic variability respectively. The results of PCA used in the study have revealed the presence of high level of genetic variation existing in the population panel and explains the traits including colour parameters (L* and chroma) and micronutrient (Mn and Fe) contents contributing for this variability. The character Fe content also showed high values for genetic variability, heritability coupled with high genetic gain and thus could serve as an important trait for the selection of superior genotype. Thus, the characters, colour parameters and Fe content coming together in PC1 offer opportunity for its utilization in rice breeding with better nutritional quality.

Genetic relationship among different genotypes of pigmented rice

Figure 1 represents the dendogram of 78 indigenous pigmented rice genotypes of NE India showing their relationship as revealed by UPGMA cluster analysis. The mean Euclidean distance of the all rice genotypes ranges from 1.155 to 9.840, indicating sufficient genetic diversity existing among the rice genotypes. Four groups were well resolved in terms of morphological characteristics. Group I comprises of 20 different genotypes which were having comparatively higher Zn and TEAC contents but lower Fe content. Group II has 12 different genotypes including the highest Fe containing genotype Naga-A from Nagaland whereas rests were with comparatively lower Fe content. In terms of Zn and TEAC contents, the genotypes within this group had comparatively higher values. Similarly, Group III and Group IV comprises of 29 and 17 genotypes respectively. Group III had genotypes with comparatively higher Zn and TEAC contents but with lower Fe content whereas Group IV had genotypes with comparatively lower Fe, Zn and TEAC contents. It was observed that different clusters were characterized with desirable attributes for different traits along with high genetic diversity. So selection of parents from different clusters to use in recombination breeding can be made to develop variety with desirable combination of grain quality characters.

Thus, it could be concluded that more emphasis should be given to the characters Fe, TPC and TEAC contents with high

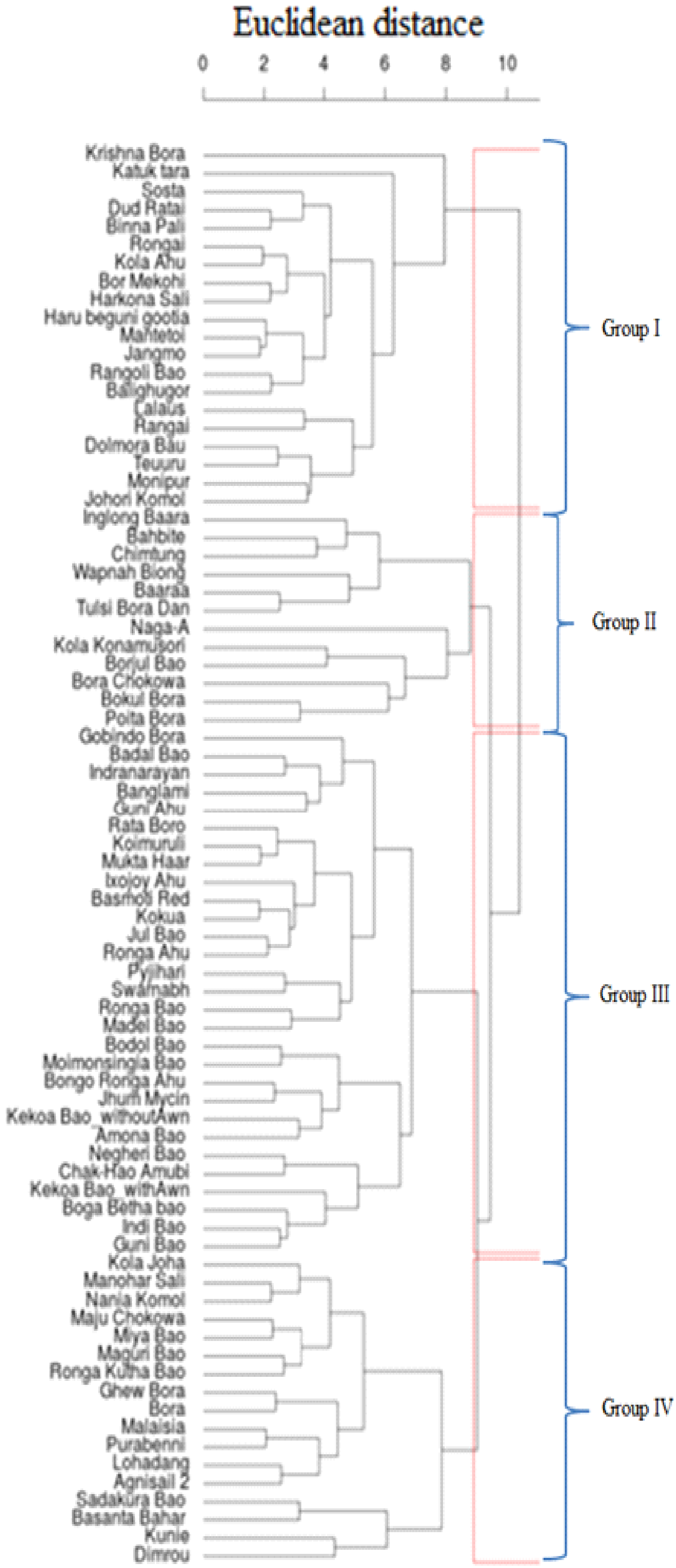

Fig.1 Dendogram of 78 Indigenous pigmented rice genotypes of NE India.

Table 2. ANOVA for grain quality characters in pigmented rice genotypes of NE India

Source of variations	Mean sum of squares of characters																
	df	L*	a*	b*	Chroma	Hue Angle	Length	Breadth	L/B ratio	Ash content	Amylose	Zn	Mn	Fe	Cu	TPC	TEAC
Replicates	2	0.560	3.394	1.001	2.867	0.003	0.302	0.012	0.039	0.170	5.670	0.258	0.306	0.108	0.223	8.576	41.699
Treatments	77	101.996**	20.662**	34.292**	34.458**	0.122**	1.014**	0.209**	0.433**	0.284**	66.968**	0.578**	1.797**	1.317**	0.189**	1258.850**	156.098**
Error	154	4.264	0.811	1.345	1.437	0.006	0.083	0.016	0.038	0.032	1.072	0.009	0.016	0.018	0.007	37.248	0.964

** Significant at 1% level of probability.

Table 3. Estimates of range, variability, heritability, and genetic advance as per cent of mean

Sl. No.	Characters	Range Lowest	Range Highest	GCV (%)	PCV (%)	Heritability (h2) (%)	GA as per cent of mean (5%)
1	L*	42.48	68.14	10.59	11.26	88.43	20.52
2	a*	1.23	12.06	40.67	43.09	89.08	79.08
3	b*	2.93	19.33	29.86	31.64	89.09	58.06
4	Chroma	3.19	22.22	25.41	27.02	88.46	49.24
5	Hue Angle	0.70	1.49	18.97	20.25	87.75	36.60
6	Length (mm)	4.73	7.43	9.71	10.93	78.93	17.77
7	Breadth (mm)	1.63	2.90	11.20	12.54	79.72	20.59
8	L/ B_ratio	1.98	3.42	14.10	15.99	77.78	25.62
9	Ash Content (%)	0.72	2.16	22.27	26.16	72.48	39.06
10	Amylose (g)	4.47	25.67	29.52	30.23	95.35	59.38
11	Zn (mg/100g)	0.61	2.91	30.03	30.74	95.45	60.43
12	Mn (mg/100g)	0.42	4.90	51.92	52.63	97.33	105.53
13	Fe (mg/100g)	0.14	4.57	82.33	83.99	96.09	166.26
14	Cu (mg/100g)	0.06	1.63	45.40	47.94	89.67	88.55
15	TPC (mg GAE/100g)	10.55	79.83	33.82	35.33	91.62	66.68
16	TEAC (mg TEAC/100g)	5.50	54.40	32.19	32.49	98.17	65.69

Table 4. Genotypic correlations among different characters in rice

Sl. No.	Parameters	L*	a*	b*	Chroma	Hue Angle	Length (mm)	Breadth (mm)	L/ B ratio	Ash Content (%)	Amylose (g)	Zn (mg/ 100g)	Mn (mg/ 100g)	Fe (mg/ 100g)	Cu (mg/ 100g)	TPC (mg GAE /100g)	TEAC (mg TEAC /100g)
1	L*	1	-0.457**	0.756**	0.553**	0.873**	0.0523**	0.146	-0.101	-0.018	-0.19	-0.316**	0.028	-0.082	-0.017	-0.425**	-0.149
2	a*		1	0.130	0.432**	-0.730**	0.185	0.198	-0.034	-0.055	0.067	0.214	0.042	0.146	0.109	0.400**	0.121
3	b*			1	0.948**	0.565**	0.184	0.208	-0.065	-0.018	-0.263*	-0.113	0.166	0.049	0.062	-0.176	0.061
4	Chroma				1	0.277*	0.223*	0.248*	-0.067	-0.044	-0.215	-0.043	0.158	0.093	0.085	-0.044	0.080
5	Hue Angle					1	-0.0213	-0.034	-0.006	0.054	-0.251*	-0.231*	0.138	-0.049	0.005	-0.459**	-0.011
6	Length (mm)						1	0.120	0.588**	-0.053	-0.153	-0.119	0.179	-0.016	-0.202	0.128	0.040
7	Breadth (mm)							1	-0.727**	0.117	0.220*	-0.237*	-0.176	0.001	-0.410**	-0.038	-0.210
8	L/ B ratio								1	-0.114	-0.265*	0.095	0.264*	-0.003	0.172	0.117	0.180
9	Ash Content (%)									1	-0.064	0.052	0.336**	0.370**	0.057	-0.075	-0.139
10	Amylose (g)										1	-0.131	-0.369**	-0.182	-0.105	-0.017	-0.045
11	Zn (mg/ 100g)											1	0.300**	0.049	0.343**	0.181	0.040
12	Mn (mg/ 100g)												1	0.360**	0.124	-0.099	0.054
13	Fe (mg/ 100g)													1	0.204	-0.144	0.006
14	Cu (mg/ 100g)														1	0.033	0.044
15	TPC (mg GAE/100g)															1	0.108
16	TEAC (mg TEAC/100g)																1

**, * Significant at 0.05 and 0.01 level of probability, respectively.

Table 5. Principal components of analysis of 16 different characters of 78 pigmented genotypes of NE India.

Component Variable	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7
Eigene Value (Root)	2.88666	2.45667	1.93519	1.36214	1.3121	1.18924	0.9546
% Var. Exp.	28.0416	15.3542	12.0949	8.51336	8.20062	7.43272	5.96622
Cum. Var. Exp.	28.0416	33.3958	45.4907	54.0041	62.2047	69.6374	85.6037
L*	0.41951	0.08635	0.3367	0.22787	0.11612	0.15309	0.1415
a*	-0.3005	-0.09591	0.47565	-0.0481	-0.04958	0.11005	0.17491
b*	0.26244	-0.20143	0.33684	0.2047	0.30338	-0.07193	-0.37253
Chroma	0.46788	0.08735	0.04541	0.23547	-0.13234	-0.05767	0.10995
Hue Angle tan-1b/a	0.09057	-0.19245	-0.43428	-0.2222	0.30732	-0.02318	0.38953
Length (mm)	-0.0764	-0.05894	0.39247	-0.162	-0.12689	-0.45913	0.41204
Breadth (mm)	-0.1424	0.31763	0.30936	-0.3719	0.0414	0.2542	-0.11398
L/B ratio	0.23905	0.09656	-0.18028	-0.0086	-0.50598	-0.43694	-0.03089
Ash Content (%)	0.34204	-0.09889	-0.08716	-0.3094	-0.07984	0.22404	-0.37147
Amylose (g)	-0.1299	0.40882	-0.19593	-0.0953	0.1144	0.1349	0.07182
Zn (mg/100g)	-0.1847	-0.42098	-0.05594	0.14464	-0.1766	0.18238	-0.18206
Mn (mg/100g)	0.15593	-0.39632	0.11675	-0.3824	0.01675	-0.13347	0.07021
Fe (mg/100g)	0.13766	-0.31178	0.02169	-0.4583	-0.07097	0.13459	-0.0045
Cu (mg/100g)	-0.0463	-0.35742	-0.07534	0.35756	-0.0752	0.37637	0.38403
TPC (mg GAE/100g)	-0.3595	-0.18642	-0.03009	0.13799	-0.24619	-0.20005	-0.33999
TEAC (mg TEAC/100g)	-0.1086	-0.1162	-0.06511	0.07422	0.61968	-0.4121	-0.13695

to moderate genotypic variance, high to moderate heritability and greater genetic gain for selection. There is an urgent need to study the yield and quality characters of the pigmented rice genotypes of North east India. The informations obtained from the present study may be utilized for adopting breeding plan for improvement of grain quality characters in pigmented rice genotypes of NE India**.**

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