



Genetic Variability and Diversity in Rice Cultivars of North Bank Plain Zone of Assam for Traits Associated with Grain Yield and Adaption under Moisture Stress

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Authors' contributions

This work was carried out in collaboration among all authors. Author ASNA designed the study, performed the experiment wrote the protocol, and wrote the first draft of the manuscript. Author MKS supervised and made the final presentation of the manuscript. Author DDS managed the analyses of the study, conducted the literature searches and statistical analysis. Authors MPN, NSD and JCT performed the laboratory analysis, collected and tabulated the data. Author SDD did the statistical analysis and software handling. All authors read and approved the final manuscript.

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ABSTRACT

Fifty four rice cultivars from North Bank Plain Zone (NBPZ) of Assam were assessed for their genetic variability and diversity with respect to yield and traits associated with adaptation under moisture stress with a view to formulate hybridization strategies for further genetic improvement. Genotypes were evaluated following a completely randomized design with two replications under PVC pipes at the experimental field of BN College of Agriculture, Biswanath Chariali, Assam. A higher magnitude of phenotypic and genotypic coefficient of variation was recorded for root volume, root dry weight, root length density, filled grains per panicle, shoot dry weight, root length,

root-shoot ratio and grain yield per plant. High heritability coupled with higher genetic advance was registered for root dry weight, root length density, root volume, root-shoot ratio, root length and grain yield per plant. D^2 analysis revealed that the genotypes could be distributed into a group of eight clusters with maximum distance between cluster III and cluster V (845.71). Root volume was found to contribute highest towards divergence (12.83%). Out of all the clusters, cluster IV with an intra cluster distance of 370.76 consisted of maximum number of accessions (17). Genotypes based on the *inter se* genetic distance and *per se* performances of specific traits were identified for undertaking hybridization programme. The implication of the diversity pattern elucidated for breeding varieties for moisture stress adaptation were discussed. Hybridization programme may be undertaken between the identified genotypes having *inter se* genetic diversity belonging to diverse clusters. Thus it could be expected to obtain desirable segregants out of the hybridization programme for further genetic improvement of rice in the region.

Keywords: Genetic variability; genetic diversity; rice; North Bank plain zone of Assam; moisture stress.

1. INTRODUCTION

Rice (*Oryza sativa* L.) is a noble crop mostly grown and consumed in Asia, where 60 per cent of the Earth's human population and two third of the World's poor live [1]. It is unique crop with its ability to grow under wide range of hydrological environment [2]. The crop is grown from about five meters water depth (below mean sea level) to even the hilltops at about 3050 meters above sea level having no stagnation of water [3]. Its adaptability ranges from the tropical climate of Sri Lanka and Africa to the temperate climate of South Korea and Japan [4]. The crop is cultivated in diverse ecosystems like upland, rainfed lowland, flood-prone, and irrigated. Rice crop consumes a relatively huge quantity of water during its growth period compared to other crops [5]. About 5000 litres of water is required to produce 1 kg of rice grain [6].

Under the current global water crisis, water is thus, considered as a major limiting factor in rice production. Reduced water supply to the crop or a condition of water stress not only affects the grain yield but also adversely affects the grain quality. With the advent of climate change, even in the high rainfall zone of Assam, intermittent water crisis has been affecting rice yield in recent years [7]. Root characteristics are, therefore, appears to be of paramount consideration under such water deficit situation. This investigation was, therefore, carried out on the currently cultivated varieties of the North Bank Plain Zone of Assam with a view to assess their diversity with respect to some root traits which are related with moisture stress adaptation as well as traits relate to grain yield. Thus, it is aimed at to arrive at the strategy to formulate an effective hybridization programme in order to obtain

desirable segregants for obtaining further genetic improvement of rice in the region.

2. MATERIALS AND METHODS

The materials for the present investigation consisted of a set of 54 rice cultivars (Table 1) comprising of 51 winter rice cultivars from farmers' fields of North Bank Plain Zone of Assam representing all the administrative blocks of the zone along with three upland rice genotypes. The investigation was carried out at the experimental field of Biswanath College of Agriculture, Biswanath Chariali, represented by the latitude of 26°15'N, 77°45'N, the longitude of 92°42'E, 95°30'E and altitude of 104 m MSL. The crop for the present investigation was raised during the Kharif season of 2019. The experiment was carried out using PVC (Poly Vinyl Chloride) tubes of one m length and 20 cm in diameter. With two replications, the experiment was carried out using Completely Randomized Design. The same soil media was employed across the experimental units to guarantee that the experimental units were homogeneous (PVC tubes). Five to six seeds were directly sown into each PVC pipes. Upon germination and seedling establishment, three well-spaced seedlings were retained and others were discarded. To impose a natural periodic moisture stress, the experiment was conducted in a rainfed environment. To quantify and understand the genetic variability, observations were recorded for 15 quantitative traits *viz.*, days to 50 per cent flowering, days to maturity, plant height (cm), effective tillers per plant, filled grains per panicle, root length (cm), root volume (cm³), root dry weight (g), shoot dry weight (g), root-shoot ratio, total chlorophyll content, chlorophyll stability index, root length density, proline content and grain yield per plant.

The data obtained were subjected to analysis of variance following standard protocol given by Panse and Sukhatme [8]. The mean sum of squares obtained from the analysis of variance was subjected to estimation of genetic parameters of variation as per Singh & Choudhury [9]. Estimates of variability parameters, heritability and genetic advance were calculated using standard methods of Burton and Devane [10], Lush [11] and Johnson et al., [12]. In order to understand the nature and magnitude of diversity prevailing in the rice genotypes, the 15 quantitative characters involving five root related characters were assessed for diversity based on the D^2 analysis (Mahalanobis, 1936). Grouping of the genotypes and estimation of contribution of traits towards diversity was performed by Tocher's method as suggested by Rao [13] and as described in Singh & Choudhury [9].

3. RESULTS AND DISCUSSION

The analysis of variance revealed that the mean sum of squares due to genotypes was significant for all the 15 traits. This indicated the presence of significant variation among all the genotypes and there appeared ample scope for selection of promising lines from the set of rice genotypes for yield and other moisture stress adaptive traits. The magnitude of variability indicated that the cultivars under the investigation were of much diverse in nature.

Several investigators in the past reported the presence of significant variability in rice germplasm for these traits. The present findings find co-linearity with the findings of Zheng et al. [14] and Hemamalini [15], who also observed significant variability for grain yield and root related component traits in rice. Such studies were, however, very meager in the rice germplasm of the region under consideration of present study. Thus, further dissection of the nature and magnitude of this variation in genetic terms would be meaningful. The estimates of various genetic parameters of variation are presented in Table 2. Highest genotypic and phenotypic coefficient of variances (GCV and PCV) was observed for root volume followed by root dry weight, root length density and grain yield per plant. PCV and GCV were classified as suggested by Shivasubramanian and Menon [16] into low (0 – 10%), Moderate (10.1 – 20%) and High (>20%). High GCV and PCV were observed for filled grains per panicle, root volume, root length, root dry weight, shoot dry weight, root-

shoot ratio, root length density and grain yield per plant. Ganapathy et al. [17] also observed high GCV and PCV in regards to traits viz., root length, root volume, root length density, root dry weight and root-shoot ratio in an experiment conducted under conditions of PVC pipes. PVC pipes grown crop. Moderate estimates of GCV and PCV were observed for plant height, effective tillers per plant, proline content, days to 50 *per cent* flowering and days to maturity. Nithya et al. [18] also reported moderate values for plant height, tiller number, days to 50 *per cent* flowering and relative water content. Total chlorophyll content and chlorophyll stability index on the other hand showed low estimates of GCV and PCV. Khriedinuo et al. [19] also observed low values of GCV and PCV for chlorophyll stability index. Higher values of GCV and PCV indicated that the germplasm exhibits relatively higher magnitude of variance with respect to these traits. This indicated possibilities of selection response for these traits. Presence of high magnitude of variation is also not the sole criterion for effectiveness of selection [20]. Therefore, estimation of heritability and genetic advance are also required to arrive at a more reliable conclusion [21].

Heritability was classified as suggested by Robinson et al. [22] into low (0 – 30%), moderate (30.1 – 60%) and high (> 60%). The genetic advance as per cent of mean was categorized as suggested by Johnson et al. [12] as low (0 - 10%), moderate (10.1 – 20%) and high (>20%). For variables such as root dry weight, root length density, root volume, root-shoot ratio, root length, and grain yield per plant, strong heritability with high genetic progress as a percent mean was observed (Table 2). Hemamalini [15] also observed similar trend with respect to high heritability and genetic advancement as *per cent* mean for root number, root volume and root dry weight. This suggested preponderance of additive gene action in the expression of these characters. Simple selection scheme would be effective in order to obtain genetic gain for these traits.

High heritability associated with moderate genetic advance as *per cent* mean was observed for days to 50 *per cent* flowering and days to maturity. As also reported earlier by Islam et al. [23] and Sabesan et al. [24], these traits are also governed by considerable magnitude of additive gene action. This indicated possibility of obtaining a reasonable response to selection in these traits owing to their high transmissibility

even if the genetic advance and GCV was moderate [25,26].

In order to understand the nature and magnitude of genetic diversity in 54 genotypes of rice, the mean data obtained for the 15 quantitative characters were subjected to the analysis of Mahalanobis' generalized distance (D^2). Based on D^2 values, 54 genotypes were grouped into five clusters (Fig. 1). Khatun et al. [27] and Worede et al. [28] calculated a similar clustering pattern for 43 and 24 upland rice genotypes, respectively. Out of the 54 genotypes, three genotypes were present in cluster I, eight genotypes in cluster II, 16 genotypes in cluster III, 17 genotypes in cluster IV and 10 genotypes in cluster V. The inter - cluster D^2 values also ranged widely with a minimum value of 192.42 between cluster I and cluster II and a maximum value of 845.71 between cluster III and cluster IV (Table 3). The intra - cluster distance varied from 62.83 in cluster I to a maximum of 629.93 in cluster V. This revealed the presence of considerable diversity existed even within a cluster. Cluster III with 16 genotypes and cluster IV with 17 genotypes were the most divergent groups with a maximum inter-cluster distance (845.71). Therefore, intercrossing between these genotypes may be expected to yield better recombinants. Sandhyakishore et al. [29] and Chandra et al. [30] also suggested to undertake intercrossing between the genotypes of clusters separated by large inter-cluster distances to achieve higher heterotic recombinants.

As a component of genetic diversity studies, per cent contribution of the traits towards diversity was calculated. Among the 15 quantitative characters studied, the most important character contributing to the divergence was root volume followed by grain yield per plant, root dry weight and root length density (Table 4).

The presence of the wide genetic diversity with respect to grain yield and the root traits related to adaptation for moisture stress in the cultivars of the NBPZ of Assam appears to be significance for breeding rice varieties for resilience to climate change leading to periodic moisture stress experienced recently. The spectrum and magnitude of genetic variability obtained in segregating generation is the function of genetic distance between the parents. Thus, the set of cultivars showed potential for selection of desirable parents in the above direction. However, while selecting diverse genotypes for hybridization programme their yield potential

should not be overlooked [31] While planning a hybridization programme, therefore, we should emphasize in one hand, the *inter se* genetic distance and on the other hand the *per se* performance of the genotypes for specific traits [6].

In the above considerations genotypes were identified for inclusion in hybridization programme. Out of 54 rice genotypes evaluated, the genotype Haccha belonging to cluster V was the earliest to attain 50 *per cent* flowering. It also exhibited the highest root- shoot ratio. Saru Jahinga belonging to cluster IV had the highest number of effective tillers per plant along with the highest root dry weight and root length density. This cultivar being a traditional photoperiod sensitive variety adapted to the native environment appears to be a promising parent contributing towards moisture stress tolerance [32-34]. Maximum root length and root volume were recorded for the genotypes Vasudev and Jaibangla respectively belonging to cluster IV. Filled grains per panicle was found to be highest in Bhogali followed by Bahadur. These two genotypes too belong to cluster IV. Ronga Joha of cluster II had the highest grain yield per plant followed by Bhogali.

Based on the mean performance of the genotypes, the earliness of Haccha appears to be advantageous and can be utilized in crossing programme with Saru Jahinga (effective tillers, root dry weight and root length density), Vasudev and Jaibangla (root length and root volume), Bhogali (filled grains per panicle) and Ronga Joha (grain yield) to produce recombinants with considerable higher yield and moisture stress tolerance. Better performances with respect to root length and filled grains per panicle was recorded for Bairing and Guni Dhan belonging to cluster III which are having the highest inter cluster distance with cluster V ($D^2 = 845.71$). Hence, hybridization between these genotypes with Haccha (cluster V) would yield short duration heterotic segregants. In this case, higher root length of Bairing would add to better tolerance to moisture stress through greater moisture absorption during water deficit condition. Also, Guni Dhan (cluster III) with higher number of filled grains per panicle could be used as parent in hybridization programme with genotypes having higher intensities of traits related to moisture stress tolerance. Likewise, utilization of Ronga Joha as one of the parents for crossing with the genotypes with better root traits might yield desirable high yielding

segregants under moisture stress environment. Thus, an efficient hybridization programme might be formulated out of the above consideration

which would pave the way for obtaining basic genetic materials to undertake further selection and crop improvement programme.

Table 1. List of 54 indigenous rice cultivars taken for the investigation

Sl. No.	Genotype	Place of Collection	Sl. No.	Genotype	Place of Collection
1	Bais Muthi	Udalguri	28	Biriabhonga Bao	Lakhimpur
2	Chapar Aijung	Darrang	29	Sok Maichu	Karbi Anglong
3	Kola Joha	Darrang	30	Komol Dhan	Sonitpur
4	Ranjit 1	Darrang	31	Bora	Sonitpur
5	Solpona	Dhemaji	32	Ranjit 2	Udalguri
6	Sulsuli Bao	Dhemaji	33	Mala	Biswanath
7	Boga Joha	Dhemaji	34	Prasadbhog	Biswanath
8	Basanti Sali	Dhemaji	35	Bishnuprasad	Biswanath
9	Biyoi Sali	Dhemaji	36	TTB-404	Biswanath
10	Kosu Sali	Dhemaji	37	Kunkuni Joha	Biswanath
11	Kon Joha	Dhemaji	38	Bhogali	Biswanath
12	Maguri Dhan	Dhemaji	39	Luit	Biswanath
13	Kokua Bao	Dhemaji	40	Agni Sali	Biswanath
14	Guni Dhan	Dhemaji	41	Ranikajol Joha	Biswanath
15	Jaldubi	Dhemaji	42	Moinagiri	Biswanath
16	Suwagmoni	Dhemaji	43	Bahadur	Biswanath
17	Ronga Joha	Dhemaji	44	Dehangi	Biswanath
18	Malbhog Dhan	Dhemaji	45	Kanaklata	Biswanath
19	Aampakhi	Dhemaji	46	Jaibangla	Biswanath
20	CheniSakowa	Lakhimpur	47	Panindra	Biswanath
21	Betguti	Dhemaji	48	Boga Aijung	Biswanath
22	Gumraj	Dhemaji	49	Haccha	Haflong
23	Saru Jahinga	Dhemaji	50	Vasudev	Biswanath
24	Bor Jahinga	Dhemaji	51	Maibee	Karbi Anglong
25	Nepali Sokowa	Dhemaji	52	Bairing	Karbi Anglong
26	RangaSali	Dhemaji	53	Vandana	Karbi Anglong
27	Til Bora	Dhemaji	54	Inglongkiri	Karbi Anglong

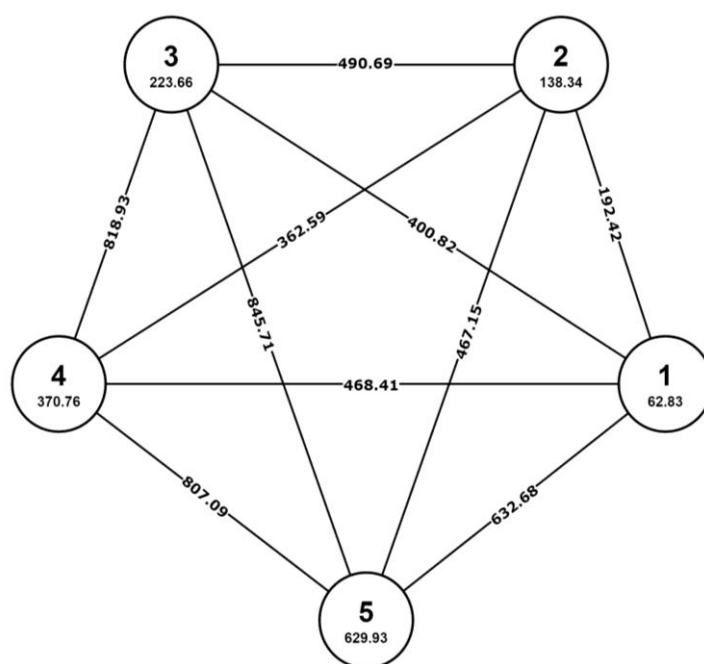


Fig. 1. Mahalanobis Euclidean Distance

Table 2. Genetic parameters of variation for 15 quantitative traits in rice under moisture stress situation

Character	Mean	SE(m)	Range	GV	PV	EV	GCV (%)	PCV (%)	H _{bs}	GA (%)
Days to 50 percent flowering	114.54	0.97	69 - 144	223.82	225.69	1.87	13.06	13.12	99.17	26.80
Days to maturity	146.79	1.34	102 - 174	222.91	226.48	3.56	10.17	10.25	98.43	20.79
Plant Height	114.66	1.73	64.28 - 161.94	508.95	514.96	6.01	19.68	19.79	98.83	40.29
Effective tillers per plant	9.50	0.88	4 - 16	3.42	4.96	1.54	19.47	23.44	69.03	33.33
Filled grains per panicle	84.11	7.64	22 - 182	1018.07	1134.79	116.72	37.93	40.05	89.71	74.02
Root length	37.40	2.22	15.44 - 63.42	109.66	119.55	9.88	28.00	29.23	91.73	55.24
Root volume	23.91	1.98	6.5 - 59.5	157.98	165.83	7.85	52.58	53.87	95.27	105.72
Root dry weight	14.56	0.74	4.18 - 30.36	42.95	44.04	1.09	45.01	45.57	97.53	91.56
Shoot dry weight	44.30	1.49	15.94 - 83.74	232.55	236.98	4.43	34.43	34.75	98.13	70.25
Root-Shoot ratio	0.33	0.02	0.19 - 0.52	0.01	0.01	0.01	26.98	27.82	94.07	53.91
Total Chlorophyll content	1.69	0.06	1.24 - 1.87	0.01	0.01	0.01	4.66	6.65	49.17	6.74
Chlorophyll Stability Index	76.27	1.33	66.92 - 83.62	7.46	11.02	3.56	3.58	4.35	67.72	6.07
Root length density	0.14	0.01	0.04 - 0.29	0.01	0.01	0.01	45.01	45.57	97.53	91.56
Proline content	52.61	1.73	32.00 - 97.95	85.78	91.78	6.00	17.60	18.21	93.46	35.06
Grain yield per plant	13.63	1.56	3.69 - 34.69	36.39	41.28	4.89	44.28	47.16	88.16	85.64

Where,
 GV : Genotypic Variance GCV : Genotypic Coefficient of Variance GA : Genetic Advance as per cent mean
 PV : Phenotypic Variance PCV : Phenotypic Coefficient of Variance SE(m) : Standard Error of mean
 EV : Environmental Variance H_{bs} : Heritability in Broad Sense

Table 3. Clustering pattern along with average inter and intra cluster distances for yield and root related characters

Clusters	Genotypes	I	II	III	IV	V
I	Gumraj, Kanaklata, Kola Joha	62.83	192.42	400.82	468.41	632.68
II	Ronga Joha, Bor Jahinga, Malbhoog Dhan, Solpona, Boga Joha, Bishnuprasad, Panindra, Aampakhi	192.42	138.34	490.68	362.59	467.15
III	BasantiSali, Jaldubi, MaguriDhan, KosuSali, Mala, SokMaichu, KokuaBao, Sulsuli Bao, Boga Aijung, Bairing, Maibee, BiriabhongaBao, GuniDhan, Ranjit 1, Ranikajol Joha, Luit	400.82	490.68	223.66	818.93	845.71
IV	Ranjit 2, Kunkuni Joha, Kon Joha, Moinagiri, RongaSali, Biyoisali, Suwagmoni, Bora, Betguti, Til Bora, Saru Jahinga, Jaibangla, Prasadbhog, Bahadur, KomolDhan, Bhogali, Vasudev	468.41	362.59	818.93	370.76	807.09
V	Nepali Sokowa, Agni Sali, Vandana, TTB-404, CheniSakowa, BaisMuthi, Inlongkiri, ChaparAijung, Dehangi, Haccha	632.68	467.15	845.71	807.09	629.93

* Diagonal values indicate intra cluster distances; * Above and below diagonal values indicate inter cluster distances

Table 4. Per cent contribution of each character towards divergence in rice genotypes evaluated under low-moisture stress condition using PVC Pipes

Sl. No.	Character	Contribution (%)
1	Days to 50 per cent Flowering	3.13
2	Days to Maturity	2.44
3	Plant Height	4.71
4	Effective Tillers per plant	5.58
5	Filled Grains per Plant	9.54
6	Root Length	6.96
7	Root Volume	12.83
8	Root Dry Weight	10.85
9	Shoot Dry Weight	8.28
10	Root-Shoot Ratio	6.63
11	Total chlorophyll content	1.58
12	Chlorophyll Stability Index	1.04
13	Root Length Density	10.85
14	Proline Content	4.34
15	Grain yield per Plant	11.23
	Total contribution	100

4. CONCLUSION

The present study indicated the presence of significant variability and elucidated the genetic diversity amongst the cultivated rice varieties of North Bank Plain Zone of Assam. In view of the advent of climate change and recently experienced drought spells, the elucidation of diversity and identification of genotypes as donors for different traits related with grain yield as well as moisture stress tolerance, particularly the root traits would facilitate further breeding programme for rice improvement in the region. The findings of the study revealed the *per se* performances of the rice cultivars as well as their *inter se* genetic distances, which will help in planning hybridization programme in order to obtain desirable segregants.

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ETHICAL APPROVAL

There is no any involvement of ethical issues regarding the report on the manuscript.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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