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## Research Article

### Pattern of genetic diversity in indigenous *Ahu* rice germplasm of Assam

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#### Abstract

The north-eastern part of India including Assam is one of the key centres of diversity of cultivated rice. Among the diverse varietal types, *Ahu* group of varieties with their evolutionary significance being intermediate between *indica* and *japonica* deserves attention for their detailed evaluation and utilisation in crop improvement programme. This work was attempted to elucidate the pattern of genetic variation and genetic diversity in a set of 147 indigenous *Ahu* rice genotypes of Assam grown under rainfed upland direct seeded condition. Among the 13 traits under study, the highest genotypic coefficient of variation was exhibited by primary branches per plant followed by secondary branches per plant and grain yield. Heritability in broad sense was the highest for grain L: B ratio followed by grain width and grain length. More than 90% heritability in broad sense was, observed for all the traits except effective tillers per plant, panicle length and grain yield. The highest genetic advance as per cent of mean was observed for primary branches per plant followed by secondary branches per plant and grain yield. Hence, selection for these traits would be most effective for further genetic improvement. At the intermediate linkage distance, four main and nine sub clusters were obtained by Euclidean cluster analysis. Cluster III b was the largest containing 35 entries, which was followed by cluster I c containing 32 entries. The variety Chidon *Ahu* remained distinct from all other entries and belonged to cluster I b. Based on *per se* performances of the genotypes and their *inter se* distance, promising genotypes were suggested for hybridization in order to obtain desirable segregants for further genetic improvement of *Ahu* rices.

**Keywords:** Genetic variation, genetic divergence, *Ahu* rice, rainfed upland

#### INTRODUCTION

Rice (*Oryza sativa* L.) being the staple food of about 50 per cent people worldwide, occupies an important place amongst the cultivated cereals. Rice is the most important cereal for the people of south-east Asia where about 90 per cent of the people consume rice and it is their staple food. India is endowed with a large number of cultivated and wild rice genotypes in different eco-geographical regions of its vast territorial land. Out of the different rice growing areas, Assam and adjoining states of northeast India, which is the prime centre of diversity of *Oryza sativa*, comprise a very rich region having

enormous forms of cultivated rice. Only a tiny fraction of the available diversity of rice in the region was utilized in varietal development (Baruah and Das, 1995).

Rice germplasm of north-east India is not only endowed with genetic diversity but also represents a wealth of valuable genes (Sharma *et al.*, 1971; Das *et al.*, 1981). Continuous rice cropping through ages in the varying land situations of the region and differential preferences of rice types by various tribes and communities resulted in adaptive selection and development of multitude of

cultivated varieties for specific adaptation (Das, 1997). A large number of cultivated varietal groups are known to exist in the region as identified by their adaptation to different eco-geographical situation, seasons, grain types and endosperm quality to suit different ethnic preferences (Baruah and Das, 1995).

The entire north-east India is endowed with hundreds of photoperiod insensitive traditional varieties of rice which are cultivated during February / March to June / July either as dry broadcast under rainfed upland or transplanted crop depending on water availability. This group of varieties popularly known as *Ahu* are characterized by photoinensitivity, early maturity, tolerance to periodic moisture stress and poor yield (1000 kg/ha). They are intermediate between the *indica* and *japonica* subspecies of rice (Das, 1997). However, These rices of Assam have not received due attention for their improvement as well as for their utilisation in breeding programmes (Sarma *et al.*, 2004). Hence, there is significance for detail characterisation of this diversity for evolutionary point of view and for utilisation in rice improvement. In the present investigation an attempt was made to elucidate the variability and diversity pattern of a set of 147 *Ahu* rice genotypes of Assam.

#### MATERIALS AND METHODS

The experiment was carried out during *Ahu* season ( Feb/March - June/July) of 2019 & 2020 with 147 rice genotypes belonging to *Ahu* group of rice varieties including IR 64, CH 63 and Annada as checks under direct seeded situation of rainfed upland in the research field of B N College of Agriculture, AAU, Biswanath Chariali, Assam. The experiment was laid out in a randomized block design with three replications. Each plot consisted of five rows of three meter length. Seeds were direct sown in line with 20 cm inter row spacing maintaining 5 cm seedling to seedling distance for assessment of individual plant performance and the crops were raised following the recommended package of practices under rainfed upland condition of Assam.

Ten plants were tagged randomly in each plot avoiding border rows for recording data on grain yield and yield attributes. Seed yield was recorded on randomly taken one meter length of crop row. Plant height was measured from the ground level to the panicle tip of mother culm. Five plants were randomly selected from each plot, to record the yield attributes *viz.*, plant height, effective tillers, panicle length, panicle weight, primary and secondary branches per panicle, spikelets per panicle, grain weight, grain length and width. The days required from sowing to 50% flowering and maturity was recorded on plot basis. The data over seasons were pooled and subjected to the analysis of variance of RBD design with three replications following Panse and Sukhatme (1967). The mean sum of squares obtained from ANOVA analysis were subjected to estimation of genetic parameters of

variation as per Singh and Choudhury (1988). Estimates of variability parameters, heritability and genetic advance were calculated using standard methods of Burton and Devane (1953) and Johnson *et al.* (1955). The mean data set pooled over the years were subjected to diversity analysis using Euclidian Cluster Analysis following single linkage rule (Sneath and Socol, 1973) and using the software STATISTICA.

#### RESULTS AND DISCUSSION

Analysis of variance revealed significant mean sum of squares for all the 13 traits under study indicating wide variability in the set of 147 rice genotypes under study. The estimates of genetic parameters of variation are presented in **Table 1**. Highest Genotypic variance was observed for the attribute number of filled spikelets per panicle followed by plant height and days to maturity. Similar pattern was also observed for variance due to phenotype which indicated good agreement between the phenotypic observations with the genotypic values. Mere studying the magnitude of variance does not justify the comparison of variability exhibited by different traits. Estimation of coefficient of variation which takes into account the mean of each characters, gives the real basis for comparison. In this investigation, highest genotypic coefficient of variation was exhibited by primary branches per plant followed by secondary branches per plant and grain yield. There was good agreement between the genotypic coefficient of variation and phenotypic coefficient of variation indicating less influence of environmental variance. Mere presence of high magnitude of variation does not indicate the effectiveness of selection (Burton, 1952). Here lies the essence of estimation of heritability and genetic advance (Sarma and Richharia, 1995). Heritability in broad sense was highest for grain L : B ratio followed by grain width and grain length. More than 90% heritability in broad sense was, observed for all the traits except effective tillers per plant, panicle length and grain yield. Genetic advance as *per cent* of mean was observed highest for primary branches per plant followed by secondary branches per plant and grain yield. High heritability coupled with high genetic advance indicates effectiveness of selection (Johnson *et al.*, 1959 and Gandhi *et al.*, 1964). Based on the above observation it may be predicted that selection for the traits, primary branches per plant followed by secondary branches per plant and grain yield would be most effective for further genetic improvement in the set of germplasm under study. The traits under study in general had high to moderate heritability and genetic advance which indicated involvement of both additive and non-additive gene actions. These results are accordance with Jayasudha and Sharma (2010).

The variability spectrum generated in the segregating generation depends on the genetic distance between the parents. The wider the genetic distance between the parents, wider is the variability generated in the segregating generation. The 147 rice genotypes were

**Table1. Genetic parameters of variation for 13 quantitative traits in rice under aerobic environment**

Genetic parameters	Days to 50% flowering	Days to maturity	Plant height (cm)	Effective tillers per plant	Panicle length (cm)	Number of primary branches per plant	Number of secondary branches per plant	Filled spikelets per panicle	100-grain weight (g)	Grain length (mm)	Grain width (mm)	Grain L:B ratio	Grain yield per metre row length (g)
Maximum	118.00	156.00	140.40	8.00	26.30	13.4	37.6	164.20	3.57	9.50	3.50	3.52	108.41
Minimum	65.00	93.00	66.50	4.00	16.00	5.6	6.5	44.80	0.95	4.01	2.02	1.23	15.91
Mean	99.36	139.24	105.84	5.75	19.69	9.5	21.4	101.06	1.89	6.12	3.07	2.01	50.24
Phenotypic variance	232.23	311.09	318.97	0.95	4.12	14.8	59.7	497.10	0.20	1.28	0.06	0.21	263.98
Genotypic variance	227.12	297.41	302.70	0.81	3.64	14.2	54.5	454.35	0.20	1.27	0.06	0.21	197.46
PCV(%)	15.34	12.67	16.87	16.95	10.31	40.50	36.11	22.06	23.82	18.47	7.80	22.85	32.34
GCV (%)	15.17	12.39	16.44	15.67	9.69	39.67	34.50	21.09	23.67	18.40	7.78	22.83	27.97
Heritability (bs) %	97.80	95.60	94.90	85.50	88.30	95.95	91.29	91.40	98.70	99.30	99.50	99.80	74.80
Genetic advance	30.70	34.74	34.91	1.72	3.69	7.60	14.53	41.98	0.91	2.31	0.49	0.95	25.04
Genetic advance (% of mean)	30.90	24.95	32.99	29.85	18.75	80.04	67.90	41.54	48.44	37.77	15.98	46.97	49.83
CV	2.27	2.66	3.81	6.45	3.53	8.15	10.66	6.47	2.72	1.54	0.55	1.02	16.23
SEm	0.98	1.20	1.34	0.56	0.78	0.87	1.32	8.56	0.08	0.15	0.07	0.06	5.85

subjected to genetic diversity analysis following Euclidean cluster analyses based on single linkage rule. The diversity pattern obtained from the analysis is presented in the form of dendrogram (**Fig. 1**). At the intermediate linkage distance, we obtained four diverse main clusters which were further divided into nine sub clusters out of the 147 entries. Cluster III b was the largest cluster containing 35 entries, which was followed by Cluster I c containing 32 entries (**Table 2**). The variety Chidon ahu remained distinct from all other entries and belonged to cluster I b. Clusters mean values for different traits were calculated and presented in **Table 3**. Cluster II a was identified with highest cluster mean values for grain yield (GY), panicle length (PL), and spikelets per panicle (SP). In contrast to this, cluster IV b exhibited the lowest mean values for these traits. The cluster I c had lowest mean value for days to maturity. Clusters II b and III a exhibited highest mean values for primary branches per plant and secondary branches per plant. The highest mean number of effective tillers per plant was observed in cluster II b while lowest was observed for I b. Plant height was lowest in cluster I b while, it was highest in I a. The cluster I b exhibited highest mean values for grain weight, grain length and grain length-breadth ratio (L:B). Lowest grain weight was exhibited by cluster I a.

Clusters were obtained from the dendrogram prepared on the basis of Euclidean distance following UPAGMA linkage rule. Such clustering was used by many workers

in studying genetic diversity with respect to morphological as well as molecular variation in various crops including rice (Mohapatra *et al.*, 1993; Sarma *et al.*, 2015; Parasar *et al.*, 2017; Sarma *et al.*, 2019). Grouping of genotypes through the method of dendrograms as followed in this study had been observed to be in good agreement with Tocher's method following D<sup>2</sup> analysis and canonical root method commonly followed in genetic diversity analysis (Mohapatra *et al.*, 1993).

Clustering pattern of the present study revealed the presence of wide diversity in the set of *Ahu* rice genotypes with respect to various traits related with grain yield. Dendrogram obtained for the set of traits indicated that varieties could be reasonably classified into several clusters based on the traits evaluated. Earlier workers (Das *et al.*, 1981; Baruah *et al.*, 1994) also classified *Ahu* rice germplasm of Assam which also indicated the presence considerable diversity in *Ahu* rices. Similar analysis of diversity was also made by Banumathi *et al.* (2010) The findings of the present investigation would therefore, very well supplement the information available on the pattern of diversity in *Ahu* rices of Assam.

The wide grouping of the varieties would facilitate for isolation of diverse genotypes with respect to characteristics of interest. It is however important that while selecting diverse genotypes for hybridization

Table 2. Composition of different clusters involving 147 *Ahu* rice genotypes

Cluster	S. No.	Genotype	Cluster	S. No.	Genotype	Cluster	S. No.	Genotype	
Cluster Ia	1	Nilazi I	Cluster IIb	47	IR 64	Cluster IIIb contd.	97	Hasakumra II	
	2	Maibee II		48	Annada		98	Jubali	
	3	Maibee I		49	Titabor local		99	Bijor II	
	4	Bahmori		50	Koejeira II		100	Bijor I	
	5	Bizor III		51	Duhiguni		101	AS 100	
	6	Durshiahu II		52	Koejeira I		102	AS 75	
	7	As 1194		53	Dogaronga II		103	Kolaahu	
Cluster Ib	8	Chidonahu		54	AS 192		104	Banglami II	
				55	Noga ahu		105	Kajoliahu	
Cluster Ic	9	Sesamthat		56	Meghiahu I		106	Bairing	
	10	Kolamanik		57	AS 320		107	Durshiahu I	
	11	Garem III	58	AS 180/2	108	AS 1195			
	12	Ikoraguni II	59	Guniahu II	109	Rongagutia II			
	13	Haripua	60	Iharsal	110	AS 69-70			
	14	Guniahu I	61	AS 105	111	Ahujohall			
	15	Saraituni	62	Rongdoi II	Cluster IVa	112	Swarnamohan		
	16	Chenga ahu	63	Daokola maghi		113	Begonbishi		
	17	Betguti I	64	AS317		114	Rongajira		
	18	NDR 97	65	Menors ahu		115	Rongadoria I		
	19	Basantabahar	66	Kolagoria		116	Rogagutia I		
	20	Malsira	67	AS 39		117	Paromaahu		
	21	Goalbhog	68	Nipak		118	Koijapuri I		
	22	Gorumoina	69	Nilazi II		119	Koijapuri II		
	23	Ikoragunil	70	Maibee III		120	Rikhjoi I		
	24	Hufaahu	71	Gunidhan		121	BNAS 6		
	25	Gobarguni	72	Cheniahu		122	AS 323		
	26	Gorupodia ahu	73	BNAS 5		123	Koimurali II		
	27	Koimurali I	74	AS 206		124	BNAS 2		
	28	Hasakumra I	75	Cheniahu I		125	TTB 182		
	29	Bongaloni	76	AS 36		126	Saruronga ahu		
	30	Panjasali	77	Heera		127	Ikra III		
	31	BNAS 7	78	Kanua		128	Ikra II		
	32	Bogaahu	79	Kanchi	129	Ikra I			
	33	Jaibangla II	80	Bongalahu	130	Aijuri			
	34	Jaibangla I	81	Betgutiahu II	131	Dogaronga I			
	35	Bizor III	82	Kolamaghi	132	Sarimohia ahu II			
	36	AS 1196	83	AS 209	133	Sarimohia ahu I			
	37	Majenichamba	84	SD 98	134	CH 63			
	38	AS 178/3	85	Himalay	135	Rikhjoi II			
	39	As 313	86	AS 34	136	Dubaichenga			
	40	AS 152	87	Banglami I	137	Ahujoha I			
	Cluster Ila	41	TTB 360	Cluster IIIa	88	Roso	Cluster IVb	138	Rongadoria II
		42	Padunoniahu II		89	Meghiahu II		139	BNAS 4
		43	Malbhogl		90	Khoijoi		140	BNAS 3
		44	Tinimohia		91	Rongadoria		141	AS 330
		45	Kosamoni		92	Malbhog II		142	AS 69/70
		46	Garem II		93	Padumoniahu I		143	AS 490
					94	Garem I		144	AS 36/20
					95	Bijor I		145	Rongdoi I
		96	AS 191	146	Chanali				
				147	Ahujam				

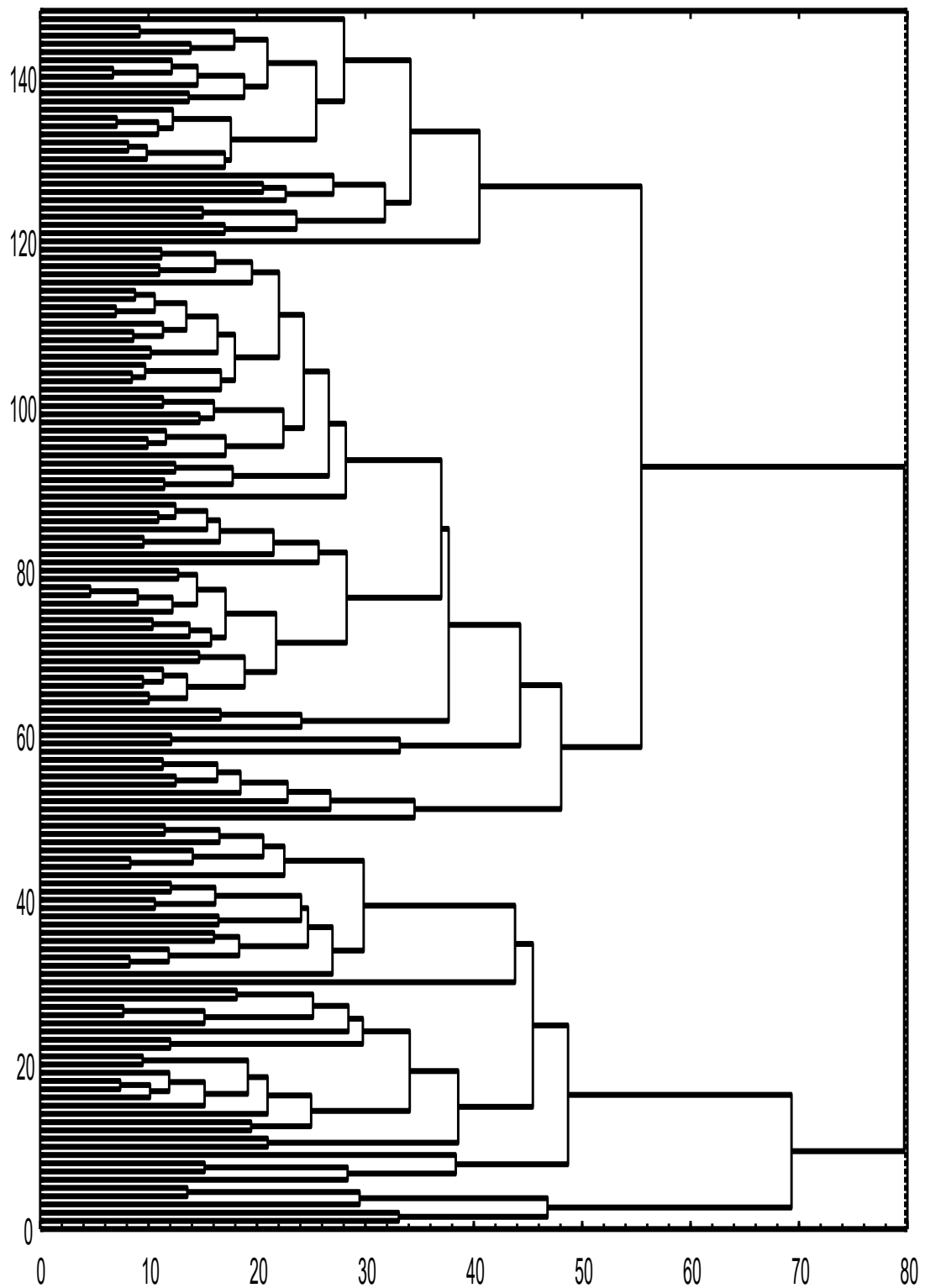


Fig. 1. Dendrogram based on Euclidian distance and UPGMA

Table 3. Cluster mean values for different yield and yield attributing traits

Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	Effective tillers per plant	Panicle length (cm)	Number of primary branches per plant	Number of secondary branches per plant	Filled spikelets per panicle	100-grain weight (g)	Grain length (mm)	Grain width (mm)	Grain L:B ratio	Grain yield per metre row length (g)
Ia	92.86	121.00**	120.57**	7.86	25.83	7.88	22.97	163.64	2.21*	7.24	2.41*	3.06	14.69
Ib	93.00**	121.00**	80.60*	5.60*	23.56	8.06	20.89	128.80	2.89**	8.13**	2.55	3.19**	11.20
Ic	83.32*	111.30*	111.20	7.54	24.13	7.65	26.04	142.00	2.28	6.98	2.59	2.77	14.72
IIa	90.83	119.67	119.67	8.20	26.33**	6.95	18.31*	200.52**	2.32	6.83	2.44	2.87	20.93**
IIb	86.31	115.33	106.54	9.25**	24.98	12.60**	22.51	183.55	2.29	7.03*	2.53	2.90	19.86
IIIa	83.22	112.61	114.35	7.07	20.62	6.20*	27.62**	92.89	2.39	7.03	2.50	2.85	10.82
IIIb	85.30	113.50	108.87	8.58	22.70	6.80	27.15	119.50	2.38	7.11	2.56	2.85	13.99
IVa	88.32	117.00	118.45	7.72	24.62	6.40	21.51	154.57	2.41	6.79*	2.75**	2.51*	15.61
IVb	84.00	112.20	110.54	8.45	19.96*	6.50	26.30	81.48*	2.48	6.91	2.66	2.61	10.46*

\*\* = Highest cluster mean, \* = Lowest cluster mean

programme, the *per se* performance of the genotypes should not be overlooked (Singh *et al.*, 1987). An insight into the cluster mean values for different traits would be helpful in identifying genotypes having desirable *per se* performance as well as belonging to diverse clusters.

Therefore, selection of genotypes having desirable *per se* performance for the traits under consideration and belonging to different clusters should be practiced in order to incorporate them in hybridization programme. Based on the genetic diversity as well as *per se* performance genotypes could be identified useful for hybridization for various traits. Thus, genotypes selected for various traits were, Padumoni Ahu, Ikra I and Ikra II for grain yield; Khoijoi for grain yield and effective tillers; Kosamoni for grain yield, spikelets per panicle and panicle length; Tinimohia Ahu, TTB 360 and Malbhog I for spikelets per panicle; Malbhog II and Kola Ahu for grain weight; Himalay, Maibee II and Titabor Local for grain length; Rikhjoi II for panicle length; Boga Ahu for panicle length, earliness and grain length; Kanua, Kanchi, Jaibangla and AS 192 for dwarfness, Chidon Ahu for dwarfness, grain weight and grain length; Aijuri for grain length, Basantbahar for grain length, lower grain width and high L:B ratio and Chenga Ahu for grain width. These varieties belonging to different clusters and having desirable *per se* performances for various traits could be hybridized in order to obtain desirable segregants for further *Ahu* rice improvement programme.

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