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 photoinsensitivity, 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 Socal, 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
Table 1. 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 (PCV of mean) | 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                        |

subjects 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 dendogram (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 dendogram prepared on the basis of Euclidian 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 dendograms as followed in this study had been observed to be in good agreement with Tocher’s method following D² 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. Dendogram 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 | 47 | 51 | Duhuguni | 97 | Hasakumra II |
|         | 3 | Khejaria | 48 | 52 | Khejaria II | 98 | Jubali |
|         | 4 | Malbhog | 49 | 53 | Dogaronga II | 99 | Bijor II |
|         | 5 | Malsira | 50 | 54 | AS 192 | 100 | Bijor I |
|         | 6 | Panjasali | 51 | 55 | AS 180/2 | 101 | AS 100 |
|         | 7 | Panjasali | 52 | 56 | AS 197 | 102 | AS 75 |
|         | 8 | Panjasali | 53 | 57 | AS 181 | 103 | AS 75 |
|         | 9 | Panjasali | 54 | 58 | AS 195 | 104 | Kolaahu |
|         | 10 | Panjasali | 55 | 59 | AS 196 | 105 | Kolaahu |
|         | 11 | Panjasali | 56 | 60 | AS 197 | 106 | Kolaahu |
|         | 12 | Panjasali | 57 | 61 | AS 199 | 107 | Kolaahu |
|         | 13 | Panjasali | 58 | 62 | AS 200 | 108 | Kolaahu |
|         | 14 | Panjasali | 59 | 63 | AS 201 | 109 | Kolaahu |
|         | 15 | Panjasali | 60 | 64 | AS 202 | 110 | Kolaahu |
|         | 16 | Panjasali | 61 | 65 | AS 203 | 111 | Kolaahu |
|         | 17 | Panjasali | 62 | 66 | AS 204 | 112 | Kolaahu |
|         | 18 | Panjasali | 63 | 67 | AS 205 | 113 | Kolaahu |
|         | 19 | Panjasali | 64 | 68 | AS 206 | 114 | Kolaahu |
|         | 20 | Panjasali | 65 | 69 | AS 207 | 115 | Kolaahu |
|         | 21 | Panjasali | 66 | 70 | AS 208 | 116 | Kolaahu |
|         | 22 | Panjasali | 67 | 71 | AS 209 | 117 | Kolaahu |
|         | 23 | Panjasali | 68 | 72 | AS 210 | 118 | Kolaahu |
|         | 24 | Panjasali | 69 | 73 | AS 211 | 119 | Kolaahu |
|         | 25 | Panjasali | 70 | 74 | AS 212 | 120 | Kolaahu |
|         | 26 | Panjasali | 71 | 75 | AS 213 | 121 | Kolaahu |
|         | 27 | Panjasali | 72 | 76 | AS 214 | 122 | Kolaahu |
|         | 28 | Panjasali | 73 | 77 | AS 215 | 123 | Kolaahu |
|         | 29 | Panjasali | 74 | 78 | AS 216 | 124 | Kolaahu |
|         | 30 | Panjasali | 75 | 79 | AS 217 | 125 | Kolaahu |
|         | 31 | Panjasali | 76 | 80 | AS 218 | 126 | Kolaahu |
|         | 32 | Panjasali | 77 | 81 | AS 219 | 127 | Kolaahu |
|         | 33 | Panjasali | 78 | 82 | AS 220 | 128 | Kolaahu |
|         | 34 | Panjasali | 79 | 83 | AS 221 | 129 | Kolaahu |
|         | 35 | Panjasali | 80 | 84 | AS 222 | 130 | Kolaahu |
|         | 36 | Panjasali | 81 | 85 | AS 223 | 131 | Kolaahu |
|         | 37 | Panjasali | 82 | 86 | AS 224 | 132 | Kolaahu |
|         | 38 | Panjasali | 83 | 87 | AS 225 | 133 | Kolaahu |
|         | 39 | Panjasali | 84 | 88 | AS 226 | 134 | Kolaahu |
|         | 40 | Panjasali | 85 | 89 | AS 227 | 135 | Kolaahu |
|         | 41 | Panjasali | 86 | 90 | AS 228 | 136 | Kolaahu |
|         | 42 | Panjasali | 87 | 91 | AS 229 | 137 | Kolaahu |
|         | 43 | Panjasali | 88 | 92 | AS 230 | 138 | Kolaahu |
|         | 44 | Panjasali | 89 | 93 | AS 231 | 139 | Kolaahu |
|         | 45 | Panjasali | 90 | 94 | AS 232 | 140 | Kolaahu |
|         | 46 | Panjasali | 91 | 95 | AS 233 | 141 | Kolaahu |
|         | 47 | Panjasali | 92 | 96 | AS 234 | 142 | Kolaahu |
|          |     |             |        |     |             |        |     |             |
Fig. 1. Dendogram 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                     |
| lc       | 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                     |
| lla      | 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**                    |
| llb      | 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                     |
| llia     | 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                     |
| llb      | 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                     |
| lVa      | 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                     |
| lVb      | 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; Ajouri 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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