

Morphological characterization of Brinjal genotype of Assam using multivariate analysis

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ABSTRACT

The experiment was carried out to evaluate the genetic diversity, correlation, and path coefficient analysis between twenty-three brinjal genotypes during the summer season of 2019 at Horticultural Research Farm, Assam Agricultural University. The twenty-three brinjal genotypes were grown in randomized complete block design with three replications. The analyses of variance revealed significant variation at a genotypic level for all the sixteen characters except one i.e, fruit length which indicates that the genotypes are diverged genetically. Longai oblong (G3) genotype has shown the maximum yield per plant, which may be due to the highest number of primary branches. From the path coefficient analysis, it was found that the highest positive direct effect was of days to 50% fruiting (1.100), followed by days to first fruiting (0.263), fruit volume (0.217), days to 50% flowering (0.199) and fruit pedicel length (0.190). For these characters, direct selection would be useful in crop improvement. Based on D^2 analysis the twenty-three genotypes were grouped into 5 clusters. The inter-cluster D^2 value was observed to be maximum (329.67) between clusters III and IV followed by between cluster I and IV with D^2 value of 284.76. This is indicative of diverse clusters which can be utilized for producing superior heterotic combinations. The values of the PCs explained all the characters influencing about 77.6% of the genotypic variability, while the first two PCs explained 58.8% of the variability. Based on the relationship of characters and genotypes to the PC 1, it can be concluded that the genotypes G3, G5, G7, G10, and G19 can be selected for breeding purposes in the brinjal improvement program for the Assam condition.

Keywords- Genotype, Heritability, D-square, Path analysis, Principle component, brinjal

Introduction

Vegetables are good sources of vitamins, carbohydrates, proteins, and minerals. Consuming vegetables improves the overall well-being of a person. They have various health benefits. Since vegetables are rich in antioxidants and phytochemicals, they help in controlling inflammation. The other benefits include improved blood pressure, better eyesight, good skin, reduced risk of heart disease, cancer, and increased immunity. Brinjal (*Solanum melongena* L.), which hails from the nightshade family of plants is rich in fiber and low in calories. This helps in regulating blood sugar levels and controls the absorption of glucose. A study has found that phenolics present in the brinjal act as inhibitors of enzymes involved with type 2 diabetes [1]. Brinjals are said to possess antioxidant properties that promote a healthy heart [2]. Several studies have shown the anti-cancer benefit of brinjal. One such study by Cham (2011) has found the presence of solasodine rhamnosyl glycosides (SRGs) in brinjal peel which is believed to treat skin cancer. Other benefits of brinjal include improved cognitive function, skin health, aid in weight loss, promote eye health, enhanced bone health, treat Anemia and prevent birth defects. Apart from the health benefits to the consumers, brinjal

is a boon to the growers as well. From a farmer's perspective, in comparison to field crops, vegetable farming is a promising venture. This is so because vegetables are of very short duration that can be easily grown in diversified agro-climatic conditions. The income generated is also comparatively high. As per the National nutrition guidelines 'recommendation, a person should consume on average, 300 g of vegetables daily. Therefore, cultivating brinjal which is considered as a superfood can earn huge returns for the farmers. Brinjal is a vegetable crop where one can find immense diversity in its morphological characteristics. There is variation in the number of seeds a brinjal fruit contains, plant stature, the colour of the leaves, flowers, fruits, the shape, color distribution of the fruit etc. In India, we will find diversified varieties of brinjal differing in size, shape, and color of fruits [3]. India is the center of origin for the brinjal crop and with the existing variations in the brinjal crop opens up avenues for crop improvement for any stakeholders – plant breeders, agricultural institutes, seeds companies, etc. Despite the prospects of brinjal having economic as well as nutritional importance, the efforts in brinjal breeding are still inadequate. And because of this reason, its production is lower

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in comparison with other solanaceous crops [4]. For increasing productivity, the first and foremost objective of brinjal is to develop high-yielding varieties. Keeping all these in view, the present investigation was carried out with the objective study variability analysis for the traits adaptive to the summer season.

Material and Methods

The experiment was carried out to evaluate the genetic diversity, correlation, and path coefficient analysis between twenty-three brinjal genotypes (Table 1) during the summer season of 2019 at Horticultural Research Farm, Assam Agricultural University, Jorhat is situated at an altitude of 116 above mean sea level, 26.7509° North latitude and 94.2037° east longitude. The experimental area was quite uniform in respect of topography and fertility. The twenty-three brinjal genotypes were grown in a randomized complete block design with three replications (Table 1). Each genotype was planted in five rows of 1.5-meter length spaced 20 cm apart with one seedling per hill. Gap filling was done within a week in order to maintain a uniform plant population. A fertilizer dose of 60 kg N, 20 kg P₂O₅, and 40 kg K₂O was applied as per recommendation for Kharif rice. The entire dose of P₂O₅ and K₂O along with half dose of N was applied as basal dose at the time of final field preparation; the remaining amount of nitrogen was applied in two equal splits and was applied at the time of active growth stages. Standard agronomic practices were adopted for normal crop growth. The following observations were plant Height (cm), plant spread (cm), number of primary branches per plant, leaf blade length, leaf blade width, days to first flowering, days to 50% flowering, days to first fruiting, days to 50% fruiting, fruit pedicel length (cm), fruit length (cm), fruit circumference (cm), fruit volume (cc), number of fruits per plant, fruit weight (g) and fruit yield per plant (kg) recorded on five randomly chosen plants of each genotype per replication.

Statistical analyses

Analysis of variance for the traits was done considering replication and genotype as fixed effects [5] in MS Excel 2007. Genetic parameters were estimated by the formula given by Burton, 1952 for GCV and PCV, Hanson, Robinson, and Comstock (1956) for heritability, and Allard (1960) for expected genetic advance as percent of mean in MS Excel 2007. Mahalanobis D^2 and PCA analysis was done using 'R' software.

Result and Discussion

ANOVA

The analyses of variance which are presented in Tables 2a and 2b revealed significant variation at a genotypic level for all the sixteen characters except one i.e, fruit length which indicates that the genotypes have diverged genetically. Considerable variation in eggplant germplasm has been reported in studies by [6, 7 & 8].

Mean performance

Means regarding yield and yield attributing traits and their comparison are given in Tables 3a and 3b. The present result revealed that plant height was highly significantly affected due to various brinjal genotypes. The plant height ranged from 48.08 to 70.98 cm. The genotype SLL was found lowest plant height, whereas genotype JC1 had the highest plant height. The genotype LLP showed the early flowering and Tezpur local showed the late flowering. The number of branches is the most important yield component in brinjal. The effective and fruit-bearing branches play an important role in enhancing the final

yield. The number of primary branches varies from genotype to genotype depending upon the genetic potential of a genotype. In the present study the number of branches was significantly affected by the various genotypes. The highest branches (9.31) were produced by Longai oblong followed by Green Streaked (9.11), KB4 (8.92), and HRS4 (8.46). Similarly, MLC-1 and Naboneeta had shown very poor performance by showing only 6.44 and 6.51, primary branches per plant respectively. The highest fruit bearing genotype was KB 4. The highest fruit length (22.13 cm) was found in Longai Long. Fruit weight is an important yield parameter and is vary from genotype to genotype. KB-4 genotype showed the highest fruit weight (152.24 g). Longai oblong genotype has shown the maximum yield per plant, which may be due to the highest number of primary branches.

Genetic Parameters

Data on range, mean, GCV, PCV, Heritability, and Genetic Advance for 17 traits in 33 eggplant genotypes are presented in Table 4. It has been observed that the range for all the characters implies the incidence of diversified genotypes. The characters under study have shown that the three highest range of variability were of fruit volume (16.67 – 179.78 cc), fruit weight (29.52 – 152.24 g) and fruit yield per plant (1.35 – 3.98 kg). A sound awareness of genetic variability which is present in a population is essential for the successful development of quantitative traits. The characters with great variability have more scope for further improvement [9]. The genotypic coefficient of variability ranged from 6.65% (Number of primary branches per plant) to 42.66% (Fruit volume). High estimates of GCV were recorded for fruit volume (42.66%), fruit weight (38.44%), fruit yield per plant (32.32%), plant spread (26.90%), fruit circumference (25.89%), and number of fruits per plant (24.74%). Similar results were observed by [10] for number of fruits per plant, [11] for fruit weight, and [12] for a number of fruits per plant, fruit circumference and fruit yield per plant. The range of the phenotypic coefficient of variability (PCV) was from 7.35% (Days to 50% fruiting) to 44.96% (Fruit volume). High estimates of PCV were observed for eight characters which were fruit volume (44.96%), fruit weight (42.36%), fruit yield per plant (36.58%), plant spread (31.35%), fruit circumference (30.72%), number of fruits per plant (26.44%), fruit length (24.93%) and fruit pedicel length (20.87%). High PCV for the number of fruits per plant was also reported by [10 & 12]. Evaluation of variability factors revealed that there was lot of variation present among the genotypes studied. The value of the phenotypic coefficient of variation (PCV) was found to be higher than the genotypic coefficient of variation (GCV) for all the characters studied in the present study, which is indicative of the considerable influence of environmental factors on the performance of genotypes. Similar results were also reported in Brinjal by [13, 14 & 15].

Both high GCV and PCV were manifested by fruit volume, fruit weight, fruit yield per plant, plant spread, fruit circumference and number of fruits per plant which is suggestive of greater variability for these traits which were governed by additive genes and also indicative that the parents chosen on the basis of these characters may be further utilized in crossing program for acquiring superior transgressive segregants. In the present study, broad sense heritability was found high for all the characters except for fruit pedicel length (60%), leaf blade width (37%), and leaf blade length (48%) which were found to be moderate heritability and plant height (36%), fruit length (16%) which was observed to be with low heritability. The

characters which manifested high heritability were fruit volume (90%), days to 50% flowering (88%), number of fruits per plant (87%), days to first flowering (86%), days to first fruiting (85%), fruit weight (82%), days to 50% fruiting (80%), fruit yield per plant (78%), plant spread (73%), fruit circumference (71%). High heritability for a number of fruits per plant, fruit weight, and fruit yield per plant were also reported earlier by [16, 17 & 18]. High heritability is indicative of the low influence of environmental factors on the expression of the traits which allows breeders to select a genotype for further improvement program [19]. Genetic advance refers to the degree of gain obtained in a character under the circumstances of specified selection pressure. In crop improvement programs, high heritability does not all the time show evidence of high genetic advance. It is the high heritability estimates with high genetic advance together that render the most appropriate condition for selection [20]. In the present investigation, high heritability coupled with high genetic advance was observed for the traits, plant spread, fruit circumference, number of fruits per plant, fruit weight, fruit volume and fruit yield per plant. Several earlier reports also recorded high heritability and high genetic advance estimates for a number of fruits per plant, and fruit weight which is akin to the present findings [12, 16 & 21]. These results are suggestive of the presence of additive genes in the traits and support reliable crop improvement through a selection of those traits.

Character interrelationship

In any breeding program, it is a prerequisite to understanding the magnitude of genetic variability of yield contributing attributes, association between them and their relation with yield. The nature and extent of the association between yield and its component traits are essential for reasonable selection in advance generations. Linkage of genes or pleiotropy of genes is responsible for correlations between character pairs and thus, selection of one trait greatly influences the other linked or pleiotropically affected traits. The correlation coefficient also helps to identify characters with little or no importance in the selection program [22]. The Pearson correlation coefficients among the 17 characters are presented in Figure 1. The current study revealed that the characters Plant height (0.685), Plant Spread (0.447), Number of primary branches per hill (0.570), Leafblade length (0.536), number of fruits per plant (0.462) and fruit weight (0.644) exhibited significant positive correlation with fruit yield plant⁻¹. Maximum significant negative correlation with fruit yield plant⁻¹ was revealed in days to first flowering (-0.821), days to 50% flowering (-0.834) and days to 50% fruiting (-0.787). The results were in close harmony with Patel et al. (2015).

Path coefficient analysis

The path coefficient analysis is presented in Table 5 Through the path coefficient analysis, it was found that the highest positive direct effect was of days to 50% fruiting (1.100), followed by days to first fruiting (0.263), fruit volume (0.217), days to 50% flowering (0.199) and fruit pedicel length (0.190). The positive direct effect of fruit length was also studied by [23] and days to first flowering, fruit length on yield by [24]. For these characters, the direct selection would be useful in crop improvement given that most of these characters were observed to have a positive coefficient of correlation in improving the fruit yield per plant. Similar results in brinjal have also been reported by [9, 25 & 26]. The residual effect was observed to be 0.0329 which indicates

that 99.96% variation had been examined. It further indicated that some other factors which have not been considered in this study contributed to fruit yield and hence, besides the characters under study, other traits may also be considered during the selection of genotypes for high yield.

Genetic Diversity

In the present study, the twenty-three genotypes of brinjal were subjected to genetic divergence analysis where significant difference for the characters was observed. The analysis of variance for dispersion and Wilk's test is presented in Table 6. The value of 'V' statistics which was estimated through Wilk's test exhibited significant differences among the genotypes for all the sixteen characters. The twenty-three genotypes were grouped into 5 clusters (Table 7) based on the relative magnitude of D² statistics and using Tocher's method given by [27]. The genotypes were grouped into the various clusters in such a manner that genotypes within each cluster had smaller D² statistic than in another cluster. Clustering pattern revealed that among all the five clusters, cluster I was observed to consist of a maximum number of genotypes (12). Clusters II and III had equal number of genotypes i.e., four. While cluster IV had two Genotypes, cluster V was a solitary cluster with only one genotype. Genotype in solitary cluster signifies the uniqueness of that genotype for the majority of the traits. Using the genotype in the hybridization program will ensure breeding material with high diversity. Similar studies were done by [28, 29 & 30] in brinjal.

The intra and inter-cluster D² values was studied in the present investigation and presented in Table 8 The intra-cluster D² values portray the variation among the genotypes within the same cluster. It was for cluster IV (109.55) that the highest intra-cluster distance was observed, followed by cluster III (72.07), cluster I (55.53) and cluster II (53.62). Higher intra-cluster distance shows the existence of some diversity within the genotypes of the same cluster. Similar intra-cluster variation was also reported by [31, 32 & 33]. In order to maintain the broad genetic base, it is resourceful to evade using genotypes of the same cluster as parents during the hybridization program. The inter-cluster D² value was observed to be maximum (329.67) between clusters III and IV followed by between cluster I and IV with D² value of 284.76. This is indicative of diverse clusters which can be utilized for producing superior heterotic combinations as recommended by [34]. The crossing between superior genotypes of the above diverse cluster pairs (i.e. between cluster III and IV and between I and IV) may provide desirable transgressive segregants for developing high-yielding varieties.

The cluster means data with regard to five clusters inclusive of all the 16 characters are presented in Table 9. Superior cluster was the cluster whose character's average mean was found better than the others. Cluster II was found to be superior to the rest of the clusters for the characters, plant spread (72.67), a number of primary branches per plant (8.65), leaf blade length (15.16), leaf blade width (7.93), fruit pedicel length (7.51), fruit weight (125.66), fruit yield per plant (3.69). The characters denoting the earliness such as days to first flowering (57.50), days to 50 % flowering (65.50), days to first fruiting (64.84), days to 50% fruiting (73.00) were obtained in cluster IV with the lowest mean. Cluster IV also showed superiority in respect to the characters, fruit length (19.76), and fruit volume (144.73). Cluster V was found to be superior for the characters, plant height (62.74), and fruit circumference (20.70). The percent

contribution of the sixteen characters was presented in Table 9. The preference of the parents and their selection in crop improvement primarily depends on the contribution of the characters to divergence. In the present investigation, the highest contribution percent was manifested for days to 50% flowering (46.70%) followed by days to first flowering (39.60%) and fruit volume (3.76%). The genotype, *Longai Purple Long* was recorded for the least mean to days to first flowering (56.67), 50% flowering (64.67) and fruit volume (179.78) and therefore can be used as a parent in the hybridization program.

Principle component analysis

Principal Component Analysis (PCA) is a powerful tool in modern data analysis because it is a simple, non-parametric method for extracting relevant information from confusing data sets. With minimal effort, PCA provides a roadmap for how to reduce a complex data set to a lower dimension to reveal the sometimes hidden, simplified structures that often underlie it. It reduces the dimensionality of the data while retaining most of the variation in the data set. PCA accomplishes this reduction by identifying directions, called principal components (PCs), along which the variation in the data is maximal [35]. In the present investigation, PCA was performed for 23 brinjal genotypes and presented in Table 10. A total of 16 principal components (PCs) were obtained, but only four PCs that exhibited eigenvalues > 1 were measured as significant. The rest of the non-significant PCs (eigenvalue < 1) were not worthy of further interpretation. The values the PCs explained all the characters influencing about 77.6% of the genotypic variability, while the first two PCs explained 58.8% of the variability (Table 10 and Figure 2). Scree plot explained the percentage of variation associated with each principal component obtained by drawing a graph between eigenvalues and principal component numbers. The PC1 showed 40.9% variability with eigenvalue 6.54 which then declined gradually. An elbow type line is obtained which after 5th PC tended to straight with little variance observed in each PC. From the graph, it is clear that the maximum variation was observed in PC1 (Figure 3). PC 1 accounted for 40.9% of total variability and it was positively contributed by the characters fruit yield per plant (0.371), plant height (0.277), fruit weight (0.258), leaf blade length (0.221), number of Primary branches per plant (0.220) and number of fruits per plant (0.207) while days to 50% flowering (-0.363), days to first flowering (-0.360), days to first fruiting (-0.359) and days to 50% fruiting (-0.354) contributed negatively. PC 2 accounted for 17.9% of the total variability. The positively related traits were leaf blade width (0.506), plant spread (0.314), no of primary branches per plant (0.282), fruit circumference (0.272), fruit volume (0.269) and number of fruits per plant (-0.338) were negatively related to PC 2. PC 3 contributed 10.6% to total variability and the characters plant spread (0.353), number of fruits per plant (0.353), and fruit volume (-0.597) contributed to PC 3's positive and negative respectively. PC 4 contributed 8.2% total variance. The characters namely plant height, plant spread, number of primary branches per plant, number of fruits per plant, and fruit volume together in different principal components. Thus, the prominent characters placed together in different principal components and explaining the variability have the tendency to remain together [36]. This may be taken into consideration during the utilization of these characters in the brinjal breeding program. The length of the vector is based on the contribution of the character to the principal component (Figure 2). Moreover,

the angle of the character vectors is reflecting the correlation of variables. If the angle between two trait vectors is 90 (an obtuse angle), indicates a positive correlation. The two vectors in the 2nd quadrant viz., fruit circumference, plant spread, number of primary branches per plant, leaf blade length, fruit weight, and fruit yield per plant were highly correlated variables. Similarly, the vectors in 1st quadrant days to first flowering, days to 50% flowering, days to first fruiting, and days to 50% fruiting were highly correlated variables. These ten variables are also strongly correlated with the first principal component by the factor loading values. If the angle between two traits is > 90 (an obtuse angle), indicates a negative correlation. While if the angle is equivalent to 90 indicates that no correlation between the characters. It concluded that by comparing the ten genotypes, the genotypes G3, G5, G7, G10 and G19 were superior genotypes and had positive interaction with the character's fruit circumference, plant spread, number of primary branches per plant, leaf blade length, fruit weight, and fruit yield per plant. Genotypes with a high positive principal component score for PC 1 were G22 (1.519) followed by G10 (1.346), G3 (1.333), G7 (1.259), and G19 (1.031) (Table 11). Solaiman et al. (2014) reported that fruit width, fruit weight, and fruit yield per plant were important traits contributing to the divergence of the genotypes. While [37] concluded that in eggplant plant height, fruit length and fruit diameter should be kept average to obtain maximum fruit yield. The role of fruit yield in eggplant was more important in genetic divergence [38]. Overall, it was observed that fruit circumference, plant spread, number of primary branches per plant, leaf blade length, fruit weight, fruit yield per plant, days to first flowering, days to 50% flowering, days to first fruiting and days to 50% fruiting had high influence on the PC 1 and the genotypes G3, G5, G7, G10 and G19 had high principal component score for PC 1. Based on the relationship of characters and genotypes to the PC 1, it can be concluded that the genotypes G3, G5, G7, G10, and G19 can be selected for above said characters for breeding purposes in the brinjal improvement program for Assam condition.

Conclusions

The clustering pattern of D^2 analysis of twenty-three brinjal genotypes also confirmed the quantum of diversity present in the brinjal germplasm of Assam and offer scope for its exploitation through breeding for yield improvement. PCA helps us to identify the traits which have a great impact in the phenotype of different landraces of brinjal, and this is very much important in the selection procedure of the breeding program. Overall, it was observed that fruit circumference, plant spread, number of primary branches per plant, leaf blade length, fruit weight, fruit yield per plant, days to first flowering, days to 50% flowering, days to first fruiting, and days to 50% fruiting had high influence on the PC 1 and the genotypes G3, G5, G7, G10 and G19 had high principal component score for PC 1. Based on the relationship of characters and genotypes to the PC 1, it can be concluded that the genotypes G3, G5, G7, G10, and G19 can be selected for above said characters for breeding purposes in the brinjal improvement program for Assam condition.

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Author Contribution

Study Design: A.S. and S.G.; Data collection: B.I.; Manuscript draft preparation: B.I. and D.B.; Data Analysis: D.B. and H.V.; Data interpretation: B.I.; D.B and M.J.; Manuscript review: A.S.; S.G.; and D.B.; Supervision: A.S. and S.G.

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Conflict of interest

The authors declare that they have no conflict of interest related to the subject of research.

Table 1: Name of the genotypes and the source

| Entry Number | Name of the Entry | Source |
|--------------|----------------------------|-------------------------------------|
| G1 | Green Streaked | HRS, Kahikuchi, AAU, Jorhat |
| G2 | Singimari Local Long (SLL) | Dept. of Horticulture , AAU, Jorhat |
| G3 | Longai Oblong | HRS, Kahikuchi, AAU, Jorhat |
| G4 | Longai Long | HRS, Kahikuchi, AAU, Jorhat |
| G5 | HRS 4 | HRS, Kahikuchi, AAU, Jorhat |
| G6 | Hashim Local | HRS, Kahikuchi, AAU, Jorhat |
| G7 | Balijana | HRS, Kahikuchi, AAU, Jorhat |
| G8 | ABB5(1) | Dept. of Horticulture , AAU, Jorhat |
| G9 | ABB5(2) | Dept. of Horticulture , AAU, Jorhat |
| G10 | KB4 | HRS, Kahikuchi, AAU, Jorhat |
| G11 | Tezpur Local | Tezpur, Assam |
| G12 | MZ1 | Mizoram |
| G13 | Barpeta | HRS, Kahikuchi, AAU, Jorhat |
| G14 | Naboneeta | Dept. of Horticulture , AAU, Jorhat |
| G15 | M1 | HRS, Kahikuchi, AAU, Jorhat |
| G16 | M2 | HRS, Kahikuchi, AAU, Jorhat |
| G17 | ML2 | HRS, Kahikuchi, AAU, Jorhat |
| G18 | Longai Purple Oblong (LOP) | HRS, Kahikuchi, AAU, Jorhat |
| G19 | Longai Purple Long (LLP) | HRS, Kahikuchi, AAU, Jorhat |
| G20 | Manipur Local -1 (MLC-1) | HRS, Kahikuchi, AAU, Jorhat |
| G21 | Manipur Local -3 (MLC-3) | HRS, Kahikuchi, AAU, Jorhat |
| G22 | JC1 | HRS, Kahikuchi, AAU, Jorhat |
| G23 | Green Streaked | HRS, Kahikuchi, AAU, Jorhat |

Table 2a. Analysis of variance for different morphological traits in the 23 genotypes of brinjal

| Source of Variations | df | Plant Height (cm) | Plant Spread (cm) | Number of Primary Branches Per Plant | Leaf Blade Length (cm) | Leaf Blade Width (cm) | Days to First Flowering | Days to 50% Flowering | Days to First Fruiting |
|----------------------|----|-------------------|-------------------|--------------------------------------|------------------------|-----------------------|-------------------------|-----------------------|------------------------|
| Replicates | 2 | 12.60 | 168.39 | 0.54 | 30.86 ** | 2.99 | 9.23 | 8.54 | 5.06 |
| Genotype | 22 | 102.43 * | 712.86 ** | 1.75 * | 12.54 ** | 2.88 * | 89.57 ** | 105.34 ** | 89.39 ** |
| Error | 44 | 37.69 | 75.89 | 0.97 | 3.28 | 1.04 | 4.35 | 4.23 | 4.92 |
| C.V. | | 10.89 | 16.08 | 12.79 | 13.73 | 15.13 | 3.21 | 2.80 | 3.05 |

* - Significant at 5% level, ** - Significant at 1% level

Table 2b. Analysis of variance for different morphological traits in the 23 genotypes of brinjal

| Source of Variations | df | Days to 50% Fruiting | Fruit Pedicel Length (cm) | Fruit Length (cm) | Fruit Circumference (cm) | Number of Fruits Per Plant | Fruit Weight (g) | Fruit Volume (cc) | Fruit Yield Per Plant (kg) |
|----------------------|----|----------------------|---------------------------|-------------------|--------------------------|----------------------------|------------------|-------------------|----------------------------|
| Replicates | 2 | 6.83 | 0.96 | 16.96 | 5.19 | 7.35 | 176.63 | 19.16 | 0.05 |
| Genotype | 22 | 91.99** | 4.37 ** | 20.87 | 41.78 ** | 526.21 ** | 3693.33 ** | 3764.68 ** | 2.25 ** |
| Error | 44 | 6.87 | 0.78 | 13.08 | 5.01 | 23.71 | 245.98 | 134.09 | 0.19 |
| C.V. | | 3.24 | 13.09 | 22.77 | 16.55 | 9.31 | 17.79 | 14.20 | 17.15 |

* - Significant at 5% level, ** - Significant at 1% level

Table 3a: Comparative Mean performance for yield and yield related traits of 23 genotypes
****lower case letter are significant different based on Tukey's honestly test**

| Genotype | Plant Height (cm) | Plant Spread (cm) | Number of Primary Branches Per Plant | Leaf Blade Length (cm) | Leaf Blade Width (cm) | Days to First Flowering | Days to 50% Flowering | Days to First Fruiting |
|----------------|---------------------|-------------------------|--------------------------------------|------------------------|-----------------------|-------------------------|-----------------------|------------------------|
| Green Streaked | 56.43 ^{ab} | 91.69 ^a | 9.11 ^a | 14.96 ^{abc} | 7.79 ^a | 64.00 ^{bcd} | 72.00 ^{bcd} | 71.33 ^{bcd} |
| SLL | 48.08 ^b | 62.48 ^{bcd} | 7.31 ^a | 13.4 ^{abc} | 7.39 ^a | 70.33 ^{ab} | 79.33 ^a | 78.33 ^a |
| Longai Oblong | 63.24 ^{ab} | 62.34 ^{bcd} | 9.31 ^a | 14.36 ^{abc} | 7.73 ^a | 60.33 ^{de} | 68.33 ^{de} | 68.67 ^{def} |
| Longai Long | 54.31 ^{ab} | 74.94 ^{abc} | 7.91 ^a | 11.96 ^{abc} | 6.70 ^a | 58.33 ^{de} | 66.33 ^{de} | 65.67 ^{ef} |
| HRS 4 | 63.58 ^{ab} | 77.48 ^{ab} | 8.46 ^a | 16.25 ^{ab} | 8.60 ^a | 67.00 ^{abc} | 75.00 ^{abc} | 74.33 ^{abcd} |
| Hashim Local | 52.48 ^{ab} | 43.60 ^{efgh} | 7.55 ^a | 10.41 ^c | 6.31 ^a | 70.33 ^{ab} | 79.33 ^a | 78.00 ^{ab} |
| Balijana | 63.38 ^{ab} | 59.15 ^{bcd} | 7.73 ^a | 15.05 ^{abc} | 7.58 ^a | 58.00 ^{de} | 66.00 ^{de} | 65.67 ^{ef} |
| ABB5(1) | 54.57 ^{ab} | 62.15 ^{bcd} | 7.42 ^a | 15.55 ^{abc} | 8.33 ^a | 69.00 ^{ab} | 78.00 ^{ab} | 76.33 ^{ab} |
| ABB5(2) | 55.20 ^{ab} | 54.13 ^{bcd} | 8.31 ^a | 14.23 ^{abc} | 6.34 ^a | 69.00 ^{ab} | 78.00 ^{ab} | 76.67 ^{ab} |
| KB4 | 52.70 ^{ab} | 73.72 ^{abcd} | 8.92 ^a | 13.97 ^{abc} | 6.94 ^a | 58.33 ^{de} | 66.33 ^{de} | 66.67 ^{ef} |
| Tezpur Local | 52.26 ^{ab} | 46.57 ^{defgh} | 7.31 ^a | 13.54 ^{abc} | 7.36 ^a | 71.33 ^a | 80.33 ^a | 78.33 ^a |
| MZ1 | 48.75 ^b | 50.34 ^{bcd} | 7.53 ^a | 15.64 ^{abc} | 8.43 ^a | 69.67 ^{ab} | 78.67 ^a | 77.00 ^{ab} |
| Barpeta | 63.98 ^{ab} | 57.07 ^{bcd} | 6.76 ^a | 11.38 ^{abc} | 5.71 ^a | 59 ^{de} | 67.00 ^{de} | 66.67 ^{ef} |
| Naboneeta | 55.03 ^{ab} | 51.24 ^{bcd} | 6.51 ^a | 11.76 ^{abc} | 5.94 ^a | 70.67 ^a | 79.67 ^a | 77.67 ^{ab} |
| M1 | 55.04 ^{ab} | 51.95 ^{bcd} | 7.60 ^a | 10.43 ^c | 6.13 ^a | 69.33 ^{ab} | 78.33 ^{ab} | 78.00 ^{ab} |
| M2 | 57.09 ^{ab} | 53.43 ^{bcd} | 6.75 ^a | 13.67 ^{abc} | 5.65 ^a | 61.67 ^{cde} | 69.67 ^{cde} | 69.00 ^{cdef} |
| ML2 | 51.28 ^b | 32.28 ^{gh} | 7.20 ^a | 10.33 ^c | 5.63 ^a | 68.00 ^{abc} | 77.00 ^{ab} | 75.00 ^{abcd} |
| LOP | 62.74 ^{ab} | 28.87 ^h | 7.66 ^a | 13.18 ^{abc} | 6.74 ^a | 58.00 ^{de} | 66.00 ^{de} | 66.00 ^{ef} |
| LLP | 56.75 ^{ab} | 41.50 ^{efgh} | 7.80 ^a | 14.19 ^{abc} | 6.10 ^a | 56.67 ^e | 64.67 ^e | 64.00 ^f |
| MLC-1 | 57.73 ^{ab} | 46.34 ^{efgh} | 6.44 ^a | 11.41 ^{abc} | 6.05 ^a | 70.67 ^a | 79.67 ^a | 79.33 ^a |
| MLC-3 | 52.19 ^{ab} | 48.33 ^{cdefgh} | 7.89 ^a | 10.87 ^{bc} | 5.92 ^a | 70.33 ^{ab} | 79.33 ^a | 77.67 ^{ab} |
| JC1 | 70.98 ^a | 46.37 ^{defgh} | 8.24 ^a | 16.71 ^a | 5.91 ^a | 58.33 ^{de} | 66.33 ^{de} | 65.33 ^{ef} |
| SM-6-7 | 48.60 ^b | 29.75 ^{sh} | 7.51 ^a | 10.24 ^c | 5.49 ^a | 68.33 ^{ab} | 77.00 ^{ab} | 75.67 ^{abc} |

Table 3b: Comparative Mean performance for yield and yield related traits of 23 genotypes
****lower case letter are significant different based on Tukey's honestly test**

| Genotype | Days to 50% Fruiting | Fruit Pedicel Length (cm) | Fruit Length (cm) | Fruit Circum. (cm) | Number of Fruits Per Plant | Fruit Weight (g) | Fruit Volume (cc) | Fruit Yield Per Plant (kg) |
|----------------|-----------------------|---------------------------|---------------------|------------------------|----------------------------|-------------------------|------------------------|----------------------------|
| Green Streaked | 79.67 ^{bcd} | 5.71 ^c | 13.99 ^{ab} | 21.39 ^a | 56.33 ^{bc} | 119.38 ^{abc} | 87.66 ^{cdef} | 3.41 ^{abc} |
| SLL | 87.67 ^{ab} | 5.73 ^c | 17.48 ^{ab} | 16.4 ^{abcd} | 46.67 ^{bcd} | 112.32 ^{abcd} | 59.00 ^{defgh} | 2.21 ^{bcd} |
| Longai Oblong | 77.00 ^{de} | 7.23 ^{bc} | 17.30 ^{ab} | 17.33 ^{abc} | 48.00 ^{bcd} | 146.04 ^{ab} | 105.00 ^{bc} | 3.98 ^a |
| Longai Long | 73.33 ^e | 6.91 ^{bc} | 22.13 ^a | 10.21 ^{def} | 46.00 ^{bcd} | 118.11 ^{abc} | 109.67 ^{bc} | 2.75 ^{abcd} |
| HRS 4 | 82.33 ^{abcd} | 10.84 ^a | 14.23 ^{ab} | 13.68 ^{bcd} | 48.33 ^{bcd} | 115.61 ^{abc} | 92.00 ^{cde} | 3.69 ^a |
| Hashim Local | 87.00 ^{ab} | 6.54 ^{bc} | 15.51 ^{ab} | 9.37 ^{def} | 42.00 ^{cde} | 79.47 ^{cdefg} | 77.00 ^{cdefg} | 1.98 ^{defg} |
| Balijana | 74.00 ^e | 6.24 ^{bc} | 15.47 ^{ab} | 17.39 ^{abc} | 46.67 ^{bcd} | 121.60 ^{abc} | 92.55 ^{bcd} | 3.66 ^a |
| ABB5(1) | 84.33 ^{abc} | 6.17 ^c | 15.96 ^{ab} | 15.05 ^{abcd} | 42.00 ^{cde} | 95.10 ^{cde} | 102.67 ^{bc} | 1.95 ^{defg} |
| ABB5(2) | 84.67 ^{abc} | 5.14 ^c | 15.89 ^{ab} | 7.97 ^{ef} | 45.00 ^{bcd} | 29.60 ^h | 55.44 ^{fgh} | 1.44 ^{fg} |
| KB4 | 75.00 ^{de} | 5.73 ^c | 15.86 ^{ab} | 14.97 ^{abcde} | 82.00 ^a | 152.24 ^a | 45.00 ^{ghi} | 3.66 ^a |
| Tezpur Local | 86.67 ^{ab} | 7.30 ^{bc} | 16.1 ^{ab} | 11.39 ^{cdef} | 52.00 ^{bcd} | 85.37 ^{cdef} | 61.00 ^{defg} | 1.88 ^{efg} |
| MZ1 | 85.00 ^{abc} | 5.98 ^c | 19.97 ^{ab} | 10.52 ^{cdef} | 40.67 ^{de} | 61.37 ^{efgh} | 95.33 ^{bcd} | 1.66 ^{efg} |
| Barpeta | 75.00 ^{de} | 6.63 ^{bc} | 16.3 ^{ab} | 11.66 ^{cdef} | 75.33 ^a | 111.50 ^{abcd} | 16.67 ⁱ | 2.88 ^{abcde} |
| Naboneeta | 86.33 ^{ab} | 7.60 ^{bc} | 16.53 ^{ab} | 15.94 ^{abcd} | 51.67 ^{bcd} | 37.67 ^{fgh} | 102.33 ^{bc} | 1.95 ^{defg} |
| M1 | 86.67 ^{ab} | 6.90 ^{bc} | 16.17 ^{ab} | 14.06 ^{bcd} | 43.00 ^{bcd} | 32.40 ^{gh} | 63.33 ^{defg} | 2.11 ^{cdefg} |
| M2 | 77.00 ^{cde} | 6.26 ^{bc} | 8.94 ^b | 7.11 ^f | 76.67 ^a | 29.52 ^h | 24.33 ^{hi} | 2.88 ^{abcde} |
| ML2 | 83.00 ^{abcd} | 6.44 ^{bc} | 12.06 ^{ab} | 10.86 ^{cdef} | 55.33 ^{bcd} | 76.76 ^{cdefgh} | 58.33 ^{efgh} | 1.74 ^{efg} |
| LOP | 74.00 ^e | 6.60 ^{bc} | 14.9 ^{ab} | 20.70 ^{ab} | 57.33 ^b | 79.79 ^{cdefg} | 127.67 ^b | 3.31 ^{abcd} |
| LLP | 72.67 ^e | 7.01 ^{bc} | 17.23 ^{ab} | 14.33 ^{bcd} | 46.00 ^{bcd} | 82.87 ^{cdef} | 179.78 ^a | 3.56 ^{ab} |
| MLC-1 | 88.00 ^a | 6.48 ^{bc} | 19.10 ^{ab} | 13.55 ^{cdef} | 50.00 ^{bcd} | 74.73 ^{cdefgh} | 90.00 ^{cdef} | 1.61 ^{efg} |
| MLC-3 | 83.33 ^{abc} | 5.52 ^c | 13.07 ^{ab} | 11.81 ^{cdef} | 32.00 ^e | 97.33 ^{bcd} | 104.33 ^{bc} | 1.87 ^{efg} |
| JC1 | 73.00 ^e | 8.97 ^{ab} | 16.32 ^{ab} | 9.92 ^{def} | 77.33 ^a | 105.46 ^{abcde} | 46.33 ^{ghi} | 3.48 ^{ab} |
| SM-6-7 | 83.33 ^{abc} | 6.97 ^{bc} | 14.71 ^{ab} | 15.50 ^{abcd} | 42.67 ^{bcd} | 63.92 ^{defgh} | 80.11 ^{cdefg} | 1.35 ^g |

Table 4: Genetic parameters for 16 characters of twenty three genotypes

| Characters | General Mean | Range | GCV% | PCV% | Heritability h ² (b.s) | GA as a percent of mean |
|--------------------------------------|--------------|-------------|-------|-------|-----------------------------------|-------------------------|
| Plant Height(cm) | 56.37 | 48.08-70.98 | 8.24 | 13.66 | 0.36 | 10.25 |
| Plant Spread (cm) | 54.16 | 28.87-91.69 | 26.90 | 31.35 | 0.73 | 47.57 |
| Number of Primary Branches Per Plant | 7.71 | 06.44-09.31 | 6.65 | 14.41 | 0.21 | 6.33 |
| Leaf Blade Length (cm) | 13.19 | 10.24-16.71 | 13.31 | 19.13 | 0.48 | 19.09 |
| Leaf Blade Width (cm) | 6.73 | 05.49-08.60 | 11.67 | 19.10 | 0.37 | 14.68 |
| Days to First Flowering | 65.07 | 56.67-71.33 | 8.19 | 8.80 | 0.86 | 15.71 |
| Days to 50% Flowering | 73.58 | 64.67-80.33 | 7.89 | 8.37 | 0.88 | 15.32 |
| Days to First Fruiting | 72.67 | 64.00-79.33 | 7.30 | 7.92 | 0.85 | 13.88 |
| Days to 50% Fruiting | 80.83 | 72.67-88.00 | 6.59 | 7.35 | 0.80 | 12.18 |
| Fruit Pedicel Length (cm) | 6.73 | 5.14-10.84 | 16.26 | 20.87 | 0.60 | 26.10 |

| | | | | | | |
|-----------------------------------|-------|--------------|-------|-------|------|-------|
| Fruit Length (cm) | 15.88 | 8.94-22.13 | 10.15 | 24.93 | 0.16 | 8.51 |
| Fruit Circumference (cm) | 13.53 | 7.11-21.39 | 25.89 | 30.72 | 0.71 | 44.93 |
| Number of Fruits Per Plant | 52.30 | 32.00-82.00 | 24.74 | 26.44 | 0.87 | 47.71 |
| Fruit Weight(g) | 88.18 | 29.52-152.24 | 38.44 | 42.36 | 0.82 | 71.87 |
| Fruit Volume (cc) | 81.55 | 16.67-179.78 | 42.66 | 44.96 | 0.90 | 83.38 |
| Fruit Yield Per Plant(kg) | 2.57 | 01.35-03.98 | 32.32 | 36.58 | 0.78 | 58.80 |

Table 5: Path analysis of the 16 traits of 23 brinjal genotypes

| Characters | PH | PS | NPBPP | LBL | LBW | DFP | D50F | DFFr | D50Fr | FPL | FL | FC | NFPP | FW | FV | correl |
|----------------------|--------------|--------------|--------------|--------------|--------------|-------|-------|--------------|--------------|--------------|-------|-------|-------|--------------|--------------|--------|
| PH | 0.110 | 0.021 | 0.018 | 0.022 | 0.001 | 1.261 | - | - | - | 0.100 | 0.017 | - | 0.030 | 0.054 | - | 0.68** |
| PS | 0.013 | 0.186 | 0.042 | 0.022 | 0.033 | 0.343 | - | - | - | 0.009 | - | - | 0.009 | 0.098 | - | 0.45** |
| NPBPP | 0.024 | 0.095 | 0.082 | 0.023 | 0.026 | 0.734 | - | - | - | 0.016 | - | - | 0.001 | 0.108 | 0.035 | 0.57** |
| LBL | 0.048 | 0.083 | 0.039 | 0.050 | 0.039 | 0.680 | - | - | - | 0.052 | - | - | 0.014 | 0.061 | 0.023 | 0.54** |
| LBW | 0.002 | 0.107 | 0.037 | 0.034 | 0.057 | - | - | - | - | 0.027 | - | - | - | 0.083 | 0.052 | 0.290 |
| DFP | - | - | -0.029 | - | 0.003 | - | - | - | - | - | - | - | - | - | - | - |
| D50F | 0.068 | 0.031 | 0.016 | 0.003 | 2.064 | 0.198 | 0.261 | 1.082 | 0.020 | 0.012 | 0.003 | 0.037 | 0.089 | 0.027 | -0.820 | |
| DFFr | - | - | -0.030 | - | 0.003 | - | - | - | - | 0.009 | 0.003 | - | - | - | - | - |
| D50Fr | 0.068 | 0.034 | 0.017 | 0.003 | 0.199 | 0.261 | 1.082 | 0.024 | 0.009 | 0.003 | 0.003 | 0.037 | 0.090 | 0.027 | -0.830 | |
| DFFr | 0.067 | 0.029 | -0.028 | 0.017 | 0.003 | 2.055 | 0.198 | 0.263 | 1.091 | 0.025 | 0.006 | 0.003 | 0.037 | 0.086 | 0.028 | -0.810 |
| D50Fr | 0.066 | 0.027 | -0.030 | 0.017 | 0.004 | 2.031 | 0.195 | 0.261 | 1.100 | 0.024 | 0.004 | 0.002 | 0.035 | 0.086 | 0.030 | -0.790 |
| FPL | 0.058 | 0.009 | 0.007 | 0.014 | 0.008 | 0.221 | - | - | - | 0.190 | - | 0.000 | 0.008 | 0.024 | 0.019 | 0.360 |
| FL | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| FC | 0.014 | 0.039 | 0.025 | 0.007 | 0.021 | 0.392 | - | - | - | - | - | - | - | 0.074 | 0.093 | 0.390 |
| NFPP | 0.049 | 0.025 | 0.001 | 0.011 | - | 1.137 | - | - | - | - | - | - | - | - | - | - |
| FW | 0.032 | 0.097 | 0.047 | 0.016 | 0.025 | 0.980 | - | - | - | 0.024 | - | - | 0.013 | 0.187 | 0.018 | 0.64** |
| FV | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| FV | 0.003 | 0.019 | 0.013 | 0.005 | 0.014 | 0.261 | 0.024 | 0.034 | 0.152 | 0.017 | 0.101 | 0.007 | 0.039 | 0.015 | 0.217 | 0.160 |
| Residual are 0.03294 | | | | | | | | | | | | | | | | |

Table 6: Wilks' Lamda for testing the simultaneous significance of mean difference and Analysis of dispersion

| WILKS TEST | | | | | |
|---------------------------------------|------------------|----------------|--------------|-----------|-------------|
| Determinant of Error Matrix | | | 1.51E+15 | | |
| Determinant of Error + Variety Matrix | | | 0.00E+00 | | |
| Wilk's Criterion | | | | | |
| M | 45.5V statistics | 0 | | | |
| Degree of Freedom | 352Probability | 1 | | | |
| ANOVA for DISPERSION | | | | | |
| Source of Variations | df | Sum of Squares | Mean Squares | F Ratio | Probability |
| Varieties | 22 | -1.51E+15 | -6.85E+13 | -1.96E+00 | 0.02982 * |
| Error | 43 | 1.51E+15 | 3.51E+13 | | |
| Total | 65 | 0.00E+00 | 0.00E+00 | | |

Table 7: Distribution of the 23 genotypes into 5 different Tocher's clusters

| Cluster | Number of notypes | Name of Genotypes |
|-------------|-------------------|---|
| Cluster I | 12 | ABB5(1), MZ1, Hashim Local, MLC-1, Tezpur Local, Nabaneeta, ML2, ABB5(2), M1, Singimari Local Long, SM-6-7, MLC-3 |
| Cluster II | 4 | Longai Oblong, Balijana, Green Streaked, HRS 4 |
| Cluster III | 4 | KB4, Barpeta, M2, JC1 |
| Cluster IV | 2 | Longai Long, LPL |
| Cluster V | 1 | Longai Purple Oblong |

Table 8: Intra (bold) and inter (above diagonal) distances D2 among the 5 different Tocher's clusters

| Cluster | I | II | III | IV | V |
|---------|-------|--------|--------|--------|--------|
| I | 55.53 | 182.03 | 272.78 | 284.76 | 255.94 |
| II | | 53.62 | 143.89 | 176.22 | 124.79 |
| III | | | 72.07 | 329.67 | 198.33 |
| IV | | | | 109.55 | 204.7 |
| V | | | | | 0 |

Table 9: Mean values for the different Tocher's clusters

| Characters | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V | % contribution to divergence |
|--------------------------------------|-----------|------------|-------------|------------|-----------|------------------------------|
| Plant Height (cm) | 52.60 | 61.66 | 61.19 | 55.53 | 62.74 | 0.60 |
| Plant spread (cm) | 48.26 | 72.67 | 57.65 | 58.22 | 28.87 | 1.14 |
| Number of primary branches per plant | 7.38 | 8.65 | 7.67 | 7.86 | 7.66 | 0.26 |
| Leaf blade length (cm) | 12.32 | 15.16 | 13.93 | 13.08 | 13.18 | 0.72 |
| Leaf blade width (cm) | 6.61 | 7.93 | 6.05 | 6.40 | 6.74 | 0.31 |
| Days to first flowering | 69.75 | 62.33 | 59.33 | 57.50 | 58.00 | 39.60 |
| Days to 50% flowering | 78.72 | 70.33 | 67.33 | 65.50 | 66.00 | 46.70 |
| Days to first fruiting | 77.33 | 70.00 | 66.92 | 64.84 | 66.00 | 0.32 |
| Days to 50% fruiting | 85.50 | 78.25 | 75.00 | 73.00 | 74.00 | 0.23 |
| Fruit pedicel length (cm) | 6.40 | 7.51 | 6.90 | 6.96 | 6.60 | 0.90 |
| Fruit length (cm) | 16.20 | 15.27 | 14.42 | 19.76 | 14.91 | 0.00 |
| Fruit circum. (cm) | 12.70 | 17.45 | 10.92 | 12.27 | 20.70 | 1.15 |
| Number of fruits per plant | 45.25 | 49.83 | 77.83 | 46.00 | 57.33 | 2.28 |
| Fruit weight (g) | 70.50 | 125.66 | 99.68 | 100.49 | 79.79 | 1.02 |
| Fruit volume (cc) | 79.07 | 94.30 | 33.08 | 144.73 | 127.67 | 3.76 |
| Fruit yield per plant (kg) | 1.81 | 3.69 | 3.23 | 3.16 | 3.31 | 0.00 |

Table 10: Eigen value, contribution of variability and factor loadings for the principal component

| | Principle component (PC) | | | |
|--------------------------------------|---|---------------|---------------|--------------|
| | PC1 | PC2 | PC3 | PC4 |
| Eigenvalues | 6.54 | 2.869 | 1.695 | 1.312 |
| Proportion | 0.409 | 0.179 | 0.106 | 0.082 |
| Cumulative Proportion | 0.409 | 0.588 | 0.694 | 0.776 |
| Characters | Factor loading value after varimax rotation | | | |
| Plant Height (cm) | 0.277 | -0.116 | 0.094 | 0.422 |
| Plant spread (cm) | 0.16 | 0.314 | 0.353 | -0.251 |
| Number of primary branches per plant | 0.22 | 0.282 | 0.097 | -0.178 |
| Leaf blade length (cm) | 0.221 | 0.246 | 0.269 | 0.214 |
| Leaf blade width (cm) | 0.092 | 0.506 | 0.184 | 0.053 |
| Days to first flowering | -0.36 | 0.167 | 0.167 | 0.086 |
| Days to 50% flowering | -0.363 | 0.161 | 0.155 | 0.079 |
| Days to first fruiting | -0.359 | 0.173 | 0.16 | 0.064 |
| Days to 50% fruiting | -0.354 | 0.178 | 0.163 | 0.065 |
| Fruit pedicel length (cm) | 0.111 | 0.033 | 0.153 | 0.727 |
| Fruit length (cm) | 0.016 | 0.245 | -0.277 | 0.037 |
| Fruit circum. (cm) | 0.124 | 0.272 | -0.249 | -0.116 |
| Number of fruits per plant | 0.207 | -0.338 | 0.352 | -0.112 |
| Fruit weight (g) | 0.258 | 0.231 | 0.052 | -0.225 |
| Fruit volume (cc) | 0.05 | 0.269 | -0.597 | 0.217 |
| Fruit yield per plant (kg) | 0.371 | 0.047 | 0.035 | 0.053 |

Table 11: First two Principle Component Score

| Genotype | PC1 | PC2 | Genotype | PC1 | PC2 |
|----------------|--------|--------|-----------|--------|--------|
| Green Streaked | 0.873 | 1.446 | Barpeta | 0.743 | -1.732 |
| SLL | -0.752 | 1.011 | Naboneeta | -0.993 | -0.185 |
| Longai Oblong | 1.333 | 1.126 | M1 | -0.981 | -0.181 |
| Longai Long | 0.802 | 0.257 | M2 | 0.139 | -2.29 |
| HRS 4 | 0.741 | 1.497 | ML2 | -0.893 | -1.208 |
| Hashim Local | -1.08 | -0.157 | LOP | 0.957 | -0.515 |
| Balijana | 1.259 | 0.3 | LLP | 1.031 | -0.209 |
| ABB5(1) | -0.398 | 1.305 | MLC-1 | -1.098 | -0.096 |

| | | | | | |
|--------------|--------|--------|--------|--------|--------|
| ABB5(2) | -0.875 | -0.147 | MLC-3 | -0.947 | 0.109 |
| KB4 | 1.346 | -0.082 | JC1 | 1.519 | -1.205 |
| Tezpur Local | -0.871 | 0.334 | SM-6-7 | -1.043 | -0.585 |
| MZ1 | -0.814 | 1.208 | | | |

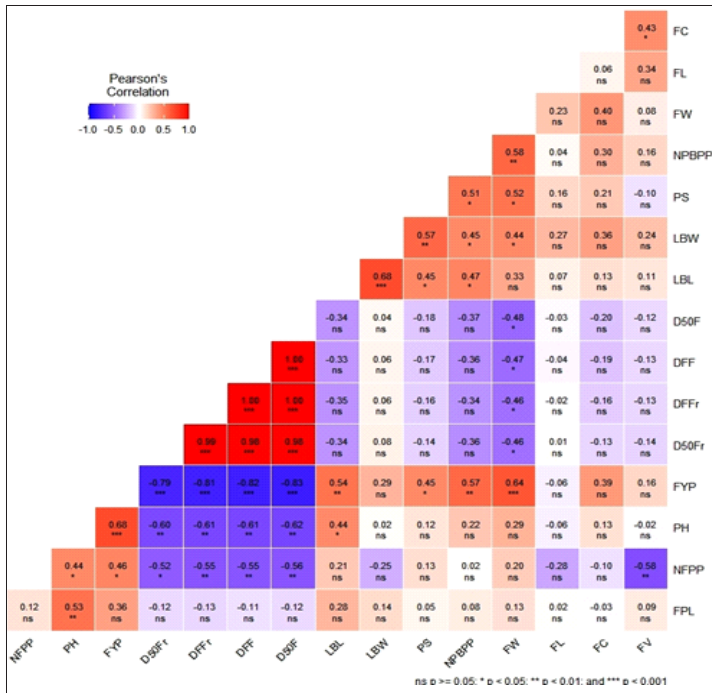


Figure 1: Pearson correlation of 16 traits of 23 brinjal genotypes of Assam

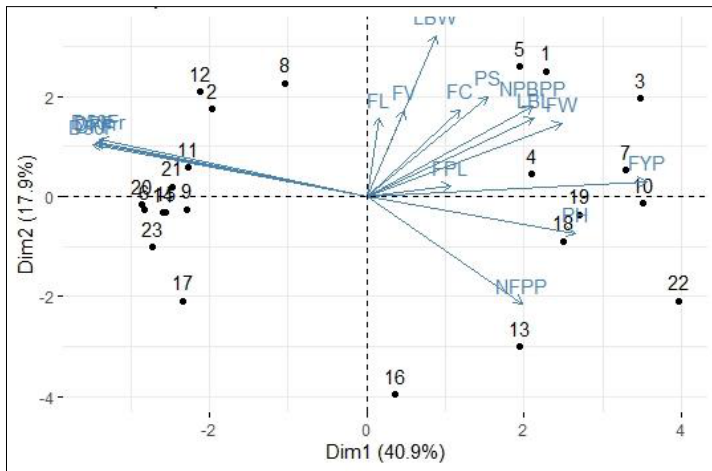


Figure 2: Distribution of genotypes and variables across first two components

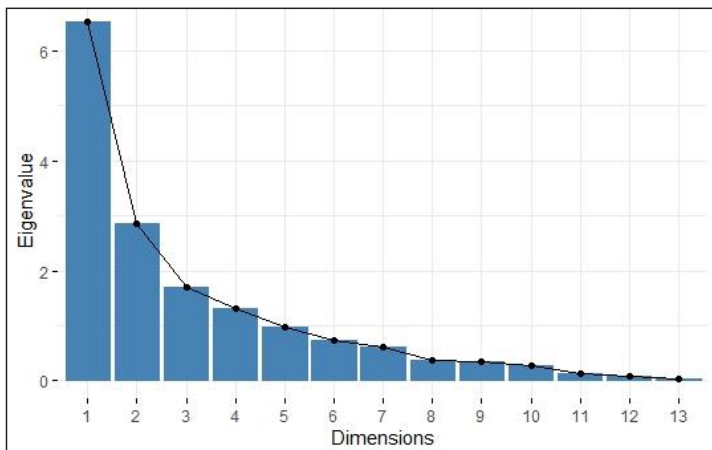


Figure 3: Scree plot showing Eigen value variation

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