Available online at **www.ijpab.com**

DOI: http://dx.doi.org/10.18782/2320-7051.5505

ISSN: 2320 – 7051

Int. J. Pure App. Biosci. **6 (1):** 915-919 (2018)

International Journal of Pure & Applied Bioscience

Research Article

OPEN ACCESS

Genetic Divergence in Wild Brinjal (*Solanum gilo*) Genotypes of North Eastern Region

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Received: 22.08.2017 | Revised: 29.09.2017 | Accepted: 5.10.2017

ABSTRACT

Fifteen genotypes of wild brinjal (Solanum gilo) were evaluated for genetic diversity using Mahalanobis D^2 statistics foe various morpho physiological traits during 2015-2016. The data on 19 physiological traits were recorded and on the basis of Mahalanobis' D^2 statistics, all the 15 genotypes of the present study were grouped into four clusters. Maximum number of genotypes (6) were included in clister III followed by cluster I (5) and remaining clusters with two genotype each. Considering the inter cluster distances, it was highest between cluster II and III (12829.31) whereas it was lowest between cluster I and II (3933.95). Among the 19 characters studied, protein content, total carbohydrate, steroid content, total phenol, fruit yield per plant and number of fruits per plant contributed maximum towards the total divergence and were found to be responsible for primary differentiation.

Key words: *Solanum gilo, Genetic divergence, Hierarchical cluster analysis.*

INTRODUCTION

Solanum gilo is commonly known as bitter brinjal. It is an important indigenous leaf and fruit vegetable in tropical Africa; cultivated and consumed largely in Africa[9]. It is important for production in marginal areas and for the genetic improvement of *Solanum melongena*[10]. Wide variations exists within and between the species including variation in characters like diameter of corolla, petiole length, leaf blade width, plant branching, fruit shape and color[1]. The fruits are round, the top and bottom are flattened out and have grooved portions with a length of 5-6 cm and a width of 6-7 cm. It has very tiny seeds and its stalk is curved or erect[3]. This species of garden egg have bitter tastes and is cultivated in the same way with other species. The fruit turn red or orange in color when ripened. Although bitter brinjal is cultivated in all the state of North Eastern Region of India but there is no improved variety that can be recommended to the farmers for its commercial cultivation in the region. Therefore, assessment of genetic diversity among the genotypes is important for planning a systematic approach for crop improvement.

Cite this article: Sanga, L., Pandey, A.K., Warade, S.D., Hazarika, B.N. and Singh, S., Genetic Divergence in Wild Brinjal (*Solanum gilo*) Genotypes of North Eastern Region, *Int. J. Pure App. Biosci.* **6(1):** 915-919 (2018). doi: http://dx.doi.org/10.18782/2320-7051.5505

It has become possible to quantify magnitude of genetic diversity among germplasm with the help of advanced biometrical methods such as multivariate analysis[6], based on Mahalanobis'[4], D^2 statistics.

MATERIAL AND METHODS

Fifteen wild brinjal (*Solanum gilo*) genotypes were collected from different part of the North eastern region of India and cultivated at research farm of department of Vegetable Science, College of Horticulture and Forestry, Central Agricultural University, Pasighat, Arunachal Pradesh, India during 2015 to 2016. The genotypes were collected from different parts of North Eastern Region. The experiment was laid out in Randomized Block Design (RBD) with 15 genotypes and 3 replications. Observations regarding quantitative characters and biochemical components *viz*., plant height (cm), days to first flowering (50%), days to first fruit set (50%), days to first harvest, fruit girth (cm), fruit length (cm), fruit weight (g), number of fruits per plant, fruit yield per plant (kg), total carbohydrate (mg/100g), solasodine content (mg/100g), total phenol (mg/100g), ascorbic acid content (mg/100g), total alkaloid (mg/100g), steroid content (µg/100g), flavonoid content (mg/100g), terpenoid content (mg/100g), phytosterol content (%) and protein content (mg/100g) were recorded on five randomly selected plants in each replication.

The genetic divergence among the genotypes was computed by means of Mahalanobis' D^2 statistics.

Intra and inter cluster distance, cluster means and contribution of each trait to the divergence were estimated as suggested by Singh and Chaudhary[7].

RESULTS AND DISCUSSION

The ANOVA revealed significant differences among the fifteen genotypes for nineteen characters indicating the existence of sufficient amount of diversity among the genotypes.

The 15 genotypes were grouped into four clusters using Tocher's method with a criterion that the intra cluster average D^2 values should be less than the inter-cluster D^2 values.

Based on D^2 value, 15 genotypes were grouped in to 4 clusters. Out of the 4 clusters, cluster III was largest group comprising of 6 genotypes, followed by cluster I with 5 genotypes; cluster II and IV were containing 2 genotypes each (Table1). The tree like structure called dendrogram was constructed based on clustering by Tocher's method (Fig .1).

The average intra and inter cluster D^2 values were presented in table 2. The intra and inter cluster distances revealed that inter cluster distance was greater than intra cluster distance. The intercluster D^2 value was maximum (12829.31) between cluster II and III. The minimum (3933.95) distance was observed between cluster I and II which indicated close relationship among the two genotypes whereas Intra cluster distance was observed and it was found highest in cluster III (3053.33) followed by cluster IV (1342.92), cluster I (1126.39) and cluster II (218.77).

The per cent contribution towards genetic divergence by all the nineteen contributing characters is presented in table 3. The knowledge on characters influencing divergence is an important aspect to a breeder. The genetic diversity among 15 genotypes was measured by employing D^2 statistic. Out of 19 characters studied; protein content contributed maximum percent to the diversity (31.10%) followed by total carbohydrate (28.57%), steroid content (12.38%), total phenol (0.95%), fruit yield per plant (0.74) and number of fruits per plant (0.57).

The cluster mean values for nineteen characters are presented in table 4. The mean values obtained for varying number of genotypes in each cluster, although, cannot be compared statistically, but to get a relative idea of diversity among the clusters they are compared. Based on the range of means for each character, it became possible to know; the characters influencing the divergence. It also helps to categorize the cluster under high fruit yield per plant bearing groups or according to their average performance for a particular character *viz*., clusters II, IV, I, and III. Cluster II (CHFG-5 and CHFG-8) recorded highest fruit yield per plant because it has higher side of values for number of fruits per plant. While the lowest values for these traits were recorded by cluster III formed the lowest performing group for yield. Similarly, it helps to categorize the cluster under high biochemical component bearing groups. Cluster IV (CHFG-4 and CHFG-9) recorded highest biochemichal components.

Genetic divergence among 15 genotypes revealed that cluster II with genotype (CHFG-5 and CHFG-8) and cluster IV (CHFG-4 and CHFG-9) were more divergent. Hence, genotype in this cluster can be utilized for improvement programme as donor parent.

Among the characters studied, protein content, total carbohydrate, steroid content, total phenol, fruit yield per plant and number of fruits per plant were the potent characters which contributed maximum divergence and playing dominant role in the improvement of brinjal. The results were in agreement with the findings of Patel *et al*.[5], Singh *et al*.[7], and Das *et al*,[2], in brinjal.

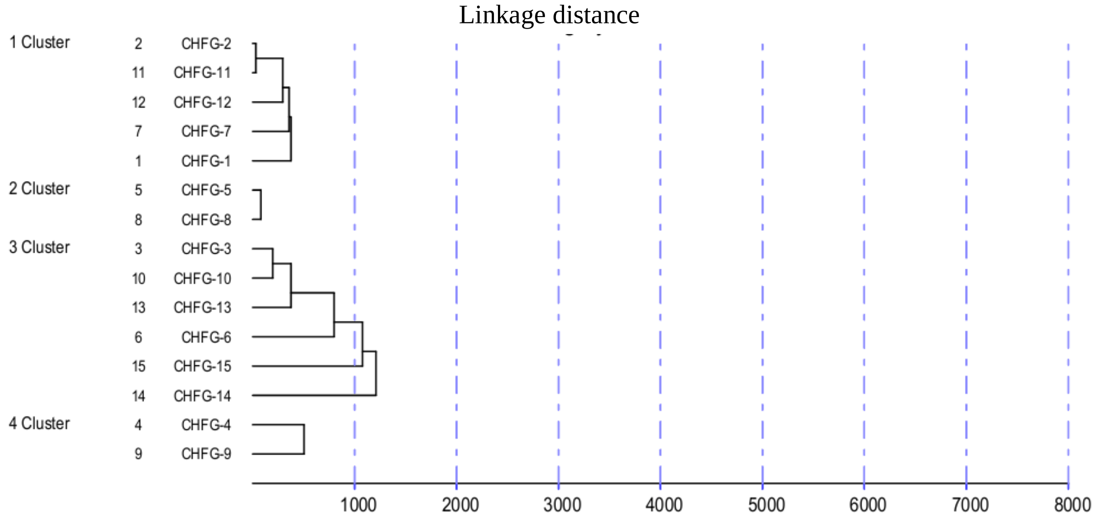

Fig. 1: Tree diagram showing 15 genotypes of wild brinjal for nineteen studied characters using hierarchical cluster analysis (Tocher's method)

Table 1: Clustering pattern of 15 genotypes by Tocher's method

Cluster	Number of genotypes	Genotypes
Cluster I	5	CHFG-2, CHFG-11, CHFG-12, CHFG-7, CHFG-1
Cluster II	2	CHFG-5, CHFG-8
Cluster III	6	CHFG-3, CHFG-10, CHFG-13, CHFG-6, CHFG-15, CHFG-14
Cluster IV	2	CHFG-4, CHFG-9

Table 2: Average Inter and Intra Cluster distances (D^2) for 15 wild brinjal genotypes

Cluster number	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	**1126.39**	3933.95	7970.16	8948.91
Cluster II		**218.77**	12829.31	8004.50
Cluster III			**3053.33**	8062.15
Cluster IV				**1342.92**

Table 3: Percentage contribution of nineteen characters towards diversity in wild brinjal

Character	Contribution (%)
Plant height (cm)	0.00
Days to first flowering (50%)	0.00
Days to first fruit set (50%)	0.00
Days to first harvest	0.00
Fruit girth (cm)	0.00
Fruit length (cm)	0.00
Fruit weight (g)	0.00
Number of fruits per plant	0.57
Fruit yield per plant (kg)	0.74
Total carbohydrate (mg/100g)	28.57
Solasodine content (mg/ 100g)	0.00
Total phenol (mg/100g)	0.95
Ascorbic acid content (mg/100g)	0.00
Total alkaloid (mg/100g)	0.00
Steroid content (µg/100g)	12.38
Flavonoid content (mg/100g)	0.00
Protein content (mg/100g)	31.10

Table 4: Mean values of clusters for nineteen characters studied in wild brinjal

Cluster number	Plant height (cm)	Days to first flowering (50%)	Days to first fruit set (50%)	Days to first harvesting	Fruit girth (cm)	Fruit length (cm)	Fruit weight (g)	Number of fruits per plant	Fruit yield per plant (kg)
Cluster I	54.56	64.27	75.53	88.07	4.37	2.79	25.93	70.67	1.83
Cluster II	49.78	64.83	75.83	88.83	2.92	2.43	21.48	92.67	1.99
Cluster III	54.97	68.22	79.44	92.83	3.05	2.59	20.31	71.33	1.44
Cluster IV	58.78	66.83	78.17	91.00	4.49	2.83	27.42	71.17	1.95

Cluster number	Total carbohydrate (mg/100g)	Solasodine content (mg/100g)	Total phenol (mg/100g)	Ascorbic acid content (mg/100g)	Total alkaloid (mg/100g)	Steroid content (µg/100g)	Flavonoid content (mg/100g)	Terpenoid content (mg/100g)	Phytosterol content (%)	Protein content (mg/100g)
Cluster I	326.46	14.99	20.27	13.99	3.74	178.76	11.80	2.46	7.01	152.69
Cluster II	353.66	9.64	16.45	10.67	3.70	174.38	11.73	2.36	6.67	150.67
Cluster III	343.12	23.16	21.83	11.98	3.36	188.39	10.98	2.20	6.56	138.04
Cluster IV	368.71	24.41	26.50	16.27	4.56	189.15	13.23	3.08	7.99	156.48

CONCLUSION

The genotypes of outstanding mean performance from these clusters will be useful in development of high yield with better quality.

Acknowledgement

The authors are thankful to Dean, College of Horticulture & Forestry, Central Agricultural University, Pasighat, Arunachal Pradesh for providing all kinds of help during present investigation.

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