Original Research Article

Study of genetic divergence in fenugreek (*Trigonella foenum-graecum* L.)

Abstract

A research work on genetic divergence, analysis was estimated in 75 genotypes of fenugreek (*Trigonella foenum-graecum* L.) grown in an Augmented Block Design during *Rabi* season of 2019-20 at Main Experiment Station of Department of Vegetable Science Acharya Narendra Deva University of Agriculture and Technology, Ayodhya. The objective of this study was to characterize morphological differences and yield related traits among 75 fenugreek accessions. Genetic diversity among 75 fenugreek genotypes (*Trigonella foenum-graecum* L.) was assessed. The estimation of genetic diversity among tested genotypes was highly significant, which got grouped into 8 clusters with cluster VI comprising maximum genotypes. Maximum intra-cluster distance (31.23) was observed in cluster V followed by cluster IV (15.51). Similarly maximum inter cluster distance was recorded between the cluster V and VIII (111.88) followed by cluster III and VIII (111.81) respectively. Although maximum cluster means for seed yield traits was recorded for cluster V and III respectively, suggesting a wide range of diversity for most of the economic traits that would enable breeder to identify the genotypes with suitable traits to be used in direct selection and also in improvement programme for broadening the genetic base. 75 accession showed distinguished variation in the dendrogram for all the studied parameters.

Keyword: Augmented, Cluster, divergence, fenugreek.

Introduction: -

Fenugreek (Trigonella foenum-graecum L.) is a dicotyledonous, annual autogamous crop. It is diploid species, populary grown by its localism name "Methi", belongs to the family "fabaceae". It originated from Mediterranean region (Duke et al. 1981). The word "*Trigonella*" is a Latin ward, having meaning from little tringle; refers to its triangular shape of flower. The species name "*foenum-graecum*" means "Greek-hay" indicated that it was used as a forage crop in the past. Fenugreek is a native of West Asia and South- Eastern Europe. The genus *Trigonella* comprises of 50 species mostly of Mediterranean and oriental origin. It is self-pollinated crop and its chromosome number 2n=16. It is an important spices and condiment crop grown for both seed as well as leaves purpose. It is grown widely in part of North India and cultivated in all over the subcontinent for its green leaves and seeds. There are two species of the genus *Trigonella* which are of economic importance, *viz. T. foenum graecum* L., the common methi and *T. corniculata*, the kasthuri methi. It is an annual herb reaching to a height of approximately 90.0 cm. Leaves are light-green and are pinnately trifoliate. The flowers are papilionaceous nature. Fruits are long, narrow, legumes, tapering and curved and with a slender point which contain small extremely furrowed seeds. The flowers are white are yellow in colour. Anthesis takes place with a peak at 11.30am and normally between 9am and 6pm. Fenugreek seeds are used as dietary proteins and have antipyretic, antidiabetic digestive, lactogogue, hypolipidemic, and cholesterol reducing properties (Srinivasan 2014). Spices value of fenugreek is a valuable source of several highly desirable biologically active compounds such asdiosgenin, trigonelline and other most valuable bioactive constituents present in fenugreek. India has been well known as land of spices since very long time period of recorded history. The history of Indian spices crops is well known to be dates back to the inception of human enlightenment. Moreover, references are also available with regard to the Indian spices and their use in Vedas (6000 B.C.) by Manu (4000B.C.). Among the seed spices from an important group of crop which are extensively grown throughout the country as pure or intercrop, both under rain-fed and irrigated condition. These crops play an important role in our national economy. However, national domestic need and the export target beyond 2000 A.D., their production requirement is 3-4 folds, up-gradation of the existing level.

As fenugreek is considered one of the minor crops, the genetic resources of these indigenous underutilized species face rapid destruction owing to erosion of traditional farming culture, change of traditional food habits and the introduction and adaptation of high yielding crops (Zahoor, 2007). In fact, the availability of fenugreek germplasm is low or almost scanty in gene banks (Hymowitz, 1990; Ellison et al., 2006). It is a matter of great concern that fenugreek accessions (land races) are affected by climate change impact or by the decrease of agricultural land. It is therefore required to characterize, document and develop strategies to preserve the valuable resources of indigenous fenugreek species from extinction.

Genetic divergence is the procedure in which two or more populations of an inherited species accumulate independent genetic changes (mutation) through time, offen after the population have become reproductively isolated for some period. Assessment of genetic divergence in fenugreek germplasm is important for long term crop improvement programme. Undoubtedly, the study of the genetic diversity of fenugreek genotypes is not only important for germplasm conservation but also in selecting the parents for breeding purposes. The biological variations in an organism are combined response of genotypic, phenotypic and environmental components. Of which the genotypic variation is of great importance from crop improvement point of view (Mazzucato et al., 2008) and consists of heritable (additive) and non-heritable (dominance and epistatic components).

Material and Methods

Experiment was conducted at Main Experiment Station of Vegetable Research Farm at Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya (U.P.) in well leveled field having proper facility of drainage. Geographically Narendra Nagar falls under humid sub-tropical climate and is located in between 24.470 and 26.560 N latitude and 82.120 and 83.980 E longitude at an altitude of 113 m above from sea level in the Gangetic Alluvial plains of eastern Uttar Pradesh. There are total Seventy five genotypes including 3 checks of fenugreek were collected from Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj) Ayodhya, Uttar Pradesh. The check varieties were Hisar Sonali (C.C.S.H.A.U., Hisar, Haryana), Pua Early Bunching (IARI, New Delhi) and NDM-1(A.N.D.U.A.T., Kumarganj, Ayodhya, Uttar Pradesh). The present experiment was carried out in Augmented Block Design. The material involved in the experiment comprised of 75 selected germplasm of fenugreek among which three were the checks. Each genotype consisted of two row spaced 30 cm apart with plant to plant spacing of 10 cm. Observation were recorded for eleven different characters of fenugreek i.e. Days to 50% flowering , Plant height (cm) , Plant height (cm) , Primary branches per plant , Secondary branches per plant , Days to maturity , Pods per plant , Length of pod (cm) , Seeds per pod , 1000-seed weight (g) , Seed yield per plant (g) , Seed yield (q/ha). Data were subjected to analysis of genetic divergence given by (Spark, 1973 and Beale, 1969). The detailed description among different cluster are given under K- mean clustering of standardized data was used to identify the more significant level of discrimination between the cluster for each of variable.

Result and Discussion

The results obtained from the present investigation as well as relevant discussion have been summarized as under. Selection of suitable parent plays an important role in a successful genetic divergence analysis. Various methods are available for estimating genetic diversity. Seventy five genotypes of fenugreek taken for Euclidian analysis were differed significantly with regard to the characters under study and showed marked divergence, when taking all 11 characters together. Average intra and inter cluster distance were calculated and presented in the table 1. Intra cluster distance showed divergence among the genotype within a cluster while inter cluster distance showed relative divergence among the cluster. The cluster mean for 11 characters among the eight clusters are also presented in table 2.

4.7.1. Distribution of genotypes into different clusters

The 75 genotypes were grouped into eight distinct non-overlapping clusters. Cluster VI had highest number of genotypes (26) followed by cluster IV (13), cluster II (12), cluster I (8) cluster III (7), cluster VII (6) and V (2) and cluster VIII (1). The distribution pattern of genotypes between different clusters also resulted that there is no geographical parallism in the grouping of genotypes, indicating that genotype of different geographical origin may grouped together or vice-versa. Similar findings have been also reported by Sulochana *et al.* (2018), Meena *et al.* (2021), Al-Maaman *et al.* (2020).

4.7.2. Average intra and inter-cluster distance

The estimates of intra and inter-cluster distance for ten clusters have been given in Table 2. The maximum intra-cluster distance was recorded for cluster V (31.23) followed by cluster IV (15.51), cluster II (14.32), cluster VII (11.86), cluster VI (11.04), cluster III (9.67), cluster I (5.45) while lowest intra-cluster distance were recorded in cluster VIII (0.00).

Maximum inter-cluster distance was found between cluster V and cluster VIII (111.88), followed by cluster III and cluster VIII (111.81), cluster II and cluster VIII (93.80), cluster I and cluster VIII (93.04), cluster IV and cluster VIII (91.53), cluster VII and cluster VIII (86.12), cluster VI and cluster VIII (82.97), cluster V and cluster VII (40.83), cluster II and cluster V (35.76) cluster IV and cluster V (32.71), cluster V and cluster VI (32.05) cluster III and cluster V(31.89), cluster V and V (31.23).

The minimum inter cluster distance found between cluster I and cluster II (14.88) followed by cluster I and cluster VI (15.45). The higher inter-cluster distance indicated greater genetic divergence between the genotypes of those clusters, while lower inter-cluster values between the clusters suggested that the genotypes of the clusters were not much genetically diverse from each other. Similar findings have been also reported by Sulochana *et al*. (2018), Meena *et al.* (2021), Al-Maaman *et al.* (2020).

4.7.3. Cluster means:

The cluster means for different traits indicated considerable differences between the clusters as indicated in Table 3.

Cluster I showed maximum mean value for the plant height (105.43). Cluster II showed maximum mean value for seeds per pod (21.68) followed by seed yield per plant (7.05). Cluster III showed maximum mean value for days to maturity (135.55) followed by days to 50% flowering (84.53), length of pods (14.33), secondary branches per plant (7.40), primary branches per plant (3.98). Cluster V showed maximum mean value for seed yield q/ha (16.24) followed by 1000-seed weight (10.05) and showed minimum mean value for days to maturity (130.71) followed pods per plant (31.67), length of pods (10.87) ,seed yield per plant (5.29) s. Cluster VI showed minimum mean value for seed yield q/ha (14.42). Cluster VII showed maximum mean value for pods per plant (50.05). Cluster VIII showed minimum mean value for days to 50% flowering (75.24) followed by plant height (69.55), seeds per pod (16.31), 1000-seed weight (7.65), secondary branches per plant (5.00), primary branches per plant (2.00). Similar findings have been also reported by Sulochana *et al.* (2018), Meena *et al.* (2021), Al-Maaman *et al.* (2020).

Table 1. Clustering pattern of seventy five genotypes of fenugreek

Cluster no.	**No. of genotype**	**Genotypes**
1	**8**	NDM-11, NDM-36, NDM-96, NDM-131, NDM-71, NDM-111, NDM-140, NDM-31
2	**12**	NDM-13, NDM-133, NDM-38, NDM-73, NDM-98, NDM-17, NDM-117, NDM-54, NDM-76, NDM-40, NDM-100, NDM-119
3	**7**	NDM-12, NDM-132, NDM-37, NDM-72, NDM-97, NDM-151, NDM-152
4	**13**	NDM-18, NDM-92, NDM-51, NDM-32, NDM-56, NDM-19, NDM-53, NDM-120, NDM-139, NDM-77, NDM-94, NDM-116, NDM-138
5	**2**	NDM-118, Hisar Sonali
6	**26**	NDM-14, NDM-134, NDM-136, NDM-137, NDM-20, NDM-39, P.E.B., NDM-1, NDM-135, NDM-52, NDM-78, NDM-57, NDM-91, NDM-58, NDM-75, NDM-35, NDM-15, NDM-34, NDM-16, NDM-93, NDM-55, NDM-112, NDM-60, NDM-115, NDM-95, NDM-99
7	**6**	NDM-33, NDM-59, NDM-79, NDM-80, NDM-113, NDM-114
8	**1**	NDM-74

Table 2: Inter and Intra cluster D^2 value for eight cluster in fenugreek

Clusters	**Cluster 1**	**Cluster 2**	**Cluster 3**	**Cluster 4**	**Cluster 5**	**Cluster 6**	**Cluster 7**	**Cluster 8**
Cluster 1	**5.45**	14.88	21.88	16.24	29.52	15.45	23.35	93.04
Cluster 2		**14.32**	28.81	23.31	35.76	20.39	25.76	93.80
Cluster 3			**9.67**	23.48	3.89	34.25	30.57	111.81
Cluster 4				**15.51**	32.71	18.06	24.45	91.53
Cluster 5					**31.23**	32.05	40.83	111.88
Cluster 6						**11.04**	16.61	82.97
Cluster 7							**11.86**	86.12
Cluster 8								**0.00**

Table- 3: Intra cluster group mean for eight characters in fenugreek germplasm

Cluster	**Days to 50% flowering**	**Plant height (cm)**	**Primary branches per plant**	**Secondary branches per plant**	**days to maturity**	**No. of Pods per plant**	**Length of pod (cm)**	**Seeds/pod**	**1000 seed weight**	**Seed yield per plant (g)**	**Seed yield (q/ha.)**
Cluster-1	78.56	105.43	3.36	5.39	132.16	35.98	14.29	19.34	8.81	6.11	14.65
Cluster-2	77.47	88.79	2.88	5.80	132.14	34.66	13.75	21.68	8.37	7.05	15.13
Cluster-3	84.53	87.30	3.98	7.40	135.55	47.58	14.33	20.07	9.19	5.95	15.76
Cluster-4	82.28	83.60	3.13	5.79	134.73	34.27	12.88	17.96	8.47	5.60	14.62
Cluster-5	77.74	73.35	3.12	7.00	130.71	31.67	10.87	18.13	10.05	5.29	16.24
Cluster-6	75.93	82.04	2.63	5.58	131.34	34.81	12.15	17.20	8.16	5.72	14.42
Cluster-7	75.87	74.62	2.66	6.15	131.74	50.05	13.25	16.89	7.96	6.10	14.52
Cluster-8	75.24	69.55	2.00	5.00	132.25	34.42	13.35	16.31	7.65	5.80	14.74

IV. Percent contribution in genetic divergence in fenugreek

The highest percent contribution in genetic divergence in fenugreek was recorded by plant height (60.18) followed by pods per plant (24.43), days to 50% flowering (8.97), length of pod (3.93), seeds per pod (1.55), secondary branches per plant (0.11), seed yield quintal per ha (0.11) Based on primary branches per plant (0.001), 1000-seed weight (0.001), seed yield per plant (0.001) was found to contribute negligible. The result for some of the traits also reported by Sulochana *et al.* (2018), Meena *et al.* (2019).

Table 4: Percent contribution in genetic divergence in fenugreek

S.N.	Source	Contribution %
1	Days to 50% flowering	8.97%
2	Plant height	60.18%
3	Primary branches/plant	0.001
4	Secondary branches/plant	0.11%
5	Days to maturity	0.72%
6	No. of pods/plant	24.43%
7	Length of pods(cm)	3.93%
8	Seeds/pod	1.55%
9	1000-seed weight	0.001
10	Seed yield/plant(g)	0.001
11	Seed yield (q/ha)	0.11%

References:

Al-Maamari, I.T.; Khan, M.M.; Al-Sadi; A.M.; Iqbal, Q. and Al-Saddy, N. Morphological characterization and genetic diversity of fenugreek (*Trigonella foenum-graecum* L.) accessions in *Oman*. Bulgarian J. of Agric. Sci. 2020;26(2): 375-383.

Beale, E.M.L. Euclidean cluster analysis. *Bull. Int. Stat. Inst*. 1969;43: 92-94.

Duke, J. A, Reed C F and Weder P. *Trigonella foenum graceum* L. Handbook of Legumes of World Economic Importance. Duke J A (Eds). Plenum Press, New York. 1989.

Ellison, W., Liston, A., Steiner, J., Williams, W. & Taylor, N. Molecular phylogenetics of the clover genus (*Trifolium-Leguminoseae*). *Mol. Phylogenet. Evol*. 2006;39: 688-705.

Hymowitz, T. Grain legumes. In: Janick, J. and J.E. Simon (eds.). Advances in new crop. Timber Press, Portland, OR, 1990;54- 57.

Mazzucato, A., Papa, R., Bitocchi, F., Mosconi, P., Nanni, L.,Negri, V., Picarella, M. E., Siligato, F., Soressi, G. P., Tiranti, B. & Veronesi, F. (). Genetic diversity, structure and marker-trait associations in a collection of Italian tomato (*Solanum lycopersicum* L.) landraces. *Theor. Appl. Genet*. 2008;5:657-669.

Meena, R. S., Choudhary, S., Verma, A. K., Meena, N. K., & Mali, S. C. Estimates of genetic variability, divergence, correlation and path coefficient for morphological traits in fenugreek (Trigonella foenum-graecum L.) genotypes. *Legume Research-An International Journal*. 2021;44(3):281-286.

Spark, D. N.. Euclidean cluster analysis. Algorithm AS 58. *Appl. Stat*. 1973;22:126-130.

Srinivasan K. Antioxidant potential of spices and their active constituents. *Critical Review of Food Science and Nutrition*. 2014;54:352–72.

Sulochana, J.; Kumar, D.; Masuthi, A.; Naika, M.B.N.; Tatagar, M.H. and Koulagi, S. Estimation of genetic diversity in fenugreek (*Trigonella foenum-graecum* L.) genotypes for productivity traits. *Int. J. of Chem. Stud*. 2018;6(5):2701-2703.

Zahoor, A. Country report on plant genetic resources for food and agriculture. *Pakistan Agricultural Research Council,* 2007;79.