An experimental 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.

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Introduction

Fenugreek (*Trigonella foenum-graecum* L.) is an annual herb, autogamous and dicotyledonous in nature. It is, popularly known as “Methi”, belongs to the family “fabaceae” and consist diploid chromosome. It seems to be it is originated from Mediterranean region (Duke et al. 1981). The Genus name “*Trigonella*” is derived from a Latin word, which means little triangle; indicated to shape of its triangular flower. The word “*foenum-graecum*” means “Greek-hay” refers that in past it was used as a forage crop by farmers. The origin place of Fenugreek is West Asia and South- Eastern Europe (Ecocrop, 2017; Alaoui, 2005).

There are 50 species comprises in the genus *Trigonella* in which maximum are originated form Mediterranean and oriental origin. Fenugreek is autogamous or self-pollinated crop and consists 2n=2x=16 chromosome number (Frayer, 1930). It is cultivated for both leaves purpose as well as seed and play important role in spices and condiment crop. It is cultivated hugely in North India part and grown in all over the subcontinent for its high value green leaves and also for seeds (Singh *et al.,* 2017). The common methi (*T. foenum graecum* L.) and kasthuri methi (*T. corniculata*), are the only two species which have economic importance in the genus *Trigonella*. Fenugreek is attaining to a height of approximately 90.0 cm. Its leaves are trifoliate pinnately and light green in colour. The flowers of fenugreek are white or yellow in colour and papilionaceous nature. Fruits are yellow pods long, narrow, aromatic, tapering and curved and with a slender point which consists small highly furrowed brown seeds. Opening of flower takes place mostly at 11.30 am and usually between 9am and 6pm (Singh *et al*, 2019). Its seeds have antipyretic, antidiabetic digestive, lactogogue, hypolipidemic, and cholesterol decreasing attributes and used as a dietary proteins (Srinivasan 2014).

Fenugreek is a valuable source of a number of highly desired physiologically active chemicals, including diosgenin, trigonelline, and other highly useful bioactive components. Since the beginning of written history, India has a long and illustrious history as a land of spices. It is common knowledge that Indian spice crops have existed since the dawn of civilization. Additionally, there are allusions to Indian spices and their use in the Vedas (6000 B.C.) by Manu (4000 B.C.) (Prakash *et al.* 2020). Among the seed spices from a significant variety of crops that are widely farmed throughout the nation as pure or intercrop, both under rain-fed and under irrigation. The economy of our country is significantly influenced by these crops. However, domestic national needs and the export target beyond 2000 A.D., their production requirement is 3-4 folds, up-gradation of the existing level (Singh *et al.* 2019).

The genetic resources of these indigenous underutilized species are in danger of being rapidly destroyed because of the deterioration of traditional agricultural practices, changes in traditional eating patterns, and the introduction and adaptation of high yielding crops, even though fenugreek is thought to be a vital component of minor crops. (Zahoor, 2007). In fact, the availability of fenugreek germplasm is low or almost scanty in gene banks (Hymowitz, 1990; Ellison *et al.*, 2006). The fact that fenugreek accessions (land races) are impacted by climate change or the shrinking amount of arable land is a major cause for concern. As a result, it is necessary to characterize, record, and create methods to protect the priceless resources of native fenugreek species from extinction.

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Genetic divergence is the process through which two or more populations of an inherited species assemble distinct genetic changes (mutations) over time, frequently following the population's temporary isolation from one another in terms of reproduction. For long term crop improvement programme evaluation of genetic divergence in fenugreek germplasm is most important. Undoubtedly, the assessment of the genetic diversity is not only important for germplasm conservation but also in parent selection 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). Keeping in view of the above all facts, the present investigation entitled "Study of genetic diversity, in fenugreek (*Trigonella foenum-graecum* L.)" has been planned with the objectives of to estimate the genetic divergence (D^2) among the genotypes for various traits.

Material and Methods

This experiment was examined 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 with proper drainage facility. Geographically, Narendra Nagar is in the Gangetic Alluvial Plains of eastern Uttar Pradesh, between 24.470° and 26.560° N latitude and 82.120° and 83.980° E longitude, at an altitude of 113 m above sea level, and it has a humid subtropical climate.

Experimental Details-

In this experiment there are total 75 genotypes of fenukgreek including 3 checks which are maintain by ANDUAT, Ayodhya were collected for examination from Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj) Ayodhya, Uttar Pradesh. Three check varieties were Hisar Sonali, Pua Early and NDM-1 which are taken form (C.C.S.H.A.U., Hisar, Haryana), Bunching (IARI, New Delhi) (A.N.D.U.A.T., Kumarganj, Ayodhya, Uttar Pradesh), respectively. The present investigation was carried out in Augmented Block Design.

Every genotypes were comprise of two row spaced 30 cm apart with plant to plant spacing of 10 cm. Observation were recorded for eleven different traits of fenugreek i.e. Days to 50% flowering, Plant height (cm), Days to maturity, Secondary branches per plant, Primary

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branches per plant, Pod Length (cm), Number of Pods per plant, 1000-seed weight (g), Seeds per pod, Seed yield per plant (g), Seed yield (q/ha).

Table 1. Genotypes passport data in table

NDM-11	NDM-54	NDM-97	NDM-140
NDM-12	NDM-55	NDM-98	NDM-151
NDM-13	NDM-56	NDM-99	NDM-152
NDM-14	NDM-57	NDM-100	Hisar Sonali
NDM-15	NDM-58	NDM-111	P.E.B.
NDM-16	NDM-59	NDM-112	NDM-1
NDM-17	NDM-60	NDM-113	
NDM-18	NDM-71	NDM-114	
NDM-19	NDM-72	NDM-115	
NDM-20	NDM-73	NDM-116	
NDM-31	NDM-74	NDM-117	
NDM-32	NDM-75	NDM-118	
NDM-33	NDM-76	NDM-119	
NDM-34	NDM-77	NDM-120	
NDM-35	NDM-78	NDM-131	
NDM-36	NDM-79	NDM-132	
NDM-37	NDM-80	NDM-133	
NDM-38	NDM-91	NDM-134	
NDM-39	NDM-92	NDM-135	
NDM-40	NDM-93	NDM-136	
NDM-51	NDM-94	NDM-137	
NDM-52	NDM-95	NDM-138	
NDM-53	NDM-96	NDM-139	

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Through non-hierarchical Euclidean cluster analysis, the genetic divergence among 75 genotypes, including checks placed in augmented design, was investigated. **(Beale, 1969; Spark, 1973**).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

Following is a summary of the findings from the current study as well as relevant discussions. 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 inter and intra cluster distance were calculated and exhibited in the table 2. 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 3.

4.7.1. Clustering of genotypes:-

The 75 genotypes of fenugreek were grouped into 8 distinct non-overlapping clusters. Highest number of genotypes (26) were found in Cluster VI pursued by cluster IV (13), cluster II (12), cluster I (8) cluster III (7), cluster VII (6) and V (2) and cluster VIII (1). The pattern of genotypes distribution among various clusters also resulted that there is none geographical parallism in the genotypes grouping, denoting that genotypes of various geographical origin may be grouped along 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. Intra and inter cluster distance average:-

Estimation of intra and inter-cluster distance for ten clusters have been given in Table 3. Cluster V (31.23) were observed as a maximum intra-cluster distance pursued 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 cluster VIII (0.00) have consist lowest intra-cluster distance.

Inter-cluster distance maximum value was found between cluster V with cluster VIII (111.88), pursued by cluster III with 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 I and II cluster (14.88) pursued by I and VI cluster (15.45). Lower inter-cluster values between the clusters meant that the genotypes of the clusters were not significantly genetically different from one another, but higher inter-cluster distances indicated greater genetic divergence between the genotypes of

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those clusters. Same findings were also founded by Sulochana *et al.* (2018), Meena *et al.* (2021), Al-Maaman *et al.* (2020).

4.7.3. Cluster means:

The cluster means for various traits denoted that there were considerable differences between the clusters as shown in table 4.

Cluster I exhibited maximum mean value for the plant height (105.43). Maximum mean value for seeds per pod (21.68) exhibited by Cluster II followed by seed yield plant^{-1} (7.05). Cluster III exhibited higher mean value for days maturity (135.55) pursued by days to 50% flowering (84.53), length of pods (14.33), secondary branches per plant (7.40), primary branches plant^{-1} (3.98). Cluster V exhibited higher mean value for total seed yield q/ha (16.24) pursued 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 plant^{-1} (5.29). Cluster VI showed minimum mean value for seed yield q/ha (14.42). Cluster VII exhibited higher mean value for pods plant^{-1} (50.05). Cluster VIII showed lower 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).

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Table 2. Clustering pattern of seventy five genotypes of fenugreek

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Cluster no.	No. of genotype	Genotypes
I	**8**	NDM-11, NDM-36, NDM-96, NDM-131, NDM-71, NDM-111, NDM-140, NDM-31
II	**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
III	**7**	NDM-12, NDM-132, NDM-37, NDM-72, NDM-97, NDM-151, NDM-152
IV	**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
V	**2**	NDM-118, Hisar Sonali
VI	**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
VII	**6**	NDM-33, NDM-59, NDM-79, NDM-80, NDM-113, NDM-114
VIII	**1**	NDM-74

Table 3: Inter and Intra cluster D^2 value for eight cluster in fenugreek

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	**5.45**	14.88	21.88	16.24	29.52	15.45	23.35	93.04
Cluster II		**14.32**	28.81	23.31	35.76	20.39	25.76	93.80
Cluster III			**9.67**	23.48	3.89	34.25	30.57	111.81
Cluster IV				**15.51**	32.71	18.06	24.45	91.53
Cluster V					**31.23**	32.05	40.83	111.88
Cluster VI						**11.04**	16.61	82.97
Cluster VII							**11.86**	86.12
Cluster VIII								**0.00**

Table- 4: 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- II	77.47	88.79	2.88	5.80	132.14	34.66	13.75	21.68	8.37	7.05	15.13
Cluster-III	84.53	87.30	3.98	7.40	135.55	47.58	14.33	20.07	9.19	5.95	15.76
Cluster-IV	82.28	83.60	3.13	5.79	134.73	34.27	12.88	17.96	8.47	5.60	14.62
Cluster- V	77.74	73.35	3.12	7.00	130.71	31.67	10.87	18.13	10.05	5.29	16.24
Cluster-	75.93	82.04	2.63	5.58	131.34	34.81	12.15	17.20	8.16	5.72	14.42

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VI											
Cluster-VII	75.87	74.62	2.66	6.15	131.74	50.05	13.25	16.89	7.96	6.10	14.52
Cluster-VIII	75.24	69.55	2.00	5.00	132.25	34.42	13.35	16.31	7.65	5.80	14.74

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IV. Percent contribution in genetic divergence in fenugreek

The highest percent contribution in genetic divergence in fenugreek was observed in plant height (60.18) pursued by pods plant^{-1} (24.43), days to 50% flowering (8.97), length of pod (3.93), seeds per pod (1.55), secondary branches plant^{-1} (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 founded by Sulochana *et al.* (2018), Meena *et al.* (2019).

Table 5: Percent contribution in genetic divergence in fenugreek

S.N.	**Source**	**Contribution Percentage**
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%

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Conclusion:

With the help of result of present investigation it can be concluded that there exists ample variation with in the germplasm of fenugreek**.** Maximum inter-cluster distance was obserevd between cluster V and cluster VIII. Crossing among genotypes of cluster VIII and cluster VI may give rise desirable F1/segregates in future.

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