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Genetic Diversity for Yield and its Component Traits in Fenugreek (*Trigonella foenum-graecum* L.)

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Abstract Genetic divergence in thirty five genotypes of fenugreek was assessed by using Mahalanobis D^2 statistics. The experiment was carried out during *rabi* of 2014-15. The genotypes were grouped into four clusters. The cluster I contained the highest number of genotypes while, the clusters II, III and IV were monogenotypic. The maximum inter cluster distance was noticed between the cluster III and IV and minimum between cluster II and III. The highest intra-cluster distance was observed in the cluster I. Among all the characters studied, seed yield per hectare contributed maximum amount towards genetic divergence. The study indicated that for obtaining heterotic response as well as better segregants intermating between genotypes of diverse clusters may be undertaken in breeding programs for improving yield and quality traits.

Keywords Cluster, D^2 technique, Fenugreek, Genetic diversity, *Trigonella foenum-graecum*.

Introduction

Fenugreek (*Trigonella foenum-graecum* L.) commonly known as methi or menthya, belongs to the family Fabaceae is one of the most prominent seed spice. In India, fenugreek is grown in about 93,090 hectares with an annual production of about 1,12,845 tones. Fenugreek is a multipurpose crop being used as a spice, vegetables, fodder and a medicinal plant. Its leaves are rich source of proteins, minerals and vitamins. The seed of fenugreek is generally used in blends of curry powder, pickles and meat product. Seeds are rich in essential amino acids and trigonilline for which fenugreek is well known for medicinal uses. Seeds are also reported to contain steroid 'diosgenin' which is used in the preparation of contraceptives.

Genetic divergence is an important factor in any crop improvement program for obtaining high yielding variety. Selection of parents based on genetic divergence is a pre-requisite in a heterosis breeding. Thus, precise information on the nature and degree of genetic divergence helps plant breeders in choosing the diverse parents for purposeful hybridization. The use of D^2 statistic of multivariate analysis gives an understanding of genetic diversity in the crop. D^2 measures the degree of diversity and determines the relative proportion of each component traits to the total divergence. There are few studies on genetic divergence in fenugreek and hence the present study aims at assessing the genetic divergence among 35 genotypes of fenugreek.

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Table 1. Grouping of fenugreek genotypes based on D^2 values.

Sl. No.	Cluster	Name of genotypes	Number of genotypes
1	I	DFC 1, DFC 2, DFC 3, DFC 5, DFC 6, DFC 7, DFC 8, DFC 9, DFC 10, DFC 11, DFC 12, DFC 13, DFC 14, DFC 15, DFC 16, DFC 17, DFC 19, DFC 20, DFC 21, DFC 22, DFC 23, DFC 24, DFC 25, DFC 26, DFC 27, DFC 28, DFC 29, Pant ragini, Gujarat methi 2, Ajmer methi 1, Ajmer methi 2, Lam M 2	32
2	II	Pusa early bunching	1
3	III	DFC 4	1
4	IV	DFC 18	1

Materials and Methods

The experimental material comprised of 35 genotypes from different research stations and local collections and were grown in a completely randomized block design with two replications at Spice Unit, Main Agricultural Research Station, University of Agricultural Sciences, Dharwad (Karnataka) during *rabi* season of 2014-15. The planting was done with a row to row spacing of 30 cm and plant to plant spacing of 10 cm. All recommended agronomic practices and plant protection measures were followed timely for successful raising the crop. The data on days to 50% flowering and days to maturity was recorded on plot basis, while, five plants were tagged at random to record data on important growth and yield contributing characters, which were analyzed by the standard statistical methods. The genetic divergence was estimated using the D^2 statistic [1] and the population was grouped into clusters by following the Tocher's method [2].

Results and Discussion

The multivariate analysis based on D^2 values among 35 genotypes revealed that all the genotypes can be grouped into four clusters on the assumption that genotypes within the cluster have similar D^2 values among themselves than those from groups belonging to two different clusters (Table 1). Cluster I was the largest having 32 genotypes, while clusters II, III and IV were monogenotypic. Similar results were also reported by earlier workers, where thirty six genotypes grouped into six clusters [3]. Similarly, forty genotypes grouped into nine clusters [4]. The clustering pattern of the genotypes showed that genetic diversity was not related to geographic diversity. Such a type of constellation of germplasm proves that the collection made were genetically viable for different characters. The clustering pattern of the strains revealed that there was no close correspondence between geographical distribution and genetic divergence as estimated by the D^2 statistic.

Average intra and inter cluster distance of four clusters are presented in Table 2. The inter-cluster distances were greater than intra-cluster distances, revealing considerable amount of genetic diversity among the genotypes. Cluster I showed maximum intra-cluster distance (D^2 = 244.34). Inter cluster distances varied from 1030.87 to 7591.07. Cluster III and IV showed maximum inter cluster distance (7591.07) followed by clusters II and IV (7091.41) followed by cluster I and II (2388.07) and cluster I and III (2214.47), indicating wide divergence among these clusters. This also suggests that the genetic architecture of the genotypes in one cluster differs entirely from those included in the other cluster. Hence, it is suggested that inter-mating between the genotypes included in these diverse clusters may give high heterotic re-

Table 2. Average intra and inter cluster D^2 values of fenugreek genotypes.

Cluster distances	I	II	III	IV
I	244.34	2388.07	2214.47	1922.79
II		0	1030.87	7091.41
III			0	7591.07
IV				0

Table 3. Percent contribution of various characters towards diversity in fenugreek genotypes.

Sl. No.	Characters	Times ranked 1st	Percent contribution
1	Plant height at 30 DAS	9	1.51
2	Plant height at 60 DAS	8	1.34
3	Plant height at 90 DAS	0	0
4	Number of branches at 30 DAS	0	0
5	Number of branches at 60 DAS	8	1.34
6	Number of branches at 90 DAS	1	0.17
7	Number of leaves at 30 DAS	17	2.86
8	Number of leaves at 60 DAS	0	0
9	Number of leaves at 90 DAS	9	1.51
10	Leaf area	23	3.87
11	Chlorophyll content	3	0.5
12	Herbage yield per plant	0	0
13	Herbage yield per sq m	2	0.34
14	Dry matter per plant	2	0.34
15	Days to 50% flowering	0	0
16	Days to maturity	40	6.72
17	Number of pods per plant	12	2.02
18	Pod length	24	4.03
19	Pod width	44	7.39
20	Number of seeds per pod	6	1.01
21	Hundred seed weight	27	4.54
22	Seed yield per plant	6	1.01
23	Seed yield per hectare	339	56.97

Table 4. Cluster means for various characters in fenugreek genotypes.

Cluster	I	II	III	IV
Plant height 30 DAS (cm)	16.71	1.8	22.9	15.8
Plant height 60 DAS (cm)	57.56	24.4	70.1	62.6
Plant height 90 DAS (cm)	72.12	45.2	78.7	79
No. of branches 30 DAS	3.23	4.2	3.7	3.7
No. of branches 60 DAS	9.13	14.7	7.1	5.9
No. of branches 90 DAS	10.44	15.9	8.4	9.1
No. of leaves 30 DAS	18.66	23.5	20.2	17.55
No. of leaves 60 DAS	77.88	65.5	57.8	61.9
No. of leaves 90 DAS	35.71	94.33	54	32.5
Leaf area (cm^2)	7.39	6.2	8.96	6.59
Chlorophyll content	55.38	49.56	54.3	53.87
Herbage yield / plant (g)	16.9	21.1	18.58	14.52
Herbage yield/ sqm (kg)	0.58	0.74	0.65	0.51
Dry matter / plant (g)	3.36	4.79	4.33	2.64
Days to 50% flowering	41.66	56	41	41
Days to maturity	84.64	109	87.5	82.5
No. of pods per plant	38.93	40.5	41.45	50.6
Pod length (cm)	10.34	9.59	10.46	11.02
Pod width (mm)	3.6	3.54	3.42	3.34
No. of seeds per pod	14.48	13.6	14.96	15.54
100 seed weight (g)	1.72	1.11	1.7	1.61
Seed yield per plant (g)	6.77	3.35	7.1	8.0
Seed yield per hectare (q)	29.28	20.16	35.25	29.87

sponse and thus better segregants. The lowest inter cluster distance was noticed between cluster II and III (1030.87) followed by cluster I and IV (1922.79) indicating the close relationship among the genotypes included in these clusters. Thus crossing of genotypes from these two clusters may not produce high level of heterotic expression in the F_1's and broad-spectrum of variability in segregating (F_2) populations. Similar results were reported earlier by Banerjee and Kole [5].

The contribution of individual characters to the divergence was worked out in terms of number of times it appeared first (Table 3). Total seed yield per hectare (56.97%) contributed maximum to the genetic diversity among the genotypes followed by pod width (7.39%), days to maturity (6.72%), hundred seed weight (4.54%), pod length (4.03%), leaf area (3.87%), number of leaves at 30 DAS (2.86%), number of pods (2.02%), plant height at 30 DAS (1.51%), number of leaves at 90 DAS (1.51%), number of branches at 60 DAS (1.34%), plant height at 60 DAS (1.34%), seed yield per plant (1.01%), number of seeds per pod (1.01%), chlorophyll content (0.5%), herbage yield per sq m (0.34%) and dry matter per plant (0.34%) whereas other characters did not contribute to the diversity. The results are in agreement with Banerjee and Kole [5] who reported the greater contribution for plant height, seed yield per plant and number of seeds per pod and similar results were obtained for plant height, pods per plant, test weight, seed yield per plant and branches per plant in divergence by Banerjee and Kole [5].

The existence of diversity among the genotypes was also assessed by considerable amount of variation in cluster mean for different characters (Tables 4 and 5). The genotypes in cluster IV and I were the early maturing. The genotypes in cluster I, III and IV were tallest and cluster II had the dwarf genotype. Maximum number of branches per plant was recorded in the cluster II. The higher herbage yield per plant was recorded by the genotypes in clusters II and III. Genotypes in clusters VI had the highest number of pods per plant, pod length, pod width, number of seeds per pod, seed yield per plant. The genotypes comprising of cluster I (1.72 g) showed highest hundred seed weight followed by cluster III. High seed yield per hectare was shown by the genotype in cluster III (35.25 q) followed by cluster IV (29.87 q).

Genetically distant parents usually are able to produce higher heterosis. The clustering pattern could be utilized in choosing parents for cross combinations which is likely to generate the highest possible variability for effective selection of various economic traits [6]. Keeping in this view, the findings from present study indicated that the cluster III and IV, II and IV and I and II showed higher distance between them. Parental material selection from these clusters would give high manifestation of heterosis as well as spectrum of variation when they are hybridized.

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