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# Genetic divergence in fenugreek (*Trigonella foenum-graecum* L.) germplasm

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**Abstract**

Thirty six genotypes of fenugreek (*Trigonella foenum-graecum* ) were studied at Jobner (Rajasthan) for their genetic divergence following $D^2$ analysis. The study indicated that the genotypes were grouped into six clusters and there was lack of parallelism between genetic and geographic diversity. Intra cluster distance was highest in cluster I followed by cluster II. Inter cluster distance was maximum between cluster IV and II followed by III and II. Among the 10 characters studied for genetic divergence, fat content contributed the maximum accounting for 70.3% of total divergence, followed by plant height (8.6%). The study indicated that for obtaining heterotic response as well as better segregants, inter-mating between genotypes of diverse clusters may be undertaken in breeding programmes for improving yield and quality traits.

**Keywords:** $D^2$ statistic, genetic divergence, fenugreek, *Trigonella foenum-graecum*.

The development of new varieties in crop plants is mainly governed by the magnitude of genetic diversity and the extent of variability available for the desired characters. The nature and magnitude of genetic divergence in a population is essential for selecting diverse parents which upon hybridization leads to greater opportunity for crossing over which release latent variation by breaking up the predominantly repulsion phase linkages. 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. Information on these aspects in fenugreek is limited and hence the need for identifying the genotypes having better performance for yield and quality traits and which belong to diverse parents. The present investigation was hence undertaken to determine the genetic diversity in 36 genotypes of fenugreek (*Trigonella foenum-graecum* L.).

Thirty six genotypes (derived from recombination and mutation of the germplasm collected from various districts of Rajasthan) of fenugreek including five standard checks were grown in a completely randomized block design with three replications at SKN College of Agriculture, Jobner (Rajasthan) during *rabi* season 2000–01. Jobner is situated at 27° 05′ North latitude and 75° 28′ East lon-

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**Table 1.** Distribution of 36 fenugreek genotypes in 6 clusters based on $D^2$ values

| Cluster | Genotype | No. of genotypes |
|---|---|---|
| I | AL-8, RTP-10, UM-305, AL-47, RTP-5, Local, AL-106, AL-1, AL-103, Rmt-303, RTP-6, AL-2, Rmt-143, RTP-8, RTP-7, NS-4, AL-49, Rmt-1, AL-18, AL-51, NS-7, RTP-11, RTP-1, RTP-2 | 24 |
| II | AL-21, AL-48, AL-31, RTP-4, AL-83, NS-5, NS-1 | 7 |
| III | RTP-9 | 1 |
| IV | AL-45 | 1 |
| V | NS-2, NS-3 | 2 |
| VI | NS-6 | 1 |

gitude at an altitude of 427 m above MSL in Jaipur District of Rajasthan. Each plot consisted of two rows of 4 m length with plant spacing of 30 cm x 10 cm. Ten plants were selected at random from each plot for recording observations on 10 characters. The genetic divergence was estimated using the Mahalanobis $D^2$ statistic (1936) and the population was grouped into clusters by following the Tocher's method described by Rao (1952).

The analysis of variance for each individual showed highly significant differences among the genotypes for all the characters studied. The pooled divergence for all the characters within the genotypes, tested by the Wilk's criterion $X^2$ (1415 at 350 df ) was significant. Hence, the analysis of genetic divergence among genotypes used in the study was considered relevant.

The multivariate analysis based on $D^2$ values among 36 genotypes revealed that all the genotypes can be grouped into six clusters (Table 1). Among these, cluster I consisted of 24 genotypes, followed by cluster II (7) and cluster V (2); clusters III, IV and VI were monogenotypic. The results indicated that genetic divergence is not related to geographical diversity and may possibly be due to varietal diversity among the genotypes due to diversity of their pedigree along with natural and directional selection pressure for certain agronomic traits. Similar results were also reported by Mathur (1992) and Kole &

**Table 2.** Average intra and inter cluster $D^2$ values in 6 clusters of fenugreek

| Cluster | I | II | III | IV | V | VI |
|---|---|---|---|---|---|---|
| I | **6.211**(2.492) | 12.329(3.511) | 10.288(3.207) | 12.114(3.480) | 11.142(3.337) | 9.872(3.142) |
| II | | **5.220**(2.284) | 20.309(4.506) | 22.440(4.737) | 17.479(4.181) | 14.985(3.871) |
| III | | | **0.00** | 5.704(2.388) | 9.680(3.111) | 12.988(3.603) |
| IV | | | | **0.00** | 13.746(3.707) | 12.858(3.585) |
| V | | | | | **0.00** | 14.975(3.869) |

Values in bold are intra cluster distances; Values in parenthesis indicate D values

**Table 3.** Contribution of various characters to divergence in fenugreek

| Character | Times ranked 1st | Contribution (%) |
|---|---|---|
| Days to 50% flowering | 17 | 2.7 |
| Plant height | 54 | 8.6 |
| Primary branches plant$^{-1}$ | 7 | 1.1 |
| Pods plant$^{-1}$ | 24 | 3.8 |
| Pod length | 4 | 0.6 |
| Seeds pod$^{-1}$ | 6 | 0.9 |
| Test weight | 16 | 2.5 |
| Seed yield plant$^{-1}$ | 37 | 5.9 |
| Protein content | 16 | 2.5 |
| Fat content | 449 | 71.3 |

Mishra (2002) in fenugreek. Genetic drift and selection forces under diverse environments could cause greater diversity than geographical distance (Bhatt 1970; Kole *et al*. 2003).

The inter-cluster distances were greater than intra-cluster distances, revealing considerable amount of genetic diversity among the genotypes (Table 2). Cluster I showed maximum intra-cluster distance. Intra-cluster distance is the main criterion for selection of genotypes using $D^2$ analysis. Inter-cluster distance varied from 5.704 to 22.440. Minimum inter-cluster $D^2$ value was observed between clusters IV and III (5.704) indicating the close relationship among the genotypes included in these clusters. Maximum inter-cluster value was observed between clusters IV and II (22.44) indicating maximum divergence between the genotypes of these clusters. The inter-cluster $D^2$ values were also higher between the clusters III and II (20.309), clusters V and II (17.479) and clusters VI and II (14.985) and V (14.975). Hence, it is suggested that inter-mating between the genotypes included in these diverse clusters may give high heterotic response and thus better segregants.

The contribution of individual characters to the divergence was worked out in terms of number of times it appeared first (Table 3). Fat content (%) contributed maximum towards genetic divergence, followed by plant height, seed yield plant$^{-1}$ and seeds pod$^{-1}$. Cluster means for 10 characters revealed that genotypes included in cluster V showed maximum seed yield plant$^{-1}$, pod length, seeds pod$^{-1}$ and test weight with early flowering and tall plants (Table 4). Genotypes in cluster IV had maximum number of primary branches plant$^{-1}$ and protein content (%) in the dwarf plant type. Genotypes in clusters II and VI had the highest fat content (%) and pods plant$^{-1}$ combined with late flowering, respectively. It can, therefore, be concluded from the present study that hybridization among genotypes of these cluster combinations is expected to enhanced variability in fenugreek for the targeted traits. Selection of parents from diverse clusters in breeding programmes

**Table 4.** Cluster mean values for 10 characters in fenugreek

| Cluster | Days to 50 % flowering | Plant height | Primary branches plant$^{-1}$ | Pods plant$^{-1}$ | Pod length | Seeds pod$^{-1}$ | Test weight | Seed yield plant$^{-1}$ | Protein content | Fat content |
|---|---|---|---|---|---|---|---|---|---|---|
| I | 61.362 | 36.762 | 3.839 | 17.472 | 8.710 | 14.520 | 12.435 | 2.374 | 21.623 | 5.095 |
| II | 62.111 | 39.489 | 3.811 | 19.178 | 8.211 | 13.850 | 12.605 | 2.324 | 16.776 | 9.335 |
| III | 60.000 | 40.500 | 3.900 | 14.233 | 8.933 | 13.867 | 13.020 | 2.821 | 25.545 | 1.556 |
| IV | 59.667 | 35.233 | 4.133 | 18.000 | 9.000 | 14.067 | 13.457 | 1.983 | 28.472 | 1.081 |
| V | 53.333 | 59.800 | 2.400 | 18.467 | 9.600 | 15.467 | 13.899 | 3.221 | 24.233 | 3.471 |
| VI | 59.333 | 36.000 | 4.067 | 38.467 | 6.853 | 10.200 | 11.563 | 2.115 | 18.908 | 5.201 |

has been suggested by many workers in pulse crops (Singh & Singh 1995; Kumar *et al*. 1998) for exploiting non additive gene action.

This will provide an opportunity to select better recombinants for various characters and thereby creating large variability for these characters in fenugreek.

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