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

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Abstract

Genetic divergence among 22 genotypes of fenugreek (*Trigonella foenum-graecum*) was esti-mated for 8 quantitative characters using Mahalanobis's D^2 statistic and the genotypes were grouped into 6 clusters. Cluster I consisted of maximum number of 13 genotypes followed by 4 and 2 genotypes in clusters II and III, respectively. Three clusters were monogenotypic. Clustering pattern of genotypes was not related to geographical differentiation. Inter-cluster distance was highest between clusters III and VI and lowest between clusters II and VI while, intra-cluster distance was highest in cluster III. Plant height, pods plant^{-1}, days to flowering and test weight were the major forces for divergence.

Key words: D^2 statistics, fenugreek, genetic divergence, quantitative characters, *Trigonella foenum-graecum*.

Study of genetic divergence is important in crop improvement programmes and multi-variate analysis by means of Mahalanobis's D^2 statistic for estimating genetic divergence have been emphasized by many workers (Anand & Murty 1968; Arunachalam 1981; Anand & Rawat 1984). The more diverse the parents within overall limits of fitness, the greater are the chances of obtaining higher amount of heterotic expression in F_1 and broad spectrum of variability in segregating generations (Anand & Murty 1968). There are few studies on genetic divergence in fenugreek (Mathur 1992; Kole & Mishra 2002) and hence the present study aims at assess-ing the genetic divergence among 22 geno-types of fenugreek (*Trigonella foenum-graecum* L.).

The experimental material consisted of 22 genotypes of fenugreek (Table 1). The geno-types of JF series and GJ-1 were collected from Main Spices Research Station, Jagudan (Gujarat), while Sonali was from Hissar (Haryana) and NC and IC series were from National Bureau of Plant Genetic Resources, New Delhi. The field experiment was con-ducted at the Agriculture Farm, Institute of Agriculture, Visva-Bharati University, Sriniketan (23°39' N 87°42' E, 58.9 m MSL) (West Bengal), with these genotypes in a ran-domized block design with three replications during *rabi* (November–March) 2002–03. Each plot consisted of five rows of 3 m length with inter- and intra-row spacing of 20 cm and 5 cm, respectively. A uniform fertilizer dose of 25:50:50 kg $N:P_2O_5:K_2O$ ha^{-1} was applied and

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normal agronomic practices were followed. Observations were taken on five randomly selected plants in each replication for eight quantitative characters. The genotypes were grouped into different clusters following Tocher's method as described by Rao (1952).

Analysis of variance showed significant differences among genotypes for all the eight characters. Wilk's Lambda criterion (ë = 0.165 x 10^{-4} and V = 528.55 with 168 d.f.) revealed highly significant differences among the genotypes for the pooled effect of all the characters. The D^2 value ranged from 3.28 (between JF-20 and GJ-1) to 348.27 (between JF-14 and NC 66847). Based on relative magnitude of D^2 values, the genotypes were grouped into six clusters. Cluster-I comprised of maximum number of genotypes (13) followed by cluster II (4) and cluster III (2). Clusters IV, V and VI were monogenotypic (Table 1). The distribution pattern of genotypes in different clusters indicated that genetic divergence was not related to geographical differentiation. Many genotypes of close geographic proximity fell in different clusters and vice-versa. Similar results have been reported in fenugreek by Mathur (1992) and Kole & Mishra (2002). The tendency to form such type of clustering ignoring geographical boundaries showed that regional isolation was not the only factor contributing to diversity in natural populations

(Rao *et al.* 1980). Clustering of genotypes from different eco-geographic locations into one cluster could be attributed to the possibility of free exchange of breeding materials. However, unidirectional selection, practiced for a particular trait or a group of linked traits in several places may produce similar phenotype, which can aggregate into one cluster irrespective of their geographic region (Singh & Gupta 1968). Formation of different clusters among the genotypes of common geographic origin may be due to their parentage, developmental traits, past history of selection and different out-crossing rates (Arnold *et al.* 1996).

The statistical distance represents the index of genetic diversity among the clusters (Table 2). The study revealed that the average intra-cluster distance (D^2) varied from 0 in clusters IV, V and VI to 25.58 in cluster III. The maximum inter-cluster distance (D^2) 323.68 was found in clusters IV and VI, followed by clusters II and IV (305.10), clusters II and V (285.76), clusters III and VI (266.73), clusters V and VI (265.44), clusters I and VI (179.22), clusters I and II (178.06) and so on. This indicated considerable amount of divergence within and between the clusters. It would, therefore, be logical to effect crossing between genotypes separated by considerable statistical distance.

Table 1. Distribution of 22 genotypes of fenugreek into various clusters

Cluster	No. of genotypes	Genotype
I	13	JF-1, JF-5, JF-6, JF-7, JF-8, JF-9, JF-11, JF-18, JF-20, JF-22, JF-23, GJ-I, Sonali
II	4	JF-13, NC-66847, IC-143822, IC-143839
III	2	JF-17, JF-21
IV	1	JF-14
V	1	JF-15
VI	1	IC-143828

Table 2. Average intra- and inter-cluster D^2 values in fenugreek

Cluster	I	II	III	IV	V	VI
I	15.44	178.06	43.64	50.73	41.88	179.22
II		18.18	236.04	305.10	285.76	28.97
III			25.58	38.79	56.77	266.73
IV				0	42.46	323.68
V					0	265.94
VI						0

Table 3. Cluster means of eight quantitative characters in fenugreek

Cluster	Plant height (cm)	Branches plant^{-1}	Days to flowering	Pods plant^{-1}	Pod length (cm)	Seeds pod^{-1}	Test weight (g)	Seed yield plant^{-1} (g)
I	43.17	5.75	53.67	11.39	6.86	09.68	17.16	1.89
II	33.02	6.56	70.00	13.66	6.67	10.78	12.44	1.83
III	52.53	5.61	53.00	15.20	6.68	09.46	14.70	2.13
IV	52.92	5.69	51.00	09.00	6.04	10.00	17.53	1.36
V	48.78	4.50	53.67	11.27	6.17	09.31	20.87	2.16
VI	32.64	6.93	70.33	14.67	7.28	10.66	16.23	1.98
Relative contribution (%)	16.47	10.93	13.88	14.09	8.57	10.23	13.76	12.04

Cluster means for different characters revealed that cluster I showed moderate to high values for almost all the characters (Table 3). Cluster II had the highest value for seeds pod^{-1}; cluster III exhibited the highest value for pods plant^{-1}; cluster IV showed maximum value for plant height; cluster V had maximum value for test weight and seed yield. Mean values were the highest for branches plant^{-1}, days to flowering and pod length in cluster VI. Relative contribution to the total divergence was highest for plant height followed by pods plant^{-1}, days to flowering, test weight, seed yield plant^{-1} and branches plant^{-1}. The results are in agreement with Mathur (1992) for test weight and branches plant^{-1} and Kole & Mishra (2002) for test weight, grain yield and branches plant^{-1}.

Considering genetic divergence, relative importance of characters in determining the yield in this particular population and *per se* performance of the genotypes as well as cluster means, crossing between the intra-cluster genotypes JF-11 x JF-22 and JF-15 x Sonali within cluster I and inter-cluster genotypes between JF-7 x NC 66847 (cluster I x II), GJ-1 x NC-66847 (cluster I x II), JF-9 x JF-17 (cluster I x III), JF-9 x JF-15 (cluster I x V), NC-66847 x JF-15 (cluster II x V) and JF-14 x JF-17 (cluster III x IV) are most likely to yield a considerable amount of heterosis in F_1 generation and to provide a wide spectrum of recombinants in segregating generations.

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