



Research Article

GENETIC DIVERGENCE ANALYSIS IN FENUGREEK [*Trigonella foenum-graecum* (L.)]

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Abstract: Forty genotypes of fenugreek [*Trigonella foenum-graecum* (L.)] were evaluated at Agronomy Instructional Farm, S. D. Agricultural University, Sardarkrushinagar during rabi-2019 to estimate genetic diversity existing among them by using Mahalanobis's D^2 statistic. The genotypes were grouped into four clusters. Out of four clusters, maximum number of 32 genotypes are in cluster I. Cluster II is the second largest with 5 genotypes followed by cluster III with two genotypes. The cluster IV having single genotype. The pattern of distribution of genotypes into various clusters was at random indicating that geographical and genetic diversity were not related. Among the genotypes, pattern of group showed significant differences. Inter cluster distance was maximum between cluster II and III followed by cluster II and IV. Intra cluster distance was maximum recorded in cluster I followed with cluster II. Among the ten characters studied in divergence, number of branches per plant, harvest index (%), days to flowering, number of pods per plant and test weight (g) contributed maximum toward total genetic divergence suggested these characters should be taken into consideration while selecting parents to hybridization.

Keywords: Fenugreek, D^2 statistic, Genetic Divergence, *Trigonella foenum-graecum* (L.)

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Introduction

Trigonella foenum-graecum (L.) is commonly known as Methi in hindi, belong to family fabaceae. An important non spice use of fenugreek is as a potential source of diosgenin. Fenugreek is considered to have originated in the Mediterranean region in parts of Asia [1]. The species name "*foenum-graecum*" means "Greek hay" indicating its use as a forage crop in the past. Fenugreek is widely cultivated in warm temperate and tropical regions of the Mediterranean, Europe and Asia. India is the largest producer, exporter of seed spices in the world. During 2018-19, fenugreek was cultivated in an area of 122 thousand hectares with an annual production of 189 thousand MT [2]. Fenugreek has a long history of use as a medicinal herb. It is extensively used in both Indian Ayurvedic medicines and traditional Chinese medicines [3]. In herbal medicine it is used in the treatment of diabetes [4]. The crop species has long been used as a galactagogue to promote lactation in weaning mothers and to promote weight-gain in women [5]. It is one of the crops in which every part is consumed in one or other forms. Its tender leaves are consumed as leafy vegetables; grain has carminative property and is also an important ingredient of several ayurvedic medicines. Fenugreek seeds are used as condiments and flavouring food preparations. The success of any plant breeding programme largely depends on the existence of diversity among the genotypes [6]. Genetic diversity helps in the choice of parents for crossing programme for yield maximization. Hence, the present investigation was carried out to determine the genetic diversity of 40 genotypes of fenugreek.

Material and methods

Forty genotypes along with two check entries viz., GM 1 and GM 2 of Fenugreek received from Seed Spices Research Station, S. D. Agricultural University, Jagudan and evaluated at the agronomy instructional farm, Sardarkrushinagar, Banaskantha district of North Gujarat during rabi season, 2019 in a Randomized Block Design with four replications.

Every entry was sown in double rows upto 4.0 meter length having a spacing of 45 cm x 10 cm. Five competitive plants were selected randomly from each replication of each plot and recorded the observation on average basis for seed yield per plant, plant height, days to flowering, days to maturity, number of branches per plant, number of pods per plant, pod length, number seeds per pod, test weight and harvest index. The genetic divergence was estimated using the Mahalanobis D^2 statistic [7]. The population was grouped into clusters by following the Tocher's method [8].

Result and Discussion

Multivariate analysis using wilk's criterion was carried out to test the difference among forty fenugreek genotypes. Wilk's criterion was highly significant. Eventually, the differences among genotypes are also highly significant. Mahalanobis's D^2 statistic was computed between all possible pairs of forty fenugreek genotypes and the genetic diversity present among the genotypes was assessed.

The composition of clusters is given in [Table-1]. The results indicated that a maximum number of diverse genotypes (32 genotypes) appeared in cluster I, cluster II composed of 5 genotypes, cluster III composed of 2 genotype and clusters IV composed by single genotype. The distribution pattern revealed that genotypes from different geographic regions are grouped in same cluster. Similarly, the genotypes from same geographic regions are scattered in different clusters. Hence, it could be concluded that there is no association between geographic diversity and genetic diversity. These results were in accordance with [9] and [10].

The intra and inter cluster D^2 values were presented in [Table-2] and [Fig-1]. The Maximum intra cluster D^2 value was 229.96 for cluster I followed by 81.43 for cluster II and 64.32 for cluster III, while it was zero for cluster IV.

Table-1 The distribution of forty genotypes of fenugreek into four different clusters on the basis of Mahalanobis D^2 statistic

Cluster	Number of genotypes	Name of genotypes
I	32	JFg 224, JFg 268, UM 126, LFC 72, AFG 7, NDM 82, HM 425, PM 1, Hisar Sonali, FGK 138, JFg 13-04, Anantpur, JFg 7, JFg 13, JFg 15, JFg 77, JFg 80, JFg 52, JFg 148, JFg 178, JFg 179, JFg 180, JFg 181, JFg 183, JFg 184, JFg 185, JFg 191, JFg 194, JFg 195, JFg 196, GM 1 and GM 2
II	5	LFC 90, NDM 79, HM 257, RM 204 and RMT 361
III	2	UM 294 and AFG 8
IV	1	Kasuri methi

Table-2 Average Intra and Inter – cluster (D^2) value for forty genotypes of fenugreek

Cluster	I	II	III	IV
I	229.96	376.42	800.9	947.14
II		81.43	1469.29	1137.9
III			64.32	1622.16
IV				0

Table-3 Contribution of ten characters under study to total divergence

Characters	Number of times ranked first	% Contribution towards divergence
Plant height (cm)	54	6.92
Days to flowering	98	12.56
Days to maturity	31	3.97
Number of branches per plant	283	36.28
Number of pods per plant	93	11.92
Pod length (cm)	4	0.51
Number of seeds per pod	18	2.31
Test weight (g)	86	11.03
Seed yield per plant (g)	5	0.64
Harvest index (%)	108	13.84

Table-4 Cluster mean value for forty genotypes of fenugreek

Cluster	PH	DF	DM	BPP	PPP	PL	SPP	TW	SYP	HI
I	68.18	54.92	126.93	4.97	42.04	11.60	13.06	15.07	8.78	33.05
II	63.76	52.55	122.25	4.71	53.09	11.13	12.39	14.71	9.94	36.39
III	74.31	50.38	123.25	6.05	40.10	10.17	11.76	15.27	7.97	29.20
IV	71.88	70.50	144.00	3.08	126.06	1.73	4.46	9.73	5.52	20.43

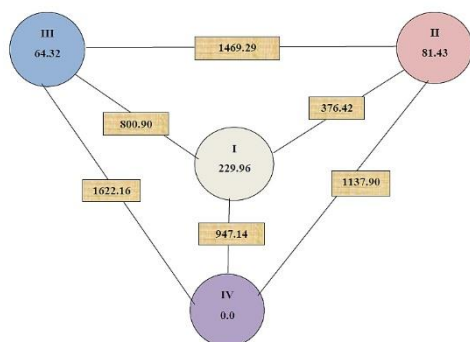
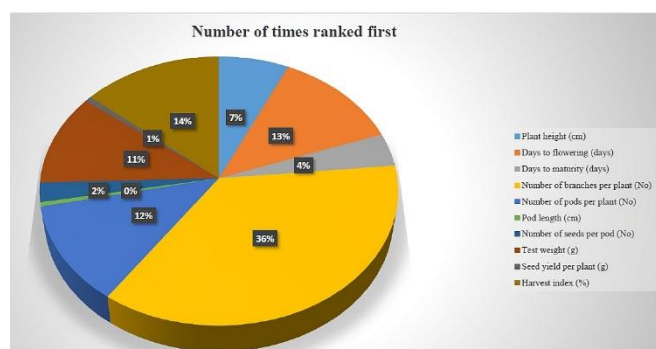
Fig-1 Cluster diagram of average Intra and Inter-cluster (D^2) value for forty genotypes of fenugreek

Fig-2 Contribution of ten characters under study to total divergence

The high intra cluster distance was observed for cluster IV because it contained single genotype. The high intra cluster distance in cluster I indicated the presence of wide genetic diversity among the genotypes. The maximum inter cluster D^2 value was observed between cluster III and IV (1622.16) followed by cluster II and III (1469.29). Minimum inter cluster D^2 value was depicted between cluster-I and II (376.42). Based on these studies crosses may be made between genotypes of cluster III (UM 294 and AFG 8) and cluster IV (Kasuri methi) followed by cluster II (LFC 90, NDM 79, HM 257, RM 204 and RMT 361) and III (UM 294 and AFG 8) to obtain new desirable recombinants in fenugreek.

The per cent contribution of various character towards the expression of genetic divergence as present in [Table-3] and [Fig-2] indicated that the traits viz., number of branches per plant (36.28%), harvest index (13.84%), days to flowering (12.56%), number of pods per plant (11.92) and test weight (11.03%) had major contribution towards genetic divergence in the present material. Similar results for one or more characters were reported by [11-16].

Cluster means for all the ten characters are presented in [Table-4]. The results clearly indicated appreciable difference among cluster mean for most of the yield attributes. The genotypes of cluster II recorded maximum seed yield per plant, harvest index and dwarf plant type with early maturity. Genotypes of cluster III had maximum number of branches per plant, test weight and tall plants with early flowering. Genotypes of cluster IV had recorded maximum number of pods per plant with late flowering and maturity. Cluster mean value of pod length and number of seeds per pod are recorded highest in cluster I.

Conclusion

Number of branches per plant, harvest index (%), days to flowering, number of pods per plant and test weight (g) contributed maximum toward total genetic divergence suggested these characters should be taken into consideration while selecting parents for hybridization.

Hybridization among genotypes of these cluster combination is expected to enhance variability in fenugreek for the target characters to obtain better and desirable recombinants.

Application of research: The research study more useful to plant breeder/scientist for development of new desirable high yielding recombinants of fenugreek variety for benefit to farmer.

Research Category: Genetics and Plant Breeding

Abbreviations: DF= Days to flowering, PH= Plant height (cm), PL= Pod length, BPP= Number of branches per plant, PPP= Number of pods per plant, SPP= Number of seeds per pod, DM= Days to maturity, TW= Test weight (g), HI= Harvest index (%), SYP= Seed yield per plant (g)

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Study area / Sample Collection: Agronomy Instructional Farm, Sardarkrushinagar, North Gujarat

Cultivar / Variety / Breed name: Forty different genotypes of Fenugreek

Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.
Ethical Committee Approval Number: Nil

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