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

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Abstract
The present investigation was carried out on twenty genotypes of fenugreek for the estimation of genetic divergence. All the genotypes under study are grouped into four clusters. Cluster analysis of the genotypes indicate that hybridization between genotypes from cluster III and cluster IV for these characters can produce better segregants in segregating populations.

Keywords: Genetic Divergence, Fenugreek.

Introduction

Fenugreek (*Trigonella foenum-graecum* L.), plant is widely distributed throughout the world. It belongs to the family Fabacecae, having chromosome number $2n = 2x = 16$. It is an annual herb indigenous to the countries bordering on the eastern shores of the Mediterranean. It is cultivated as a leafy vegetable, condiment, seed spice and as a medicinal plant. The seeds are used as spices worldwide, whereas the leaves are used as green leafy vegetables in the diet. It is one of the principle odorous constituent of curry powder in India. Fenugreek seeds are used to treat flatulence, dysentery, enlargement of lever span, gout, headache, deafness, baldness, leucorrhoea, back pain, mouth ulcer, abdominal pain, kidney problem, hernia, beriberi, chapped lips, diabetes, colic, dropsy, spleen, heart disease, obesity, etc. (Jain *et al.,* 2013) [4]. It is an erect hairy annual reaching 30-60 cm (1-2 ft.). The plant has three part leaves, the long slender stems bear tripartite, toothed, grey-green or light green ovate leaves. The sessile axillary flowers are white or pale yellow. The thin, sword-shaped pods with a curved beak-like tip, each carrying 10-20 small hard yellowish-brown seeds, which are smooth and oblong each grooved across the corner giving them a hooked look (Helambe and Dande, 2012) [3].

Material and Methods

The present investigation was carried out at the College of horticulture Veer Chandra Singh Garhwali Uttarakhand University of Horticulture and Forestry during February to June 2016. The altitude of the experimental site is about 1900 m above mean sea level at a longitude of 78.990 E and latitude of 30.0560 N. (Anon., 2012) [1]. Each plot consists of four rows with spacing of 30X10 cm and all the recommended practices were followed. Observations were recorded on five randomly selected plants from each of the plot for twelve characters. Genetic diversity between clusters based on correlation matrix was computed based on multivariate analysis using Mahalanobis D^2 statistic (Mahalanobis, 1936) [10]. The important traits in each principal component that significantly contributed to the variation observed were identified as suggested by (Johonson and Wichern, 1988) [7]. Based on the squared distances (D^2), clustering of genotypes was done using Tocher's method as described by (Singh and Chaudhary, 1999) [12]. Squared distance (D^2) for each pair of clusters combinations was computed as per (Singh and Chaudhary, 1999) [12].

Result and Discussion

Divergence analysis is a technique used to categorize genotypes that are similar into one group and others into different groups. D-square statistics (D2) developed by Mahalanobis (1936) [10], has been used to classify the divergent genotypes into different groups. Further, grouping of genotypes based on Tocher's method will be more useful in choosing reliable parents for obtaining superior segregants. The value of D^2 statistics (Mahalanobis, 1936) [10] has been demonstrated effective in choosing the parental stocks for cross breeding of fenugreek (Wojo *et al.,* 2015) [13].

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The distribution pattern of genotypes in different clusters indicated that the cluster was based genetic divergence rather than geographical diversity i.e. Genetic drift and selection forces under diverse environments could cause greater diversity than geographical diversity (Jain *et al.,* 2011) [6]. It might be due to diversity of their pedigree along with natural and direction pressure for certain agronomic traits (Jain *et al.,* 2011) [6]. Similarly, the distribution pattern of Fenugreek genotypes in different clusters indicated that genetic divergence not related to geographical differentiation (Kole and Saha, 2009; Jain *et al.,* 2011) [8, 6]. Genotypes grouped into the same cluster presumably diverge little from one another as the aggregate characters are measured. Generally, maximum genetic segregation and genetic recombination is expected from crosses that involve parents from the clusters characterized by significant distances. Following this, genetic divergence in the 20 genotypes of fenugreek used in the present studies was worked-out to identify the potential parents to be involved in the hybridization program for trait specific improvement or selecting better segregants. On the basis of performance of various traits, 20 genotypes of fenugreek were grouped into four clusters. Maximum number of genotypes was arranged in cluster-I (8) and other three clusters II, III and IV contained five, six and one genotype respectively. The intra cluster distance was highest in cluster III and lowest in cluster IV. Since, crossing of genotypes belonging to same cluster will not expect to yield superior hybrids or segregants, inter cluster distances were also worked-out. The highest inter cluster distance was recorded between cluster III and IV and lowest was observed between cluster I and II. Inter cluster distance was maximum between cluster III and IV indicating that hybridization between genotypes from cluster III and IV can be utilized for getting the superior recombinants/transgressive segregants in segregating generations in fenugreek. So, hybridization between genotypes from cluster III and cluster IV for these characters can produce better segregants in segregating populations. The findings are in close agreement with (Banerjee and Kole, 2004) [2], (Jain *et al.,* 2006) [5], (Kole and Goswami, 2015) [9] and (Wojo *et al.,* 2015) [13].

Table 1: Average intra and inter cluster distance (D^2)

Clusters	I	II	III	IV
I	2.167			
II	2.747	2.175		
III	3.511	3.003	2.742	
IV	7.950	7.725	8.810	2.154

Conclusion
Cluster analysis of the genotypes indicate that hybridization between genotypes from cluster III and cluster IV for these characters can produce better segregants in segregating populations.

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