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

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Abstract

Fifty germplasm of fenugreek (*Trigonella foenum-graecum* L.) along with five checks namely Hisar Suvarna, Hisar Sonali, RMt-361, RMt-1 and AFg-3 were evaluated in Augmented Block Design in five blocks during Rabi 2013-2014 at the research farm of ICAR-National Research Centre on Seed Spices, Tabiji, Ajmer (Rajasthan) to estimate genetic divergence. Analysis of variance revealed significant variability for most of the traits. The 55 genotypes under study were grouped into 5 clusters using Rohlf methods analysis. The intra cluster distance ranged from 18.89 (cluster III) to 35.88 (cluster IV). The inter cluster distance were higher between cluster V and others, while and minimum between cluster IV and III. Whereas, the intra cluster distance was maximum for cluster IV.

Key Words : Fenugreek, *Trigonella foenum-graecum*, gernetic divergence

Introduction

Fenugreek (*Trigonella foenum-graecum* L.) is an annual diploid species, belonging to the sub-family "Papilionaceae" of the family "Fabaceae". Fenugreek is native to the countries bordering the Eastern shores of Mediterranean, extending to Central Asia. It is an important condiment crop grown for both seed as well as leaves purpose, largely in North India during *Rabi* season. Fenugreek is an important spice crop due to its multitudinous uses. Fenugreek are extensively used as fresh leaves (green leafy vegetable), chopped leaves (flavouring agent), sprouts (salad), micro greens (salad), pot herbs (decoration), seeds (spice, condiments or medicines), extracts and powders (medicines). The seeds and leaves of fenugreek are widely known for its culinary properties for flavouring food preparations to enhance the taste of meat, poultry and vegetables (Peteropoulos, G.A. 5). Fenugreek seeds are used to treat flatulence, dysentery, enlargement of lever span, gout, headache, deafness, baldness, vata disease, leucorrhoea, back pain, mouth ulcer, abdominal pain, kidney problem, hernia, beri-beri, chapped lips, diabetes, colic, dropsy, spleen, heart disease, obesity, etc (Rathore *et. al.* 6). Fenugreek is widely cultivated in India, Iran, Nepal, Bangladesh, Pakistan, North Africa, East Africa, Ukraine South East Asia, Russia, Greece, Argentina, Egypt, France, Spain, Turkey, Morocco and China (Kakani and Anwer, 4). In India the fenugreek growing states are Rajasthan, Gujarat, Tamil Nadu, Madhya Pradesh, Maharashtra, Haryana, Uttar Pradesh and Punjab.

A quantitative estimation of genetic diversity guides the breeder for rapid progress of the breeding programme. The selection of agronomical suitable diverse parents for hybridization is important for getting desired recombinants segregating generations. Divergence analysis is a useful tool in quantifying the degree of divergence between biological population at genotypic level and also to assess relative contribution of different components to the total divergence both at intra and inter-cluster levels.

Material and methods

The experimental material for the present investigation consisted of 50 diverse genotypes from different geographic and genetic origin and five checks *viz.*, (Hisar Suvarna, Hisar Sonali, RMt-1, RMt-361 and AFg-3). These checks are locally used famous high yielding improved varieties. The experiment was laid out in an Augmented Design in five blocks with ten test entries and five checks in each block. The plot size was of 0.5 m x 2 m with row to row spacing of 50 cm and plant to plant spacing was 5-10 cm. All recommended agronomic practices and plant protection measures were followed timely for successful raising of the crop. Observation on the characters were recorded on five randomly selected plants from each testing germplasm at the time of maturity except days to 50 per cent flowering and days to 75 percent maturity, which was recorded on the whole plot basis.

To estimate the variation among the germplasm and checks, analysis of variance was carried out as per the

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procedure suggested by Federer (2). The genetic divergence among 50 genotypes was estimated based on the weighted mean values calculated. Genetic distance was estimated by using NTSys pc ver 2.01e software (Rohlf, 7). Genetic distance coefficient was calculated in euclidean distance based on which dendrogram was drawn using SAHN Sub programme of NTSys pc software.

Results and discussion

Analysis of variance was carried out for each character separately and has been presented in Table 1. Analysis of variance revealed that there was no significant differences among blocks as block effect was non-significant for the characters viz. days to 50 percent flowering, days to 75 percent maturity, plant height, primary branches per plant, secondary branches per plant, number of pods on main stem, number of pods per plant, pod length, shelling percent, number of seeds per pod, test weight and seed yield per plant. Analysis of variance showed significant differences among entries (germplasm + checks). The mean sum of squares due to entries was significant for the characters viz. days to 50 percent flowering, number of pod on main stem, number of pods per plant, pod length, shelling percent, number of seed per pod, test weight and seed yield per plant. It was non-significant for days to 75 percent maturity, plant height, primary branches per plant and secondary branches per plant. Analysis of variance revealed significant difference among checks also.

Rohlf method was used to estimate genetic divergence among 55 genotypes of fenugreek. The generalized Rohlf values were calculated for each pair of genotypes in all possible combination using dendrogam (Fig. 1). All the genotypes were grouped in to five clusters (Table 2). Maximum numbers of genotype i.e. 45 were included in cluster III. Cluster I, cluster II, and cluster IV had 4, 3 and 2 genotype, respectively. While, cluster V had only one genotypes. Inter and intra cluster distances among 5 clusters were computed and have been given in the (Table 3). The intra cluster distance ranged from 18.89 to 35.88. The maximum intra cluster distance was recorded for cluster IV (35.88), whereas minimum intra cluster distance was recorded for cluster III (18.89), which accommodated maximum germplasm lines. Cluster V have maximum inter distance with all other clusters. Whereas the cluster IV have minimum inter cluster distance with cluster III (11.09). The clustering pattern using Rohlfs methods indicate that distributing of germplasm lines into different clusters did not follow any

Table 1: Analysis of variance for different characters

Sources of variation	D f	Days to 50% flowering	Days to 75% maturity	Plant height	Primary branches per plant	Secondary branches per plant	No. of pods on main stem	No. of pods per plant	Pod length	Shelling %	No. of seeds per pod	Test weight	Yield per plant
Block (Eliminating check + Var.)	4	0.554	0.302	41.331	0.829	1.572	0.430	2.393	0.169	6.526	0.320	0.152	0.245
Entries (Ignoring Block)	54	14.97**	2.072	50.202	0.572	2.769	3.008*	99.288**	0.229*	73.855**	3.454**	5.301**	9.374**
Checks	4	36.59**	2.1	49.690	1.169*	2.396	9.698**	91.071**	0.006	64.617**	7.463**	2.260**	21.996**
Germplasm	49	13.508**	2.101	48.898	0.520	2.704	2.396	84.80**	0.238*	73.957**	3.197**	5.641**	7.165**
Checks vs. Germplasm	1	0.24	0.54	116.124	0.721	7.437*	6.242*	842.061**	0.7004**	105.856*	0.035	0.837	67.160**
Error	16	1.085	2.524	47.826	0.381	1.453	1.343	7.944	0.0805	12.755	0.547	0.320	1.060

** Significant at p = 0.01, * Significant at p = 0.05

Table 2: Distribution of fenugreek germplasm lines in five cluster

Clusters	Number of lines	Genotype
I	4	JFg-13, NDM -43, HM -258, HM -273
II	3	RM -27, RM -70, NDM -45
III	45	RM t-1, RM -191, RM -194, J Fg-250, NDM -61, AM -295, NDM -72, RM -203, HM -277, HM -282, AM -293, NDM -48, NDM -37, NDM -69, J Fg-49, AM -190, H. Sonali, RM t-361, A Fg-3, HM -259, H. Suverna, AM -300, AM -301, AM -304, J Fg-235, NDM -13 JFg-201, HM -267, J Fg-266,HM -280, AM -298 J Fg-240, RM-196, HM -278, NDM -74, HM -281
IV	2	RM 28, NDM 67
V	1	HM - 271

Table: 3: Inter and intra cluster distance between clusters

Cluster	I	II	III	IV	V
I	**22.29**	11.39	18.28	23.68	53.95
II		**26.65**	21.28	26.67	56.95
III			**18.89**	11.09	56.35
IV				**35.88**	61.74
V					**0**

specific trend and germplasm lines of divers origin clustered into different clusters. Similar type of results were also obtained by Jain et al. (3) . Five clusters were formed with cluster III having maximum numbers of germplasm. Clusters IV and V had minimum numbers of germplasm.

A comparison of the mean value of thirteen characters of different clusters has been presented in Table 4. Considerable differences in cluster mean values were evident for all the characters. Cluster I had highest mean value for secondary branches per plant (7.66) and days to 50 percent flowering (56.78), which is not desirable, but lowest mean value for days to 75 percent maturity (133.80) which is desirable, plant height (74.25), primary branches per plant (4.92), number of pods on main stem (12.76), number of pods per plant (43.03) and seed yield per plant (4.12). Cluster II had highest mean value for days to 75 percent maturity (135.73) which is late, lowest mean value for shelling percent (42.39), number of seeds per pod (11.73) and test weight (10.35). Cluster III had highest mean value for plant height (88.55), number of pods per plant (54.77) and seed yield per plant (8.76). The cluster IV had highest mean value for primary branches per plant (5.37), number of pods on main stem (14.42), pod length (11.26), number of seeds per pod (15.09), while lowest mean value for days to 75 percent maturity (133.80) which is desirable. The cluster V had highest mean values for shelling percent (94.35) and test weight (15.10), but lowest mean value for secondary branches per plant (5.44) and pod length (9.90). Banerjee and Kole (1) reported that plant height, pods per plant, days to flowering and test weight were the major forces for divergence.

Maximum intra cluster distance was recorded in cluster IV (35.88), while lowest intra cluster distance was recorded in cluster number III (18.89), which accommodated maximum germplasm lines. Whereas, inter cluster distance was highest in cluster V with other clusters, while lowest inter cluster distances were observed in cluster IV to III.

Table 4: Cluster mean value for different characters in fenugreek germplasm

Clusters No.	Day to 50% Flowering	Days to 75% Maturity	Plant height	Primary branches	Secondary branches	Pods on main stem	Pods /plant	Pod length	Shelling (%)	No. of seeds /pod	Test weight	Yield per plant
I	56.78	133.80	74.25	4.92	7.66	12.76	34.03	10.76	61.14	11.86	14.48	4.12
II	53.35	135.73	83.81	5.06	6.92	13.16	46.50	11.03	42.39	11.73	10.35	5.01
III	55.06	133.87	88.55	5.31	7.33	13.10	54.77	10.88	62.28	14.03	14.26	8.76
IV	52.48	133.80	87.07	5.37	6.56	14.42	48.40	11.26	43.95	15.09	12.23	7.89
V	53.48	134.00	87.65	4.61	5.44	13.98	36.38	9.90	94.35	13.64	15.10	4.44

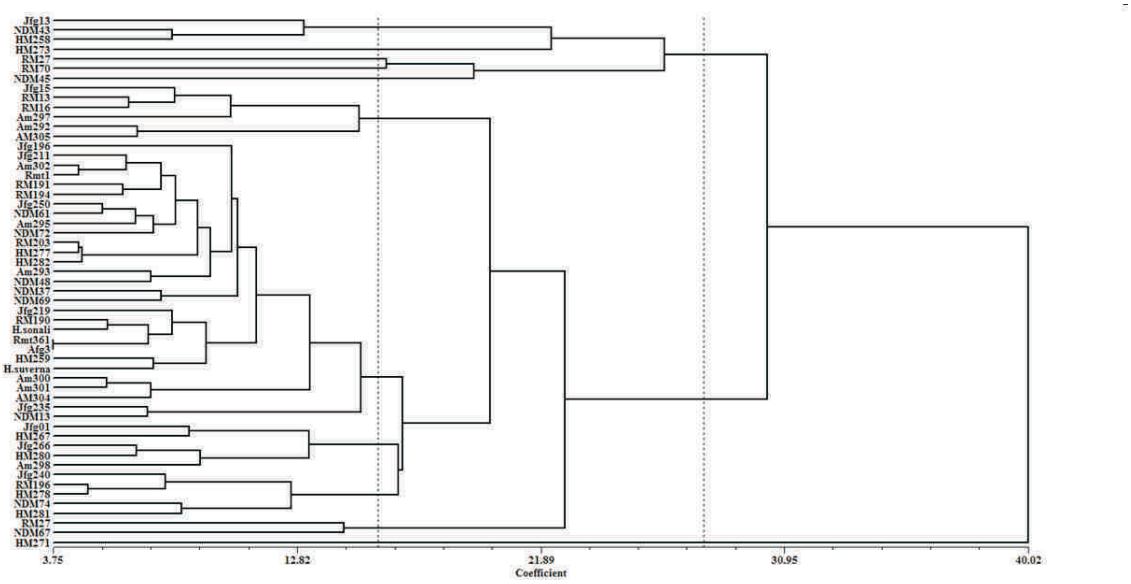

Fig 1: Euclidean Dendrogram

Thus, it can be recommended that for crossing programme parents should be taken from cluster IV and V or cluster III and V to generate higher variability and higher probability for getting transgressive segregates.

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