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Assessment of genetic variability of fenugreek (*Trigonella foenum-graecum* L.) genotypes under *Tarai* conditions of Uttarakhand

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Abstract
Fenugreek (*Trigonella foenum-graecum* L.), is an important annual herb belongs to the Fabaceae family and it is one of the important leafy vegetable cum spice crop. Its leaves and seeds have been extensively used for medicinal purposes. In this study, thirty seven genotypes of fenugreek were planted in Randomized Block Design (RBD) with three replications and evaluated for sixteen different traits viz., number of primary branches per plant, number of leaves per plant at 30 DAS, number of leaves per plant at 45 DAS, number of leaves per plant at 60 DAS, plant height, days to first flowering, node of first flowering, days to 50 per cent flowering, days to seed maturity, number of pods per plant, pod length, pod width, number of seeds per pod, thousands seed weight, green leaf yield per plant and seed yield per plant. Analysis of variance (ANOVA) revealed highly significant differences among the studied genotypes for all the traits, suggesting the presence of substantial level of genetic variations among all the genotypes. High GCV, PCV, heritability and genetic advance as per cent of mean was observed for characters like number of leaves per plant at 45 days after sowing, number of leaves per plant at 60days after sowing, number of pods per plant, thousands seed weight, leaf yield per plant and seed yield per plant which indicates that these traits were govern by additive genes and selection will be highly effective for these quantitative traits.

Keywords: Genetic Variability, Genotypic Coefficient of Variance, Phenotypic Coefficient of Variance, Heritability, Genetic Advance, Genetic advance as per cent of mean.

Introduction
Fenugreek (*Trigonella foenum-graecum* L.) commonly known as "Methi" is an important seed spice crop and is largely grown in India during *rabi* season. It is an annual herb belonging to the family fabaceae. It is a self-pollinated diploid species with chromosome number of 2n = 16 (Frayer, 1930) [7]. Fenugreek is a dicotyledonous crop with light green, pinnately trifoliate leaves (Srinivasan, 2006) [21] and yellow-white papilionaceous flowers. Fenugreek has two species of economic importance viz., *T. foenum graecum*, the common Methi and *T. Corniculata*, the kasuri methi. Fenugreek is believed to be originated from South-Eastern Europe and Western Asia and India is a leading nation as a producer and consumer of the crop. Among the major producing states of fenugreek seeds, Rajasthan ranks first followed by Madhya Pradesh and Gujarat.

In India and other countries of the Mediterranean region, it is primarily used as a spice crop (Acharya *et al.*, 2008) [1] to increase the flavour and nutritive value of food. Its fresh tender leaves and stems are consumed as curried vegetable. For medicinal and cosmetic purpose, its leaf and seed is used to prepare extract and powder. Its seed powder is used for bio fortification of wheat flour and then the flour can be used in *chapatti* & *halva* making. Fenugreek has an exceptional nutritional and pharmaceutical profile. Fenugreek leaves and shoots are qasuite rich in protein, iron, calcium, carotene and ascorbic acid (Farooqi *et al.*, 2003) [6] as well As minerals and vitamins (Rao and Sharma, 1987) [14]. It is an important ingredient of several ayurvedic medicines. Fenugreek seeds are used to reduce blood glucose and cholesterol levels (Souvaire *et al.*, 1991) and to cure various diseases *viz.*, flatulence, dysentery, diarrhea, enlargement of lever span, gout, headache, deafness, baldness, leucorrhoea, back pain, mouth ulcer, abdominal pain, kidney problem, hernia, beriberi, chapped lips, diabetes, dropsy, heart disease, obesity, etc.

In India very less research work has been done on fenugreek and there were only few research institutes that are actively engaged in its improvement. In order to increase its seed yield extensive studies are required by plant breeders. For the success of any crop improvement program presence of genetic variability is must as the crosses between the diverse parents results in trans Gressive segregation. The selection is also effective only if there is presence of additive gene effects. In this context the study of various variability parameters *viz.*, genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as per cent of mean, becomes very important. Various variability parameters of diverse fenugreek genotypes were evaluated so that improved genotypes can be selected as and high yielding cultivars can be developed.

Material and Methods

Thiry six genotypes of fenugreek (*Trigonella foenum-graecum* L.) along with one check (Pusa Early Bunching) were grown in Randomized Block Design with three replications and evaluated for genetic variability at Pantnagar Centre for Plant Genetic Resources (PCPGR) of GBPUA&T, Pantnagar, Uttarakhand during *rabi* season of 2016-17. The experimental material was sown at a spacing of 30 cm between row to row and 10 cm between plant to plant. The observations were recorded on five randomly selected plants for sixteen quantitative characters *viz.*, number of primary branches per plant, number of leaves per plant at 30 DAS, number of leaves per plant at 45 DAS, number of leaves per plant at 60 DAS, plant height, days to first flowering, node of first flowering, days to 50 per cent flowering, days to seed maturity, number of pods per plant, pod length, pod width, number of seeds per pod, thousands seed weight, green leaf yield per plant and seed yield per plant. The ANOVA was analysed by using the formula of Panse and Sukhatme (1967). GCV and PCV were calculated by using the formula of Burton and De Vane (1953) [4], heritability by using formula of Burton and De Vane (1953) [4] & Allard (1960) [2], genetic advance as per the formula given by Robinson *et al.* (1949) [15] and genetic advance as per cent of mean was evaluated as per the formula provided by Johnson *et al.* (1955) [9].

Result and Discussion

(a). Analysis of Variance (ANOVA)

Analysis of variance (ANOVA) was carried out in Randomized Block Design (RBD) in three replication for thirty seven genotypes of fenugreek for sixteen different traits (Table 1). The Mean Sum of Squares (MSS) due to genotypes was found to be highly significant for all the traits under study indicating the presence of sufficient amount of genetic variability for all these traits. This genetic variability present in the genotypes can be exploited for development of superior varieties. Similar results were0obtained by Singh and Kakani (2017) [18], Singh and Naula (2017) [17] and Yadav *et al.* (2017) [13].

Table 1: Analysis of variance for different quantitative characters in fenugreek

		Mean Sum of Squares															
S.V.	**df**	**PBP**	**NLP (30 days)**	**NLP (45 days)**	**NLP (60 days)**	**PH**	**DFF**	**NFF**	**DTF 50%**	**DMs**	**NPP**	**PL**	**PW**	**NSP**	**1000 SW**	**LY/P**	**SY/P**
R	2	0.033	0.05	34.09**	21.44	20.01	0.18	0.09	0.38	3.25	50.87*	2.05*	0.10*	0.36	2.11	0.27	12.39**
T	36	0.97**	13.72**	242.91**	1,751.07**	229.12**	11.42**	2.04**	12.84**	14.61**	2,026.98**	0.86*	0.08**	7.29**	9.07**	11.38**	26.61**
E	72	0.168	1.578	6.492	9.241	7.344	1.745	0.117	1.591	1.206	15.034	0.483	0.033	0.168	0.700	0.248	2.379

** significant at 1%, * significant at 5%

Here, PBP= number of primary branches per plant, NLP= number of leaves/plant at 30 days, 45 days & 60 days after sowing, PH= Plant Height (cm), DFF= Days to first flowering, NFF= Node of first flowering, DTF50%= Days to 50% flowering, DMs= Days to seed maturity, NPP= number of pods per plant, PL= Pod length (cm), PW= Pod width (mm), NSP= Number of seed per pod, 1000 SW= Seed Weight (g), LY/P= Green leaf yield per plant (g), SY/P= Seed yield per plant (g).

(b). Phenotypic and genotypic coefficient of variation (PCV & GCV)

The results obtained for Genotypic and Phenotypic coefficient of variation revealed that in general the phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the traits under study. The genotypic coefficient of variation was recorded highest for leaf yield per plant followed by number of leaves per plant at 60 DAS, number of pods per plant, seed yield per plant, number of leaves per plant at 45 DAS and thousands seed weight (Table 2). Similar results of high GCV for number of pods per plant were also reported by Prajapati *et al.* (2007) [13], for number of leaves per plant at 60 DAS by Hosa math *et al.* (2017) [8] for Thousands seed weight by Panwar *et al.* (2018) [12]. Moderate GCV values were recorded for plant height, node of first flowering, number of leaves per plant at 30 DAS, primary branches per plant. Characters like number of seeds per pod, pod width, pod length, days to first flowering, days to 50% flowering and days to seed maturity showed lower magnitude of GCV. Low estimates of GCV for days to 50% flowering were also reported by Sharma and Sastry (2008) [16] and Singh *et al.* (2016) [19].

Phenotypic coefficient of variation was recorded highest for leaf yield per plant (42.20%), number of leaves per plant at 60 DAS, seed yield per plant, number of pods per plant, number of leaves per plant at 45 DAS, thousands seed weight (Table 2). Similarly high PCV for number of leaves per plant at 60 DAS was also reported by Hosa math *et al.* (2017) [8], for number of pods per plant by Yadav *et al.* (2017) [13], for seed yield per plant by Dashora *et al.* (2011) [5] for thousands seed weight by Wojo *et al.* (2016) [22]. Characters such as plant height, number of leaves per plant at 30 DAS, node of first flowering, primary branches per plant, pod width, number of seeds per pod showed moderate estimates of PCV. Moderate estimates of PCV for plant height and primary branches per plant were also reported by Banerjee and Kole (2004) [3]. Lower magnitude of PCV was reported for pod length, days to first flowering, days to 50% flowering and days to seed maturity. Low PCV for days to 50% flowering by also reported by Singh *et al.* (2016) [19].

Table 2: Estimates of genetic parameters of variation for the different characters of fenugreek genotypes

S. No.	Characters	Mean	Range	Genotypic Coefficient of Variance	Phenotypic Coefficient of Variance	Heritability (%)	Genetic Advance	Genetic Advance as per cent of mean (%)
1	PBP	4.29	2.63-5.73	12.08	15.40	61.54	0.84	19.53
2	NLP (30 days)	14.25	10.03-18.67	14.12	16.65	71.97	3.52	24.68
3	NLP (45 days)	39.11	26.00-62.73	22.70	23.61	92.39	17.58	44.94
4	NLP (60 days)	76.85	45.70-151.33	31.35	31.60	98.43	49.25	64.08
5	PH	52.75	31.47-68.16	16.30	17.09	90.96	16.89	32.03
6	DFF	71.43	66.67-77.33	2.52	3.12	64.90	2.98	4.17
7	NFF	5.28	3.22-6.44	15.17	16.49	84.58	1.52	28.73
8	DTF 50%	88.36	83.67-94.67	2.19	2.62	70.21	3.34	3.78
9	DMs	136.93	134.67-144.00	1.54	1.74	78.75	3.87	2.82
10	NPP	85.33	43.24-144.55	30.35	30.69	97.81	52.76	61.83
11	PL	9.59	8.60-10.97	3.73	8.15	20.98	0.34	3.52
12	PW	1.67	1.23-2.01	8.02	13.44	35.57	0.17	9.85
13	NSP	15.62	13.30-19.03	9.87	10.21	93.39	3.07	19.64
14	1000 SW	8.03	5.67-11.84	20.80	23.27	79.95	3.08	38.32
15	LY/P	4.72	1.84-11.09	40.86	42.20	93.74	3.84	81.49
16	SY/P	10.45	4.34-17.40	27.20	30.94	77.25	5.15	49.24

(c) Heritability and Genetic Advance

High estimates of heritability was obtained for number of leaves per plant at 60 DAS followed by number of pods per plant, leaf yield per plant, number of seeds per pod, number of leaves per plant at 45 DAS, plant height and node of first flowering (Table 2). High estimates of heritability for number of pods per plant were also reported by Hosa math *et al.* (2017) [8], for plant height by Lodhi *et al.* (2015) [10]. Moderate values was recorded for thousands seed weight, days to seed maturity, seed yield per plant, number of leaves per plant at 30 DAS, days to 50% flowering, days to first flowering and primary branches per plant while lower estimates observed for pod width and pod length. Highest genetic advance as per cent of mean was obtained for leaf yield per plant followed by number of leaves per plant at 60 DAS, number of pods per plant, seeds yield per plant, number of leaves per plant at 45 DAS, thousands seed weight, plant height, node of first flowering and number of leaves per plant at 30 DAS. Similarly results for high0genetic advance0as per cent of mean0was reported for number of pods per plant by Kaila shchandra *et al.* (2000) and for plant height by Panwar *et al.* (2018) [12]. The characters viz. number of seeds per pod and primary branches per plant showed moderate values while pod width, days to first flowering, days to 50% flowering, pod length and days to seed maturity recorded with lower estimates of genetic advance as per cent of mean.

High heritability0coupled with0genetic advance0as per cent of mean was reported for number of leaves per plant 45 DAS, number of leaves per plant 60 DAS, plant height, node of first flowering, number of pods per plant and leaf yield per plant. Similar results was also obtained for number of pods per plant by Prajapati *et al.* (2007) [13] and Yadav *et al.* (2017) [13], for plant height by Lodhi *et al.* (2015) [10] and Panwar *et al.* (2018) [12], for thousands seed weight by Banerjee and Kole (2004) [3] and similarly for seed yield per plant by Singh and Kakani (2017) [18]. High heritability along with high genetic advance is an important parameter for selection. Characters showing high heritability coupled with genetic advance are most responsive to selection as these characters are controlled by additive genes. In such condition selection will be highly effective and responsive.

Conclusion

The results of the present investigation revealed that the studied genotypes of fenugreek are significantly different from each other and there is sufficient amount of genetic variability which can be exploited for improvement of the fenugreek. The characters like number of leaves per plant at 45 days after sowing, number of leaves per plant at 60days after sowing, number of pods per plant, thousands seed weight, leaf yield per plant and seed yield per plant, exhibited high GCV, PCV, heritability and genetic advance as per cent of mean, and therefore selection for such traits will be of merit value while doing selection for superior genotypes.

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