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Deciphering genetic variability in fenugreek (*Trigonella foenum-graecum* L.) genotypes

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Abstract
Seed spices are hidden treasure of India in which fenugreek (*Trigonella foenum-graecum* L.) is one of them having medicinal, industrial and economical importance. For deciphering the amount of genetic variability and heritability coupled with genetic advance as percent mean the present study was carried out planting 38 genotypes in RBD experimental design having three replications at instructional farm, college of agriculture, Jodhpur (Rajasthan) at the time of *Rabi* 2024-25. ANOVA revealed significant variability for all the 13 traits. The greatest values of phenotypic and genotypic coefficient of variance, along with heritability and genetic advance as a percent of the mean, were observed for the number of pods plant-1, seed yield plant-1, harvest index, and oil content. Determining that this straight forward selection would effectively enhance these characteristics.

Keywords: Fenugreek, genotypes, variability, heritability, genetic advance

Introduction

India is the country famous for its spice's richness and in the list of such Indian spices, fenugreek is one of the seed spices, botanically called as *Trigonella foenum-graecum L.* (2n = 2x = 16) and in India popularly pronounced as "methi", belongs to family Leguminosae and the crop is being consumed as a leafy vegetable and as a whole seed. Climatic conditions favor growth of fenugreek is having temperature range between of 20°C to 25°C. The centers of origin of the crop are the Indian sub-continent and the eastern Mediterranean region (Vavilov, 1926) [37]. The mode of pollination in fenugreek is self-pollination and germination of seed take place in hypogeal manner. Fenugreek's importance is not only as a spice, it has many medicinal properties also, that helps in lowering the blood sugar level, decreasing cholesterol level because of presence of an alkaloid called "Diosgenin" and neuroprotective because of an alkaloid called "Trigonelline" and has anti-carcinogenic properties, anti-fungal properties, the consumption of fenugreek on daily basis helps in curing gastrointestinal disorder. Because of the presence of "Saponin" in fenugreek it considered as steroidal significant crop. Fenugreek constitute both macro as well as micro nutrients like in 100 grams of fenugreek it contains 26.2 g of protein etc. (Gupta *et al.* 1989) [13]. Oil derived from fenugreek seeds used to promote hair health and growth, researchers suggest it can strengthen hair from roots, improve scalp health because the oil contain compound like "Lecithin" which moisturizes and conditions the scalp. Fenugreek covered 1.58 lac ha area in India and 0.77 lac ha area in Rajasthan with overall all production of 2.49 lac tons in India, in which Rajasthan is the second largest producer having production of 1.02 lac tons after Madhya Pradesh (Anonymous 2023-24). However, the dominance of high yielding varieties has led to reduction in genetic variability which ultimately makes the crop susceptible to different biotic and abiotic stresses. For overcoming this harm germplasm evaluation is crucial to maintain the genetic variability for further crop improvement.

Therefore, in order to examine the growth characteristics and seed yield parameters of fenugreek in the context of Jodhpur, Rajasthan the present study has been conducted.

Materials and methods

Location

The study was carried during Rabi-2024–2025 at the College of Agriculture's instructional farm in Jodhpur, Rajasthan, which is roughly ten kilometers from the Jodhpur train station. Geographically, it is situated at an elevation of 231 meters above mean sea level between latitudes 26° 15' N and 26° 45' North and longitudes 73° 00' E and 73° 29' East. This area is located in Rajasthan's agroclimatic zone IA, or the Arid Western Plains Zone.

Table 1: List of fenugreek genotypes.

Genotype	Name of Genotypes	Source	Genotype	Name of Genotypes	Source
G1	UM-3	SKNAU, Jobner	G20	UM-23	SKNAU, Jobner
G2	UM-4	SKNAU, Jobner	G21	UM-24	SKNAU, Jobner
G3	UM-5	SKNAU, Jobner	G22	UM-25	SKNAU, Jobner
G4	UM-6	SKNAU, Jobner	G23	UM-26	SKNAU, Jobner
G5	UM-7	SKNAU, Jobner	G24	UM-27	SKNAU, Jobner
G6	UM-8	SKNAU, Jobner	G25	UM-28	SKNAU, Jobner
G7	UM-9	SKNAU, Jobner	G26	UM-29	SKNAU, Jobner
G8	UM-10	SKNAU, Jobner	G27	UM-30	SKNAU, Jobner
G9	UM-11	SKNAU, Jobner	G28	AM-71	NRCSS, Ajmer

G10	UM-12	SKNAU, Jobner	G29	AM-108	NRCSS, Ajmer
G11	UM-13	SKNAU, Jobner	G30	AM-280	NRCSS, Ajmer
G12	UM-14	SKNAU, Jobner	G31	AM-281	NRCSS, Ajmer
G13	UM-15	SKNAU, Jobner	G32	AM-282	NRCSS, Ajmer
G14	UM-17	SKNAU, Jobner	G33	AM-284	NRCSS, Ajmer
G15	UM-18	SKNAU, Jobner	G34	AM-293	NRCSS, Ajmer
G16	UM-19	SKNAU, Jobner	G35	AM-310	NRCSS, Ajmer
G17	UM-20	SKNAU, Jobner	G36	RMT-143	SKNAU, Jobner
G18	UM-21	SKNAU, Jobner	G37	RMT-305	SKNAU, Jobner
G19	UM-22	SKNAU, Jobner	G38	AFG-3	NRCSS, Ajmer

Experimental details and data analysis

The experimental material comprises 38 fenugreek genotypes (**Table 1**) that were organized in a randomized block design with three replications, planted at a spacing of 30 x 10 cm². All suggested practices were implemented to cultivate a healthy crop, and essential steps were taken to control pests and diseases. The characters under study are days to 50 percent flowering, days to maturity, plant height (cm), number of primary branches plant-1, number of pods plant-1, pod length (cm), number of seeds pod-1, 1000-seed weight (g), biological yield plant-1 (g), harvest index (%), seed yield plant-1 (g), protein content (%) and oil content (%) in which the data were collected from five randomly chosen plants of each genotype in every replication for all traits, except for days to 50 percent flowering and days to maturity, which were recorded on a plot basis. Protein is estimated using calculation nitrogen through Kjeldahl unit method (J. Kjeldahl, 1883) [17] and oil content through Soxhlet apparatus (F. Soxhlet, 1879) [36]. The data obtained through field trial on fenugreek for thirteen characters were statistically analyzed with the help of WINDOSTAT Version 9.3 software.

The analysis of variance was performed using a RBD experimental design for each character, according to the conventional statistical methodology described by Panse and Sukhatme (1985).

Analysis of variance enables the calculation of components of variance which are genotypic, environmental, and phenotypic variance, where genotypic variance was computed based on Johnson *et al.* (1955) [16] and phenotypic variance was derived following Comstock and Robinson (1952) [5]. The variance component also allows for the computation of genotypic and phenotypic coefficients of variation using the formula given by Lush (1949) [20]. Heritability (h^2) in the broad sense was determined utilizing the formula suggested by Johnson *et al.* (1955) [16].

Result and discussion

Analysis of variance revealed that all the genotypes had highly significant mean sum of squares for all the thirteen characters (Table 2). The significant differences in all the characters of the material under study indicated that there was a sufficient genetic variability in the experimental material which can be applied in further fenugreek improvement programme. A comparison of coefficient of variation revealed that the phenotypic coefficient of variation was greater than the genotypic coefficient of variation for all characters (Table 3), indicating that environment had an effect on character expression. These findings were in accordance with (Gurjar *et al.,* (2016); Panwar *et al.,* 2017; Yadav *et al.,* 2024) [14, 28, 39].

Table 2: Analysis of Variance (ANOVA) showing mean sum of squares for yield and its contributing characters in fenugreek.

Source of variation	df	DF (days)	DTM (days)	PH (cm)	NPB	NP	PL (cm)	NSP	1000-SW (g)	BY (g)	HI (%)	PC (%)	OC (%)	SY (g)
Replication	2	0.53	6.87	7.19	0.32	29.15	0.01	0.6	0.16	6.25	3.57	0.37	0.003	1.18
Treatment	37	36.23**	294.17**	49.21**	3.16**	551.95**	1.35**	9.28**	12.05**	91.71**	108.37**	15.20**	4.31**	13.68**
Error	74	1.89	3.56	13.47	0.20	14.09	0.11	0.64	0.33	4.88	9.04	0.19	0.002	0.79

*, ** Significant at 5% and 1% probability level of significance respectively.

DF = Days to 50 % flowering, DTM = Days to maturity, PH = Plant height, NPB = Number of primary branches plant -1, NP = Number of pods plant-1, PL = Pod length, NSP = Number of seeds pod-1, 1000-SW = 1000 seed weight, BY = Biological yield plant-1, HI = Harvest index, PC = Protein content, OC = Oil content, SY = Seed yield plant-1.

High GCV and PCV estimates recorded for traits like oil content, seed yield plant-1, number of pods plant-1, harvest index and biological yield plant-1.

The observed substantial genetic variability in these traits suggested that selecting for them would be effective. This is because the effectiveness of selection is directly related to the degree of variation contained within the group being studied similar findings were earlier observed by (Sharma and Sastry 2011; Patahk *et al.,* 2014; Shivraj *et al.,* 2023) [33]. Moderate GCV and PCV values were observed for number of primary branches plant-1, 1000-seed weight, plant height and number of seeds pod-1 and biological yield plant-1 which were earlier reported by (Panwar *et al.,* 2017; Mishra *et al.,* 2021; Khairiya *et al.,* 2023) [21, 28, 31].

Character such as protein content, pod length, days to 50 percent flowering and days to maturity showed low GCV and PCV which were aligning with the results of (Dashora *et al.,* 2011; Bhatt *et al,.* 2019) [2, 6].

Table 3: Mean, range, variability, heritability (h^2) and genetic advance as per cent of mean of thirteen characters in fenugreek.

Characters	Mean	Range		Coefficient of variation		Heritability (%)	GA as per cent of mean (%)
		Min	Max	GCV (%)	PCV (%)		
Days to 50 percent flowering	49.57	44.66	60.66	6.82	7.36	85.8	13.02
Days to maturity	124.7	120	132	1.73	2.30	56.9	2.703
Plant height (cm)	76.35	53.73	90.40	12.66	13.55	87.4	24.40

Number of primary branches plant-1	5.83	4.93	10.40	17.01	18.72	82.6	31.84
Number of pods plant-1	46.33	24.26	85.46	28.89	30.01	92.7	57.31
Pod length (cm)	8.37	7.20	10.20	7.67	8.67	78.2	13.98
Number of seeds pod-1	15.82	12.58	20.58	10.72	11.86	81.7	19.95
1000-seed weight	13.91	8.01	18.13	14.20	14.80	92.1	28.06
Seed yield plant-1 (g)	7.17	4.33	13.06	28.90	30.48	84.3	54.68
Biological yield plant-1 (g)	27.7	20.80	41.33	19.41	20.99	85.6	36.99
Harvest index (g)	26.04	14.08	35.12	22.09	24.93	78.5	40.33
Protein content (%)	28.99	22.76	33.29	7.71	7.86	96.3	15.93
Oil content (%)	3.15	1.26	6.23	37.97	38.01	99.8	78.14

Heritability can be a very good indicator of character transmission from parents to offspring (Falconer, 1989) [8] and measuring genetic advance can truly indicate overall genetic improvement under selection for qualities influenced by polygenes. The characters with high heritability with high genetic advance as percent mean were reported for plant height, number of primary branches plant-1, number of pods plant-1, 1000-seed weight, seed yield plant-1, biological yield plant-1, harvest index and oil content proves that these characters are likely to be governed by additive gene and direct selection will be effective for improvement of these characters. Similar findings were reported by (Patahk *et al.*, 2014; Kumar *et al.*, 2020; Shekhawat *et al.*, 2023) [19, 32]. High heritability along with moderate genetic advance as percent mean was observed for days to 50 percent flowering, pod length, number of seeds pod-1 and protein content. Similar results were drawn by (Panwar *et al.*, 2017; Bhatt *et al.*, 2019; Singh *et al.*, 2022) [2, 4, 28]. Moderate heritability along with low genetic advance was reported for days to maturity and results were in accordance to the (Fikreselassie *et al.*, 2013; Yadav *et al.*, 2018; Khairiya *et al.*, 2023) [9, 31, 40].

Conclusion

The maximum values of GCV and PCV observed for the trait of oil content demonstrated significant phenotypic and genotypic variability among the genotypes, indicating a strong potential for selection response, ultimately enhancing production in the fenugreek crop. The traits number of pods plant-1, seed yield plant-1, biological yield plant-1, harvest index, and oil content observed high genetic variability, high heritability along with high genetic advance as percent mean revealed the pre dominance of additive gene action and selection might be beneficial in next generations for these characters.

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