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## Analysis of genetic variability in fenugreek (*Trigonella foenum-graecum* L.) germplasm

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### Abstract

A set of 208 germplasms of fenugreek (*Trigonella foenum-graecum* L.) was evaluated in augmented randomized complete block design in four blocks and eight check varieties during *Rabi* 2016-17 at the research farm of S.K.N. College of Agriculture, Jobner. Analysis of variance revealed significant differences among the accessions and checks for all the characters except seeds per pod in checks. The highest percentage of PCV and GCV was observed for seed yield per plant, pods per plant, branches per plant, 1000-seed weight and plant height which indicates the presence of high amount of genetic variability for these characters. The high estimates of heritability along with high genetic advance were found for seed yield per plant, pods per plant, 1000-seed weight and plant height indicating predominance of additive gene effects for these traits. Hence, these characters were used for further improvement in yield of fenugreek.

**Keywords:** Augmented, fenugreek, genetic advance, germplasm, heritability

### Introduction

Fenugreek (*Trigonella foenum-graecum* L.) is a self-pollinated diploid species with chromosome number of  $2n = 16$  (Frayer, 1930) [1]. The fenugreek also known as “Methi” is an important leafy vegetable cum seed spices belongs to the sub family Papilionaceae of the family Fabaceae. The place of origin of fenugreek supposed to between iran and north India (smith, 1982) [2]. Fenugreek seed contains carbohydrates (48%), proteins (25.5%), mucilagenous matter (20.0%), fats (7.9%) and saponins (4.8%) (Rao and Sharma, 1987) [3]. The seed also contains major nutrients like P, K and minor nutrients like Ca, Fe and Na and amino acid like leucine, valine, lysine and phenylalanine besides cellulose and hemicelluloses and, saponin. The fenugreek seeds are bitter in taste due to presence of an alkaloid known as “Trigonellin”. A potential use of fenugreek is for extraction of diosgenin. Diosgenin is a steroid precursor, which is used as a basic material in the synthesis of sex hormones and contraceptives. Fenugreek seeds are high in soluble fibre, which helps lower blood sugar by slowing down digestion and absorption of carbohydrates. The success of crop improvement depends upon the magnitude of genetic variability existing in the population and the extent to which the desired characters are heritable. Presence of genetic variability in a population is of primary importance for a successful breeding programme. Studies on genetic variability with the help of suitable biometrical tools such as variability, heritability, genetic advance gives us an idea about the extent of genetic variability present in the population. Heritability is a suitable measure for assessing the magnitude of genetic portion of total variability and genetic advance aids to make improvement in crop by selection for various characters. It is an index of transmissibility of a character from parents to their off springs. Thus, study of heritability coupled with genetic advance is more useful in predicting the resultant effect of selection.

### Material and Methods

The 208 accessions were evaluated in an augmented block design during *Rabi* season (2016-2017) at Agronomy Farm, S.K.N. College of Agriculture, Jobner (20° 6' N, 75° 25' E and 420 m above sea level). The material was divided into 4 blocks. Each group of 52 accessions was assigned to each block. Eight check varieties i.e. RMt-1, RMt-143, RMt-303, RMt-305, RMt-351, RMt-361, RMt-354 and RMt-365 were also assigned randomly to each block. Each accession and check was sown in a single row plot. Each row was 3.0 m long and spaced 30 cm apart.

Plant to plant distance was kept to 10 cm by thinning. At the time of maturity data were recorded on five randomly selected plants, which was tagged before flowering from each plot to record the data on plant height, branches per plant, pods per plant, pod length, seeds per pod 1000-seed weight and seed yield while, data on days to 50 per cent flowering and days to maturity were however, recorded on whole plot basis. The average value of five plants for various characters was used for statistical analysis. The analysis of variance was calculated as per the method suggested by Federer [4]. The phenotypic and genotypic coefficient of variation was estimated using the following formulae proposed by Burton and Johnson et al. [5-6]:

$$PCV = \frac{\sqrt{\sigma^2_p}}{\bar{X}} \times 100$$

$$GCV = \frac{\sqrt{\sigma^2_g}}{\bar{X}} \times 100$$

Where,  $\sigma^2_g$  = genotypic variance,  $\sigma^2_p$  = phenotypic variance and  $\bar{X}$  = overall mean of the character.

Heritability in broad sense was calculated by the formula given by Hanson et al. [7]:

$$\text{Heritability (h}^2_{bs}\text{) in percentage} = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,  $\sigma^2_g$  = genotypic variance and  $\sigma^2_p$  = phenotypic variance.

The expected genetic advance was calculated by the following formula as suggested by Johnson et al. [6]:

$$\text{Genetic advance (GA)} = h^2.k.\sigma_p$$

While, genetic advance as percentage of mean was obtained by the following formula:

$$\text{GA as \% of mean} = \frac{GA}{\bar{X}} \times 100$$

Where,  $h^2$  = heritability in proportion,  $k$  = standardized selection differential which is generally taken as 2.06 at 5% selection intensity,  $\sigma_p$  = phenotypic standard deviation,  $\bar{X}$  = the general mean of the character and GA = genetic advance.

## Results and Discussion

The analysis of variance revealed that significant amount of variability was present in the accessions for all the characters viz., days to 50% flowering, days to maturity, plant height, branches per plant, pods per plant, pod length, seeds per pod, 1000-seed weight and seed yield per plant. These are in agreement with the earlier reports of Sharma and Sastry, Dashora et al., Jain et al., Wojo et al. [8-11]. The block effect was significant for all the characters indicating the sensitivity of accessions to the environment. The check varieties showed significant differences for all the characters except seeds per pod, it indicated that checks themselves were diverse.

Estimates of genotypic and phenotypic variance indicated that in general the phenotypic variances were higher than genotypic variance it means that the apparent variation is not only due to genotypes but also due to the influence of environment. The variances of various characters were compared on the basis of coefficient of variation. In the

present investigation similar trend was observed for all the characters indicating a positive effect of environment on the characters expression. Higher GCV (genotypic coefficient of variation) and PCV (phenotypic coefficient of variation) were recorded for yield per plant, pods per plant, branches per plant, 1000-seed weight and plant height. Such results were also reported by Datta et al. and Prajapati et al. [12-13]. The GCV and PCV were moderate for days to 50% flowering, pod length and seeds per pod, whereas low for days to maturity, which are in agreement with the earlier report of Kumari et al. [14]. The results revealed that the differences between genotypic and phenotypic coefficient of variations were low and this is expected in augmented design. In an augmented design, the error component used is based on checks which are repeated in blocks. This often is very limited; hence the difference is very limited. The closeness of the estimates of genotypic and phenotypic coefficient of variation indicated that these characters were least affected by the environment.

The response to selection depends upon the relative magnitude of heritable variation present in relation to the phenotypic variation. Thus, in order to judge how effectively selection can be practiced, it is desirable to partition the observed variability into its heritable and non heritable components. The broad sense heritability estimates along with genetic advance were also determined. Since in augmented design only the error variance of check varieties could be subtracted from the variance of accessions, a portion of it may be confounded with the genotypic variance used for calculating the heritability. Therefore, caution should be exercised in interpreting the estimated of heritability values as they represent only the upper limit of heritability.

The estimates of heritability were higher for days to 50% flowering, pods per plant, plant height, days to maturity, 1000-seed weight, seed yield per plant and pod length, indicating that these characters are less influenced by environment and direct selection for these yield contributing traits would be effective for future improvement in yield. Similar results were obtained by Gangopadhyay et al. [15] and Sharma et al. [16]. Moderate heritability (50-70%) was observed for branches per plant which is in agreement with the findings of Sarada et al. [17] and Jain et al. [10]. Low heritability was observed for seeds per pod. Similar result was found in the findings of Dashora et al. [9].

In the present investigation, genetic advance as percentage of mean was also estimated in order to determine the relative merits of different characters that can be further utilized in selection programme. The expected genetic advance expressed as percentage of mean was observed to be high for seed yield per plant followed by pods per plant, 1000-seed weight and plant height, which are in accordance with the earlier reports of Singh [18] and Sarada et al. [17]. In the present study, moderate genetic advance was observed for days to 50% flowering, pod length and branches per plant. Low genetic advance was observed for days to maturity and seeds per pod, which is in agreement with earlier reports of Singh et al. [19].

High heritability (broad sense) coupled with high genetic advance as percentage of mean was observed for the characters viz., seed yield per plant, pods per plant, plant height and 1000-seed weight which is in agreement with earlier reports of Gangopadhyay et al. [15], Dashora et al. [9] and Verma et al. [20] which indicated that most likely the heritability was due to additive gene effects and selection may

be effective for these characters. Days to maturity showed high heritability with moderate genetic advance, which are in accordance with the earlier report of Prajapati *et al.* [13]. The high heritability accompanied with low genetic advance was recorded for days to 50% flowering and pod length which indicated that the presence of non-additive gene action, whereas moderate heritability coupled with moderate genetic

advance was observed for branches per plant, which is in agreement with Jain *et al.* [10]. The low heritability coupled with low genetic advance was estimated for seeds per pod, which was earlier reported by Balai *et al.* [21] which indicated that the character is highly influenced by environment effects and selection would be ineffective.

**Table 1:** Analysis of variance for different characters

Source of variation	d.f.	Days to 50% flowering	Days to maturity	Plant height (cm)	Branches per plant	Pods per plant	Pod length (cm)	Seeds per pod	1000-seed weight (g)	Seed yield per plant (g)
Blocks (b-1)	3	19.189**	9.789**	916.139**	10.655**	1051.475**	9.275**	10.214**	1.816**	12.770**
Entries (c+g)-1	215	7.897**	4.907**	73.357**	0.688*	99.422**	0.916**	1.695	1.708**	2.944**
Checks (c-1)	7	7.196**	7.929**	418.840**	1.039*	264.080**	1.151**	0.822**	2.765**	5.600**
Accessions (g-1)	207	7.945**	4.828**	61.926**	0.677**	94.284**	0.908**	1.729*	1.667**	2.838**
Checks v/s Accessions	1	2.878*	0.208	21.117	0.407	10.421	0.911	0.667	2.896**	6.189**
Error (b-1)(c-1)	21	0.542	0.857	10.683	0.331	10.581	0.257	0.926	0.316	0.551
Genotypic variance (V <sub>g</sub> )		7.403	3.971	51.243	0.347	83.703	0.651	0.803	1.351	2.287
Phenotypic variance (V <sub>p</sub> )		7.945	4.828	61.926	0.667	94.284	0.908	1.729	1.667	2.838
Error variance (V <sub>e</sub> )		0.542	0.857	10.683	0.331	10.581	0.257	0.926	0.316	0.551

\*\*Significant at P=0.01, \*Significant at P=0.05

**Table 2:** General mean, range, genotypic and phenotypic coefficients of variation, heritability (broad sense) and genetic advance as percentage of mean for different characters in Fenugreek

S. No.	Characters	Mean	Range	Genotypic coefficient of variation (GCV)	Phenotypic coefficient of variation (PCV)	Heritability in Broad sense (%)	Genetic advance as percentage of mean
1	Days to 50% flowering	50.72	47.94-70.06	5.36	5.56	93.18	10.67
2	Days to maturity	107.80	104.00-118.00	1.85	2.04	82.26	3.46
3	Plant height (cm)	66.74	42.23-89.31	10.73	11.79	82.75	20.10
4	Branches per plant	4.73	2.43-8.11	12.45	17.39	51.23	18.29
5	Pods per plant	35.86	15.86-69.08	25.51	27.08	88.78	49.52
6	Pod length (cm)	10.00	7.44-13.08	8.07	9.52	71.71	14.03
7	Seeds per pod	15.03	10.25-18.49	5.96	8.75	46.44	8.34
8	1000-seed weight (g)	10.62	5.78-14.26	10.95	12.16	81.06	20.29
9	Seed yield per plant (g)	5.48	2.25-10.39	27.61	30.76	80.58	50.91

## Conclusion

The analysis of variance indicated that the accessions had significant variability with respect to all the characters namely days to 50% flowering, days to maturity, plant height, branches per plant, pods per plant, pod length, seeds per pod 1000-seed weight and seed yield. The genotypic and phenotypic coefficient of variation were higher for *viz.*, seed yield per plant, pods per plant, branches per plant, 1000-seed weight and plant height, while moderate for days to 50% flowering, pod length and seeds per pod and low for days to maturity.

The estimates of heritability (broad sense) were high for days to 50% flowering, pods per plant, plant height, days to maturity, 1000-seed weight, pod length and seed yield indicating that less influence by environment and direct selection for these yield contributing traits would be effective for future improvement in seed yield in fenugreek.

High heritability (broad sense) coupled with high genetic advance expressed as percentage of mean was observed for the characters *viz.*, plant height, pods per plant, 1000-seed weight and seed yield per plant, while days to maturity showed high heritability with moderate genetic advance. The high heritability and low genetic advance was recorded for days to 50% flowering and pod length. The moderate heritability coupled with moderate genetic advance was estimated for branches per plant, while seeds per pod showed low heritability and low genetic advance.

Out of 208 accessions, 17 accessions *viz.*, UM-110, UM-55,

UM-169, UM-183, UM-162, UM-111, UM-71, UM-27, UM-35, UM-69, UM-98, UM-103, UM-113, UM-118, UM-146, UM-167, UM-221 were found better to the best check variety on the basis of seed yield per plant.

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