

## Assesment of genetic variability in fenugreek (*Trigonella foenum-graecum* L.) using augmented design

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### ABSTRACT

Forty-one genotypes of fenugreek (*Trigonella foenum-graecum* L.) were evaluated for variability, heritability and genetic advance at Research Farm, MPUAT, Udaipur during *rabi*, 2010-11 in augmented design. High estimates of phenotypic and genotypic coefficient of variation were recorded for pods per plant, branches per plant and seed yield which indicates the presence of high amount of genetic variability for these characters. The difference between PCV and GCV were high for pod length and seeds per pod indicating that these traits were much influenced by the environment, while the differences between PCV and GCV were less for test weight, days to 50 % flowering and pods per plant. High heritability estimates along with high genetic advance as per cent of mean was observed for pods per plant, branches per plant, test weight and seed yield indicating predominance of additive gene effects for these traits. It was concluded that improvement in the seed yield of fenugreek is possible through selection for pods per plant, branches per plant, test weight and seed yield

**Key words:** Augmented design, Fenugreek, Genetic advance, Heritability, Variability.

### Lkkj k'k

eFkh ds 41 tuunD; ka dh fofokrk , oa vupf'kdka dk v?; ; u o"kl 2010&11 ea mn; ij ds Nf"k fo'o fo | ky; ea fd; k x; kA ijh{k.k ea ih-l h-oh- , oa th-l h-oh- Qfy; k; i fr i kSkk] 'kk [kkvka i fr i kSkk rFkk cht mRi knu ea T; knk ik; k x; k] tks buea vkupf'kd fofokrk dks n'kkzk gA ih-l h-oh- , oa th-l h-oh- ea vf/kd vrj Qyh dh yEckbz , oa ftLkl sl kfcg gkrk gSfd bu xqkka ea okrkj.k dk iHkko T; knk iMrk gA tcfD i fr 1000 nkuk okj] 50 i fr'kr Qy vkus dk le; rFkk i fr i kSkk Qfy; ka ea ih-l h-oh- , oa th-l h-oh- ds chp varj cgq de Fkka bl l s; sfl ) gkrk gSfd eFkh ea cht l qkkj ds fy, Qfy; ka i fr i kSkk] 'kk [kkvka i fr i kSkk kk 1000 nkuka dk Hkkj , oa cht mit ds xqkka ds p; u ij /; ku nsuk pkfg, A

### INTRODUCTION

Fenugreek (*Trigonella foenum-graecum* L.; 2n=16) is one of the important seed spice crop of India, belongs to the family Fabaceae. It is indigenous to Western Asia and Southern Europe and is now cultivated mainly in India, Pakistan, France, Argentina and North African countries. The crop is gaining importance among seed spices because of its demand in the international market. The low productivity of fenugreek is mainly due to non-availability of suitable high yielding varieties for various agro-climatic regions.

To formulate efficient breeding programme, knowledge about the presence of genetic variability for yield and yield component traits is essential. Superior genotypes can

be isolated by selection, if considerable genetic variability exists in the population. Besides genetic variability, heritability and genetic advance reflecting the genetic gain is also important to understand crop behaviour. Limited information is available in this direction on fenugreek. Keeping this in view, an attempt was made to study the genetic variability, by determining the magnitude of phenotypic coefficient of variation (PCV), genetic coefficient of variation (GCV), heritability ( $h^2$ ) estimates in broad sense and expected genetic advance of different biometric traits in 41 genotypes using augmented design.

### MATERIALS AND METHODS

The experimental materials consisted of 41 diverse genotypes. Six checks viz., RMt 1, RMt 143, RMt 303, RMt

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305, Rmt 351 and Hisar Sonali randomized as per augmented design (Petersen,1). The experiment was laid during *rabi*, 2010-11 at the Research Farm, Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur (Rajasthan). Each genotype was planted in four rows of 5 m length at a distance of 30 cm from row to row and 10 cm within the row. Recommended cultural practices were followed and five competitive plants from each genotype were tagged and data were recorded. The characters included for the present study were days to 50 % flowering, plant height, branches per plant, pods per plant, pod length, seeds per pod, test weight and seed yield. The data was analysed using Indostat ver 8 software. The phenotypic and genotypic coefficient of variation was worked out as per Burton (1) and heritability (broad sense) and genetic advance were determined following the methodology of Johnson *et al.* (3)

### RESULTS AND DISCUSSION

The analysis of variation indicated significant differences among genotypes for most of the traits studied indicating presence of significant variability in the materials. The range, mean and standard error of mean, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability ( $h^2$ ) in broad sense and genetic advance (GA) as per cent of mean for various characters are presented in Table 1. The range of variability indicated the existence of variability for all the characters. In general, PCV values were relatively higher than respective GCV values indicating influence of environment on the expression of the character. The GCV estimates helps in the measuring the range of genetic variability present for the respective quantitative

trait. The GCV value ranged from 2.22 % for days to 50 % flowering to 32.88 % for pods per plant. High estimates of GCV were recorded for pods per plant, branches per plant and seed yield which indicates the presence of high amount of genetic variability for these characters.

These results are in agreement with the earlier findings for pods per plant reported by Chandra *et al.*(2), Raje *et al.* (6), Sarada *et al.*(8) and Prajapati *et al.* (5) and for seed yield by Rakesh & Korla (7) and Prajapati *et al.* (5). In general, the difference between PCV and GCV were high for pod length and seeds per pod indicating that these traits were much influenced by the environment, while the differences between PCV and GCV were less for test weight, days to 50 % flowering and pods per plant indicating that these traits were not much influenced by the environment, thus suggesting ample scope for improvement.

Heritability estimates in broad sense gives an idea of efficiency of selection on the basis of phenotypic performance, but to assess selection effect more accurately in predicting the resultant effect of selection on phenotypic expression, genetic advance was also computed because high broad sense heritability is not associated with higher genetic gain. High heritability was obtained for pods per plant (96.96 %), test weight (87.61 %), branches per plant (75.33 %) and plant height (70.65 %) while it was moderate for days to 50 % flowering (65.93 %) and seed yield (65.70%). In corollary to high heritability estimates, high estimates of genetic advance as per cent of mean was observed for pods per plant, branches per plant, test weight and seed yield indicating predominance of additive gene effects for these traits. Similar finding

**Table 1.** Range, mean, phenotypic and genotypic coefficient of variation, heritability and genetic advance as per cent of mean of various characters in 41 genotypes of fenugreek.

Characters	Range	Mean $\pm$ SEM	PCV (%)	GCV (%)	Heritability (%)	Genetic advance as % of mean
Days to 50% flowering	49.0- 54.0	50.5 $\pm$ 0.66	2.74	2.22	65.93	3.72
Plant height (cm)	86.7-116.7	104.7 +11.60	6.02	5.06	70.65	8.76
Branches per plant	4.0-6.7	5.4 + 0.11	12.38	10.74	75.33	19.21
Pods per plant	13.0-62.0	33.1 + 4.58	33.44	32.88	96.69	66.61
Pod length (cm)	8.7-12.7	10.5 $\pm$ 0.81	9.60	4.38	20.79	4.11
Seeds per pod	13.0-20.7	17.1 $\pm$ 1.89	9.71	5.44	31.43	6.29
Test weight (g)	11.8-16.6	13.8 $\pm$ 0.15	7.96	7.45	87.61	14.37
Seed yield (kg/ha)	1584-2884	2239 + 277.82	11.56	9.37	65.70	15.64

was observed for pods per plant by Prajapati *et al.* (5) for pods per plant and seed yield; Rakesh & Korla (7) and Raje *et al.* (6) for pods per plant

The present study indicated the presence of wide range of variability for pods per plant, branches per plant, test weight and seed yield. Therefore, selection should be based on these characters in order to achieve greater productivity in this crop.

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