



P-ISSN: 2349-8528

E-ISSN: 2321-4902

IJCS 2018; 6(4): 153-156

© 2018 IJCS

Received: 28-05-2018

Accepted: 29-06-2018

Aman KumarDepartment of Vegetable
Science, NDUAT, Kumarganj,
Faizabad, Uttar Pradesh, India**VP Pandey**Department of Vegetable
Science, NDUAT, Kumarganj,
Faizabad, Uttar Pradesh, India**Vipin Kumar Maurya**Department of Vegetable
Science, NDUAT, Kumarganj,
Faizabad, Uttar Pradesh, India**Devesh Tiwari**Department of Vegetable
Science, NDUAT, Kumarganj,
Faizabad, Uttar Pradesh, India**Sriom**Department of Vegetable
Science, NDUAT, Kumarganj,
Faizabad, Uttar Pradesh, India**Correspondence****Aman Kumar**Department of Vegetable
Science, NDUAT, Kumarganj,
Faizabad, Uttar Pradesh, India

Genetic variability, heritability & genetic advance in fenugreek (*Trigonella foenum-graecum* L.)

Aman Kumar, VP Pandey, Vipin Kumar Maurya, Devesh Tiwari and Sriom

Abstract

The present investigation was executed at Main Experiment, Station of Department of Vegetable Science, Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Faizabad, during *Rabi* 2016-17. A set of 124 germplasm of fenugreek (*Trigonella foenum-graecum* L.) was evaluated in augmented block design in four blocks with four check varieties to determine nature of variability, heritability and genetic advance. Observations were recorded on 10 quantitative characters *viz.*, days to 50% flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, pods per plant, length of pods, seeds per pod, 1000-seed weight and seed yield per plant.

The analysis of variance revealed significant differences among the genotypes for all the characters except days to maturity. Based on mean performance most promising genotypes *viz.*, NDM-98, NDM-120, NDM-117, NDM-58, NDM-96, NDM-101, NDM-106, NDM-71, NDM-77 and NDM-116 were found as most promising genotypes for high yield per plant. High magnitude of variability was observed in case of seed yield per plant followed by pods per plants, secondary branches per plant, primary branches per plant, length of pods, 1000 seeds weight, plant height and seeds per pod. The high estimates of heritability was observed in Seed yield per plant followed by primary branches per plant, pods per plants, secondary branches per plants, length of pods, plant height. Seeds per pods, 1000 seeds weight and days to 50% flowering. Moderate genetic advance observed in plant height and pods per plant while low genetic advance recorded for rest of traits.

Keywords: Fenugreek, variability, heritability, GCV, PCV

Introduction

Fenugreek (*Trigonella foenum-graecum* L.) is one of the oldest spices crop of the world and grown for its medicinal values. It is a self-pollinated, diploid species having chromosome number $2n = 2X = 16$ (Frayer, 1930). The fenugreek, also known as "Methi", is an important leafy vegetable cum seed spices belongs to the sub family Papilionaceae of the family Fabaceae. Fenugreek is supposed to be originated in between Iran and North India (Smith, 1982) [8].

The generic name, *Trigonella*, comes from Latin meaning 'little triangle', in reference to the triangular shape of the small yellowish-white flowers. The genus *Trigonella* comprises 50 species of the Mediterranean and oriental origin. There are two species of the genus *Trigonella*, which are economically importance, *viz.* *Trigonella foenum-graecum* or the commonly called "Common Methi" and *Trigonella corniculata* or the "Kasuri methi". *Trigonella foenum-graecum* is an annual herb and plants are semi-erect, tall, moderately branched with bold, typically yellow grains. Plants of *Trigonella corniculata* are bushy green, the flowers are bright orange yellow medium sized and pods are small and sickle shaped.

India has been known as land of spices since very early period of recorded history. The history of Indian spices is known to be dates back to the beginning of human civilization. Moreover, references are also available with regard to Indian spices and their use in Vedas (6000 B.C.) by Manu (4000 B.C.). Fenugreek is the third largest seed spice in India after coriander and cumin. India occupies a prime position among the fenugreek growing countries in the world. Its wild forms are found growing in north western India. Argentina, Egypt, Southern France, Morocco, Spain, Turkey, China, Pakistan and Lebanon are the leading countries for fenugreek production. However, in India it is mainly grown in Rajasthan, Madhya Pradesh, U.P., Gujarat and Punjab.

Rajasthan claims the monopoly in production accounting for about 80% of fenugreek produce in the country. During 2017 the Indian fenugreek crop had an average productivity of 1.6MT/ha covers an area of 218.00(000, ha) with production of 220.00 (000, MT) all over India (Anonymous, 2017) [1].

Fenugreek, a *Rabi* seasoncrop, can be grown under wide range of climatic conditions. It requires low temperature during early stage for better vegetative growth, while dry and relatively high temperature favours better ripening and high seed production. It can be grown on all types of well drained soils but mostly grown in sandy loam soil. Unlike other legumes, it is quite tolerant to salinity and it can be grown in black cotton soils. Stems of *Trigonella foenum-graecum* are 20-120 cm long, straight, rarely ascending, branching, usually hollow, anthocyanin tinged at base or all the way up, rarely completely green. First leaf is simple, sometimes weak trifoliate, oval or orbicular with entire margin and a long petiole. Leaf petiole thickened at the top, attenuate beyond point of attachment of lateral leaflets. Calyx is 6-8 mm, soft hairy with teeth as long as the tube, half as long as the corolla. Corolla is 13 -19 mm long, white. Standard tend backwards oblong emarginated at apex with bluish spots (these spots are absent from some genotypes), wings half as long as the standard; keel obtuse, split at base. Pods with the mucro (beak), 10-18 cm long and 3.5–5cm broad, curved, rarely straight, with transient hairs. Seeds vary from rectangular to rounded in outline, the length is 3.5-6 mm and the width 2.5-4 mm, light grayish, brown coloured, with a pronounced radicle that is half the length of the cotyledons.

Phenotypic variability changes under different environmental conditions while genetic variability remains unchanged and more useful to a plant breeder for exploitation in selection or hybridization. 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.

Materials & Methods

In the present investigation one hundred twenty four genotypes were evaluated in augmented block design with 4 checks *viz.*, Pusa Early Bunching, Hisar Sonali, NDM-19 and Rajendra Kranti at Main Experiment Station of Vegetable Research Farm of Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Faizabad (U.P.) India. The experiment was laid out in Augmented Block Design, with plot size of 2.0 × 1.2 m² with distance of 30 cm row to row and 10 cm plant to plant. Observations were recorded on 10 quantitative characters *viz.*, days to 50% flowering, days to maturity, plant height, Primary branches per plant, Secondary branches per plant, pods per plant, length of pods, seeds per pod, 1000-seed weight and seed yield per plant (gm). The analysis of variance for different characters in “Augmented Design” was done according to Federer (1956) [3]. Variability for different characters was estimated as suggested by Burton and de Vane (1953). Expected genetic advance (Ga) was estimated by the method suggested by Johnson *et al.*, (1955).

Results and Discussion

The present study revealed that the analysis of variance for ten characters is presented in table 1. The variation due to block was significant for all the characters except days to 50% flowering and days to maturity. The mean sum of square due to treatment (genotype + check) was highly significant for all the traits except days to maturity, indicating therefore significant differences among the genotypes. The check varieties showed significant differences for all the characters except days to 50% flowering and days to maturity, indicating that checks themselves were diverse. An insight into the magnitude of variability exists in a crop species of most importance, as it provides the basis of the effective selection. In general, the phenotypic coefficient of variability was higher than genotypic coefficient of variability for all the nine characters under study which indicates that environment played a considerable role in the expression of their traits.

The significant differences were observed among genotypes for all the characters studied. The higher magnitude of coefficient of variation (Table 2.) at phenotypic level observed for Seed yield per plant (30.99%) followed by pods per plants (22.72%), secondary branches per plant (17.55%), primary branches per plant (17.00%), length of pods (10.70%), 1000 seeds weight (10.56%), plant height (10.45%) and seeds per pod (9.44%). Maurya *et al.* (2013) [4], Yadav *et al.* (2013) [11], Sharma *et al.* (2015) [6] and Wojo *et al.* (2016) [10] also reported similar results in their studies. While, low GCV and PCV was observed for remaining two characters *viz.*, days to 50% flowering and days to maturity. Saha and Kole (2001) [5] also reported similar results in their studies. The data on phenotypic coefficient of variation indicated that there is a greater scope of selection for the characters that showed high range of PCV and the characters which were showing low range are least effective.

Heritability in broad sense of a character is important to the breeder since it indicates the possibility and extent to which improvement is possible through selection. It also indicates direction of selection pressure to be applied for a trait during selection because it measures relationship between parents and their progeny, hence widely used in determining the degree to which a character may be transmitted from parents to offspring. However, high heritability alone is not enough to make efficient selection in advanced generation unless accompanied by substantial amount of genetic advance (Burton and De-Vane, 1953). The genetic advance is commonly predicted as a product of heritability ratio and selection differentials. Panse and Sukhatme (1967) mentioned that where high heritability value is accompanied by high genetic advance.

The high estimates of heritability observed in seed yield per plant (99.5) followed by primary branches per plant (99.3), pods per plant (98.8), secondary branches per plant (98.7), length of pods (98), plant height (97.5), seeds per pod (95.8), 1000 seed weight (94.9) and days to 50% flowering (78.3).

High genetic advance found in plant height (16.05) and pods per plant (13.41). While low genetic advance recorded in days to 50% flowering (4.83) followed by seed yield per plant (2.95), seeds per pod (2.93), length of pods (2.39), days to maturity (2.16), secondary branches per plant (2.13), 1000 seed per plant (1.53) and primary branches per plants (1.058). The high estimates of heritability coupled with Moderate genetic advanced in per cent of mean were observed for plant height and pods per plant. Low heritability accompanied with low genetic advance observed for seed yield per plant, primary branches per plant, secondary branches per plant,

Pods per plant, length of pod, seeds per pod and 1000 seed weight. Verma *et al.* (2016) [9], Sharma *et al.* (2015) [6], Singh *et al.* (2014) [7] and Yadav *et al.* (2013) [11] also reported similar results in their studies.

While low heritability coupled with low genetic advance observed for days to maturity. Banerjee and Kole (2004) [2] also reported similar results in their studies.

Table 1: Analysis of variance for ten characters in fenugreek genotypes

Character	Source of variation					
	Block (b-1)	Treatment (c+g)-1	Check (c-1)	genotypes (g-1)	Check vs genotypes	Error (b-1)(c-1)
<i>d.f.</i>	3	123	3	119	1	9
1. Days to 50% flowering	6.09	9.60**	6.67	9.73**	14.59*	1.94**
2. Days to maturity	4.75	11.06	13.33	9.81	147.59**	6.22**
3. Plant height (cm)	200.52**	69.75**	43.44**	70.69**	630.32**	1.59**
4. Primary Branches/plant	0.33**	0.31**	0.70**	0.30**	1.17**	0.00**
5. Secondary Branches/plant	0.57**	1.44**	1.55**	1.22**	28.20**	0.01**
6. Pods/plant	104.01**	52.19**	41.36**	48.15**	875.89**	0.52**
7. Length of pod (cm)	0.52**	1.69**	2.15**	1.55**	19.95**	0.03**
8. Seeds/pod	3.05**	2.40**	2.66**	2.44**	5.92**	0.09**
9. 1000-seed weight (g)	3.37**	0.63**	0.67**	0.68**	4.22**	0.03**
10. Seed yield/plant (g)	10.36**	2.23**	0.13**	2.30**	30.80**	0.01**

** - Significant at 5 per cent probability level, * - Significant at 1 per cent probability level

Table 2: Estimates of range, grand mean, phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability in broad sense [$h^2_{(bs)}\%$], genetic advance in per cent of mean (\bar{G}_a %) for ten characters in fenugreek genotypes

Character	Range		Grand Mean (\bar{x})	PCV (%)	GCV (%)	ECV (%)	Heritability broad sense [$h^2\%$]	Genetic advance	Genetic advance in per cent of mean (\bar{G}_a %)
	Lowest	Highest							
Days to 50% flowering	64.50	79.50	71.48	4.18	3.70	1.95	78.30	4.83	6.75
Days to maturity	119.50	135.50	127.12	2.41	1.41	1.96	34.20	2.16	1.70
Plant height (cm)	55.30	102.52	76.65	10.45	10.32	1.65	97.50	16.05	21.00
Primary branches/plant	1.98	4.63	3.05	17.00	16.94	1.49	99.30	1.058	34.791
Secondary branches/plant	3.51	8.65	6.03	17.55	17.44	1.99	98.70	2.138	35.706
Pods/plant	15.12	48.09	29.27	22.72	22.58	2.49	98.80	13.417	46.242
Length of pod (cm)	8.34	13.71	11.11	10.70	10.59	1.51	98.00	2.392	21.603
Seeds/pod	11.78	19.95	15.76	9.44	9.24	1.93	95.80	2.935	18.643
1000-seed weight (g)	5.83	11.10	7.45	10.56	10.29	2.38	94.90	1.536	20.659
Seed yield/plant (g)	2.21	8.12	4.68	30.99	30.92	2.10	99.50	2.955	63.547

References

- Anonymous. Data base National Horticulture Board, Gurgaon, Haryana, India, 2017.
- Banerjee A, Kole PC. Genetic variability, correlation and path analysis in fenugreek (*Trigonella foenum graecum* L.). Journal of Spices and Aromatic Crops. 2004; 13(1):44-48.
- Federer WT. Augmented design "Hawaii Planters" records. 1956; 55:191-208.
- Maurya BP, Yadav BK, Yadav AK, Yadav PK. Studies on variability, heritability and genetic advance in fenugreek (*Trigonella foenum graecum* L.). Biochemical and Cellular Archives. 2013; 13(2):311-313.
- Saha A, Kole PC. Genetic variability in fenugreek grown in sub-humid lateritic belt of West-Bengal. Madras Agricultural J. 2001; 88(4-6):345-348
- Sharma N, Shekhawat AS, Nagariya NK. Genetic variability in fenugreek (*Trigonella foenum-graecum* L.). Annals of Biology. 2015; 31(1):94-96.
- Singh MK, Naik A, Singh BM. Genetic variability, heritability, genetic advance and correlation coefficient analysis studies in fenugreek (*Trigonella foenum-graecum* L.). Annals of Biology. 2014; 30(3):542-544.
- Smith A. Selected materials for turmeric, coriander seed, cumin seed, fenugreek seed and curry powder. Tropical Product Institute. 1982; 165:7-45.
- Verma P, Solanki RK, Dhasora A, Kakani RK. Genetic variability in Fenugreek (*Trigonella foenum-graecum* L.) as expressed under South Eastern region of Rajasthan State. International J Seed Spices. 2016; 6(1):93-95
- Wojto AA, Alamerew S, Nebiyu A, Menamo T. Genotype and phenotype variability studies in fenugreek (*Trigonella foenum-graecum* L.). Journal of Spices and Aromatic Crops. 2016; 25(2):159-168.
- Yadav Y, Yadava PS, Pandey VP, Kumar A. Genetic variability, correlation and path co-efficient analysis studies in fenugreek (*Trigonella foenum graecum* L.). Asian Journal of Horticulture. 2013; 8(2):456-459.