



P-ISSN: 2349-8528

E-ISSN: 2321-4902

www.chemijournal.com

IJCS 2020; 8(4): 1821-1825

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Received: 01-05-2020

Accepted: 03-06-2020

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Studies on genetic variability among yield attributing traits of fenugreek genotypes

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DOI: <https://doi.org/10.22271/chemi.2020.v8.i4s.9891>

Abstract

The present study was conducted at Horticultural Complex, Vegetable Research Farm, Maharajpur, Department of Horticulture, College of Agriculture, Jabalpur (M.P.) during *Rabi* season 2016-17. The investigations revealed that the presence of considerable amount of genetic variability and mean values for all the characters have showed wide range of variability for all the morphological, phenological and qualitative traits studied. The values of phenotypic variance and phenotypic coefficient of variance were of higher magnitude than that of genotypic variance and genotypic coefficient of variance. The genotypic and phenotypic coefficient of variation was high for the characters seed yield per plant, number of pods per plant, number of branches at 90 DAS, test weight, number of leaves per plant at 30 DAS, number of branches at 60 DAS. High heritability was observed for number of leaves at 90 DAS, number of leaves at 30 DAS, number of pods per plant, shelling % and length of pods, plant height at 90 DAS, seed yield per plot and seed yield per hectare, number of branches per plant at 90 DAS, plant height at 60 DAS and plant height at 30 DAS. High estimates of GA as per cent of mean was recorded for seed yield per plant, number of pods per plant, test weight, number of leaves at 30 DAS, number of branches per plant at 90 DAS, number of leaves at 90 DAS, number of leaves at 60 DAS, and number of branches per plant at 60 DAS. High heritability coupled with high genetic advance was observed for traits like test weight, seed yield per plant, number of leaves at 30 DAS, number of pods per plant, number of leaves per plant at 30, 60, and 90 DAS.

Keywords: Fenugreek, variability, heritability, genetic advance

Introduction

Fenugreek [*Trigonella foenum-graecum* L.] also known as Methi, is an annual spice herb of the sub-family Papilionaceae of Leguminaceae. It is a small-seeded self pollinated, diploid annual legume plant with $2n=16$. An important non spice use of fenugreek is as a potential source of diosgenin. It is also known as one of the oldest medicinal plants recognized in the recorded history.

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. Burton (1952) ^[4] suggested that genetic variability along with heritability should be considered for assessing the maximum and accurate effect of selection. Johnson *et al.* (1955) ^[11] reported that heritability and genetic advance, when computed together, are more useful in predicting the resultant effect of selection. The most important among attributes of plant is its ability to yield, for rational approach of improvement of yield. Yield being a complex character, is influenced by a number of yield contributing characters controlled by polygenes and also influenced by environment. So, the variability in the collections for these characters is the sum total of heredity effects of concerned genes and the influence of the environment. Hence, it becomes necessary to partition the observed variability into heritable and non-heritable components measured as genotypic and phenotypic coefficients of variation (GCV and PCV), heritability and genetic advance expressed as per cent mean. Very little information is available in this direction on fenugreek. Keeping this in view, an attempt was made in the present investigation to assess the magnitude of variability, heritability and genetic advance for different characters in fenugreek germplasm.

Materials and Methods

The present investigation was conducted at Horticulture Research Complex, Maharajpur, Department of Horticulture, College of Agriculture, JNKVV, Jabalpur (M.P.)

Experimental material comprised of 28 genotypes consisting of 2 checks. The genotypes were collected from IISR-Calicut, Hisar, Udaipur, Jobner (Rajasthan) and Jabalpur. (Table 1). The data on days to 50% flowering and days to maturity was recorded on plot basis, while, five plants were tagged at random to record data on important growth and yield contributing characters, which were analyzed by the standard statistical methods.

Table 1: Details of treatments

S. No.	Genotypes	Source	S. No.	Genotypes	Source
1.	FGK-94	IISR, Calicut	15.	FGK-77	IISR, Calicut
2.	FGK-95	IISR, Calicut	16.	HM-282	Hisar
3.	FGK-96	IISR, Calicut	17.	UM-122	Udaipur
4.	FGK-97	IISR, Calicut	18.	ACC-01	Jabalpur
5.	FGK-98	IISR, Calicut	19.	RMT-195	Jobner, Rajasthan
6.	FGK-99	IISR, Calicut	20.	UM-231	Udaipur
7.	FGK-100	IISR, Calicut	21.	ACC-06	Jabalpur
8.	FGK-101	IISR, Calicut	22.	FGK-26	IISR, Calicut
9.	FGK-102	IISR, Calicut	23.	HM-271	Hisar
10.	FGK-103	IISR, Calicut	24.	ACC-02	Jabalpur
11.	FGK-104	IISR, Calicut	25.	RMT-186	Rajasthan
12.	FGK-105	IISR, Calicut	26.	RMT-70	Rajasthan
13.	FGK-106	IISR, Calicut	27.	Hisar Sonali (C)	Hisar
14.	UM-123	Udaipur	28.	RMT-361(C)	Rajasthan

Heritability

Heritability in broad sense refers to the proportion of genetic variation to the total observed variance in the population. It is symbolized as h^2 (BS) It has been estimated as per the formula given by Allard (1960) [1]. Heritability in broad sense is the ratio of genotypic variance to the phenotypic variance and is expressed in percentage.

Estimation of heritability was done as per the formula given by Hanson *et al.* (1956) [9].

$$h^2 \text{ (BS)} = \frac{\sigma^2_{g_i}}{\sigma^2_{p_i}} \times 100 \quad \text{or} \quad = \frac{\text{Genotypic variance of the } i^{\text{th}} \text{ character}}{\text{Phenotypic variance of the } i^{\text{th}} \text{ character}}$$

Expected genetic advance was calculated by using the method suggested by Johnson *et al.* (1955) [11] at 5% selection intensity.

Genetic advance

Genetic advance for each character was predicted by the formula given by Johnson *et al.* (1955) [11].

Genetic advance (GA) = $K \cdot P_i \cdot h^2_i$ And,

Genetic advance as percentage of mean was calculated as follows:

$$\frac{\text{Genetic advance}}{\bar{X}}$$

Where,

K = Selection intensity its value at 5% selection level is 2.06.

P_i = Phenotypic standard deviation of the i^{th} character.

h^2_i = Broad sense heritability (fraction) of the i^{th} character.

\bar{X} = General mean of the i^{th} character under consideration.

Results and Discussion

The values of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, genetic advance and genetic advance expressed as per cent mean for all the characters studied are presented in Table 2

Results indicating the values of phenotypic variance and phenotypic coefficient of variance were of higher magnitude than that of genotypic variance and genotypic coefficient of variance for all the characters indicating that the environment had an important role in influencing the expressions of the characters.

GCV AND PCV: In the present findings phenotypic coefficient of variations were observed to be higher than corresponding genotypic coefficient of variations for all the characters studied. However, the differences were narrow which implied their relative resistance to environmental variation. It also described that genetic factors were predominantly responsible for expression of those attributes and selection could be made effectively on the basis of phenotypic performance. The findings of Singh and Pramila (2009), Singh *et al.* (2012) [25], Jain *et al.* (2013) [10] and Lodhi *et al.* (2015) [13] and Singh *et al.* (2016) were similar to that of the present findings.

The magnitude of phenotypic and genotypic coefficient of variation ranged from 2.08 (%) to 21.23 (%) and 1.40 (%) to 20.38 (%). The findings were similar to Gangopadhyay *et al.* (2009), Dashora *et al.* (2011) [6], Pathak *et al.* (2014) [19], and Singh *et al.* (2016).

The genotypic and phenotypic coefficient of variation was high for the characters seed yield per plant, number of pods per plant, number of branches at 90 DAS, test weight, number of leaves per plant at 30 DAS, number of branches at 30 DAS, number of branches at 60 DAS. The findings were similar to Mori *et al.* (2016) [15] and Jain *et al.* (2013) [10]. This indicated the presence of sufficient amount of genetic variability for these traits that can be exploited by breeding procedure for the improvement of these characters.

However, it exhibited moderate PCV and GCV for characters such as days to germination, number of leaves per plant at 90 DAS, number of leaves at 60 DAS, number of seeds per pod, seed yield per plot and seed yield per plant. Similarly, Raghuvanshi and Singh (1984) [12] reported high genetic coefficients of variation for number of pods and number of branches, while Mustefa (2006) [16] reported high estimates of genotypic coefficient of variation (GCV) for seed yield plant-1, number of pods and number of secondary branches. In contrast, Sade *et al.* (1996) [24] reported a high estimate of phenotypic coefficient of variation (PCV) for seed yield plant per plant. Generally, the estimates for phenotypic coefficient of variation (PCV) were greater than genotypic coefficient of variation (GCV) for the corresponding traits. This was in agreement with the finding Wojo *et al.* (2016) [28] for pods per plant, number of secondary branches per plant, seeds per pod, as suggested by Prajapati *et al.* (2010) [20] and Verma *et al.* (2016) [27] for pods per plant, branches per plant and seed yield. This suggests presence of narrow genetic base for these traits. Improvement in these characters can be brought about by hybridization or induced variability to widen genetic base and then selecting in segregating generations. The remaining characters such as length of pod (10.28), plant height at 90 DAS (8.42), plant height at 30 DAS (8.08), plant height at 60 DAS (8.03), days to maturity (5.99), shelling % (5.84), days to first flowering (2.74), days to 50% flowering (2.08) exhibited low PCV. The results are in agreement with the

earlier reports of Lodhi *et al.* (2015) [13], Prajapati *et al.* (2010) [20] and Verma *et al.* (2016) [27]. Findings are in close harmony with results of Chandra *et al.* (2000) [5], Banerjee *et al.* (2004) [3] and Datta *et al.* (2005) [7] for days to flower initiation. Singh *et al.* (2012) [25] and Lodhi *et al.* (2015) [13] for days to 50% flowering. Low differences between PCV and GCV indicating that they are less affected by environment and comparatively stable. Thus phenotypic selection would be effective in the improvement of these characters. Low value of phenotypic and genotypic coefficient of variation indicated that there is limited scope for improvement.

Heritability

The estimate of heritability can be utilized for the prediction of genetic gain, which indicates that genetic improvement could result from the selection of best individuals. Hence, estimates of heritability are an essential pre-requisite for formulation of an effective selection method for genetic improvement.

High heritability was observed for number of leaves at 90 DAS (89.52), number of leaves at 30 DAS (89.34), number of pods per plant (87.92), shelling % (87.36) and length of pods (85.85), plant height at 90 DAS (83.00), seed yield per plot and seed yield per hectare (81.40), number of branches per plant at 90 DAS (77.87), plant height at 60 DAS (75.09) and plant height at 30 DAS (72.11).

Similar results were found by Banerjee *et al.* (2004) [3] for shelling percentage. Rakesh and Korla (2003) [23], Wojo *et al.* (2016) [28] for seed yield per plot.

High value of broad sense heritability for the above characters, expressed that they were least influenced by environmental modification. It reflected that the phenotypes were the true representatives of their genotypes and selection based on phenotypic performance would be reliable.

However, moderate heritability was observed for number of branches per plant at 60 DAS (66.46), number of seeds per pod (63.62) and days to first flowering (53.72). Whereas low heritability was observed for days to 50% flowering (45.45), number of branches per plant at 30 DAS (45.42) and days to germination (45.05). Finding of Balai *et al.* (2006) [2] is similar to that of present finding for days to 50% flowering. Similar results are reported by Kailashchandra and Singh (2000) [12] in fenugreek for days to flowering.

Genetic advance

The genetic advance is the deviation in the characters of selected population over the base population. Gain under selection or genetic advance is a measure to predict the expected progress under selection. The genetic advance helps to evaluate the selection procedures. If the value of genetic advance is more than in the succeeding generation there will be good progress over population mean.

Based on the estimate of heritability (BS) expected genetic

advance was computed on the hypothetical selection at 5 per cent best individual ($K=2.06$). Due to masking effect of environment upon characters concerned, values of genetic advance exhibited high fluctuations. Therefore, to attain relative comparison of the characters in relation to environment genetic advance as percent of mean was calculated to predict the genetic gain (Table 4.3), and were classified as high (above 20%), medium (10%-20%) and low (below 10%).

High heritability coupled with high genetic advance was observed for traits like test weight, seed yield per plant, number of leaves at 30 DAS, number of pods per plant, number of leaves per plant at 30, 60, and 90 DAS, suggested that the preponderance of additive genes. It also indicated higher response for selection of high yielding genotypes as these characters are governed by additive gene actions. The findings are in agreement to the findings of Meena *et al.* (2011) [14] and Singh *et al.* (2012) [25] for number of pods per plant and seed yield per plant. Singh (2015) [15] for number of pods per plant, Prajapati *et al.* (2010) [20] and Lodhi *et al.* (2015) [13] for test weight.

High heritability supplemented with moderate genetic advances as percentage of mean is manifested by length of pods, plant height at 90 DAS, seed yield per plot, seed yield per hectare, number of branches at 90 DAS, plant height at 30 and 60 DAS, shelling percentage and days to maturity. Similar result was reported by Pandey (2009) [18] and Pushpa *et al.* (2010) [21] for length of pod and Balai *et al.* (2006) [2] for number of leaves per plant. The results are in consonance with Yadav *et al.* (2013) [29] for pod length, plant height and number of seeds per pod, Dashora *et al.* (2011) [6] and Pandey (2009) [18] for seed yield per plot and seed yield per plant. It may infer that this character was regulated by non-additive gene action and presence of high genotypic X environmental interaction. The heritability is being exhibited due to favourable influence of environmental rather than the genotype and simple selection will not be rewarding. However this can be improved by development of hybrid or utilization of transgressive segregants in heterosis breeding programme.

Moderate estimates of heritability coupled with low genetic advance as percentage of mean have been displayed by characters like days to first flowering and days to 50% flowering. The finding is in agreement to the finding of Balai *et al.* (2006) [2].

Moderate genetic advance as per cent of mean with high or medium heritability suggesting the action of both additive and non-additive genes, thereby favoring the influence of environment in the expression of traits.

Hence, the breeder should adopt suitable breeding methodology to utilize both additive and non additive gene effects simultaneously, since varietal and hybrid development will go a long way in the breeding programmes.

Table 2: Estimates of genetic parameters of variations for various characters in fenugreek

Characters	Grand Mean	Range		Coefficient of variations		Heritability % (BS)	Genetic Advance	GA as % of mean	
		Min.	Max.	Phenotypic	Genotypic				
Days to germination	4.36	3.33	5.33	15.01	10.07	45.05	0.61	13.92	
Plant height (cm) at	30 DAS	12.82	10.81	14.82	8.08	6.86	72.11	1.54	12.01
	60 DAS	58.47	51.15	68.31	8.03	6.96	75.09	7.27	12.43
	90 DAS	89.88	73.09	101.60	8.42	7.67	83.00	12.94	14.39
No. of branches plant ⁻¹ at	30 DAS	3.01	2.33	4.00	15.79	10.64	45.42	0.44	14.78
	60 DAS	4.23	3.33	5.33	15.42	12.57	66.46	0.89	21.09
	90 DAS	5.75	4.00	8.00	19.00	16.77	77.87	1.75	30.48
No. of leaves	30 DAS	11.11	8.07	16.42	16.64	15.73	89.34	3.40	30.63

plant ⁻¹ at	60 DAS	52.52	40.09	63.85	14.06	13.40	90.92	13.82	26.32
	90 DAS	137.88	102.08	171.27	14.51	13.73	89.52	36.89	26.75
Days to first flowering		48.73	46.67	51.00	2.74	2.01	53.72	1.48	3.03
Days to 50% flowering		54.83	52.67	56.67	2.08	1.40	45.45	1.07	1.95
Number of pods plant ⁻¹		23.99	17.33	35.00	20.55	19.27	87.92	8.93	37.22
Length of pod (cm)		8.86	6.32	10.97	10.28	9.52	85.85	1.61	18.18
Number of seeds pod ⁻¹		15.55	12.74	18.92	11.13	8.88	63.62	2.27	14.58
Test weight(g)		16.19	11.29	21.21	17.71	17.48	97.32	5.75	35.51
Shelling percentage		74.24	68.59	83.90	5.84	5.45	87.36	7.80	10.50
Days to maturity		106.80	99.00	118.67	5.99	5.68	90.17	11.88	11.12
Seed Yield plant ⁻¹ (g)		8.25	5.33	12.00	21.23	20.38	92.11	3.32	40.27
Seed Yield plot ⁻¹ (kg)		1.47	1.13	1.69	10.99	9.92	81.40	0.27	18.50
Seed yield ha ⁻¹ (q ha ⁻¹)		20.47	15.73	23.50	10.99	9.92	81.40	3.77	18.44

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