

Genetic variability and character association among yield and yield contributing traits in fenugreek (*Trigonella foenum-graecum* L.) germplasm

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Abstract

Fenugreek is an important *Rabi* season seed spice crop in India. 99 fenugreek germplasm with five checks were evaluated in Augmented Block Design during *Rabi* 2019-20 at NRCSS, Ajmer experimental research farm. The characters studied were plant height (cm), number of primary branches plant⁻¹, number of secondary branches plant⁻¹, number of pods plant⁻¹, test weight (g) and seed yield plant⁻¹ (g). Data were analyzed statistically for genetic variability, correlation and path analysis for selection of superior genotypes from fenugreek germplasm. The analysis of variance showed significant variability for almost all the morphological characters in germplasm lines examined, except secondary branches plant⁻¹. The phenotypic coefficient of variance (PCV) expressed in terms of percentage were comparatively high for all the characters than genotypic coefficient of variance (GCV). This study revealed that PCV and GCV were comparatively high for seed yield plant⁻¹, number of pods plant⁻¹, number of primary branches plant⁻¹ and number of secondary branches plant⁻¹. Heritability estimates were found high for seed yield plant⁻¹, number of pods plant⁻¹, test weight and number of primary branches plant⁻¹. High estimates of heritability indicating less influenced by environment and direct selection for these yield contributing traits would be effective for future improvement in yield. Estimates of genotypic correlation coefficient is higher than their corresponding phenotypic correlation coefficient for all the characters under this study. Seed yield plant⁻¹ had significant and positive correlation with number of branches plant⁻¹, number of secondary branches plant⁻¹, number of pods plant⁻¹ and test weight at both genotypic and phenotypic level. The result of the present investigation on path coefficient analysis also revealed that number of pods plant⁻¹ (0.6211) had highest direct effect on seed yield followed by test weight (0.2132), number of primary branches plant⁻¹ (0.0685), plant height (0.0469) and number of secondary branches plant⁻¹ (0.0364). Therefore in order to increase seed yield, more emphasis should be given on positive and direct effect, selection of these characteristics would be more rewarding for fenugreek germplasm.

Key words: Correlation, fenugreek, genetic variability, heritability, path analysis.

Fenugreek (*Trigonella foenum-graecum* L.), popularly known as “Methi” is an important seed spice crop largely grown in India during *Rabi* season. In India it is mainly grown in Madhya Pradesh, Rajasthan, U.P., Gujarat and Punjab. The leading countries of fenugreek production in the world are India, Argentina, Egypt, Southern France, Morocco, Spain, Turkey, China, Pakistan and Lebanon. Fenugreek is used as food and food additive as well as in medicines. Both leaves and seeds are used which are rich in protein, vitamin A and vitamin C. Fresh tender pods, leaves and shoots are eaten as curried vegetable. The seeds are used in colic flatulence, dysentery, diarrhoea, dyspepsia, chronic cough and enlargement of liver and spleen, rickets and gout. Reducing the sugar level of the blood, it is used in diabetes in conjunction with insulin. It also lowers blood pressure.

While the medical science is well investigating fenugreek for its possible contribution to human health but it is certainly just a fraction of this multi-potential medicinal herb. As fenugreek is geographically well distributed under diverse climatic conditions, it is supposed to have large genotypic variability. In addition, being a least bred (genetically manipulated) crop hence possibility is there to have a multiple and potential allelic system against environmental stresses. However, unfortunately fenugreek has not gained particular consideration. It is the need of time to consider this crop in major research activities to discover its potential and use that information in genetic improvement as well. An extensive genomic and agronomic characterization is needed to identify the potential genes which could further facilitate in breeding programmes.

At present few high yielding varieties ruling in cultivation which often leads to genetic homogeneity. Genetic homogeneity is also well known to contribute to genetic susceptibility to biotic and abiotic stresses. In any crop breeding programme germplasm is the most important resource, it provides variability for various traits. A thorough study and evaluation of germplasm would provide an estimate about their potential value as suitable genotype for utilization in varietal development programme and it provides an opportunity to identify the superior lines with desirable yield and quality traits, which further enables to develop a high yielding variety.

Materials and method

The present study was carried out to evaluate 99 fenugreek germplasm with 5 checks (AFg-3, AFg-4, AFg-5, Hisarsonali and RMT-361). The germplasm lines with checks were sown in Augmented Block Design in *Rabi* 2019-20 at NRCSS, Ajmer experimental research farm. The study location is lying between 74° 35'39" to 74° 36' 01" Elongitude and 26° 22'12" to 26° 22' 31" N latitude with an altitude of 486 MSL. The soil of the site was sandy loam texture, poor in fertility and water holding capacity, having pH 8.0 to 8.3, EC 0.07 to 0.12 and 0.15 to 0.23% organic carbon, available N 178.5 kg ha⁻¹ (low) and P₂O₅ 12 kg ha⁻¹ (medium), K₂O 5 kg ha⁻¹ (low). Climate of the Ajmer area characterized as semi-arid. All recommended agronomic practices and plant protection measures were followed timely for successful raising the crop. Field was divided into 5 blocks to increase the homogeneity and reduce the soil heterogeneity. Blocks were divided into 2 x 3m size plots. Measurements were made at the plant level to capture the information about the variability between plants of the same accession. Observations were recorded on six quantitative characters namely, plant height (cm), number of primary branches plant⁻¹, number of secondary branches plant⁻¹, number of pods plant⁻¹, test weight (g) and seed yield plant⁻¹ (g) in each plot from 10 randomly selected plants. Every care was taken in selecting only competitive plants and avoiding border effects. The present investigation was conducted to estimate genetic variability, correlation and path analysis among yield and yield contributing traits. The recorded data were subjected to statistical analysis and analysis of variance was carried out as per the method suggested by Panse and Sukhatme (1957). The genotypic and phenotypic coefficient of variance was calculated as per the formula suggested by Burton (1952), heritability and genetic advance as per Hanson *et al.* (1956), correlation analysis as per Johnson *et al.* (1955) and path analysis

as per method suggested by Dewey and Lu (1959).

Results and discussion

The analysis of variance showed significant variability for almost all the morphological characters in germplasm lines examined, except secondary branches per plant in table 1. Similar results were also reported by Sharma *et al.* (2008), Sharma *et al.* (2015), Wojo *et al.* (2016), Kumar *et al.* (2017) and Meena *et al.* (2019).

In the present findings phenotypic coefficient of variance (PCV) was observed higher than the genotypic coefficient of variance (GCV) for all the characters. However, the differences were small which indicated their relative resistance to environmental variation in table 2. The findings of Pathak *et al.* (2014), Verma *et al.* (2016), Wojo *et al.* (2016), Choudhary *et al.* (2017) and Upadhyay *et al.* (2020) were similar to these findings. The magnitude of phenotypic and genotypic coefficient of variation ranged from 4.62% to 58.91% and 4.4% to 58.82% respectively. The results revealed that the differences between genotypic and phenotypic 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 genotypic and phenotypic coefficient of variation were high for seed yield plant⁻¹, number of pods plant⁻¹, number of primary branches plant⁻¹ and number of secondary branches plant⁻¹. These findings were similar to Prajapati *et al.* (2010), Singh *et al.* (2012), Verma *et al.* (2016) Choudhary *et al.* (2017) and Upadhyay *et al.* (2020) findings. 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, moderate PCV and GCV exhibited by characters such as plant height and test weight. Similar findings were also reported by Jain *et al.* (2013) and Choudhary *et al.* (2017).

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. The heritability in the broad sense ranged from 49.01 (number of secondary branches plant⁻¹) to 99.69 % (seed yield plant⁻¹). Heritability estimates were found high for seed yield plant⁻¹, number of pods plant⁻¹, test weight (g) and number of primary branches plant⁻¹. These findings were supported by Singh *et al.* (2012), Sharma *et al.* (2015), Wojo *et al.* (2016), Singh *et al.* (2019) and Upadhyay *et al.* (2020). High estimates of

heritability indicating less influenced by environment and direct selection for these yield contributing traits would be effective for future improvement in yield. However, moderate heritability was also observed for plant height and number of secondary branches plant⁻¹. These results are in accordance with the findings of Prajapati *et al.* (2010) and Naik *et al.* (2012). High heritability is not always an indication of high genetic gain. The expected genetic advance would be low when the heritability is mainly due to non-additive gene effect, but the genetic advance would be high when the heritability is due to additive gene effect. High heritability and high genetic advance are crucial for the improvement (genetic gain) of any character and for selection of suitable breeding method.

Genetic advance as percentage of mean ranged from 8.92 (test weight) to 121.15 (seed yield plant⁻¹). Genetic advance expressed as percentage of mean was high for the characters *viz.* number of primary branches plant⁻¹, number of pods plant⁻¹ and seed yield plant⁻¹. The characters *viz.*, number of primary branches plant⁻¹, number of pods plant⁻¹ and seed yield plant⁻¹, which recorded high heritability, also showed high genetic advance indicating the operation of additive gene action in the inheritance of these characters and giving scope for improvement through selection Naik *et al.* (2012), Singh (2014), Pathak *et al.* (2014), Verma *et al.* (2016), Meena *et al.* (2019) and Upadhyay *et al.* (2020). Genetic advance as percentage of mean was moderate for characters *viz.* plant height and secondary branches plant⁻¹. Low genetic advance as percentage of mean was shown by test weight. Moderate heritability with moderate genetic advance as percentage of mean was observed for the characters *viz.*, plant height and secondary branches plant⁻¹. Test weight, which recorded high heritability and low genetic advance indicating the non-additive gene action. These findings are in agreement to the findings of Balai *et al.* (2006). Considering the estimates of heritability and genetic advance in the present study, it is worthwhile to carry out selection in fenugreek for number of primary branches plant⁻¹, number of pods plant⁻¹ and ultimately seed yield for achieving high yield in fenugreek.

The crop yield is the consequence of a number of interactions with corresponding characters. Correlation coefficient analysis measures the mutual relationship between plant characters and determines the component characters on which selection can be made for genetic improvement of yield. When characters with direct effect on yield are chosen their interaction with

other characters is to be considered concurrently as this would indirectly impact on yield. If genotypic correlation coefficients are higher than their phenotypic correlation coefficient, it indicates genetic reason of association. When phenotypic correlation coefficients are higher than genotypic correlation coefficients, it indicates suppressing effect of the environment which modifies the expression of characters at phenotypic level. The genotypic and phenotypic correlation coefficient among yield and yield contributing characters of fenugreek germplasm are presented in table 3.

In this study the estimates of genotypic correlation coefficient is higher than their corresponding phenotypic correlation coefficient for all the characters. In agreement with the current study, higher genotypic correlation coefficients than their respective phenotypic correlation coefficients were reported by Fikreselassie *et al.* (2012) and Singh *et al.* (2019).

In the present investigation, genotypic and phenotypic correlation of seed yield plant⁻¹ had significant and positive association with branches plant⁻¹, secondary branches plant⁻¹, number of pods plant⁻¹ and test weight. The association of these characters is in the desirable direction and selection for these traits may improve the yield plant⁻¹. Similar results were reported by Balai *et al.* (2006), Sharma *et al.* (2008), Prajapati *et al.* (2010), Fikreselassie *et al.* (2012), Yogendra *et al.* (2013) and Meena *et al.* (2019). Seed yield plant⁻¹ exhibited positive and non-significant correlation with plant height. These findings are in agreement with the findings of Prajapati *et al.* (2010) and Choudhary *et al.* (2017).

A polygenic trait like seed yield is influenced by its various components directly, as well as indirectly via other traits. Path coefficient analysis helps in understanding the magnitude of direct and indirect contribution of each character on the dependent characters. Partitioning of correlation coefficient into direct and indirect effects provide information about the nature and magnitude of effects of other characters on seed yield. The result of the present investigation on path coefficient analysis are presented in (Table 4).

Path coefficient analysis revealed that no of pods plant⁻¹ (0.6211) had highest direct effect on seed yield followed by test weight (0.2132), branches plant⁻¹ (0.0685), plant height (0.0469) and secondary branches plant⁻¹ (0.0364). These results are also supported by Jain *et al.* (2013), Yogendra *et al.* (2013).

Indirect effects of no. of pods plant⁻¹ were positive and negligible via plant height, primary branches plant⁻¹, secondary branches plant⁻¹ and test weight. indirect

effects of test weight on yield were moderate positive for trait, no of pods plant⁻¹ and positive and negligible for plant height, branches plant⁻¹ and for secondary branches plant⁻¹. Plant height exhibited positive indirect effect on yield through no. of pods plant⁻¹ and test weight while negative indirect effect via number of branches plant⁻¹ and secondary branches plant⁻¹ on yield. These results are in accordance with the findings of Prajapati *et al.* (2010).

Branches plant⁻¹ exerted positive indirect effect on yield through no. of pods plant⁻¹, secondary branches plant⁻¹ and test weight. It also exhibited negative indirect effect

on yield through plant height. Secondary branches plant⁻¹ had positive indirect effect on yield via no. of pods plant⁻¹, branches plant⁻¹ and test weight. Negative effect was shown by plant height. These results are in accordance with the findings of Prajapati *et al.* (2010) and Singh and Kakani (2017).

Therefore, in order to increase seed yield plant⁻¹, focus should be given on characteristics with positive and direct effect, and balanced selection based on these characteristics would be more rewarding for fenugreek improvement in further breeding programme.

Table1: Analysis of variance for different characters in fenugreek germplasm.

Source of variation	Degree of freedom	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Number of pods per Plant	Test weight(g)	Yield(g/line)
Blocks (ignoring treatments)	4	75.77**	0.21	3.2*	424.99**	0.14**	11909.55**
Enteries (eliminating blocks)	103	27.44**	0.75**	1.9	337.67**	0.56**	12101.71**
Checks	4	77.54**	1.84**	0.56	122.26**	5.23**	3157.3**
Accessions	98	26.73**	0.71**	1.88	247.25**	0.35**	10938.17**
Check v/s Accession	1	183.97**	0.12	7.85*	11497.94**	2.74**	209391.5**
Error	16	8.67	0.12	0.96	15.93	0.02	34.33

**Significant at p = 0.01 *Significant at p = 0.05

Table 2 :Mean, genotypic and phenotypic coefficient of variation, heritability and genetic advance as % of mean for different characters in fenugreek germplasm.

S. No.	Characters	Mean	Range (min-max adjusted value)	Genotypic coefficient of variation (GCV%)	Phenotypic coefficient of variation (PCV%)	Heritability in broad sense (%)	Genetic advance as % of mean
1.	Plantheight(cm)	56.53	44.44 - 71.44	7.52	9.15	67.59	12.75
2.	Number of primary branches per plant	4.17	2.64 - 6.24	18.46	20.17	83.76	34.85
3.	Number of secondary branches per plant	7.66	4.08 - 11.68	12.55	17.92	49.01	18.12
4.	Number of pods per plant	49.02	18.88 - 95.88	31.03	32.08	93.56	61.91
5.	Test weight(g)	12.78	11.47 - 14.44	4.47	4.62	93.52	8.92
6.	Yield(g/line)	177.53	29.8 - 514.8	58.82	58.91	99.69	121.15

Table 3 :Phenotypic and genotypic correlation coefficient between different characters in fenugreek germplasm.

S. No.	Characters	Plant height (cm)	Plant height (cm)	Branches per plant	Secondary branches per plant	No. of pods/Plant	Test weight(g)	Yield(g/line)
1.	Plant height (cm)	rg	1	0.180**	-0.217**	0.135*	0.256**	0.117
		rp	1	-0.023	-0.106	0.082	0.156*	0.106
2.	Number of primary branches per plant	rg		1	0.924**	0.504**	0.213**	0.415**
		rp		1	0.719**	0.434**	0.183**	0.361**
3.	Number of secondary branches per plant	rg			1	0.835**	0.910**	0.984**
		rp			1	0.322**	0.250**	0.350**
4.	Number of pods per plant	rg				1	0.469**	0.750**
		rp				1	0.427**	0.716**
5.	Test weight(g)	rg					1	0.530**
		rp					1	0.504**
6.	Yield(g/line)	rg						1
		rp						1

**Significant at p = 0.01 *Significant at p = 0.05

Table 4 : Path coefficient analysis for yield and its contributing characters in fenugreek genotypes.

S. No.	Characters	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Number of pods per plant	Test weight(g)	Yield(g/line)
1.	Plant height (cm)	0.0469	-0.0069	-0.0055	0.0954	0.0238	0.1537
2.	Number of primary branches per plant	-0.0047	0.0685	0.0223	0.2336	0.0259	0.3456
3.	Number of secondary branches per plant	-0.0071	0.0420	0.0364	0.1185	0.0339	0.2237
4.	Number of pods per plant	0.0072	0.0258	0.0069	0.6211	0.0939	0.7549
5.	Test weight(g)	0.0052	0.0083	0.0058	0.2736	0.2132	0.5062

Residual effect = 0.6198

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Received : October 2020; Revised : November 2020;

Accepted : December 2020.