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Estimation of genetic variability, correlation and divergence studies on seed yield and its attributing characters in fenugreek (*Trigonella foenum-graecum* L.)

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Abstract

Ninety nine germplasm of fenugreek (*Trigonella foenum-graecum* L.) along with five checks were evaluated in augmented block design in five blocks at ICAR-NRCSS, Ajmer (Rajasthan) during 2019-20. Analysis of variance revealed significant variability for most of the traits. High heritability was obtained for plant height (97.02), primary branches plant⁻¹ (77.94), secondary branches plant⁻¹ (80.54), number of pods plant⁻¹ (99.55), number of seed pod⁻¹ (91.12), test weight (90.55), seed yield (99.98). Number of pods per plant and seed yield had high heritability with high genetic advance. Seed yield showed significant positive association with primary branches per plant, secondary branches per plant, no. of pods plant⁻¹, and no. of seed pod⁻¹ and 1000 seed weight. The genetic diversity among tested genotypes was assessed. The genetic divergence grouped into five clusters. The maximum inter cluster distance was observed between I & V (388.24) followed by cluster III & V (387.11).

Keywords: Fenugreek, variability, heritability, correlation, divergence

Introduction

Fenugreek (*Trigonella foenum-graecum*) is a conventional and promising medicinal herb which belongs to the Leguminosae family. *Trigonella* is a large genus in the tribe Trifoliatae of the family Fabaceae and subfamily Papilionaceae. It is a self-pollinated crop with the chromosomal number 2n=16. Fenugreek is used whole seed or powdered form, and it is frequently roasted to eliminate bitterness and enhance flavour and aroma. Seeds have a bitter flavour due to the presence of the alkaloid "Trigonelline." The existence of an asteroid called "Diosgenin," which is utilised in the manufacturing of sex hormones and contraception pills, has strengthened the importance of fenugreek, has studied the variability, character associations for different agronomic observations in fenugreek. Correlation analysis can be used to determine the strength of

association between such variables. In agricultural plants, the ultimate manifestation of yield is usually dependent on the activity and interplay of a number of essential features. In order to determine the key features, genotypic correlation coefficients provide a measure of genetic association between traits in order to identify the important traits (Pandey and Gritton, 1975). Phenotypic correlations may not always signify genetic significance and could be attributable to population structure. Conversely, phenotypic correlations are useful for describing populations, but they should be used with caution when assuming correlation, specifically beyond the test population. Crop productivity is primarily determined by yield and its component components. A substantial level of genetic variability is a prerequisite for a successful breeding programme. Similarly, understanding the degree and pattern of existing diversity in a population is critical for future crop improvement. As a result, the current study was carried out to quantify the presence of genetic divergence and morphological diversity in fenugreek for growth and yield related parameters, and to use selected lines in further improvement of the fenugreek crop.

Materials and methods: The present study was carried out during 2019-20 at the experimental fields at National Research Centre on Seed Spices Ajmer. Ninety nine germplasm of fenugreek (*Trigonella foenum-graecum* L.) collected from ICAR-NRCSS, Ajmer along with five checks namely Ajmer Fenugreek-3 (AFg-3), Ajmer Fenugreek-4 (AFg-4), Hisar Sonali, RMT-361 and Ajmer Fenugreek-5 (AFg-5) were evaluated in Augmented Block design in five blocks. A plot size of 3 x 2 meter accommodating four lines spaced 30 cm apart with row spacing of 20 cm maintained by thinning. Observations recorded for plant height, primary branches plant⁻¹, secondary branches plant⁻¹, number of pods plant⁻¹, number of seed pod⁻¹, 1000 seed weight and seed yield. Analysis of variance was carried out as per the procedure suggested by Federer. The phenotypic and genotypic coefficient of variation was worked out as per Burton and heritability (broad sense) and genetic advance were determined following the methodology of "

.Through agglomerative hierarchical clustering cluster analysis using R software, the genetic divergence among 99 genotypes, including checks placed in augmented design, was investigated. The detailed description among different cluster are given under Agglomerative Hierarchical Clustering of standardized data was used to identify the more significant level of discrimination between the cluster for each of variable.

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. Estimates of phenotypic variance, genotypic variance, phenotypic coefficient of variation and genotypic coefficient of variation are given in table 2. The genotypic coefficient of variation ranged from 6.53 to 58.86 where as phenotypic coefficient of variation ranged from 6.86 to 34.89. In this study, GCV values were lower than PCV values, indicating that environment plays an important role in expressing these characters. High heritability was obtained for plant height (97.02), primary branches per plant (77.94), secondary branches per plant (80.54), no. of pods plant⁻¹ (99.55), no. of seed pod⁻¹ (91.12), test weight (90.55), Seed Yield (99.98) which indicates that selection based on phenotypic performance would be reliable. The number of pods per plant and seed yield had high heritability and genetic advance. This indicates that heritability is most likely due to additive gene effects and selection may be effective. Various researchers have reported similar findings for detecting high heritability estimates for plant height and pod length in cluster bean (Dabas *et al.*, 1982; Gipson 1990; Kumar and Ram 2015).

Seed yield showed significant positive correlation with primary branches per plant (0.4478), secondary branches per plant (0.3779), number of pods plant⁻¹ (0.8122), number of seed pod⁻¹ (0.5165), 1000 seed weight (0.7176) (table 3). Therefore, these characteristics should be considered while making selection for yield improvement in fenugreek. These results are in accordance with the findings of for biological yield per plant and harvest index. Ninety-nine genotypes of fenugreek taken for divergence analysis

differed significantly with regard to the characters under study and showed marked divergence when taking all seven characters together. Average inter and intra-cluster distances were calculated and exhibited in table 5. The highest number of genotypes (46) was found in Cluster III pursued by cluster I (36), cluster IV (11), and cluster V (1) Intra cluster distance showed divergence among the genotype within a cluster while inter cluster distance showed relative divergence among the cluster. The cluster means for various traits denoted that there were considerable differences between the clusters as shown in table 7. Cluster II exhibited maximum mean value for number of seed pod⁻¹ (19.34). Cluster V exhibited maximum mean value for seed yield (515), maximum mean value for number of pods plant⁻¹ (95.00) and test weight (15.50). Cluster IV exhibited minimum mean value for plant height (53.90). The maximum inter cluster distance was observed between I and V (388.24) followed by cluster III and V (387.11), IV and I (188.79), III and I (7.8) (Table 6). Similar findings also reported by;

Conclusion: Number of pods plant⁻¹ and seed yield had high heritability with high genetic advance, indicates that heritability is most likely due to additive

gene effects and selection may be effective. Seed yield showed significant positive correlation with primary branches plant⁻¹, secondary branches plant⁻¹, number of pods plant⁻¹, number of seed pod⁻¹, 1000 seed weight, therefore, these characters should be considered while making selection for yield improvement in fenugreek. It can be recommended to choose parents from clusters I and V or clusters III and V for the crossing programme.

Conflicts of Interest : The authors declare no conflicts of interest.

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Table 1. Analysis of variance for different characters in fenugreek genotypes

Source of variation	Df	Plant height	Primary branches plant ⁻¹	Secondary branches plant ⁻¹	Number of pods Plant ⁻¹	Number of seed Pod ⁻¹	1000 seed weight(g)	Seed Yield (five plants) g
Block	4	85.036	0.342	2.555	625.315 **	4.009	1.278	11475.873 **
Treatment	103	26.462 **	0.753 **	2.341	351.786 **	2.023 **	0.898 **	12118.553 **
Checks	4	6.540	0.340	3.560 *	8.26	0.16	0.025	38.400
Test entry	98	26.733 **	0.707 **	2.351 *	304.394 **	2.07 **	0.783 **	10938.165 **
Check vs test entry	1	79.613 **	6.869 **	3.467	6370.287 **	4.399 **	15.588 **	176117.201 **
Error	16	3.065	0.115	0.960	9.78	0.160	0.027	34.325

Table 2. Mean, phenotypic variance, genotypic variance, phenotypic coefficient of variation, genotypic coefficient of variation, heritability in broad sense (%), and genetic advance.

Character	Range		Mean	Phenotypic variance	Genotypic variance	Phenotypic coefficient of variation	Genotypic coefficient of variation	Heritability in broad sense (%)	Genetic advance
	Mini.	Maxi.							
Plant height	45	70	56.54	26.307	25.5241	9.07	8.94	97.02	10.25
Primary branches per plant	3	6	4.19	0.688	0.536	19.77	17.45	77.94	1.33
Secondary branches per plant	4	11	7.53	2.252	1.814	19.92	17.88	80.54	2.49
Number of pods plants ⁻¹	24	95	50.47	310.073	308.675	34.89	34.81	99.55	36.11
Number of seed pod ⁻¹	14	22	16.94	2.015	1.836	8.38	8.00	91.12	2.66
1000 seed weight (g)	11.5	15.5	12.92	0.786	0.712	6.86	6.53	90.55	1.65
Seed yield (five plant) g	30	515	177.5	10916.48	10913.86	58.86	58.86	99.98	215.18

Table 3. Correlation matrix between different seed yield and other yield contributing characters.

Variables	Plant height	Primary branches plant ⁻¹	Secondary branches plant ⁻¹	Number of pods Plant ⁻¹	Number of seeds Pod ⁻¹	1000 seed weight (g)	Seed Yield (five plants) g
Plant height	1						
Primary branches plant ⁻¹	-0.0766	1					
Secondary branches plant ⁻¹	-0.0325	0.6497**	1				
No. of pods plant ⁻¹	0.0146	0.4716**	0.4121**	1			
No. of seed pod ⁻¹	-0.1552	0.3395**	0.1830	0.5070**	1		
1000 seed weight (g)	0.0875	0.3548**	0.3100	0.6042**	0.4920**	1	
Seed Yield (five plants) (g)	0.0958	0.4478**	0.3779	0.8122**	0.5165**	0.7176**	1

Table 4. Variance decomposition for the optimal classification

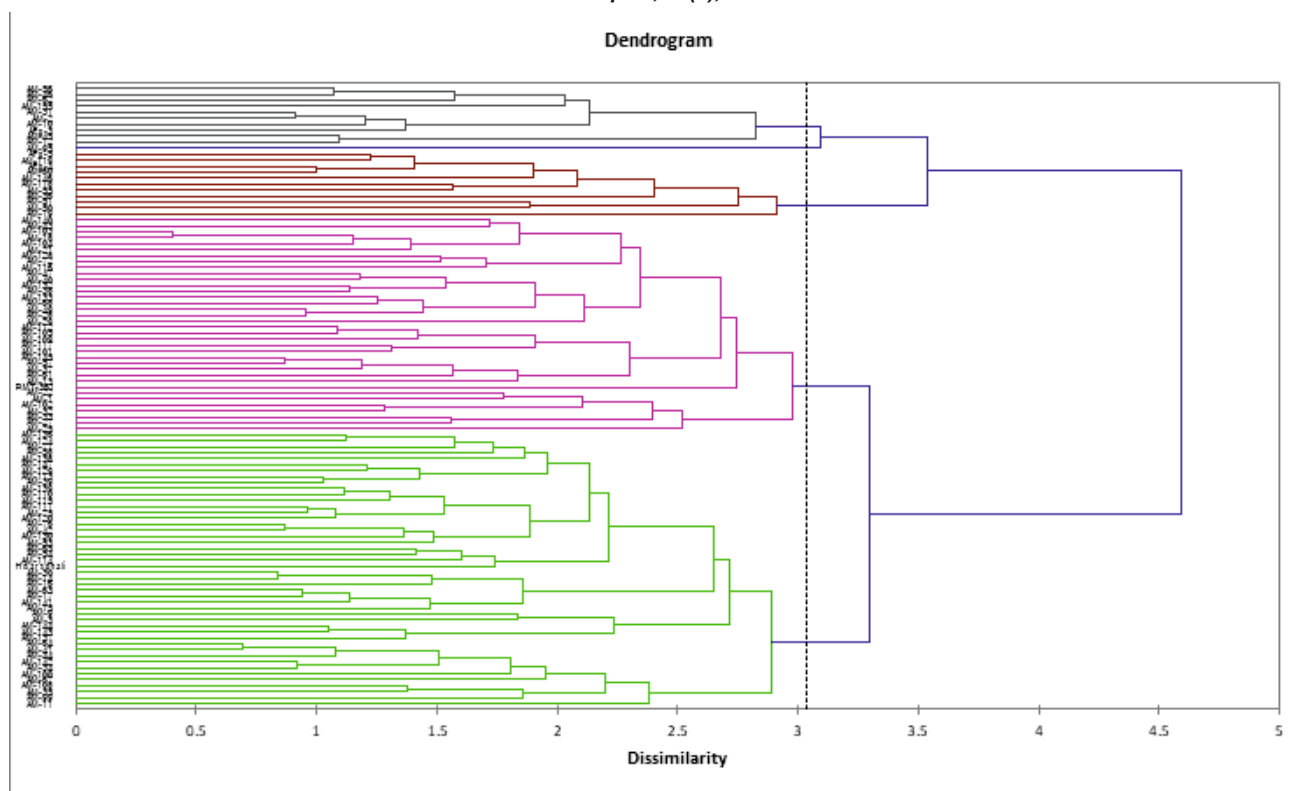
	Absolute	Percent
Within - class	2528.1512	22.46%
Between - classes	8730.4542	77.54%
Total	11258.6054	100.00%

Table 5. Clustering pattern of ninety nine genotypes of fenugreek

Cluster number	Number of genotypes	Genotypes
I	36	AM 1,AM 13,AM 18, AM 21, AM 22, AM 25, AM 27, AM 28, AM 29, AM 32, AM 33, AM-37, AM-38, AM-40, AM-43, AM-47, AM-49, AM-57,AM-61, AM-68, AM-72, AM-101, AM-102, AM-103, AM-104, AM-105, AM-109, AM-112, AM-116,AM-117, AM-128, AM-132, AM-133, AM-140, AM-145, RMT-361
II	10	AM-2, AM-10, AM-12, AM-31, AM-45, AM-46, AM-56, AM-62, AM-155, AFg -3
III	46	AM-3, AM -9,AM-11, AM -14, AM -15, AM -16, AM -17, AM -30, AM-34, AM -35, AM 39, AM-41, AM -42, AM-44, AM -53, AM -54, AM -58, AM -63,AM-64, AM-65, AM-67, AM 71, AM-75, AM-76, AM-99, AM-100, AM-108, AM-110, AM-111, AM-113, AM-114, AM-115, AM-120, AM-124, AM-129, AM-130, AM-136, AM-137, AM-138, AM-139, AM-141, AM 142, AM-143, AM-144, AM-147,Hisar sonali
IV	11	AM-19, AM -36, AM -50, AM -51, AM -55, AM -60, AM -118, AM -119, AM -146, AFg -4,AFg-5
V	1	AM-95

Table 6. Inter and Intra cluster D^2 value (by Mahalanobis method) for five cluster in fenugreek genotypes

	I	II	III	IV	V
I	0	260.34	7.82	188.79	387.91
II	260.34	0	257.43	73.21	127.74
III	7.82	257.43	0	186.33	385.10
IV	188.79	73.21	186.33	0	199.64
V	387.91	127.74	385.10	199.64	0



Dendrogram of fenugreek genotypes

Table 7. Intra cluster group mean for seven characters in fenugreek genotypes

Class	Plant height	Primary branches plant ⁻¹	Secondary branches plant ⁻¹	Number of pods Plant ⁻¹	Number of seed Pod ⁻¹	1000 seed weight (g)	Seed yield (five plants) g
I	56.7389	3.3722	5.9167	41.0667	16.7222	12.6211	130.61
II	58.1600	5.2200	8.8600	79.9000	19.3400	14.8660	372.82
III	56.5348	4.5000	8.3435	46.5087	16.4348	12.5587	130.83
IV	53.9091	4.5091	7.9091	66.9636	17.4545	13.3945	317.83
V	62.0000	6.0000	11.0000	95.0000	18.0000	15.5000	515.00

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