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Studies on Genetic Variability, Heritability and Genetic Advance for Morphological Traits in Fenugreek (*Trigonella foenum-graecum* L.) for Arid Climate of Rajasthan

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ABSTRACT

Background: Fenugreek (*Trigonella foenum-graecum* L.) is one of the oldest spices crop of the world. It is the third largest seed spice in India after coriander and cumin. It is a *Rabi* season crop, mostly grown in sandy loam soil. The present study was carried out to get better information regarding GCV, PCV, heritability and genetic advance, pre requisite for formulating an effective breeding programme.

Methods: Fifty-two accessions of fenugreek (*Trigonella foenum-graecum* L.) including four checks *viz.,* (AFg-1, AFg-2, AFg-3 and RMt-1) were evaluated in augmented complete block design (ACBD) in *Rabi* 2021-2022 for nine quantitative traits. Analysis of variance for agro-morphological characters showed in significant differences among the studied accessions indicating existence of wide variability. Adjusted mean values were used for estimation of genetic variability parameters.

Result: The high to medium magnitude of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), high heritability coupled with high genetic advance were expressed by traits *viz.,* number of branches per plant, number of pods per plant seed yield per plant and test weight. On the basis of per se performance of fifty-six accessions including checks it is concluded that selection of number of branches per plant and number of pods per plant could be effective in EC510598 and AFg-1. Likewise effective selection could be made in IC0624520 for early maturing. For pod length, accession EC510631 and for seed yield per plant EC510737, EC510536 and AFg-1 could be efficiently utilized for improvement of respective trait in fenugreek.

Key words: Fenugreek, Genetic advance, Genotypic coefficient of variation heritability, Phenotypic coefficient of variation, *Trigonella foenum-graecum* L., Variability parameters.

INTRODUCTION

Fenugreek (*Trigonella foenum-graecum* L.) is one of the important and commercial spice crop mainly cultivated for seeds and leaves and used in medicines. It is third major seed spice after cumin and coriander in India. It is popularly known as "*Methi*" and well known for its aromatic, condiment, carminative, medicinal and pharmacological properties. It is also used for nutraceuticals, it is diploid (2n=16) autogamous species belongs to family Fabaceae and sub-family Papilionaceae. Its leaves are consumed as green leafy vegetables and seeds are used for condiments and flavouring food preparations in India. Fenugreek is originated in Near East Mediterranean regions (Duke *et al*., 1981) and widely cultivated in India, Egypt, Pakistan, France, North Africa, East Africa, England, Ethiopia, Morocco and China (Mc *et al*., 2009; Kakani *et al*., 2011 and Helambe and Dande, 2012). In India, it is cultivated in Rajasthan, Gujarat, Madhya Pradesh, Uttar Pradesh, Haryana, Himachal Pradesh, Tamil Nadu and Andhra Pradesh (Maloo *et al*. 2020). Rajasthan, Gujarat and Madhya Pradesh are major fenugreek producing states contributing more than 85% production of our country.

The accessions collected are significant source of gene complex reservoir for economically important traits as they consist of untapped genetic diversity pre-requisite in formulating efficient scheme for crop breeding. The present production potential and development of superior varieties in fenugreek is impended by paucity of information about genetic variability and genetic relationship among species (Marzaugui *et al*. 2009). The maximization of seed yield, development of cultivars for early maturity and resistance to biotic and abiotic stresses are the major objectives of fenugreek breeding. Keeping in mind, knowledge of extent and pattern of the existing variability in accessions of fenugreek is indisputably essential to understand the crop biometrics and related research for further genetic improvement of fenugreek.

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MATERIALS AND METHODS

The present experiment was carried out to assess the genetic variability and character association in 52

accessions of fenugreek involving four checks *viz*., AFg-1, AFg-2, AFg-3 and RMt-1. The germplasm under study were sown in augmented randomized complete block design (Augmented RCBD) during *Rabi* 2021-22 at research field of ICAR-NBPGR, Regional Station, Jodhpur, India, which is situated at about 28°35′N, longitude of 70°18′E and an altitude of 226 meter above mean sea level. All recommended agronomic practices were adopted to raising a healthy crop. The data on days to 50% flowering and days to 80% maturity were recorded on plot basis, while five randomly selected plants from each of the entry were selected for recording the observations on plant height (cm), number of branches per plant, number of pods per plant, number of seed per pod, pod length (cm), 1000 seed weight (g) and seed yield per plant (g). Analysis of variance was calculated by method suggested by Panse and Sukhatme (1985). The estimate of genotypic variance and phenotypic variance were worked out using method suggested by Johnson *et al*. (1955). Phenotypic and genotypic coefficients of variation were calculated based on the method advocated by Burton (1952). Heritability percentage in broad sense was estimated as per the method described by Lush (1940).

RESULTS AND DISCUSSION

The analysis of variance indicating mean sum of squares showed highly significant differences among the genotypes for all the traits under study (Table 1). Adjusted block mean squares for all the traits are highly significant except days to 50% flowering. Adjusted treatment mean squares are highly significant for all the nine traits studied. It indicates that accession lines are genetically diverse from each other and there is huge scope for selection of characters from this germplasm collection for fenugreek improvement programs.

Per se performance

On the basis of adjusted mean values wide range of mean values were observed for all the studied traits. Days to 50% flowering ranged from 38.44 days to 62.44 days with mean value 53.5 days. The accessions IC0624520 has been identified with 38.44 days to 50% flowering and 92.81 days for maturity while EC510680 was late maturing accession. Plant height ranged from 29.58 cm to 64.23 cm with mean value of 47.26 cm. Accession EC510724 has been recorded highest value for plant height (67.66 cm). EC510559 exhibited highest number of branches per plant (9.96). Range of number of branches per plant varied from 3.64 to 9.96. Accession EC510598 exhibited highest value for number of pods per plant (100.38) and it ranged from 18.37 to 100.38. Range for number of seeds per pod was 6.58 to 15.97, for pod length 6.42 cm to 14.28 cm, for seed yield per plant 3.01 gm to 13.77 gm and for test weight 3.78 gm to 11.09 gm. Superior accessions were identified for various traits are given in Table 3.

Variability parameters

The difference between the values of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) is very less suggesting their relative resistance to environmental influences and consistency in its behaviour at both genotypic and phenotypic levels (Table 2). Leaf colour was recorded for all the accessions and wide range of leaf colour variation was expressed in fenugreek. Green-copper

Table 1: Mean square of nine traits in fenugreek germplasm.

Sources	DF	Days to 50% flowering	Days to 80% maturity	Plant height (cm)	No. of branches per plant	No. of pods per plant	No. of seeds/ pod	Pod length (cm)	Seed yield per plant (gm)	Test weight (gm)
Block (Ignoring treatment)	3	2.88	171.39**	156.73**	1.39*	196.17**	14.73**	12.67**	3.69**	7.28**
Treatment (Eliminating blocks)	55	22.99*	33.34**	100.81**	1.61**	307.66**	3.84**	5.56**	2.83**	2.8**
Checks	3	15.9	33.73**	14.07	2.07**	77.58**	1.37^{ns}	0.06	1.85*	3.14**
Checks + Var vs. Var	52	23.4*	33.32**	105.82**	1.59**	320.93**	3.98 **	5.88**	2.88**	2.78**
Error	9	5.9	1.17	4.43	0.22	7.86	0.66	1.05	0.32	0.12

^{ns}P>0.05; *P≤0.05; **P≤0.01.

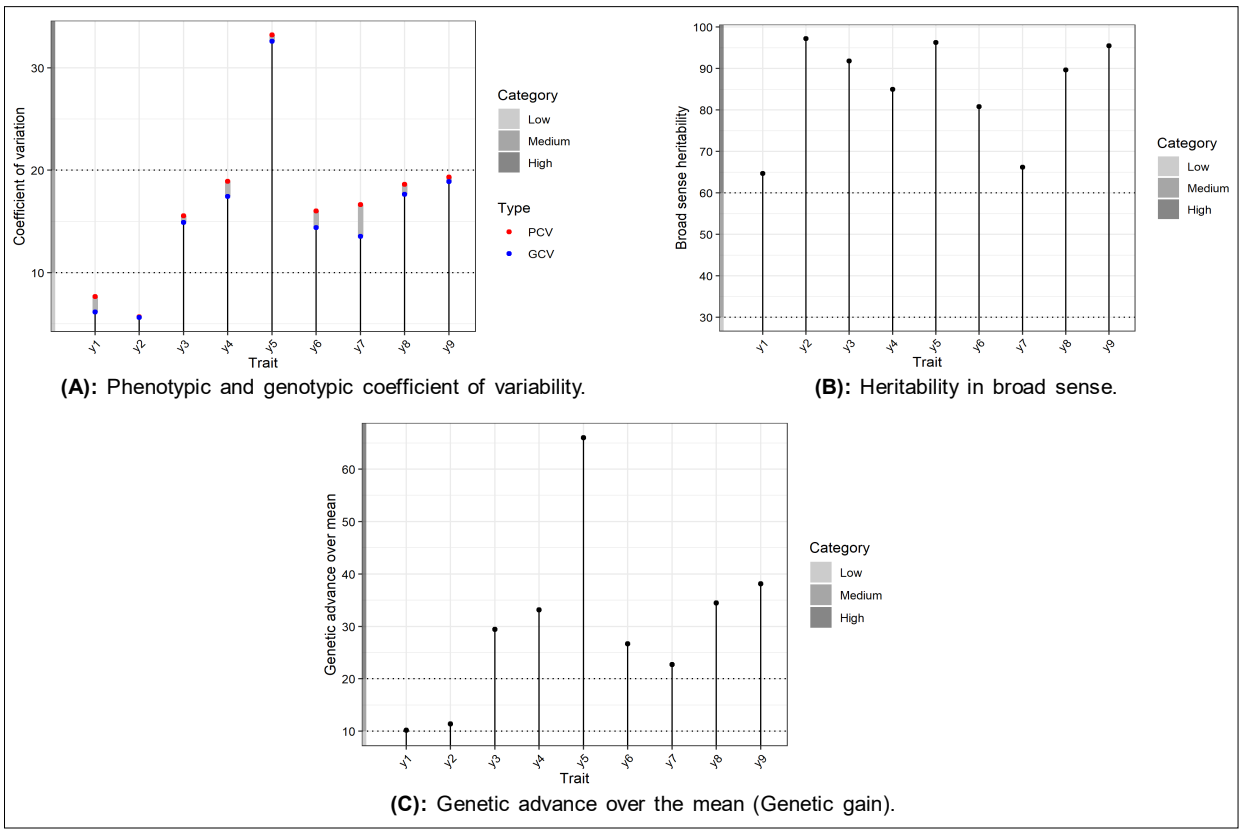
Table 2: Variability parameters of various characters in germplasm accessions of fenugreek.

Character	Range		Mean	GCV %	PCV %	Heritability (in broad sense) %	Genetic advance	Genetic gain (Genetic advance as % of mean)
	Min.	Max.						
Days to 50% flowering	38.44	62.44	53.5	6.14	7.64	64.68	5.45	10.19
Days to 80% maturity	92.81	129.06	114.29	5.6	5.68	97.21	13.02	11.39
Plant height (cm)	29.58	64.23	47.26	14.91	15.56	91.81	13.92	29.46
No. of branches per plant	3.64	9.96	6.43	17.44	18.91	84.98	2.13	33.16
No. of pods per plant	18.37	100.38	43.6	32.6	33.23	96.25	28.77	65.99
No. of seeds/pod	6.58	15.97	11.59	14.4	16.01	80.84	3.1	26.71
Pod length (cm)	6.42	14.28	10.62	13.55	16.65	66.24	2.42	22.75
Seed yield per plant (gm)	3.01	13.77	9.45	17.65	18.63	89.7	3.26	34.48
Test weight (gm)	3.78	11.09	8.26	18.9	19.35	95.47	3.15	38.10

leaf colour was observed in one accession EC510685. The magnitude of PCV was higher than GCV indicating existence of favourable influence of environment in expression of all the traits. This is accordance with finding of Naik *et al.,* (2012), Verma and Ali (2012), Mamtha *et al.,* (2017) and Panwar *et al.,* (2018). High estimates of GCV and PCV were observed for number of pods per plant. Medium value of GCV and PCV were expressed by plant height, number of branches per plant, number of seeds per pod, pod length, seed yield per plant and test weight. Lower estimates of GCV and PCV were expressed by days to 50% flowering and days to 80% maturity. These results are in agreement with the earlier findings for number of pods per plant by Meena *et al.,* (2021). The magnitude of heritability in broad sense was high for all the nine traits. Highest value of heritability in broad sense was observed for days to 80% maturity followed by number of pods per plant and test weight. Highest genetic advance was exhibited for number of pods per plant (28.77). Highest genetic gain was expressed by number of pods per plant (65.99) followed by test weight (38.10), seed yield per plant (34.48) and number of branches per plant (33.16). According to Johnson *et al.,* (1955), high heritability coupled with high genetic gain is more useful for prediction of best genotypes. High heritability

Table 3: Superior accessions identified in fenugreek.

Traits	Accessions performed superior
Days to 50% flowering	IC0624520 (38.44 days), EC510664 (44 days), EC510678 (45 days)
Days to maturity	IC0624520 (92.81 days)
Plant height (cm)	EC510576 (65.50 cm), EC510724 (67.66 cm), EC510664 (62.90 cm), EC510712 (64.30 cm), EC510717 (63.60 cm)
Number of branches per plant	EC510659 (9.96), EC510662 (7.81), EC510598 (7.94), EC510712 (7.68)
Number of pods per plant	EC510598 (100.38), EC510664 (88.13), EC510573 (94.12)
Pod length (cm)	EC5105631 (15.29 cm), EC5105681 (14.20 cm), EC5105617 (14.19 cm)
Seed yield per plant (gm)	EC510599 (12.42 gm), EC510736 (13.17 gm), EC510737 (13.77 gm), EC510741 (12.66 gm),
Leaf colour	EC510685 (Green-copper leaf colour)



(A): Phenotypic and genotypic coefficient of variability.

(B): Heritability in broad sense.

(C): Genetic advance over the mean (Genetic gain).

Fig 1: Genetic variability analysis plots.

y1: Days to 50% flowering, y2: Days to 80% maturity, y3: Plant height (cm), y4: No. of branches per plant, y5: No. of pods per plant, y6: No. of seeds/pod, y7: Pod length (cm), y8: Seed yield per plant (gm), y9: Test weight (gm).

along with high genetic gain was observed for number of branches per plant, number of pods per plant, seed yield per plant and test weight showed that these traits are governed by additive gene action to a large extent and are more amenable for phenotypic selection. High heritability coupled with moderate genetic gain was obtained for plant height, number of seeds per pod and pod length indicating these characters can also be improved by phenotypic selection. Sharma and Shastri (2008), Jain *et al.,* (2013), Verma *et al.,* (2016) and Kumar *et al.,* (2018) also reported similar results in their studies. Genetic variability analysis plots are illustrated in Fig 1a, b, c.

CONCLUSION

Within the range of accessions used in the present study, there is existence of substantial amount of genetic variability and heritability in the traits studied to warrant selection in the fenugreek accessions for breeding varieties for high seed yield in fenugreek. The high magnitude of genotypic coefficient of variation and phenotypic coefficient of variation, high heritability coupled with high genetic gain of number of branches per plant, number of pods per plant, test weight and seed yield per plant, suggest these traits could be listed in selection criteria for good parental lines in fenugreek breeding programmes. On the basis of adjusted mean values, superior accessions have been identified for early days to 50% flowering and early days to maturity is IC0624520. EC510712 found promising for two traits *viz.,* plant height (64.30 cm) and number of branches per plant (7.68). EC510598 was superior for number of branches per plant (7.94) and number of pods per plant (100.38). These superior accessions mentioned in Table 3 for various traits could be selected for yield improvement programs in fenugreek. It is concluded that genotypes IC0624517, AFg-1, EC510712, EC510598 and EC510737 could be used as divergent parental lines for greater heterotic effects and desirable transgressive segregants for seed yield and its component traits.

Conflict of interest: None.

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