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## Appraisal studies on genetic variability, heritability and genetic advance in fenugreek (*Trigonella foenum-graecum* L.)

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### Abstract

The present investigation entitled 'Studies on combining ability, heterosis and gene action in fenugreek (*Trigonella foenum-graecum* L.) for yield and quality attributing traits' at Main Experiment Station (M.E.S.) of the Department of Vegetable Science A.N.D. University of Agriculture and Technology, Kumarganj, Ayodhya (U.P.) during Rabi season of 2019-20 (Y<sub>1</sub>) and 2020-21(Y<sub>2</sub>). The experiment was conducted in a Randomized Complete Block Design (R.B.D.) with three replications on 54 genotypes (40 F<sub>1</sub> + 10 line + 4 testers). Observations were recorded for 11 characters viz., days to 50% flowering, plant height (cm), number of branches per plant, days to maturity, pods length (cm), biological yield per plant (g), harvest-index (%), number of pods per plant, number of seeds per pods, 1000-seed weight (g) and seed yield per plant (g). The findings of the present investigation revealed that genetic variability, high heritability (h<sup>2</sup>bs & ns) along with moderate genetic advance as per cent of mean were observed for most important economic traits and scope for crop improvement during the process of selection.

**Keywords:** Fenugreek (*Trigonella foenum-graecum* L.), PCV, GCV, heritability, genetic advance as per cent of mean

### Introduction

Fenugreek (*Trigonella foenum-graecum*) belongs to family Fabaceae, 2n=16. It is seed spice as well as leafy vegetable. It has been originated in Egypt. Fenugreek can be grown in the tropical and in temperate regions. It is grown from sea level up to an altitude of 2000 m. There are two species of the genus *Trigonella*, which are of economic importance, viz., *Trigonella foenum-graecum* or the commonly called "methi" and *Trigonella corniculata* or the "kasthuri methi." Fenugreek is an annual herb, 30 to 90 cm tall and has light green leaves which are pinnately trifoliate. The flowers are papilionaceous and white or yellow in colour and produces stander, beaked pods of approximately 10-15 cm long and each pod contains 10-20 small hard yellowish brown seed possessing smooth and oblong, about 3 mm long, each grooved across one corner, giving them a hooked appearance. India is also known as land of spices. India is one of the dominant producers and exporters of fenugreek. The value-added products of fenugreek such as its seeds, powder and oleoresins are exported to Europe, North America, South Africa and other Asian countries (Anonymous, 2019-20) [1]. In India, it occupies an area of about 127 thousand hectare with 184 mt productions with share of 2.4 per cent. Fenugreek is mainly grown in the states of Rajasthan, Gujarat, Punjab, Haryana, U.P., M.P. Maharashtra and Tamil Nadu. Rajasthan alone contributes nearly 60 per cent of total area and 80 per cent of total production of the crop in the country. Phenotypic variability changes under different environmental condition while genetic variability remains unchanged and more useful to a plant breeder for exploration in selection and hybridization. The genetic advance under selection is achieved when the characters under selection are highly heritable and stable and the estimate of broad sense heritability provides the index of transmissibility of characters and serves as a useful guide to the breeders for practicing selection.

### Material and Methods

The experiment was conducted on fenugreek (*Trigonella foenum-graecum* L.) at Main Experiment Station (Vegetable Research Farm), ANDUA&T (Kumarganj), Ayodhya (U.P.) India, during season of 2019-20 (Y<sub>1</sub>) and 2020-21(Y<sub>2</sub>). The experiment was conducted in a Randomized Complete Block Design (R.B.D.) with three replications and 54 genotypes (40 F<sub>1</sub> + 10 line + 4 testers). The crop was planted in row length spaced 30 cm. apart where, 10 cm.

plant to plant spacing was maintained. The experimental plant material for present investigation was comprised of 40 hybrid developed by crossing 10 line (NDM-3, NDM-4, NDM-8, NDM-10, NDM-5, NDM-63, NDM-14, NDM-23, and NDM-19 with 4 testers PEB, NDM-2, Hisar Sonali (check) and NDM-1. The observations were recorded on five plants randomly selected from each genotype in each replication on eleven characters, viz., days to 50% flowering, plant height (cm), number of branches per plant, days to maturity, pods length (cm), biological yield per plant (g), harvest-index (%), number of pods per plant, number of seeds per pods, 1000-seed weight (g) and seed yield per plant (g). The data were recorded from 40 F<sub>1</sub>'s and 10 parental lines with 4 testers on eleven characters were subjected to estimate nature and magnitude of heritability in narrow sense (Kempthorne 1957) and genetic advance as per cent of mean (Johnson *et al.* 1955).

### Result and Discussion

The coefficient of variation GCV recorded for number of branches per plant, days to 50% flowering, plant height, number of pods per plant, yield per plant, number of seed per pods, harvest index, days to maturity, test weight, pods length and biological yield recorded low GCV (<10%) in Y<sub>1</sub> values were observed which indicated that traits might be influenced by environment. number of branches per plant, days to 50% flowering, plant height, number of pods per plant, yield per plant, number of seed per pods, harvest index, days to maturity, test weight, pods length and biological yield recorded low GCV (<10%) in Y<sub>2</sub> values were observed which indicated that traits might be influenced by environment. and number of branches per plant, days to 50% flowering, plant height, number of pod per plant, yield per plant, number of seed per pods, harvest index, days to maturity, test weight, pods length and biological yield recorded low GCV (<10%) in pooled values were observed which indicated that traits might be influenced by environment. Similar results had also been reported by Yadav *et al.* (2015) [21] and Kumar *et al.* (2020) [8].

The estimates PCV were found to be moderate (10-25%) for number of branches per plant which indicated that on these traits heritable variability would not be influenced by environment. Whereas days to 50% flowering, plant height, days to maturity, pods length cm, biological yield, harvest index, number of pods per plant, number of seed pods, test weight and yield per plant recorded low PCV (<10%) values were observed which indicated that traits might be influenced by environment. in Y<sub>2</sub> Number of branches per plant, days to 50% flowering, plant height, days to maturity, pods length cm, biological yield, harvest index, number of pods per plant, number of seed pods, test weight and yield per plant recorded low PCV (<10%) values were observed which indicated that traits might be influenced by environment. In pooled Number of branches per plant moderate PCV (10-25%) which indicated that on these traits heritable variability would not be influenced by environment. whereas days to 50% flowering, plant height, days to maturity, pods length cm, biological yield, harvest index, number of pods per plant, number of seed pods, test weight and yield per plant recorded low PCV (<10%) values were observed which indicated that traits might be influenced by environment. Similar results had also been reported by Kole and Saha (2013) [5]

The heritability, which is an index of transmissibility of a character from parent to off-springs, needs to be studied in order to determine the extent to which the observed variation is inherited. But heritability alone does not give true picture of genetic improvement, likely to be made during selection in subsequent generation. It is the genetic gain which predicts the speed of genetic improvement to be effected by selecting a particular portion of the population. The effectiveness of selection for any character depends not only in the amount of variability present but also in the offspring. Heritability, which denotes the proportion of phenotypic variance that is due to genotypic variance and is transmissible from parent to off spring, is in fact an index for selection of a character. by studying the heritability, the value of a character can be assessed for formulating a breeding programme. The genetic advance under selection is achieved when the characters under selection are highly heritable and stable. Therefore, the characters with high heritability value are more important to a plant breeder than those which are less heritable. Higher the heritability of a character more effective will be the selection.

The high estimates of heritability broad -sense were recorded for eleven characters viz., plant height cm followed by days to 50% flowering and days to maturity in Y<sub>1</sub> while, days to 50% flowering followed by days to maturity and plant height in Y<sub>2</sub>, and none high heritability showed in pooled. However, moderate heritability was recorded for eleven characters viz., number of branches per plant in Y<sub>1</sub> and number of branches per plant in Y<sub>2</sub>. while, remaining characters showed low estimate of heritability in broad-sense (h<sup>2</sup><sub>bs</sub>). Similar results had also been reported by earlier workers Singh (2000) [17], Gangopadhyay *et al.* (2009) [4], Maurya *et al.* (2013) [10], Sharma *et al.* (2015) [16] and Kumar *et al.* (2020) [8].

The estimates of heritability in narrow-sense (h<sup>2</sup><sub>ns</sub>) have been classified by Kempthorne and Curnow (1961) into three categories viz., high (> 30%), medium (10-30%) and low (<10%). In the year Y<sub>1</sub>, high estimate of heritability in narrow-sense was recorded for number of pods per plant followed by pods length cm and number of branches per plant. none high heritability found in Y<sub>2</sub>. In case of pooled, high estimate of heritability in narrow-sense was recorded for biological yield g followed by pods length cm, number of pods per plant, number of seed per pods, number of branches per plant and test weight, suggested that selection would be highly effective and efficient. similar finding for high estimate of narrow sense heritability for different fenugreek traits have been also reported by Datta *et al.* (2005) [3], Kole and Saha (2013) [5], Sarada *et al.* (2008) [15], Yadav *et al.* (2013), Singh (2014) [18] and Patahk *et al.* (2014) [12]. The moderate estimate of heritability in narrow sense was observed for number of branches per plant followed by plant height cm days to 50% flowering, days to maturity, biological yield, test weight and number of seed per pod. moderate estimate of heritability in narrow-sense was recorded for biological yield followed by pods length, number of seed per pods, number of pods per plant, test weight, days to maturity, days to 50% flowering and plant height in Y<sub>2</sub> and moderate estimate of heritability in narrow sense was observed for plant height followed by days to 50% flowering and days to maturity in pooled. similar finding for moderate estimate of narrow sense heritability for different fenugreek traits have been also reported by previous workers Prajapati, *et al.* (2010) [13], Yadav *et al.* (2015) [21] and Kumar *et al.* (2018) [7].

**Table 1:** Heritability (bs & ns) genetic advance, genetic advance in per cent of mean and coefficient of variation (GCV & PCV) in Fenugreek over two seasons (Y<sub>1</sub> 2019-20, Y<sub>2</sub> 2020-21) and pooled.

Characters	Seasons	Range		Grand mean	PCV (%)	GCV (%)	Heritability in broad sense (%)	Heritability in narrow sense (%)	Genetic advance	Genetic advance in per cent of mean
		Lowest	Highest							
Days to 50% flowering	Y <sub>1</sub>	50.67	70.33	63.55	8.81	8.15	85.54	16.70	9.87	15.53
	Y <sub>2</sub>	52.67	71.33	65.37	8.04	7.48	86.58	14.51	9.38	14.34
	Pooled	57.50	69.67	64.49	8.42	4.02	22.80	16.23	2.55	3.95
Plant height (cm)	Y <sub>1</sub>	56.05	71.52	64.71	5.78	5.39	86.84	25.24	6.69	10.34
	Y <sub>2</sub>	57.08	71.62	65.80	5.61	4.99	79.09	14.24	6.01	9.136
	Pooled	60.19	69.22	65.19	5.80	2.57	19.63	18.18	1.53	2.344
Number of branches per plant	Y <sub>1</sub>	4.20	6.30	5.47	11.94	9.19	59.29	26.48	0.80	14.58
	Y <sub>2</sub>	4.30	6.23	5.43	9.93	8.23	68.74	30.71	0.76	14.06
	Pooled	4.28	6.10	5.46	10.92	6.35	33.78	31.61	0.41	3.22
Days to maturity	Y <sub>1</sub>	128.33	153.33	142.94	4.71	4.13	77.12	14.78	10.69	7.48
	Y <sub>2</sub>	128.00	151.67	142.50	4.46	4.08	83.60	18.59	10.95	7.69
	Pooled	129.00	149.83	142.78	4.63	2.69	33.79	14.91	4.60	3.22
Pod length (cm)	Y <sub>1</sub>	10.40	12.45	11.61	5.54	2.77	25.01	32.85	0.33	2.86
	Y <sub>2</sub>	10.46	12.63	11.60	4.69	2.65	31.93	26.75	0.36	3.09
	Pooled	10.73	12.19	11.59	5.23	2.35	20.12	41.57	0.25	2.17
Biological yield (g)	Y <sub>1</sub>	29.40	33.25	31.81	3.28	1.70	26.67	14.09	0.57	1.80
	Y <sub>2</sub>	29.66	32.86	31.69	2.84	1.44	25.55	28.88	0.47	1.50
	Pooled	30.13	32.85	31.73	3.16	1.17	13.70	66.65	0.28	0.89
Harvest index (%)	Y <sub>1</sub>	14.49	19.93	17.05	9.30	4.46	23.02	3.23	0.75	4.41
	Y <sub>2</sub>	14.95	19.80	17.66	8.76	4.91	31.38	1.77	1.00	5.66
	Pooled	15.68	19.32	17.35	9.03	3.64	16.22	6.25	0.52	3.02
Number of pod per plant	Y <sub>1</sub>	20.93	28.60	24.34	9.81	5.36	29.90	43.29	1.47	6.04
	Y <sub>2</sub>	21.03	28.30	24.03	8.04	5.59	48.33	21.11	1.93	8.01
	Pooled	21.17	26.72	24.17	9.01	4.91	29.70	38.02	1.33	5.51
Number of seed per pod	Y <sub>1</sub>	10.20	12.93	11.40	9.07	4.61	25.87	12.39	0.55	4.83
	Y <sub>2</sub>	10.20	12.67	11.45	7.47	3.85	26.60	22.72	0.47	4.10
	Pooled	10.48	12.63	11.40	8.32	3.15	14.34	36.24	0.28	2.46
Test weight (g)	Y <sub>1</sub>	10.50	13.13	11.75	7.93	3.83	23.29	12.99	0.45	3.80
	Y <sub>2</sub>	10.87	12.85	11.81	5.87	3.09	27.61	19.54	0.39	3.34
	Pooled	10.73	12.73	11.77	7.02	2.63	13.98	30.43	0.24	2.02
Seed yield per plant (g)	Y <sub>1</sub>	4.62	6.12	5.42	8.78	4.88	30.98	4.59	0.30	5.6
	Y <sub>2</sub>	4.79	6.23	5.59	8.37	3.09	37.04	5.36	0.37	6.39
	Pooled	5.02	6.08	5.50	8.65	3.80	19.31	6.75	0.19	3.44

The estimate Moderate of genetic advance as percent of mean was observed for days to 50% flowering followed by number of branches per plant and plant height cm in Y<sub>1</sub>, Moderate estimate of genetic advance in percent of mean was observed for days to 50% flowering followed by number of branches per plant in Y<sub>2</sub> and Moderate estimate of genetic advance in percent of mean was observed for showed none characters in pooled. similar results had also been reported by earlier workers Kole and Mishra (2006) [6] and Prajapati, *et al.* (2010) [13].

### Conclusion

The high estimates of heritability in broad sense were recorded for eleven characters *viz.*, plant height cm followed by days to 50% flowering and days to maturity in Y<sub>1</sub> while, days to 50% flowering followed by days to maturity and plant height in Y<sub>2</sub>. The estimate of high heritability in narrow-sense was recorded for number of pod per plant followed by pods length cm and number of branches per plant in Y<sub>1</sub> and high estimate of heritability in narrow-sense was recorded for biological yield (g) followed by pods length cm, number of pods per plant, number of seed per pods, number of branches per plant and test weight. Estimate of high genetic advance in per cent of mean (>20%) none traits was observed higher.

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