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Assessment of genetic variability, heritability and genetic advance in fenugreek [*Trigonella foenum-graecum* L.]

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Abstract

The current examination was laid out using 30 fenugreek genotypes at Instructional Farm, Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur during Rabi, 2020-2021 in randomized block design with three replication. The analysis of variance (ANOVA) revealed highly significant differences among the genotypes for the characters under study indicating presence of sufficient variability among the genotypes. Phenotypic Coefficient of Variation (PCV) was somewhat higher than the respective Genotypic Coefficient of Variation (GCV) for all the character reflecting that the environment had little effect on the characters. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was highest for number of pods per plant followed by number of branches per plant, seed yield per plant, biological yield per plant and harvest index. The high heritability estimates coupled with high genetic gain for number of branches per plant, protein %, and 100 seed weight.

Keywords: Genetic variability, GCV, PCV, Heritability, Genetic advance

Introduction

Fenugreek (*Trigonella foenum-graecum* L.), an annual plant belongs to the family Fabaceae, is one of the important seed spice crops of India. The crop is gaining importance among seed spices because of its demand in the international market. India is one of the major producers and exporters of fenugreek. Fenugreek is exported to Saudi Arabia, Japan, Malaysia, USA, UK, Singapore and Sri Lanka.

In India, it is mainly cultivated in the states of Rajasthan, Gujarat and Madhya Pradesh and to the limited extent in Andhra Pradesh, Tamil Nadu, Haryana, Maharashtra and Punjab covering an area of 1.33 lakh ha with an annual production and productivity of 2.03 lakh tones and 1526 kg/ha (Anonymous, 2021) [1]. Rajasthan is considered as “fenugreek bowl” of the country. In the state, it is mainly grown in the districts of Sikar, Chittorgarh, Jaipur, Nagaur and Kota covering an area of 45306 ha with a production of 59161 tons and productivity of 1418 kg/ha (Anonymous, 2020) [2].

Fenugreek seed contains carbohydrates (48%), followed by proteins (25.5%), mucilaginous matter (20%), fats (7.9%), and saponins (4.8%) (Rao and Sharma, 1987) [11]. It is a multiuse and commercially important spice crop grown for its seeds, tender shoots and fresh leaves. Fenugreek seeds and herbs are well known for their distinct aroma and slightly bitter taste. Fresh tender pods, leaves and shoots are eaten as curried vegetable. Powder of dried leaves is also used for garnishing and flavoring variety of food. It is one of the principle constituents of curry powder.

In spite of gaining a prime position among the seed spices grown in Rajasthan, its productivity is low due to non-availability of suitable high yielding varieties for various agro-climatic regions. In order to make this crop more productive and resistant to diseases and insect-pests, breeders have to launch an intensive breeding programme for releasing array of variability. In this regard, an attempt was made to study the genetic variability, by determining the magnitude of genetic coefficient of variation, heritability estimates and expected genetic advance of different biometric traits in 30 genotypes of fenugreek.

Materials and Method

Thirty genotypes of fenugreek were evaluated in a Randomized Complete Block Design with

three replications at Instructional Farm, Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur during *Rabi*, 2020-2021. In each replication, the genotypes were sown in a plot of 4.0 m x 0.90 m size accommodating two rows of 4m length spaced 30 cm apart with an intra-row spacing of 10 cm maintained by dibbling. All the recommended package of practices was followed to raise a healthy crop.

Observations were recorded on ten competitive plants from each plot per replication, for plant height, number of branches plant per plant, number of pods per plant, pod length (cm) number of seeds per pod, biological yield per plant (g), seed yield per plant (g), 100-seed weight (g), harvest index (%) and protein content (%) while for days to 50% flowering and days to maturity, the data were recorded on whole plot basis. Analysis of variance was done by the method suggested by Panse and Sukhatme (1985) [8]. The phenotypic and genotypic coefficient of variation were worked out as per Burton (1952) [3] and heritability (broad sense) and genetic advance were determined following the methodology of Johnson *et al.*, (1955) [6].

Results and Discussion

The Analysis of variance revealed significant differences among genotypes for all the traits studied indicating presence of significant variability in the materials (Table 1).

The range of variation was high for number of pods per plant (31.46 -53.13), plant height (71.2-92.53 cm), biological yield per plant (24.29-44.84 g) and harvest index (20.71-30.77%) as observed by Dashora *et al.*, (2011) [4].

The estimates of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the traits studied which is an indicator of additive effect of the environment on the expression of the trait. High magnitude of genotypic coefficient of variation was observed for number of pods per plant (16.11%) followed by number of branches per plant (14.95%), seed yield per plant (12.36%) and biological yield per plant (10.67%). The highest phenotypic coefficient of variation was recorded for number of pods per plant (18.08%), followed by number of branches per plant (15.10%), seed yield per plant (14.66%), harvest index (14.11%) and biological yield per plant (13.12%) (Table 2). High magnitude of PCV and GCV was also

observed for seed yield and biological yield by Rakesh and Korla (2003) [13], Dashora *et al.*, (2011) [4] and for pods per plant by Raje *et al.*, (2003) [12] and Dashora *et al.*, (2011) [4].

Low value of genotypic coefficient of variation was recorded for days to maturity and days to 50% flowering. Similar results were reported by Prakash *et al.*, (2020) [10], Singh *et al.*, (2019) [14], Panwar *et al.*, (2018) [9].

The difference between PCV and GCV was minimum for protein content, 100-seed weight, number of branches plant per plant, days to maturity, number of seeds per pod and pod length suggesting that these traits were least affected by environment. This observation draws support from the high value of heritability recorded for these traits.

Presence of high heritability is an important aspect for choosing the suitable trait for selection. High heritability was observed for most of the characters under study indicating the strong genetic base. High heritability was noted for number of branches per plant (97.97%), followed by protein content (97.49%), 100-seed weight (96.61%), number of seed per pod (83.15%) and days to maturity (82.78%). However, harvest index (47.63%) and days to 50% flowering (56.80%) showed low estimates of heritability.

In corollary to high heritability estimates, high estimates of genetic advance as per cent of mean was observed for number of branches per plant, protein content and 100-seed weight indicated that all these characters are governed by additive gene action and as such are expected to exhibit improvement for such traits by direct selection. These observations are in agreement with the earlier reports of Panwar *et al.*, (2018) [9], Singh *et al.*, (2019) [14], Upadhyay *et al.*, (2020) [16]. In the present study, high estimates of heritability coupled with high to moderate genetic advance as per cent of mean was observed for pod length and number of seeds per pod which may be attributed to the preponderance of additive gene action and possess high selective value and thus, selection pressure could profitably be applied on these characters for their rationale improvement (Panse, 1957). Similar kind of results were also reported by Verma *et al.*, (2016) [17] for seeds per pod. High estimates of heritability coupled with low genetic advance as per cent of mean was expressed by days to maturity inferred that this trait regulated by non-additive gene action and presence of high genotype x environment interaction.

Table 1: Analysis of variance for yield and its contributing traits in fenugreek

Source of variation	df	Mean Sum of Squares											
		Days to 50% Flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	Biological yield per plant (g)	Seed yield per plant (g)	100-seed wt. (g)	Harvest Index (%)	Protein Content (%)
Replication	2	0.41	1.23	48.94	0.03	1.08	0.14	0.77	23.47	1.48	0.00	1.78	0.12
Genotype	29	7.60**	23.99**	107.89**	1.60**	143.39**	2.00**	4.00**	55.72**	4.45**	0.03**	24.22**	9.89**
Error	58	1.54	1.56	16.17	0.01	11.43	0.15	0.25	8.13	0.53	0.00	6.50	0.08

*, ** Significant at 5% and 1%, respectively

Table 2: Genetic variability parameters for yield and its contributing traits in fenugreek

Characters	Mean	Range		GCV (%)	PCV (%)	h ² (%)	Genetic Advance	Genetic Gain (%)
		Min.	Max.					
Days to 50% flowering	50.71	48.67	53.67	2.80	3.72	56.80	2.21	4.35
Days to maturity	127.20	121.33	131	2.15	2.36	82.78	5.13	4.03
Plant height (cm)	83.34	71.2	92.53	6.63	8.20	65.41	9.21	11.05
Number of branches per plant	4.87	3.73	6.17	14.95	15.10	97.97	1.48	30.48
Number of pods per plant	41.18	31.46	53.13	16.11	18.08	79.37	12.17	29.56
Pod length (cm)	11.12	9.47	12.4	7.08	7.87	80.94	1.46	13.12
Number of seed per pod	15.18	13.27	17.1	7.36	8.07	83.15	2.10	13.82
Biological yield per plant	37.34	24.29	44.84	10.67	13.12	66.10	6.67	17.87

Seed yield per plant	9.24	7.12	11.79	12.36	14.66	71.12	1.98	21.47
100 seed weight (g)	1.35	1.13	1.51	7.80	7.94	96.61	0.21	15.80
Harvest index (%)	24.96	20.71	30.77	9.74	14.11	47.63	3.46	13.85
Protein content (%)	19.84	17.25	22.94	9.11	9.23	97.49	3.68	18.53

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