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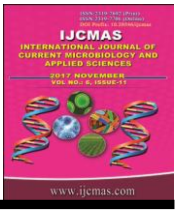

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Genetic Variability of Indian Fenugreek (*Trigonella foenum-graecum* L.) Landraces

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ABSTRACT

The present study was conducted to exhibit the presence of genetic diversity among sixty fenugreek genotypes which were collected from different geographical regions of India. Various genetic parameters like variability, heritability and genetic advance were studied during *rabi*, 2015 and 2016 in CCS HAU, Hisar at Vegetable Research Farm, Hisar. Variability for most of the characters were evaluated by mean and range values in both the years concurrently. High estimates of phenotypic and genotypic coefficients of variability were observed for seed yield and pods per plant; whereas, medium for seeds per pod and pod length; and low for days to 50% flowering in both the years. High heritability coupled with high genetic advance was observed for seed yield, pod per plant and pod length in both years indicating the existence of additive gene action and these traits could be improved by direct selection.

Keywords

Fenugreek, Variability, PCV, GCV and Heritability.

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Introduction

Fenugreek (*Trigonella foenum-graecum*), an annual plant which is native of the countries bordering Eastern shores of Mediterranean region, and locally known as Methi or Metha belongs to the family Leguminosae (Fabaceae). Both its seeds and greens are used as food, flavoured seed spice, as a vegetable for human consumption, as fodder for cattle and for pharmaceutical purposes as well. It is extensively used as fresh leaves (green leafy vegetable), chopped leaves (flavouring agent), sprouts (salad), micro greens (salad), potherbs (decoration), seeds (spice, condiments or medicines), extracts and powders (medicines). It is rich in proteins, mineral, carbohydrate and vitamins, particularly vitamin A and C. Fenugreek seeds are enriched in saponin content which has many flavoring, sweetening, antioxidant, foaming, anti-carcinogenic and antimicrobial properties. A wide range of climatic conditions to warm temperate and tropical regions of Mediterranean, Europe and Asia are favourable for growing of fenugreek. 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 (Malhotra and Vashishtha, 2008).

Rajasthan, Gujarat, Tamil Nadu, Uttar Pradesh, Haryana, Madhya Pradesh, Andhra Pradesh and Punjab are the major producers of fenugreek in India. In India, during 2011-12 this crop occupied an area of 0.97 lakh hectares and produced 1.10 lakh MT seed spice with the productivity of 1.14 MT per hectare (Anonymous, 2014).

However, in view of the low production potential of traditional fenugreek varieties, there is intense need of improvement in this crop and the major objective lies in the development of new varieties with high yield and improved yield associated traits.

Generally, success of any crop improvement program mainly depends on the magnitude of genetic variability, heritability and genetic advance of yield and its associated traits. Seed yield or productivity of any crop is mainly governed by its yield attributing characters. These attributing characters are quantitatively inherited but highly affected by environment. So, it is difficult to determine whether the observed variability of these characters is heritable or not. Therefore, to understand the extent to which the observed variations are due to genetic factors, genetic variability estimates including genotype mean, genotypic and phenotypic coefficient of variation, heritability in broad sense and genetic advance over mean. Keeping this in view, the present investigation was undertaken to assess the variability, heritability and genetic advance of the seed yield and its associated traits of fenugreek.

Materials and Methods

The experimental material comprised of sixty diverse genotypes from various origin and these genotypes were evaluated in randomised blocked design. The experiment was laid out at Vegetable Research Farm of CCS HAU, Hisar in *rabi* 2015-16 and 2016-17. The row length of each genotype was of 3 m with spacing 50 cm. Recommended agronomical practices and plant protection measures were followed timely for successful cultivation of the crop. Randomly ten competitive plants were tagged to record the observation for twelve quantitative characters namely days to 50% flowering, plant height (cm), number of pods per plant, number of branches per plant, pod length (cm), number of seeds per pod, seed yield (q/ha) and test weight. Seed yield was recorded on the plot basis and further calculated in q/ha. One thousand seeds were counted in each replication of every genotype and weighed for calculating test weight (g).

These quantitative characters were used to estimate phenotypic and genotypic coefficient of variation, heritability (broad sense) and genetic advance following the standard statistical methods. ANOVA was worked out as per the procedure given by Panse and Sukhatme (1967). The phenotypic and genotypic coefficient of variation (PCV & GCV) was calculated using the formula given by Burton and Devane (1953). Heritability (h2) in broad sense was calculated according to the method suggested by Hanson *et al.*, (1956), and the formula given by Johnson *et al.*, (1955), was used to compute genetic advance over mean (GAM).

Results and Discussion

The analysis of variance for eight characters is presented in Table 1. The mean sum of squares due to genotypes were highly significant for all the characters under study indicating presence of wide variability among the genotypes assessed, revealed that the breeder could proceed for selection in the present material.

The data relevance to genetic parameters is presented in Table 2. The character days to 50 per cent flowering was recorded when the maximum number of plants in a genotype showed fifty per cent flowering and it ranged from 52.58 to 56.34 and 51.70 to 58.49 days with the overall mean 54.38 and 55.44 in *rabi* 2015 and 2016 respectively. Low phenotypic and genotypic coefficients of variation in both years were observed, indicating that there was a less genetic diversity for this trait. Low heritability coupled with low genetic advance as percent of mean was observed for days to 50 per cent flowering, indicating that this trait could be improved through heterosis breeding since direct selection is not effective. These results are in confirmation with the findings of Kumar and Chaudhary (2003) and Sarada *et al.,* (2008).

Plant height, which was recorded at peak harvest stage, varied from 76.48 to 92.07 cm with mean of 86.5 cm in first year of observation. While, in second year plant height was varied from 72.69 to 92.31 cm with mean of 84.84 cm. These results revealed that there was a significant difference among the genotypes. Presence of moderate phenotypic and genotypic coefficients of variation for plant height indicates that there was a broad genetic variability for this character. High heritability coupled with high genetic advance over mean was exhibited in plant height, indicating that the selection of genotype for plant height in early generations would be effective. These results confirm the results of Gangopadhyay *et al.*, (2009), Singh *et al.*, (2012) and Sharma *et al.*, (2015).

The minimum number of branches per plant was recorded as 4.70 and 5.20 in year 2015 and 2016 respectively with mean of 5.21; while maximum number of branches per plant was 5.98 and 6.09 in both concurrent years with mean of 5.62. The number of branches per plant was found to have moderate phenotypic and genotypic coefficients of variation, indicating that there was a lower genetic variability for this character. Low heritability coupled with moderate genetic advance as percent of mean suggested non-additive gene action and provides limited scope for improvement of traits through selection. These observations are in agreement with the earlier reports of Singh and Pramila (2009), Dashora *et al.,* (2011) and Pathak (2014).

Table.1 Analysis of variance for different characters in fenugreek

Source of variations	df	Year	Days to 50% flowering	Plant Height (cm)	Branches per plant	Pods per plat	Pod length	Seeds per pod	Test weight	Seed yield (q/ha)
			Mean sum of squares							
Replication	2	2015	0.18	2.16	3.42	724.27	2.05	4.55	10.75	17.69
		2016	17.12	557.14	2.34	1399.17	2.68	10.97	9.61	4.32
Genotype	59	2015	13.49^{**}	174.51^{**}	1.24^{**}	387.14^{**}	1.55^{**}	14.61^{**}	4.13^{**}	33.24^{**}
		2016	15.48^{**}	403.93^{**}	0.41^{**}	486.22^{**}	4.94^{**}	7.06^{**}	13.76^{**}	67.45^{**}
Error	118	2015	3.60	39.80	0.39	68.86	0.67	2.76	1.21	1.30
		2016	4.33	35.50	0.18	69.68	0.56	2.87	12.72	1.61

Table.2 Genetic parameters for different characters in 60 genotypes of fenugreek

Characters	Years	Mean	Range	PCV	GCV	Heritability	GA	GAM
Days to 50% flowering	2015	54.38	52.58-56.34	4.83	3.34	47.78	2.58	4.75
	2016	55.44	51.70-58.49	5.11	3.47	46.2	2.7	4.87
Plant Height (cm)	2015	86.5	76.48-92.07	10.63	11.74	63.01	19.05	21.61
	2016	84.84	72.69-92.31	14.83	13.06	77.57	20.10	23.7
Branches per plant	2015	5.21	4.70-5.98	15.81	10.18	41.51	0.7	13.52
	2016	5.62	5.20-6.09	11.12	12.87	48.54	0.6	12.36
Pods per plant	2015	59.94	49.89-76.85	22.06	17.18	60.64	16.52	27.56
	2016	77.22	68.01-88.17	18.7	15.25	66.58	19.8	25.65
Pod length	2015	9.46	8.73-10.37	9.35	7.72	60.54	1.91	19.51
	2016	9.09	8.60-9.81	14.4	12.23	72.11	2.11	21.39
Seeds per pod	2015	15.36	13.29-17.31	16.87	12.93	58.83	3.14	20.44
	2016	17.07	15.47-18.86	14.07	10.83	52.62	2.38	18.11
Test weight	2015	10.44	10.45-12.82	12.92	8.62	44.6	1.35	11.87
	2016	11.44	9.34-11.79	14.44	7.61	42.65	1.19	10.88
Seed yield (q/ha)	2015	15.09	12.80-18.27	22.58	21.31	89.06	6.34	41.42
	2016	15.93	12.72-18.01	32.17	31.05	93.16	9.31	61.74

The mean value of pod length ranged from 9.46 and 9.09, with range of 8.73 to 10.37 and 8.60 and 9.81 in 2015 and 2016 respectively. Low phenotypic and genotypic coefficients of variation were recorded in year 2015 whereas in year 2016 it was recorded moderate for pod length which indicates the moderate amount of variability for pod length. High heritability was coupled with high genetic advance as percent of mean was observed for this trait, suggesting the selection of this trait in early generations would be effective. Similar findings were observed by Kumar and Chaudhary (2003) and Yadav *et al.*, (2013).

The number of pods per plant ranged from 49.89 to 76.85 and 68.01 to 88.17 with an overall mean of 59.94 and 77.22 duly in both years. The estimates of high phenotypic and genotypic coefficients of variation, indicates the occurrence of maximum diversity for this trait. Estimation of high heritability coupled with high genetic advance as per cent of mean revealed the existence of additive gene action and this trait could be improved by direct selection. These results are in confirmation with the findings of Sarada *et al.*, (2008) and Jain *et al.*, (2013).

There was a significant difference among the genotypes for number of seeds per pod, which ranged from 13.29 to 17.31 and 15.47 to 18.86 with mean value of 16.87 and 14.07 in 2015 and 2016 respectively. The moderate PCV and GCV values with higher heritability and high genetic advance as per cent of mean, indicating the existence of moderate genetic diversity and prevalence of additive gene action. This trait could be improved through direct selection. Similar results were reported by Saha and Kole (2001), Kumar and Chaudhary (2003) and Verma *et al.*, (2016).

The mean value of test weight was 10.44 and 11.44 with a range of 10.45 to 12.82 and 9.34 to 11.79 in both the years. Moderate PCV and GCV with moderate heritability and genetic advance as percent of mean was observed for test weight in both the years, indicates low genetic diversity for this trait, which could be improved through heterosis breeding since direct selection is not efficient. These results are in agreement with the results of Pathak *et al.*, (2014) and Jain *et al.*, (2013).

The seed yield ranged from 12.80 to 18.27 and 12.72 to 18.01 with mean value of 15.09 and 15.93 in year 2015 and 2016 respectively. The estimation of high phenotypic and genotypic coefficients of variation exhibits the broad genetic variability for seed yield. High heritability coupled with high genetic advance as percent of mean was observed for seed yield, indicating the preponderance of additive gene action and selection for this character in early generations would be effective. These findings were corroborated with the results of Gangopadhyay *et al.*, (2009). Fikreselassie *et al.*, (2012), Singh *et al.*, (2012), and Yadav *et al.*, (2013).

In conclusion, the analysis of variance showed significant differences among sixty germplasm of fenugreek for all characters studied indicating wider variability and high diversity among genotypes. The genotypic coefficient of variation for all characters studied was lesser than the phenotypic coefficient of variation suggesting the effects of environment in expression of these traits. High PCV coupled with high GCV, observed for pods per plant and seed yield indicates the wider variability for these traits in the germplasm studied. High heritability coupled with high genetic advance as percent of mean was observed for pods per plant, pod length and seed yield indicates the preponderance of additive gene action in the inheritance of these traits and improvement in these characters is possible through direct selection.

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