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GENETIC VARIABILITY AND MULTIVARIATE ANALYSIS IN FENUGREEK (*TRIGONELLA FOENUM-GRAECUM* L) GERMPLASM LINES

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ABSTRACT

The present study genetic variability and multivariate analysis in fenugreek (*Trigonella foenum-graecum* L.) germplasm lines, was conducted at the College of Agriculture, JNKVV, Jabalpur during 2022-2023, to explore the genetic diversity among 27 distinct fenugreek genotypes. The morphological analysis revealed significant variations in traits such as days to flowering initiation, plant height, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, number of leaves per plant, leaf area, test weight, days to maturity, yield per plant, and yield per hectare. Genotypes like AM 319, with early flowering, showed potential for faster maturity, allowing breeders to select genotypes for specific cultivation cycles. FGK-150 displayed a correlation between early flowering and taller plant height, offering further exploration avenues. The assessment of heritability and genetic advance indicated the potential for trait improvement through selective breeding and traits with high heritability and significant genetic advance, such as test weight, hold promise for enhancement, while traits like pod length, with lower genetic advance, may see limited improvement. A positive phenotypic correlation between early flowering and early maturity (0.7343) assists in selecting genotypes for specific timelines, while negative genotypic correlations, such as between plant height and days to flowering initiation (-0.593), inform breeding decisions. D² analysis elucidated that among genotypes, with higher intra-cluster distances in Clusters III and IV indicating greater diversity. The study provided a comprehensive evaluation of genetic diversity in fenugreek, to inform and enhance crop improvement strategies. The identification of diverse genotypes with desirable traits supports the development of improved fenugreek varieties, contributing to agricultural sustainability and productivity.

Key words : Fenugreek, Correlation, GCV, PCV, D² analysis.

Introduction

Fenugreek (*Trigonella foenum-graecum* L.) is an annual self-pollinated diploid species popularly grown by its vernacular name “methi”, belonging to the sub-family “Papilionaceae” of the family “Fabaceae” having chromosome number 2n=16 is grown majorly as a spice crop. The place of origin of fenugreek supposed to be between Iran and North India Smith A. (1982). Fenugreek can be grown under a wide range of climatic conditions extending widely to warm temperate and tropical regions of the Mediterranean, Europe and Asia. India is a leading producer and consumer of fenugreek for its culinary uses and medicinal application. Fenugreek

seeds and leaves are strongly aromatic and flavorful. The seeds are bitter in taste, but lose their bitterness if lightly roasted. They are rich in vitamins such as thiamin, folic acid, riboflavin, niacin, vitamins A, B₆, C and are a rich storehouse of many minerals such as copper, potassium, calcium, iron, selenium, zinc, manganese, and magnesium. Fenugreek leaves are a rich source of vitamin K as well. Fenugreek seeds are a rich source of trigonelline, lysine and l-tryptophan. The seeds also contain a large amount of saponins and fibers that may account for many of the health benefits of fenugreek like reduces cholesterol, regulates blood sugar and controls diabetes, enhances breast milk production, protects from cancer, maintains

healthy testosterone levels, aids digestion, helps with weight loss and fenugreek's use as a natural home remedy. It seed contains carbohydrates (48%), proteins (25.5%), mucilaginous matter (20.0%), fats (7.9%) and saponin (4.8%) (Rao and Sharma, 1987). The major fenugreek producing countries are India, Ethiopia, Egypt and Turkey. India is one of the major producer and exporter of fenugreek. In India, the major fenugreek growing states are Rajasthan, Gujarat, Tamil Nadu, Uttar Pradesh, Haryana, Madhya Pradesh, Andhra Pradesh and Punjab. Rajasthan is considered as "fenugreek bowl" of the country and contributes about 90% to the country's production. India leads fenugreek production worldwide with an area of ~126 thousand ha, production of 182,170 tonnes and average productivity of 1,012 kg ha⁻¹ as of 2019-20 (Nadeem *et al.*, 2023). Knowledge of genetic diversity in a crop species is fundamental to its improvement. Evaluation of genetic diversity levels among adapted, elite germplasm can provide predictive estimates of genetic variation among segregating progeny for pureline.

Fenugreek can be grown under wide range of climatic conditions. The productivity of the crop is low due to many limiting factors such as its cultivation on marginal

lands with poor fertility, lack of superior genotypes or improved cultivars for use in breeding programme to develop potential hybrids. So, there is need for development of new varieties with high productivity. The critical assessment of nature and magnitude of variability in the germplasm stock is one of the important prerequisites for formulating effective breeding methods. Improvement in any crop is proportional to the magnitude of its genetic variability present in germplasm. Greater the variability in a population, the greater chance for effective selection for desirable types (Vavilov, 1951). Yield is a complex character governed by several other yield attributing characters. Since, most of the yield attributing characters is quantitatively inherited and highly affected by environment.

The extent of variation is measured by GCV (Genotypic Coefficient of Variance) and PCV (Phenotypic Coefficient of Variance), which gives information about the variation present in the investigated characters. Heritability along with genetic advance has played a major role in determining the effective selection of experimental material for crop improvement. Selection of material based on yield attributing characters alone is not effective and efficient. So, selection based on its

Table 1 : Names of the Fenugreek Genotypes used for the study.

S. no.	Name of genotype	Source of collection
1.	FGK-139	Department of Horticulture, JNKVV, Jabalpur, Madhya Pradesh
2.	FGK-142	Department of Horticulture, JNKVV, Jabalpur, Madhya Pradesh
3.	FGK-143	Department of Horticulture, JNKVV, Jabalpur, Madhya Pradesh
4.	FGK-144	Department of Horticulture, JNKVV, Jabalpur, Madhya Pradesh
5.	FGK-145	Department of Horticulture, JNKVV, Jabalpur, Madhya Pradesh
6.	FGK-146	Department of Horticulture, JNKVV, Jabalpur, Madhya Pradesh
7.	FGK-147	Department of Horticulture, JNKVV, Jabalpur, Madhya Pradesh
8.	FGK-148	Department of Horticulture, JNKVV, Jabalpur, Madhya Pradesh
9.	FGK-149	Department of Horticulture, JNKVV, Jabalpur, Madhya Pradesh
10.	FGK-150	Department of Horticulture, JNKVV, Jabalpur, Madhya Pradesh
11.	FGK-151	Department of Horticulture, JNKVV, Jabalpur, Madhya Pradesh
12.	FGK-152	Department of Horticulture, JNKVV, Jabalpur, Madhya Pradesh
13.	FGK-153	Department of Horticulture, JNKVV, Jabalpur, Madhya Pradesh
14.	FGK-154	Department of Horticulture, JNKVV, Jabalpur, Madhya Pradesh
15.	FGK-155	Department of Horticulture, JNKVV, Jabalpur, Madhya Pradesh
16.	FGK-156	Department of Horticulture, JNKVV, Jabalpur, Madhya Pradesh
17.	AM-31	NRC Seed Spices, Ajmer, Rajasthan
18.	AM-91	NRC Seed Spices, Ajmer, Rajasthan
19.	AM-309	NRC Seed Spices, Ajmer, Rajasthan
20.	AFg-05	NRC Seed Spices, Ajmer, Rajasthan
21.	AM-115	NRC Seed Spices, Ajmer, Rajasthan
22.	AFg-03	NRC Seed Spices, Ajmer, Rajasthan
23.	AFg-04	NRC Seed Spices, Ajmer, Rajasthan
24.	AM-319	NRC Seed Spices, Ajmer, Rajasthan
25.	AM-45	NRC Seed Spices, Ajmer, Rajasthan
26.	AM-235	NRC Seed Spices, Ajmer, Rajasthan
27.	Pusa Kasturi	IARI, New Delhi

components and secondary characters could be more efficient and beneficial for the development of superior cultivars/hybrids. Therefore, generating information on the association of yield with its accrediting traits may improve the competence of selection in a breeding programme. Several measures have been employed to assess genetic diversity present among plant populations. The multivariate analysis offers the most accurate data of these measures. Among the methods with multiple variables. The generalized distance (D^2) introduced by Mahalanobis in 1956. Rajpoot *et al.* (2023) has been widely used. In order to evaluate the variety and diversity existing in pearl millet genotypes for grain yield and its accrediting features, an assessment has been undertaken in the current study.

Materials and Methods

The present investigation was conducted during *Rabi* season on twenty- seven genotypes of fenugreek which were collected from Department of Horticulture, JNKVV, Jabalpur and National Research Centre on Seed Spices, Ajmer, Rajasthan (Table 1). Field experiment was conducted on Vegetable Research Centre, Maharajpur, Department of Horticulture of Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P.), India. The Germplasm was sown in seed beds during second fortnight of October 2022 in Randomized Block Design (RBD) with a spacing of 45 cm \times 20 cm and plot size of 3.6 m \times 3m. All the standard package of practices and plant protection measures were timely adopted to raise the crop successfully. Observations were recorded for five randomly selected plants from each entry in each replication for thirteen quantitative characters including, days to 50% flowering, plant height (cm), number of branches plant, number of pods plant, number of seed per pod, pod length (cm), number of leaves, leaf area (cm²), test weight (g), days to maturity, yield plant⁻¹ and yield in kg ha⁻¹.

Results and Discussion

The genetic characteristics for the characters under study, including mean, range, PCV and GCV, heritability estimates, and anticipated genetic advance as a percentage of mean. In the present investigation, 27 diverse genotype of fenugreek were studied to assess their yield and yield attributing characters. The analysis of variance clearly indicated that there was highly significant differences among the genotypes for all the 13 characters studied as seen in Table 2. Similar result seen by Kumar *et al.* (2023). In the large differences in mean values for all the traits were observed. The trait Days to flower initiation ranged from AM 319 (30.67 days) to FGK- 148 (55 days), Days to 50 % flowering

ranged from FGK-150 (39.67 days) to FGK-143 (61.33 days), plant height ranged from Pusa Kasturi (70.4 cm) to FGK- 150 (99.19 cm), number of branches plant⁻¹ ranged from AFg 03 (4.27) to FGK-146 (7.40), number of pods plant⁻¹ ranged from AM 235 (16.53) to FGK-154 (40.13), number of seeds pod⁻¹ (9.4) in Afg-04 to (16.87) in FGK-155, Pod length (cm) ranged from FGK-142 (12.58cm) to Pusa Kasturi (5.15cm), Leaf area (cm²) ranged from AFg-03 (1.83 cm²) to FGK-152 (3.49cm²), test weight (g) ranged from (1.15 g) Pusa Kasturi to (19.95) FGK-155, Days to maturity ranged from 89.04 days (AM 304) to 144.3 days (FGK-148), Yield plant⁻¹ from (7.63 g) Pusa Kasturi to (24.35) g plant⁻¹ FGK-155, Yield (kg ha⁻¹) ranged from 1233.67 kg ha⁻¹ (Pusa Kasturi) to 2726 kg ha⁻¹ (FGK-155) as seen in Table 4. The experimental material had a wide range of variability and favourable mean performance for most of the traits investigated and these possible combinations could be exploited as potential hybrids aimed for simultaneous improvement of grain yield and other yield-attributing traits as shown in Table 4. The trait exhibits a more negligible difference between PCV and GCV values, demonstrating a high degree of genetic variability present in these characters and, consequently, greater scope for selection based on those characters. These traits are less influenced by the environment and show high genetic variability. Table 3 provides the estimates of numerous genetic parameters. A higher magnitude as indicated by the high PCV and GCV values for number of leaves, test weight, yield per plant indicating the higher magnitude of variability for these traits and consequently more scope for their improvement through selection. PCV and GCV estimates were moderate for flower initiation, days to 50% flowering, number of branches plant⁻¹, number of seeds pod⁻¹, pod length, days to maturity. This implied equal importance of additive and non-additive gene action for the traits recorded. Low GCV and PCV were recorded in plant height. These results are in conformity with the findings of Gaikwad *et al.* (2020), Panwar *et al.* (2018).

Heritability and expected genetic advance

Heritability estimates provides information on transmission of characters from parent to the progeny. Such estimates facilitate evaluation of hereditary and environmental effect in phenotypic variation and thus aid in selection. Heritability estimates are used to predict expected advance under selection so that breeders are able to anticipate improvement from different of selection intensity. Johnson *et al.* (1955) have suggested heritability estimates in association with genetic advance are much useful for selection than heritability alone. Heritability couple with genetic advance as percentage of mean was

Table 2 : Analysis of variance for different characters in Fenugreek.

Source of variation	DF	Days to flower initiation	Days to 50% flowering	Plant height (cm)	Number of branches plant ⁻¹	Number of pods plant ⁻¹	Number of seeds pod ⁻¹	Pod length (cm)
REP	2	35.3456	16.778	38.232	0.1244	3.624	7.1027	0.0468
TRT	26	102.588	120.855	139.018	2.3959	81.908	11.2781	5.1009
Error	52	13.7943	15.432	24.073	0.2834	8.135	4.4304	0.2453

Source of variation	DF	Number of leaves plant ⁻¹	Leaf area	Test weight (g)	Days to maturity	Yield plant ⁻¹	Yield (kg ha ⁻¹)
REP	2	29.16	0.1259	0.329	24.07	0.652	20479
TRT	26	1703.65	0.7157	45.178	709.89	38.689	555800
Error	52	122.2	0.1154	2.691	15.3	1.394	75514

Table 3 : Estimates of mean, range, phenotypic and genotypic coefficients of variability, heritability, genetic advance as percentage of mean for 13 quantitative traits in fenugreek.

Character	Max	Min	Mean	Coefficient of variance		Heritability (%)	G.A. %
				GCV%	PCV%		
Flowering	59	26	40.36145	13.4968	16.3421	68.21	22.9626
50% flowering	64	35	49.19277	12.0524	14.4585	69.49	20.6961
Height	101.2	61.4	84.68	7.3026	9.3184	61.41	11.7889
Branches	7.8	3.8	5.409639	15.5401	18.4033	71.30	27.0315
Pods per plant	43.2	12	23.91542	20.8145	24.0118	75.14	37.1681
Seeds per pods	28.2	8.8	12.58795	12.1430	20.8242	52.50	14.5861
Pod length	12.96	4.82	10.62046	11.9308	12.8030	86.84	22.9031
No. of leaves	158.6	38.2	77.16145	29.9591	33.2506	81.18	42.6150
Leaf area	3.81	1.19	2.554458	17.5023	21.9807	63.40	28.7072
Test weight	21.95	0.89	13.13361	28.5616	31.1576	84.03	53.9347
Days to maturity	149.52	84.89	108.788	14.0137	14.4692	93.80	27.9595
Yield per plant	26.59	6.946	15.9988	22.0644	23.2685	89.92	6.8874
Yield (kg/ha)	3080	1092	2074.12	19.2938	23.4058	67.95	32.7625

recorded for traits flower initiation, branches per plant, pods per plant, pod length, number of leaves /plant, leaf area, test weight, days to maturity, Yield (kg/ha) and moderate for seeds per pod the similar result was also obtained by Shekhawat *et al.* (2023), Singh *et al.* (2022). Correlation studies provide a natural relationship between diverse plant characters on yield and its components on the selection of genotypes for genetic improvement in yield. The genotypic and phenotypic correlation between all possible combinations of characters was estimated. Moreover, genotypic correlation coefficient was higher than their phenotypic correlation coefficient for all characters under study (Table 3).

Correlation coefficient

Phenotypic correlation coefficient

There is a significant and positive phenotypic correlation between the days to flowering initiation and the days to maturity (0.7343). Number of branches showed positive significant effect with number of pod plant⁻¹ (0.4895) followed by test weight (0.4584), number of leaves plant⁻¹ (0.4212) and number of seeds pod⁻¹ (0.0479). A significant and positive correlation (0.4283) was observed between pod length and test weight. The number of leaves per plant exhibited the highest and statistically significant positive correlation with days to maturity (0.4516), followed by yield per plant (0.4384) and test weight (0.4267). A significant and positive

Table 4 : Mean performance of twenty-seven genotypes of fenugreek for quantitative traits.

Genotypes	Days to flower initiation	Days to 50% flowering	Plant height (cm)	Branches per plant	Pods per plant	Seeds per pods	Pod length (cm)	No. of leaves	Leaf area (cm ²)	Test weight (g)	Days to maturity	Seed yield per plant (g)	Seed yield (kg/ha)
FGK-139	39.33	44.67	88.33	4.40	25.53	14.47	12.53	85.20	3.00	11.68	111.06	14.01	2266.00
FGK-142	45.33	51.33	83.00	6.20	20.00	16.33	10.88	87.07	2.20	10.83	123.46	15.90	1726.00
FGK-143	39.67	61.33	91.07	4.73	23.47	10.53	12.58	75.73	2.81	12.42	131.66	13.73	2446.33
FGK-144	41.67	41.67	82.03	5.87	21.33	10.00	10.55	82.27	2.19	14.36	110.35	14.43	2260.67
FGK-145	39.67	48.33	80.23	6.47	25.13	10.73	10.42	94.67	2.43	10.56	101.49	15.28	2431.00
FGK-146	41.33	42.00	78.83	7.40	36.67	11.93	10.77	84.27	3.11	13.38	99.48	15.28	1244.33
FGK-147	47.33	51.33	77.49	5.60	26.33	14.47	11.42	81.47	3.42	16.81	128.32	18.94	2537.33
FGK-148	55.00	60.67	70.60	5.80	19.67	10.93	10.98	78.67	2.46	11.23	144.30	12.64	1859.33
FGK-149	39.00	42.33	76.90	6.20	24.07	14.33	10.62	86.60	3.17	19.25	98.01	20.81	2352.33
FGK-150	43.33	39.67	99.19	5.33	27.07	11.87	11.23	85.13	2.55	12.92	109.22	14.86	2599.00
FGK-151	39.67	40.67	93.07	6.73	23.53	10.40	10.29	78.13	2.60	15.71	100.58	15.79	1641.33
FGK-152	43.67	41.33	77.40	5.67	24.07	12.93	12.44	155.73	3.49	16.77	121.98	19.09	2150.67
FGK-153	47.00	50.67	83.67	5.20	22.67	11.67	10.36	106.13	2.96	14.84	131.32	17.71	1921.33
FGK-154	38.00	44.67	85.03	6.60	40.13	11.20	10.42	86.07	3.10	19.81	89.12	23.45	2549.67
FGK-155	48.33	48.67	86.27	5.73	23.33	16.87	10.53	96.27	2.32	19.95	127.78	24.35	2726.00
FGK-156	47.00	52.67	82.10	6.80	27.00	11.27	10.12	96.73	2.58	18.72	125.47	21.69	2300.67
AM31	32.00	47.67	86.93	4.87	22.23	13.00	9.54	53.40	2.98	11.50	100.56	12.38	1899.67
AM91	37.00	52.33	88.53	4.93	23.83	12.47	10.82	65.13	1.87	12.08	96.15	13.42	1849.67
AM309	33.33	44.00	87.67	4.93	21.47	13.27	10.83	50.07	2.97	10.93	89.04	15.50	2557.67
AM235	39.00	51.33	91.93	4.40	16.53	12.67	10.50	48.47	2.16	10.90	98.59	14.97	2036.67
Afig05	30.67	47.00	89.33	4.73	22.27	11.33	10.46	48.73	1.86	10.21	90.18	14.60	1637.67
AM115	33.33	49.33	89.87	5.07	24.93	15.40	10.66	43.93	2.36	12.98	104.92	15.60	1623.33
Afig03	42.67	53.33	85.50	4.27	19.53	12.53	11.00	59.87	1.83	11.25	112.32	15.46	1641.33
Afig04	37.67	55.33	91.07	4.33	16.60	9.40	10.86	40.60	2.37	11.20	98.60	13.64	1732.00
AM319	30.67	59.67	89.67	4.47	16.73	10.80	11.08	71.47	2.13	11.50	91.19	13.17	1543.00
AM45	34.67	46.67	84.43	4.47	21.36	14.13	10.88	63.40	2.23	12.80	99.37	17.13	2611.33
Pusa Kasturi	42.00	59.33	70.40	4.60	27.77	11.00	5.15	64.00	1.86	1.15	97.13	7.63	1233.67
MEAN	40.31	49.19	84.84	5.40	23.82	12.43	10.66	76.64	2.56	13.18	108.58	15.98	2073.83
Min	30.67	39.67	70.40	4.27	16.53	9.40	5.15	40.60	1.83	1.15	89.04	7.63	1233.67
Max	55.00	61.33	99.19	7.40	40.13	16.87	12.58	155.73	3.49	19.95	144.30	24.35	2726.00
Sem	2.1443	2.268	2.8327	0.3074	1.6467	1.2152	0.286	6.3822	0.1962	0.9472	2.2579	0.6816	158.6544
CD at 5%	6.0852	6.4362	8.0388	0.8722	4.6731	3.4486	0.8115	18.1115	0.5567	2.6879	6.4077	1.9344	450.2337

Table 5 : Phenotypic and genotypic correlation coefficient (upper and lower diagonal respectively) correlation coefficient among seed yield and its attributing traits in fenugreek.

Characters	Days to flower initiation	Days to 50% flowering	Plant height (cm)	No. of branches	No. of pod per plant	No. of seed per pod	Pod length (cm)	No. of leaves	Leaf area (cm ²)	Test weight (g)	Days to maturity	Seed yield per plant (g)	Seed yield (kg/ha)
Days to flower initiation	1	0.1278	-0.3484	0.3294	0.1059	0.0294	0.0393	0.412*	0.1763	0.2028	0.7343**	0.2079	0.1088
Days to 50% flowering	0.1797	1	-0.1358	-0.313	-0.3393	-0.1819	-0.180	-0.258	-0.3144	-0.3619	0.2828	-0.3446	-0.1793
Plant height (cm)	-0.593**	-0.2117	1	-0.2844	-0.2034	-0.0618	0.2967	-0.366	-0.1263	0.0144	-0.2724	-0.052	0.1517
No. of branches per plant	0.4434*	-0.4821*	-0.3642	1	0.4895*	-0.0479	0.0116	0.421*	0.2997	0.4584*	0.1359	0.3855	-0.0802
No. of pod per plant	0.0792	-0.3954	-0.2087	0.666**	1	0.0218	-0.124	0.2775	0.3431	0.2583	-0.104	0.3082	0.0249
No. of seed per pod	0.135	-0.2346	-0.0169	-0.0096	-0.0532	1	0.1093	0.0544	0.0736	0.1975	0.1564	0.2928	0.092
Pod length (cm)	0.0212	-0.2231	0.3729	-0.0041	-0.1472	0.237	1	0.2405	0.3565	0.4283*	0.2814	0.2831	0.3999
No. of leaves	0.6314**	-0.3095	-0.422*	0.569**	0.3153	0.117	0.2883	1	0.387	0.4267*	0.4516*	0.4384*	0.1182
Leaf area (cm ²)	0.1575	-0.4761*	-0.2706	0.4615*	0.5024**	0.2225	0.4066*	0.5995**	1	0.435*	0.1804	0.3362	0.2922
Test weight (g)	0.2733	-0.4803	0.0882	0.575**	0.3268	0.3011	0.5176**	0.526**	0.6051***	1	0.2348	0.849**	0.3463
Days to maturity	0.896**	0.3257	-0.3466	0.1743	-0.1459	0.2084	0.307	0.5182**	0.2429	0.264	1	0.2004	0.169
Seed yield per plant	0.2982	-0.4082*	-0.0035	0.5469**	0.3548	0.5054**	0.356	0.4936*	0.4849*	0.9447**	0.2075	1	0.399
See yield (kg/ha)	0.1599	-0.2781	0.1245	-0.0369	0.0348	0.256	0.4725*	0.2394	0.2434	0.4885*	0.1951	0.5421**	1

phenotypic correlation (0.435) exists between leaf area and test weight. The correlation between test weight and yield per plant (0.8491) is both highly significant and positive.

Genotypic correlation coefficient

Number of branches showed positive significant effect with flower initiation (0.4434). Number of pod plant⁻¹ showed highly significant and positive genotypic correlation with number of branches plant per plant (0.666). A positive genotypic correlation of Number of leaves plant⁻¹ is observed with days to flower initiation (0.631) and number of branches plant⁻¹ (0.569). A significant and positive genotypic correlation of leaf area exists with number of leaves plant⁻¹ (0.5995) followed by number of pod plant⁻¹ (0.5024), number of branches plant⁻¹ (0.461) and pod length (0.4066). A highly significant and positive genotypic correlation of test weight exists with leaf area (0.6051) followed by number of branches plant⁻¹ (0.575), number of leaves plant⁻¹ (0.526), pod length (0.526). The analysis indicates that there exists statistically highly significant and positive correlation with days to flower initiation (0.896) followed by number of leaves plant⁻¹ (0.5182). A highly significant and positive genotypic correlation can be seen in yield plant⁻¹ with test weight (0.944) followed by number of branches plant⁻¹ (0.546), number of seed pod⁻¹ (0.5054), number of leaves plant⁻¹ (0.4936) and leaf area (0.484). Yield in kg ha⁻¹ recorded significant positive genotypic correlation with yield plant⁻¹ (0.542) followed by leaf area

Table 6 : Ranking and per cent contribution of characters.

Source	Times ranked 1st	Contribution %
Days to flower initiation	1	0.28%
Days to 50% flowering	8	2.28%
Plant height	5	1.42%
No. of branches plant ⁻¹	16	4.56%
No. of pod plant ⁻¹	12	3.42%
No. of seed per pod ⁻¹	2	0.57%
Pod length	30	8.55%
No. of leaves plant ⁻¹	31	8.83%
Leaf Area	10	2.85%
Test wt.	7	1.99%
Days to maturity	123	35.04%
Yield plant ⁻¹	72	20.51%
Yield (kg ha ⁻¹)	34	9.69%

Table 7 : Clustering of twenty-seven genotypes of fenugreek on the basis of genetic divergence.

Cluster	Genotypes	Genotypes
1	5	FGK152, FGK139, FGK 143, AM 319, AM91
2	4	FGK 154, FGK 146, FGK 149, FGK 147
3	4	AM 309, AM 31, Afg 04, AM235
4	4	Pusa Kasturi, FGK 153, FGK151, FGK 150
5	4	AM 115, Afg05, AM45, Afg 03
6	2	FGK148, FGK 144
7	4	FGK 145, FGK 142, FGK 155, FGK 156

(0.488) and number of seed pod⁻¹ (0.472) (Table 5). The percent contribution of individual characters toward the total divergence was found high for days to maturity (35.04%), followed by yield/ plant (20.51%), Yield/hectare (9.69%), No. of leaves/ plant (8.83%), Pod length (8.55%), No. of branches/ plant (4.56%), No. of pods/ plant (3.42%), leaf area (2.85%), Days to 50% flowering (2.28%), Test weight (1.99%), Plant height (1.42%), No. of seeds per pod (0.57%) and lowest was found in days to flower initiation (0.28%). Similar result for correlation and path was seen by Tiwari *et al.* (2024), Kole *et al.* (2023), Kumar (2023), Singh *et al.* (2022), Naik *et al.* (2012) (Table 6). The use of phenotypic data to screen breeding material for effective parents for hybridization programmes is a quick and simple technique to measure genetic diversity among genetically distinct lines. In the present investigation 27 genotypes were divided into seven distinct clusters. Cluster I had highest number of genotypes *i.e.*, 5 (FGK-152, FGK 134, FGK 143, AM 319, AM 91) followed by Cluster I, cluster III, cluster IV, cluster V, cluster VI and cluster VII each having four genotypes and cluster II included two genotypes (FGK 148, FGK 144) as shown in Table 7.

Table 8 : Cluster mean for different characters in Fenugreek genotype.

Clusters	Days to flower initiation	Days to 50% flowering	Plant height	No. of branches plant ⁻¹	No. of pod plant ⁻¹	No. of seed pod ⁻¹	Pod length	No. of leaves plant ⁻¹	Leaf area	Test wt.	Days to maturity	Yield plant ⁻¹	Yield (kg ha ⁻¹)
I	38.07	51.87	87.00	4.84	22.73	12.24	11.89	90.65	2.66	12.89	110.41	14.68	2051.13
II	41.42	45.08	79.56	6.45	31.80	12.98	10.81	84.60	3.20	17.31	103.73	19.62	2170.92
III	33.42	48.50	88.75	4.72	20.64	11.75	10.42	48.20	2.55	10.96	94.59	14.03	1956.75
IV	43.00	47.58	86.58	5.47	25.26	11.23	9.26	83.35	2.49	11.16	109.56	14.00	1848.83
V	35.33	49.08	87.28	4.63	22.02	13.35	10.75	53.98	2.07	11.81	101.70	15.70	2149.58
VI	48.33333	51.16667	76.31667	5.833333	20.5	10.46667	10.76733	80.46667	2.325	12.79667	127.3283	13.53407	2060
VII	45.08	50.25	82.90	6.30	23.87	13.80	10.49	93.68	2.38	15.02	119.55	19.31	2178.58

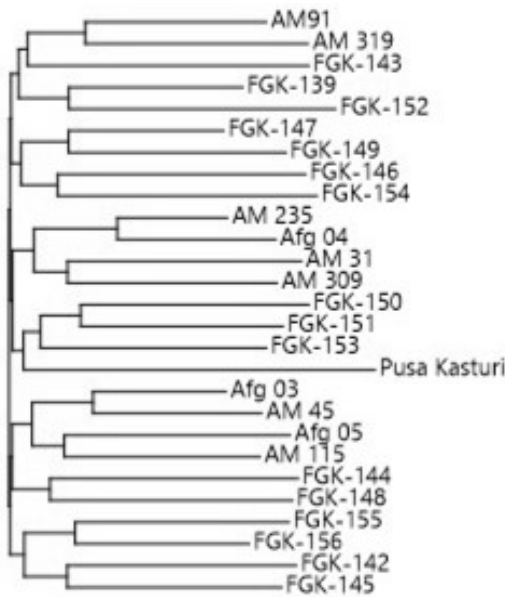


Fig. 1 : Clustering of twenty-seven genotypes of fenugreek on basis of Tocher’s method.

Table 9 : Average intra and inter cluster distance.

	I	II	III	IV	V	VI	VII
I	15.04						
II	40.456	22.65					
III	46.677	47.56	41.029				
IV	33.494	39.5656	32.983	41.029			
V	22.765	28.567	25.56	22.567	35.676		
VI	29.342	29.5455	35.676	46.677	47.56	22.65	
VII	41.029	35.676	12.456	33.494	39.5656	32.983	12.456

The existence of diversity among the genotypes was also assessed by the considerable amount of variation in the cluster means for different characters. Based upon the cluster mean performance, for flower initiation, highest mean was found in cluster VI and lowest in cluster III. Similarly for 50% flowering, highest mean was found in Cluster 1 and lowest in cluster II. For plant height, cluster III showed maximum mean (88.75) and cluster VI recorded minimum mean value (76.31). Number of branches recorded maximum cluster mean value in cluster VII (6.30) and lowest in cluster V (4.63). For number of leaves plant⁻¹, cluster VII (93.68) recorded highest cluster mean value and lowest in cluster Yield parameters including number of pod plant⁻¹, number of seeds pod⁻¹, test weight, days to maturity, yield plant⁻¹ and yield in kg ha⁻¹ were highest in Cluster II, cluster VII, cluster II, cluster VI, cluster II and cluster VII, respectively. Lowest values for yield parameters including number of pod plant⁻¹, number of seeds pod⁻¹, test weight, days to maturity, yield plant⁻¹ and yield in kg ha⁻¹ were recorded in cluster VI, cluster VI, cluster III, cluster III, cluster V and cluster IV, respectively (Table 8).

In Table 9 shows the average D² values between (intra cluster) and between (inter cluster) clusters. The Cluster III and IV (41.029) had the highest intra cluster distance, followed by Cluster V (35.676), Cluster II and cluster VI (22.65), cluster I (15.04), Cluster VII (12.06). Implying that genotypes within these clusters are more diverse in comparison to the other clusters (Fig. 1).

Highest intercluster distance shown by both clusters cluster II and II, cluster V and cluster VI (47.56), followed by clusters I and III and IV and VI (46.67), clusters I and VII, III and III, IV and IV (41.09), I and II (40.45), II and IV and V and VII (39.56), IV and VII, III and VI, V and V (35.67), I and IV and IV and VIII (33.49), III and IV and VI and VII (32.98), II and VI (29.54), I and VI (29.34), V and II (28.56), III and V (25.56), I and V (22.76), VI and VI, II and II (22.76), IV and V (22.56), I and I 15.04, III and VI (12.45) and VII and VII (12.45). Similar result was seen by Roba *et al.* (2024), Chauhan (2023), Maurya *et al.* (2023), Panwar *et al.* (2018), Yadav *et al.* (2018).

Conclusion

The morphological analysis revealed significant variations across various traits, highlighting the rich genetic diversity among the studied genotypes. This diversity offers opportunities for selecting genotypes with desirable traits tailored to specific cultivation needs. The evaluation of heritability and genetic advance further guided the selection of traits suitable for targeted improvement efforts. Correlation coefficient analysis illuminated the complex relationships between traits, both phenotypically and genotypically, providing valuable insights for breeding decisions. The D² analysis explored genetic distances and clustering patterns, aiding in the identification of genotypic groups with shared traits. These clusters provide a framework for selecting parents for hybridization strategies, aiming to harness genetic diversity for enhanced trait combinations.

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