



Genetic Variability, Heritability, Genetic Advance, Correlation Coefficient and Path Analysis of Fennel Genotypes

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ABSTRACT

Background: Fennel (*Foeniculum vulgare* Mill.) is a diploid horticultural species celebrated for its biennial or perennial life cycle. The cultivation of high yielding varieties necessitates a comprehensive understanding of the prevailing genetic diversity and the heritability of various traits. Therefore, the estimation of GCV and PCV, genetic progress and heritability, genetic advancement and correlation between seed yield and various quality is crucial.

Methods: The present investigation was conducted at College of Agriculture in Jabalpur, Madhya Pradesh during the Rabi season in 2021-2022. This study evaluated twenty four fennel genotypes using a randomized block design with three replications. The primary aim was to explore the genetic variability, heritability and genetic advancement and analyze the nature and magnitude of correlations, path coefficients and genetic divergence related seed yield and its contributing traits.

Result: The highest coefficient of variation, both GCV and PCV were recorded for number of umbels per plant, followed by number of seeds per umbel, branches per plant, seed yield per ha and per plant, test weight, plant height and number of umbellets per plant. High heritability was associated with genetic advance as a percentage of mean for traits such as number of seeds per umbel, seed yield and number of umbels per plant. Cluster V exhibited the highest intra cluster D2 followed by cluster III, both of which were polygenotypic. A thorough examination of the cluster means as well as intra and inter cluster distances and individual performances revealed that the genotypes RF 101 (check), UF 231 and RF 205 (check) stands out as superior options demonstrating significant genetic diversity. Thus, these genotypes may be utilized in future breeding programmes for creating maximum variability.

Key words: Cluster, Fennel, Genetic advance, Genetic heritability, Variability.

INTRODUCTION

Seed spices are circumscribed as those annuals whose dried fruits or seeds serve as exquisite species. They are distinguished by their pungent aroma, robust fragrance and a delightful blend of sweet and bitter flavours. (Hosseini *et al.*, 2021) Seed spices represent a very unique category of agricultural commodities that are low in volume yet high value and export-oriented. Cultivation of seed spices is increasingly recognized for its profitability, rapid growth cycle and remarkable adaptability to arid regions with minimal rainfall. Owing to its domestication, fennel has disseminated globally, establishing itself as a significant crop harnessed in both culinary and medicinal applications (Krizman *et al.*, 2022).

In India, fennel is grown over approximately 76,000 hectares, yielding an annual production of 129,350 tonnes. However, given that the majority of traits contributing to yield are quantitatively inherited and significantly influenced by environmental factors, determining the heritability of observed variability presents a challenge (Rajput *et al.*, 2022). Therefore, in addition to genetic diversity, the estimation of genotypic and phenotypic variance coefficients (GCV and PCV), genetic progress and heritability, genetic advancement and correlation between seed yield and various quality and yield attributes is crucial, as these factors lay the foundation for enhancing the efficiency of hybridization and the management of segregating populations through selections (Scariolo *et al.*,

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2022). However, there is a notable scarcity of information regarding these aspects for fennel. Consequently, the present investigation was undertaken to explore the nature and extent of genetic variability, heritability, genetic advancement and correlation for varied traits across twenty four genotypes of fennel.

MATERIALS AND METHODS

Fennel was sown in Rabi season during 2021-2022 in Randomized block design with three replications at Vegetable Research Centre, Maharajpur, Department of

Horticulture of Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P.). Twenty-four genotypes including germplasm accessions and improved varieties were selected. Before sowing, seeds were treated with thirum @ 2.5kg/ha. In November 2021, seeds were meticulously sown at a rate of 10 kg per ha and arranged in precise spacing of 45 x 10 cm and planted at a depth of 2-3 cm within well-defined rows. Ten plants were randomly selected from each plot, excluding the border rows and tagged for the purpose of recording data on various growth parameters. RF 101 and RF 205 are national check. Observations were diligently noted on tagged plants at different growth stages, encompassing developmental parameters, yield attributes and quality metrics. The mean data of the entries were subjected to variance analysis and test of significance as per method of Fisher (1918). The genotypic and phenotypic variances were calculated according to the formula.

$$\text{Genotypic variance } \sigma^2_g = \frac{\text{MSg} - \text{MSe}}{R}$$

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

Where,

MSg = Mean sum square due to genotypes.

MSe = Mean sum square due to error.

r = Number of replication.

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was calculated as per the formula suggested by Burton (1952) and Johnson *et al.* (1955). Heritability in broad sense was calculated according to the formula.

$$\text{Heritability } H(b) = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

Genotypic and phenotypic correlations among all the characters under study were estimated as per the method given by Searle (1961). The path coefficients were obtained as per the method suggested by Dewey and Lu (1959). D^2 values were derived using Tocher's method, which adeptly transforms correlated means of various traits into standard uncorrelated means. The Mahalanobis D^2 statistical distance between pairs of genotypes was computed as the aggregate of the squared differences in uncorrelated

Table 1: Mean performance of twenty four genotypes of fennel for quantitative traits.

Genotypes	Days to flowering initiation	Days to 50% flowering	Plant height (cm)	No. of primary branches	No. of umbel per plant	No. of umbelletes per umbel	No. of seeds per umbel	Test weight (g)	Seed yield/plant (g)	Seed yield (kg/ha)
HF 256	88.67	96.33	177.00	5.27	14.67	24.07	441.20	4.10	22.95	548.30
HF 192	82.67	96.67	195.67	5.40	9.33	23.47	271.33	4.97	24.16	639.00
JF 18-13	72.00	83.67	162.53	5.00	8.27	29.16	546.73	6.03	19.70	579.30
JF 18-03	73.67	82.67	169.33	5.60	10.73	26.88	429.60	6.04	20.10	615.30
UF 231	85.00	96.33	161.47	4.33	9.53	22.09	334.33	5.12	27.03	418.30
UF 230	83.33	89.67	172.93	4.47	8.20	28.80	339.80	5.21	26.37	603.00
AF 87	74.33	86.00	189.00	5.47	11.47	29.33	458.83	5.19	23.59	420.70
AF 17	81.33	95.00	168.27	4.67	8.07	26.40	370.33	5.21	23.33	530.00
RF 67	91.00	99.00	166.73	5.67	8.47	26.20	522.80	4.15	24.54	469.30
RF 101	79.00	90.00	139.60	5.73	8.80	25.42	422.50	4.20	17.86	326.70
RF 205	82.67	91.33	153.07	6.67	16.47	26.60	528.33	3.95	15.20	404.00
NDF 59	87.67	103.00	178.40	5.00	5.80	26.93	505.87	3.53	17.07	520.00
NDF 46	89.00	101.33	190.53	5.60	9.53	32.47	554.60	4.20	16.63	635.70
RF 101	85.00	95.33	127.80	6.27	16.27	22.18	213.70	4.22	21.17	577.70
RF 125	83.00	94.00	119.53	9.80	24.00	23.84	79.73	4.18	32.75	615.00
RF 143	82.00	91.67	154.47	7.07	21.07	25.28	188.80	4.23	33.14	418.30
RF 205	84.33	90.33	118.20	6.47	20.53	20.67	176.00	4.15	32.78	602.30
RF 281	85.33	94.33	116.40	7.87	21.00	20.21	173.00	4.09	17.66	420.00
RF 178	82.33	94.33	153.67	7.07	17.27	20.53	414.73	4.02	23.19	530.00
JF 1	71.67	83.00	161.73	6.20	13.20	24.27	651.67	4.12	24.38	470.30
JF 2	72.67	84.33	155.40	4.93	7.47	20.87	321.80	4.22	23.98	329.30
JF 3	71.33	85.00	152.27	3.80	5.27	15.69	179.40	4.12	26.20	403.70
Jagudan 1	81.33	94.33	150.40	4.00	4.87	20.47	147.87	3.21	17.10	327.00
Jagudan 2	83.67	95.00	140.13	4.07	4.47	19.44	143.00	3.60	23.05	355.70
Mean	81.37	92.19	157.27	5.683	11.86	24.22	350.66	4.41	23.08	489.95
Min	71.33	82.66	116.4	3.8	4.46	15.69	79.73	3.20	15.27	326.7
Max	91	103	195.66	9.8	24	29.333	651.66	6.04	33.13	639
SE(m)	1.07	1.22	3.423	0.39	0.783	1.531	4.339	0.039	0.519	3.903
C.D. at 5%	3.045	3.488	9.745	1.121	2.228	4.356	12.351	0.111	1.478	11.109

values for any two genotypes evaluated simultaneously. (Mahalanobis, 1928).

RESULTS AND DISCUSSION

In India, fennel productivity remains low owing to the dearth of high-yielding and stable varieties. A survey of the literature indicates limited genetic improvement research has been conducted on fennel. There is a lack of adequate genetic variability, limited information on the genetics of economically important traits, inadequate knowledge of population dynamics and a high degree of genotype-environment interaction.

Analysis of variance

A comprehensive analysis of variances for all characters under investigation has been compiled in the tables. The scientific findings in Table 1 stipulated a highly significant difference encompassing through the ten characters examined, in conjugation with days to flower initiation, days to 50% flowering, plant height, number of branches per plant, number of umbels per plant, number of umbellets per umbel, number of seeds per umbel, test weight, seed yield per plant and seed yield (kg/ha). This demonstrates considerable genetic variation among the genotypes.

Range and mean performance

Variability denotes the existence of differences among individuals within a plant population. Such variability is essential for the success of any crop improvement initiative. Mean performance has been depicted in a tabular form in Table 1. The initiation of flowering across varied genotypes exhibited a range from 71.33 days for JF-3 to 91 days for RF-67. The genotypes JF-1 and JF-2 demonstrated the earliest flowering initiation, occurring at 71.33 days and 72.67 days, respectively, indicating a shorter duration prior to flowering. The plants demonstrated a variation in height spanning from 116.40 cm to an impressive 195.67 cm, specifically in the RF 281 and HF-192 genotypes. Genotype NDF-46 measuring 190.54 cm was commensurable to the grand mean height of 157.72 cm.

The fennel genotypes demonstrated an average of 11.86 umbels per plant, illustrating a diverse range of variance from 4.46 in Jagudan-2 to 24.00 in RF-125. Maximum umbel production was achieved by RF-125, closely followed by RF-143 with 21.06 and RF-281 at 21.00. In terms of seed yield per plant, figures span from 15.27 g in RF-205 (Check) to 33.13 g in RF-143, yielding a mean of 23.84 g.

Table 2: Estimates of mean, range, phenotypic and genotypic coefficients of variability, heritability, genetic advance as percentage of mean for 10 quantitative traits in fennel.

Characters	Mean	Min	Max	Coefficient of variation		Heritability (%)	GA% mean
				GCV(%)	PCV (%)		
Days to flowering initiation	81.37	71.33	91.00	7.05	7.41	90.56	13.83
Days to 50% flowering	92.19	82.66	103.00	6.09	6.51	87.49	11.73
Plant height (cm)	157.27	116.40	195.67	13.92	14.43	93.17	27.69
No. of branches per plant	5.68	3.80	9.80	23.01	25.95	78.62	42.02
Number of umbel per plant	11.86	4.46	24.00	47.79	49.15	94.59	95.77
Number of umbelletes per umbel	24.22	15.69	29.33	14.65	18.29	64.19	24.19
No. of seeds per umbel	350.66	79.73	651.66	45.78	45.83	99.78	94.21
Test weight (g)	4.42	3.21	6.04	16.29	16.36	99.13	33.41
Seed yield/plant (g)	23.084	15.27	33.14	21.75	22.09	96.89	44.11
Seed yield (kg/ha)	489.95	326.70	639.00	21.52	21.56	99.59	44.24

Table 3: Phenotypic correlation coefficient among seed yield and its attributing traits in fennel.

Characters	Days to 50% flowering	Plant height (cm)	No. of primary branches	No. of umbel per plant	No. of umbelletes per umbel	No. of seeds per umbel	Test weight (g)	Seed yield/plant (g)
Days to flowering initiation	0.914**	-0.027	0.179	0.201	0.119	-0.097	-0.398	-0.041
Days to 50% flowering		0.106	0.065	0.008	0.087	-0.082	-0.449*	-0.159
Plant height (cm)			-0.485*	-0.522**	0.578**	0.606**	0.359	-0.231
No. of primary branches				0.901**	0.043	-0.157	-0.128	0.265
No. of umbel per plant					-0.069	-0.253	-0.089	0.410*
No. of umbelletes per umbel						0.658**	0.456*	-0.259
No. of seeds per umbel							0.266	-0.453*
Test weight (g)								0.101

*, ** significant at 5% and 1% level, respectively.

Coefficients of variation

Coefficients of variation referred to phenotypic and genotypic traits, accompanied with heritability and genetic advance as a percentage of the mean, are detailed in Table 2. The table illustrates significant variability among genotypes for each measured characteristic. Genotypic coefficient of variation (GCV) exhibited a range from 6.088% to 47.799%, particularly for the trait of days to 50% flowering and the number of umbels per plant, respectively. Phenotypic coefficient of variation (PCV) expressed the values of range 6.51% to 49.14%, corresponding to the traits of days to 50% flowering and the number of umbels per plant, respectively. The phenotypic coefficient of variation was generally greater than the genotypic coefficient across all traits suggesting that environmental factors significantly influence trait expression. Comparable results were observed by Meena *et al.* (2010) and Meena *et al.* (2017).

Heritability and genetic advance

Heritability range was determined in accordance to the criteria given by Johnson *et al.* (1995). Traits displaying high heritability were recognized as those with values exceeding 80%, whereas those with moderate heritability fall in between the range of 50% to 80% and the traits with low heritability were characterized by values below 50%. Estimates of the anticipated genetic improvement for various traits were calculated using a selection intensity of 5%.

Correlation coefficient

Correlation coefficient determines the impact of one variable on another which has been depicted in Table 3 and 4. Plant height demonstrated a significant positive correlation with seed yield per plant (0.899), followed by the number of seeds per umbel (0.606) and the number of umbelletes per umbel (0.578). Number of primary

Table 4: Genotypic path coefficient showing direct and indirect effects of different characters on seed yield per plant (g) in fennel.

Characters	Days to flowering initiation	Days to 50% flowering	Plant height (cm)	No. of primary branches	No. of umbel per plant	No. of umbelletes per umbel	No. of seeds per umbel	Test weight (g)	Seed yield (kg/ha)
Days to flowering initiation	-0.4586	-0.4376	0.0149	-0.086	-0.0948	-0.0636	0.0455	0.186	-0.1112
Days to 50% flowering	0.1513	0.1586	0.0167	0.0102	0.0017	0.0201	-0.0133	-0.0725	0.0285
Plant height (cm)	-0.0014	0.0044	0.0421	-0.0221	-0.0224	0.0272	0.0258	0.0153	0.0098
No. of primary branches	-0.2277	-0.0785	0.6363	-1.2146	-1.145	-0.0813	0.2001	0.1624	-0.3432
No. of umbel per plant	0.3081	0.0156	-0.7947	1.4056	1.491	-0.1008	-0.3808	-0.133	0.4082
No. of umbelletes per umbel	0.0332	0.0304	0.1548	0.016	-0.0162	0.2395	0.1716	0.1175	0.1074
No. of seeds per umbel	0.0495	0.0419	-0.3061	0.0822	0.1275	-0.3577	-0.499	-0.1327	-0.0685
Test weight (g)	0.0548	0.0618	-0.0492	0.0181	0.0121	-0.0663	-0.0359	-0.1352	-0.0592
Seed yield (kg/ha)	0.0517	0.0383	0.0494	0.0602	0.0583	0.0955	0.0293	0.0933	0.2131
Seed yield/plant (g)	-0.0391	-0.1651	-0.2358	0.2697	0.4121	-0.2873	-0.4569	0.1013	0.1847
Partial R ²	0.0179	-0.0262	-0.0099	-0.3276	0.6144	-0.0688	0.228	-0.0137	0.0394

R² = 0.4535; Residual effect = 0.7393.

Table 5: Average intra and inter cluster distance.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	17.01								
II	37.43	22.13							
III	49.34	46.72	25.13						
IV	61.51	38.13	48.89	16.19					
V	34.89	41.13	64.64	69.78	34.75				
VI	33.36	52.78	40.22	72.7	49.42	0			
VII	33.24	31.48	32.39	50.7	42.35	30.57	0		
VIII	27.74	55.63	54.57	79.73	43.6	20.23	41.26	0	
IX	32.28	61	69.75	87.78	41.54	39.59	52.42	24.95	0

branches depicted a strong positive correlation with the number of umbels per plant (0.901). Umbel number per plant showed a highly significant positive correlation with seed yield per plant (0.410). The number of umbelletes per umbel also had a highly significant positive correlation with both the number of seeds per umbel (0.658) and test weight (0.456). However, the number of seeds per umbel displayed a significant negative correlation with seed yield (-0.453) and a non-significant positive correlation with seed yield per plant (0.101). In the current study, seed yield per plant demonstrated a significant positive correlation with the number of umbels per plant and the number of seeds per umbel. Additionally, it showed a positive yet non-

significant correlation with the number of effective branches per plant, the number of umbelletes per umbel and test weight. These results suggests that these traits are pivotal in determining yield in fennel. The positive correlation of seed yield per plant aligns harmoniously with previous findings by Yadav *et al.* (2013), Kumar *et al.* (2017), Pawar *et al.*, (2018) and Shekhawat *et al.*, (2022).

Path coefficient analysis

Path coefficient analysis evaluates the connectivity of several yield relevant attributes. The number of days until flowering initiation demonstrated a negative direct impact on seed yield, quantified at -0.4586. Moreover, it showed a

Table 6: Cluster mean for different characters in fennel genotypes.

Clusters	Days to flowering initiation	Days to 50% flowering	Plant height (cm)	No. of primary branches	No. of umbel per plant	No. of umbelletes per umbel	No. of seeds per umbel	Test weight (g)	Seed yield/ plant (g)	Seed yield (kg/ha)
I	87.42	98.17	168.95	5.75	11.55	24.43	471.17	3.95	21.94	516.92
II	83.08	94.17	166.17	5.2	10.47	25.21	298.75	4.9	23.75	587.42
III	79.39	90.78	144.84	5.29	10.69	20.33	192.22	3.91	23.52	375.67
IV	83.67	92.17	118.87	8.13	22.27	22.26	127.83	4.16	32.77	608.67
V	77.25	88.42	177.85	5.42	10	29.46	497.33	5.36	20.01	562.75
VI	79	90	139.6	5.73	8.8	25.42	422.67	4.2	17.86	326.67
VII	85	96.33	161.47	4.33	9.53	22.09	334	5.12	27.03	418.33
VIII	82.67	91.33	153.07	6.67	16.47	26.6	528.33	3.95	15.27	404
IX	71.67	83	161.73	6.2	13.2	24.27	651.67	4.12	24.38	470.33

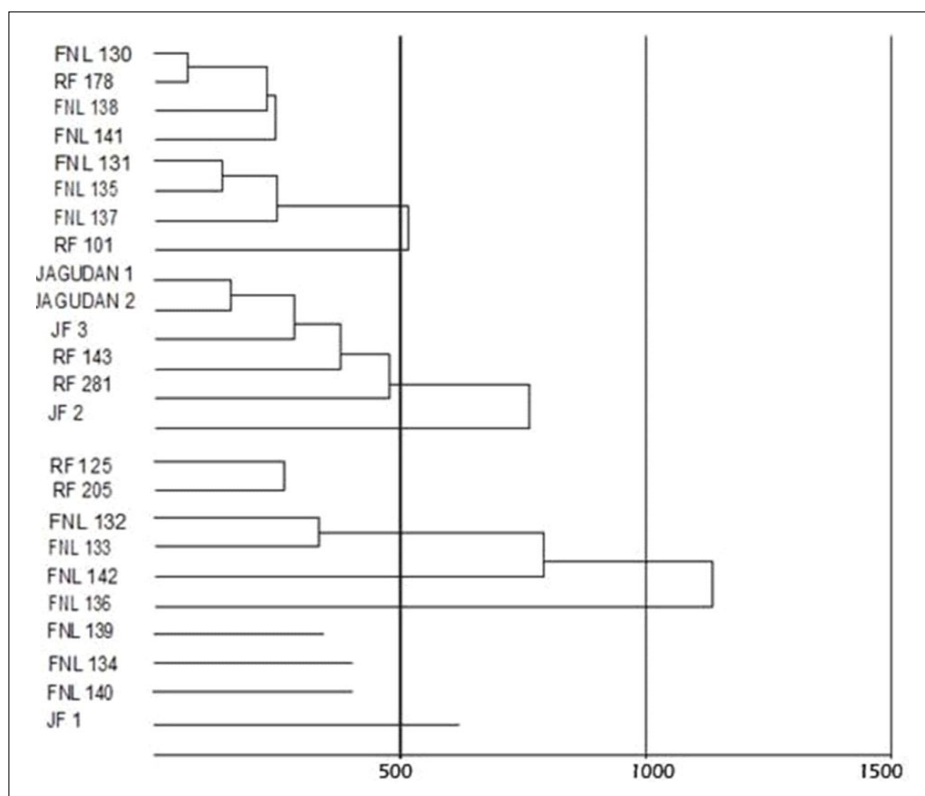


Fig 1: Clustering of twenty four genotypes of fennel on basis of Tocher's method.

positive indirect effect for various factors, such as seed yield per hectare (0.0201), plant height (0.0149) and test weight (0.186). Nonetheless, it showed a negative indirect effects via days to 50% flowering (-0.4376), the number of primary branches (-0.086), the number of umbels per plant (-0.0948) and the number of umbellets per umbel (0.0636). A direct effect of days to 50% flowering on seed yield was positive, recorded at 0.1586 and indirect positive influences were observed through the number of umbellets per umbel (0.0201), the number of umbels per plant (0.0017), seed yield in kg/ha (0.0285), the number of primary branches (0.0167) and plant height (0.0167). However, it also exhibited a negative indirect effect through seeds per umbel (0.0133) and test weight (-0.0725). Plant height contributed positively to seed yield with a direct effect of 0.0421. Its indirect negative effects were associated with the number of umbels per plant (-0.0224), the number of primary branches (-0.0221) and days to flowering initiation (-0.0014). On the other hand, it showed positive indirect effects on seed yield through seed yield in kg/ha (0.0098), the number of umbellets per umbel (0.0272), test weight (0.0153) and the number of seeds per umbel (0.0258).

The correlation coefficient's magnitude between a causal factor and its effect closely align with its direct effect. Therefore, the correlations elucidate the genuine interrelationships and indicate that direct selection of these parameters would be beneficial. These results align with the findings of Kumawat *et al.* (2020), Afshar *et al.* (2019) and Sengupta *et al.* (2014), while Cosge *et al.* (2009) and Yaldiz and Camlica (2022). highlighted the positive and significant direct effect of test weight on seed yield in fennel.

D² analysis

Intra and inter-cluster D² values

These values are depicted in Table 5. Cluster V exhibited the most substantial intra-cluster distance, succeeded by cluster III (25.13), Cluster II (22.13), Cluster I (17.01) and Cluster IV (16.19). Notably, clusters VI, VII, VIII and IX recorded no intra-cluster distance. In terms of inter-cluster divergence, Cluster IX and IV displayed the greatest distance (87.78), followed closely by Cluster VIII and Cluster IV (79.73), while Cluster V recorded the least inter-cluster distance. In the current study, 24 genotypes of fennel were categorized into nine unique, non-overlapping clusters, highlighting a significant level of diversity among the genotypes. The primary clusters identified in the genetic divergence analysis predominantly included genotypes from varied origins. However, it was also noted that the genotypes from the same origin or geographic area were often clustered together. Instances of both diverse and geographically similar genotypes being grouped within the same clusters are frequently observed. Comparable results were also documented by Choudhary *et al.*, (2017), Deswal *et al.* (2017), Meena *et al.* (2010), Jat and Chaudhary (2021), Singh *et al.*, (2022) and Prajapati *et al.*, (2022).

Cluster mean (Tocher's method)

The cluster means for the ten characters, as determined by Tocher's method are presented in Table 6 and Fig 1. It reveals a significant degree of variation across all characters examined. Specifically for the days to flowering initiation, Cluster I exhibited the highest mean at 87.42 days while Cluster IX recorded the lowest mean at 71.67 days. In terms of days to reach 50% flowering, Cluster IX again had the lowest mean at 83 days, whereas Cluster I had the highest mean at 98.17 days with Cluster III following at 62 days. Regarding plant height, Cluster V achieved the tallest average at 177.85 cm in contrast to Cluster IV which had the shortest average at 118.87 cm. Similar results were given by Choudhary *et al.*, (2017), Deswal *et al.* (2017), Meena *et al.* (2019), Jat and Chaudhary (2021), Singh *et al.*, (2022) and Prajapati *et al.*, (2022).

Grouping of genotypes

The classification of twenty four genotypes of fennel revealed in a sophisticated arrangement in Table 7 into nine distinct clusters. Cluster I, II and V each showcased a remarkable collection of four genotypes, while the Cluster III comprised six genotypes. Cluster IV included two

Table 7: Clustering of twenty four genotypes of fennel on the basis of genetic divergence.

Clusters	No. of genotypes	Genotypes
I	4	HF 256, RF 67, NDF 59, RF 178
II	4	HF 192, UF 230, AF 17, RF 101
III	6	JF 2, JF 3, JAGUDAN 1, JAGUDAN 2, RF 143, RF 281
IV	2	RF 125, RF 205
V	4	JF 18-13, JF 18-03, AF 87, NDF 46
VI	1	RF 101 (check)
VII	1	UF 231
VIII	1	RF 205 (Check)
IX	1	JF 1

Table 8: Ranking and per cent contribution of characters.

Source	Times ranked 1 st	Contribution %
Days to flowering initiation	0	0.00%
Days to 50% flowering	0	0.00%
Plant height (cm)	1	0.36%
No. of primary branches	0	0.00%
No. of umbel per plant	2	0.72%
No. of umbelletes per umbel	0	0.00%
No. of seeds per umbel	145	52.54%
Test weight (g)	29	10.51%
Seed yield /plant (g)	6	2.17%
Seed yield (kg/ha)	93	33.70%

genotypes and Clusters VI, VII VIII and IX each contained a single genotype. The findings contemplate with Tiwari *et al.*, (2024); Yadav *et al.* (2024) and Kole *et al.* (2023); Singh and Singh (2022).

Raking and per cent contribution of characters

The per cent contribution presented in Table 8 of individual characters toward the total divergence was higher for number of seeds per umbel (52.54%) which was followed by seed yield (33.70%), test weight (10.51%), seed yield per plant (2.17%), number of umbel per plant (0.72%) and plant height (0.36%). The result were in accordance to the findings of Tiwari *et al.* (2024); Yadav *et al.* (2024) and Kole *et al.* (2023); Singh and Singh (2022).

CONCLUSION

The current study concludes that fennel breeding programs should prioritize the selection of traits such as the number of primary branches, number of umbellets per umbel and the number of seeds per umbel, as these characteristics demonstrate a positive correlation with seed yield and exhibit a significant direct effect. A thorough examination of the cluster means as well as intra and inter cluster distances and individual performances revealed that the genotypes RF 101 (check), UF 231 and RF 205 (check) stands out as superior options demonstrating significant genetic diversity. These genotypes could be incorporated into future breeding programs aimed at maximizing variability in yield and yield related traits, ultimately facilitating the development of enhanced genotypes with multiple advantageous characteristics.

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Disclaimers

The views and conclusions expressed in this article are solely those of the authors and do not necessarily represent the views of their affiliated institutions. The authors are responsible for the accuracy and completeness of the information provided, but do not accept any liability for any direct or indirect losses resulting from the use of this content.

Informed consent

All animal procedures for experiments were approved by the Committee of Experimental Animal care and handling techniques were approved by the University of Animal Care Committee.

Conflict of interest

The authors declare that there are no conflicts of interest regarding the publication of this article. No funding or

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