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Genetic diversity analysis in fennel

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ABSTRACT

An experiment was conducted to study the genetic divergence of 13 fennel varieties (*Foeniculum vulgare* Mill.) using Mahalanobsis D^2 statistics. Clustering pattern indicates that varieties from the same source were distributed over different clusters. This indicated that the geographic and genetic diversity are not necessarily related, therefore the selection of varieties for hybridization should be based on genetic diversity. Estimates of intra-cluster distance ranged from 1.00-6.09. It was maximum in cluster VI and minimum in cluster II, IV and VI. Tocher's method of hierarchical cluster analysis was applied to group the varieties. The maximum inter-cluster distance between cluster III and I was 4.15 and 14.42, respectively. The varieties falling in cluster I were Hisar Swarup, GF-2, RF-101, RF-178 and RF-143, in cluster II, Rajendra Saurabha, in cluster III, Azad Saunf-1, GF-1, GF-11 and CO-1, in cluster IV, AF-1, in cluster V, RF-125 and in Cluster VI, Pant Madurika. The study suggests that clusters I & II were quite divergent from rest of the clusters and also from one another. Among the 14 characters studied for genetic divergence, 80% flowering contributed the maximum accounting for 33.33% of total divergence, followed by angle of primary branch 32.05%.

Key words: D^2 statistics, genetic divergence, *Foeniculum vulgare*.

INTRODUCTION

Fennel (*Foeniculum vulgare* Mill.) is one of the most important seed spices cultivated throughout the temperate and sub-tropical regions of the world for its aromatic seeds, which are used for culinary purpose. In India, it is mainly cultivated in Gujarat and Rajasthan and to some extent in Uttar Pradesh, Bihar, Madhya Pradesh, Punjab and Haryana. This crop has a number of industrial and medicinal uses. India is a major seed spices producer in the world. Among seed spices, only fennel contributes about 17.47% of total production. The average productivity of fennel is 528 kg/ha, however, potential productivity of fennel is only 1,000 kg/ha (Anon., 1). The development of new varieties or improvement in any crop mainly governed by the magnitude of genetic diversity and the extent of available variability for the desired characters. The nature and magnitude of genetic divergence in a population is essential for selecting diverse parents which upon hybridization leads to greater opportunity for crossing over which release latest variation by breaking up the predominantly repulsion phase linkages. The use of D^2 statistics of multivariate analysis gives an understanding of genetic diversity in the fennel. D^2 measures the degree of diversity and determines the relative proportion of each component traits to the total divergence. Information on these aspects in fennel is limited and hence there is a need for identifying the genotypes having better performance for yield and quality traits which belong to diverse parents. Therefore, the present investigation was undertaken to determine the genetic diversity in 13 fennel varieties developed at various research institutes for different agro-ecological conditions.

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MATERIALS AND METHODS

The present study was carried out in *rabi* season of 2006-07 and 2007-08 at the Research Farm of National Research Centre on Seed Spices, Ajmer (26°27'0" N, 74°38'-1" E and 460 m above sea level). The soil of experimental area is sandy loam in texture and poor in fertility and water holding capacity, having pH 8 to 8.3, EC 0.07 to 0.12 and 0.15 to 0.23% organic carbon, available N 178.5 kg ha^{-1} (low), P_20_5 12 kg ha^{-1} (medium), K_2O_5 kg ha^{-1} (low). The maximum and minimum temperature during growing season of fennel (October to April) recorded was 39° and 5°C, respectively. Total rainfall of study period was 50 mm. The annual loss through PET is 1,566 mm. The study was carried out with 13 released varieties in India of fennel namely, 'Pant Madhurika', 'Hisar Swarup', 'Rajendra Saurabha', 'Azad Saunf-1', 'GF-1', 'GF-2', 'GF-11', 'Co-1', 'RF-101', 'RF-125', 'RF-143', 'RF-178' and 'AF-1'. These varieties were developed by different research institutes situated at different agro-ecological conditions, thus have different genetical backgrounds. The experiment was laid out in randomized block

design with three replications. Plot consisted of 2 m long, 6 rows spaced 60 cm apart. Plant spacing within rows was maintained at 20 cm. The recommended package of practices was adopted for raising healthy crop. Ten plants were randomly selected from each plot and observations were recorded on days of 50% flowering, plant height (cm), number of branches, length of lower node of stem from ground, length of upper node of stem from ground, length of middle node of stem from ground, diameter of umbel, umbel plant^{-1}, umbellete umbel^{-1}, seed umbellete^{-1}, days 80% flowering, test weight (g), yield plot^{-1}. Data of both the years were pooled and genetic divergence was analysed through Winstat version 8.5. The genetic divergence was estimated using the Mahalanobis D^2, Mahanalobis (6) and the varieties were grouped into clusters by following the Tocher's method described by Rao (7).

RESULTS AND DISCUSSION

The analysis of variance shows highly significant differences among the varieties for all the characters studied. The pooled divergence for all the characters within the varieties tested by the Wilk's criterion X_2 (14413 at 176 d.f.) was significant. Hence, the analysis of genetic divergence among varieties used in the study was considered relevant. The multivariate analysis based on D^2 values of 13 varieties grouped them into six clusters (Table 2). Among these cluster I consisted of 5 varieties, followed by cluster II, (1), cluster III, (4), clusters IV, (1), cluster V (1) and cluster VI (1) were monogenotypic. The results indicated that genetic divergence is not related to geographical diversity and may possibly be due to varietal diversity among the varieties due to diversity of their pedigree along with natural and directional selection pressure for certain agronomic traits. Similar results were also

Table 1. Details of fennel varieties with respect to place of release and geographical location.

Variety	Place and state of release	Topography
Hisar Swarup	Hisar, Haryana	29°10′N 75°43′E / 29.17°N 75.72°E / 29.17; 75.72. It has an average elevation of 212 m.
RF-125	Jobner, Rajasthan	26°58′N 75°23′E / 26.97°N 75.38°E / 26.97; 75.38. It has an average elevation of 400 m.
RF-101	Jobner, Rajasthan	-do-
RF-178	Jobner, Rajasthan	-do-
RF-143	Jobner, Rajasthan	-do-
Rajendra Saurabha	Samastipur, Bihar	20.90N 86.08E. It has an average elevation of 56 m
Azad Saunf 1	Kanpur, Uttar Pradesh	26.46°N 80.33 E. It has an average elevation of 126 m
GF-2	SDAU, Gujarat	230.40N 720.30 E. It has an average elevation of 81 m
GF-1	SDAU, Gujarat	-do-
GF-11	SDAU, Gujarat	-do-
CO-1	Coimbatore, Tamil Nadu	11.16 N 76°58.21°E It has an average elevation of 411.2 m
Pant Madhurika	Pant Nagar, Uttrakhand	28.970 N 79.41 E It has an average elevation of 243.8 m
AF-1	Ajmer, Rjasthan	26° 27' 0" N, 74° 38' -1" E and 460 m above sea level

Table 2. Distribution of 13 fennel varieties in clusters based on D^2 values.

Cluster	Variety (ies)	No. of variety(ies)
I	Hisar Swarup , GF-2, RF-101, RF-178 and RF-143	5
II	Rajendra Saurabha	1
III	Azad Saunf 1, GF-1, GF-11 and Co-1	4
IV	AF-1	1
V	RF-125	1
VI	Pant Madhurika	1

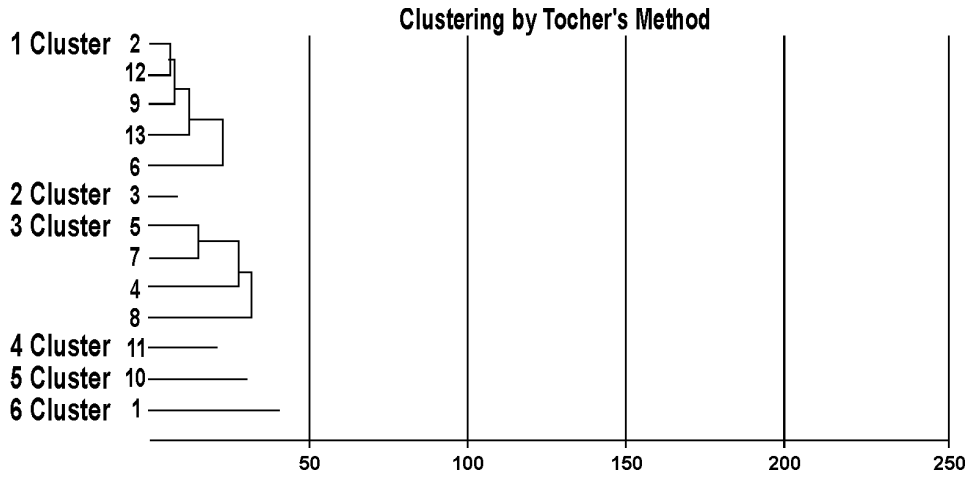

Fig. 1. Clustering of fennel varities by Tocher's method. 1. Pant Madhurika, 2. Hisar Swarup, 3. Rajendra Saurabha, 4. Azad Saunf 1, 5. GF-1, 6. GF-2, 7. GF-11, 8. Co-1, 9. RF-101, 10. RF-125, 11. AF-1, 12. RF-178, 13. RF-143.

reported by Kole and Mishra (5). Genetic drift and selection forces under diverse environments could cause greater diversity than geographical distance (Kole *et al.*, 4).

Intra-cluster distance is the main criterion for selection of genotypes using D^2 analysis. Inter-cluster distance varied from 4.38 to 12.93. Minimum inter-cluster D^2 value was observed between clusters IV and III (5.704) indicating the close relationship among the varieties included in these clusters. Maximum inter-cluster value was observed between clusters V and VI (12.93) indicating maximum divergence between the varieties of these clusters (Table 3). The inter-cluster D^2 values were also higher between the clusters III and V (12.27), clusters II and V (11.25) and clusters IV and VI (11.01). Hence, it is suggested that inter-mating between the varieties included in these diverse clusters may give high heterotic response and thus better segregants.

The contribution of individual characters to the divergence was worked out in terms of number of times it appeared first (Table 4). 80% of flowering (152.20) contributed maximum towards genetic divergence, followed by degree of angle, yield plot^{-1}, diameter of umbel, test weight and seeds umbel^{-1}. Cluster means for 14 characters revealed that genotypes included in cluster V showed maximum yield plot^{-1}, umbel plant^{-1}, length of middle node,^{1} and degree of angle with 50

Table 3. Cluster means value for 14 characters in fennel (two years pooled data).

Cluster	50%	PH	NB	Angle	LN	UN	MN	D/U	U/P	Ul/U	S/Ul	80%	TW	Y/P
I	95.6	146.5	6.7	63.9	3.5	18.3	14.6	16.4	27.9	22.2	24.3	152.2	9.2	1.2
II	96.0	133.6	6.3	60.3	3.1	18.2	13.4	15.9	19.7	21.2	24.6	148.3	9.5	0.8
III	95.5	143.4	6.3	57.1	3.4	18.0	14.2	16.1	27.2	24.7	24.7	153.3	9.6	1.2
IV	94.0	144.5	6.6	62.4	4.0	17.4	13.8	18.2	24.3	25.5	28.0	151.0	8.8	1.3
V	94.0	144.9	6.1	64.0	3.8	17.1	16.0	15.4	37.8	22.9	25.3	153.0	8.6	1.7
VI	101.0	144.5	7.0	62.0	3.3	17.3	12.8	17.0	22.8	22.1	22.7	155.0	10.4	0.7

50%: Days to 50% flowering, PH: Plant height (cm), NB: No. of branches, LN: Length of lower node of stem from ground (cm),UN: Length of upper node of stem from ground (cm), MN: Length of middle node of stem from ground (cm), D/U: Diameter of umbel, U/P: Umbels per plant, Ul/U: Umbelletes per umbel, S/Ul: Seeds per umbellete, 80%: Days to 80% flowering, TW: Test weight (g), Y/P: Yield/plot (kg).

% flowering and plant height. Genotypes in cluster IV had maximum seed umbellete^{-1}, umbellete umbel^{-1}, diameter of umbel and length of lower node of stem from ground. It can, therefore, be concluded from the present study that hybridization among varieties of these cluster combination is expected to enhanced variability in fennel for the targeted traits. Selection of parents from diverse clusters in breeding programmes has been suggested by many workers in pulse crops (Kumar, *et al*. 3) for exploiting non-additive gene action.

These studies indicated the geographic and genetic diversity are not necessarily related. Therefore, the selection of varieties for hybridization should be based on genetic diversity rather than geographic diversity. Similar results were also reported by Agnihotri (2) in fennel. Hence, it is suggested that inter-mating between the genotypes included in these diverse clusters may give high heterotic response and thus better segregants. This will provide an opportunity to select better recombinants for various characters and thereby creating large variability for these characters in the inter-clusters distances.

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Table 4. Contribution of various characters to divergence in fennel (two years pooled data).

Character	Times ranked 1st	Contribution per cent
Days to 50% flowering	0	0.00
Plant height (cm)	0	0.00
No. of branches	1	1.28
Angle of primary branches (in degree)	25	32.05
Length of lower node of stem from ground (cm)	0	0.00
Length of upper node of stem from ground (cm)	0	0.00
Length of middle node of stem from ground (cm)	2	2.56
Diameter of umbel	4	5.13
Umbel per plant	2	2.56
Umbelletes per umbel	0	0.00
Seeds per umbellete	3	3.85
Days to 80% flowering	26	33.33
Test weight (g)	4	5.13
Yield/plot (kg)	11	14.10

Table 5. Avereage inter-cluster D^2 values in six clusters of fennel varieties.

Cluster	I	II	III	IV	V	VI
I	4.38	6.69	8.61	7.27	7.00	7.60
II		0.00	7.09	5.01	11.25	7.25
III			6.09	8.35	12.27	7.87
IV				0.00	11.01	8.33
V					0.00	12.93
VI						0.00

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