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Genetic Divergence Analysis in Fennel Genotypes

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A B S T R A C T

An experiment was conducted to study a genetic divergence analysis were estimated in 19 genotypes of fennel (*Foeniculum vulgare*Mill.) grown in a Randomized Block Design (RBD) with three replications during *Rabi* season of 2016-17 at the research farm of ICAR-National Research Centre on Seed Spices, Tabiji, Ajmer (Rajasthan). Mahalanobia D^2 statistic indicated wider genetic diversity in the population. All genotypes were grouped into seven clusters on the basis of diversity. Estimates of intracluster distance ranged from 0.00-5.70. The maximum intra cluster distance was observed within cluster I (D=5.70), whereas, III, IV, V, VI and VII showed the minimum intra cluster distance (D=0.00) followed by cluster II (D=4.91). It was maximum in cluster I and minimum in cluster III, IV, V, VI and VII. Tocher's method of hierarchical cluster analysis was applied to group the varieties. The maximum inter-cluster distance between cluster V and IV was 6.51 and 14.58, respectively. The genotypes falling in cluster II were GF-11, RF-157, RAJENDRA SAURBH, RF-205, AZAD SAUNF-1, CO-1, RF-101 and GF-12, in cluster I RF-178, RF-281, GF-2, RF-143, RF-145 and RF-125, in cluster III AF-2,in cluster IV GF-1, in cluster V AF-1, in cluster VI one HISAR SWARUP, incluster VIIPANT MADURIKA. Clusters I and II showed the highest genetic distance between them. Cluster means showed that, the cluster I showed the highest mean values for plant height (150.83) and the lowest mean value for seed yield per plot (1.08). Among the 13 characters studied for genetic divergence, seed yield per plot (kg) contributed the maximum accounting for 49.12% of total divergence, followed by number of umbles per plant 29.82.

Introduction

Fennel (*Foeniculum vulgare* Mill.), belongs to family Apiaceae. It is a diploid species with chromosome number, 2n= 22 and native of Europe and Mediterranean region (Agarwal *et al.*, 2001). Seed spices include all those annuals whose dried fruits or seed are used as spices and condiment *viz.*, fennel, fenugreek, coriander, cumin, aniseed, ajwain, dill, nigella and celery etc. Among them fennel is a major seed spice crop, which is used in seed spice and culinary purposes. These seed spices play an important role in national economy. In India, Rajasthan and Gujarat are known as "seed spices bowl" and contributes more than

80% of total seed spices production. The other states where seed spices are commonly grown are Bihar, West Bengal, Uttar Pradesh, Madhya Pradesh, Orissa, Punjab, Karnataka and Tamil Nadu. Out of 31.92 lakh ha area and 61.69 lakh tonnes production of total spices presently 16.53 lakh ha of area is under seed spices cultivation with a production of 11.75 lakh tonnes annually. The seed spices contribute 10-12% of total export of spices and account for about 51.79% and 19.06% of total area and production, respectively of total spices in the country. The export of seed spices in 2015-16 was 216870 tonnes valued Rs 2617.15 crores and its global demand is increasing day by day. Indian spices and spice products are exported to more than 135 countries and leading among them are USA, Malaysia, UAE, China and UK.

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 D2 statistics of multivariate analysis gives an understanding of genetic diversity in the fennel. D2 measures the degree of diversity and determines the relative proportion of each component traits to the total divergence.

Materials and Methods

The experiment was laid out at research farm of ICAR-National Research Centre on Seed Spices, Ajmer, Rajasthan, during *rabi* season of 2016-17. The centre lies on 74^0 35' 39" E to 74^0 36' 01" longitude and 26^0 22' 12" to 26^0 22' 31" N latitude at an altitude of 460.17 m above mean sea level, in Ajmer district of Rajasthan. The region falls under agro climatic zone III of Rajasthan. The soil of research farm is sandy loam, poor in fertility and water holding capacity, having pH 8 to 8.3, EC 0.07 to 0.12 and organic carbon 0.15 to 0.23%, available N 178.5 kg ha^{-1} (low), P_2O_5 12 kg ha^{-1} (medium), K_2O 85 kg ha^{-1} (low), Ca 214.7 kg ha^{-1} (high), Mg 258 kg ha^{-1} (medium), S 27 kg ha^{-1} (medium).The maximum and minimum temperature during growing season of fennel (October to April) recorded was 32.22° and 6.72°C, respectively. Total rainfall of study period was 26.37 mm. The study was carried out with 19 released varieties in India of fennel namely, GF-11, RF-157, RAJENDRA SAURBH, RF-205, AZAD SAUNF-1, CO-1, RF-101, GF-12, RF-178, RF-281, GF-2, RF-143, RF-145, RF-125, AF-2, GF-1, AF-1, HISAR SWARUP, and PANT MADURIKA. 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 size 3× 2 m and Spacing (R×P) 50 × 25 cm. The recommended package of practices was adopted for raising healthy crop. Five plants were randomly selected from each plot and observations were recorded on days to germination, duration of king umbel anthesis, days to 50% flowering, number of primary branches per plant, number of secondary branches per plant, plant height (cm), diameter of king umbel (cm), numbers of umbels per plant, numbers of umbellets per umbel, number of seeds per umbellet, test weight (gm), seed yield per plot (kg) and essential oil (%). Data was pooled and genetic divergence was analysed through Winstat version 8.5. The genetic divergence was estimated using theMahalanobis D2, Mahanalobis and the varieties were grouped into clusters by following the Tocher's method described by Rao (1952).

Results and Discussion

The genetic diversity existing in the population helps in selecting suitable parents for the hybridization programme. Mahalanobis's D^2 statistic is employed to assess the amount of genetic diversity and a rational choice of potential parents for hybridization in breeding programme. Average linkage tends to eleven clusters with small variance and is slightly biased towards producing clusters with the some variance (Johnson and Wichern, 1996).

The results on genetic divergence are presented below. Based upon observations of thirteen characters the Mahalanobis's statistic were computed for 19 genotypes.

Based on D^2 value, the 19 genotype could be grouped in to seven clusters. The cluster pattern of these genotypes is depicted in Table 1.cluster II was the largest comprising of 8 genotypes.

The second largest cluster was cluster I containing 6 genotypes and followed by cluster III, cluster IV, cluster V, cluster VI and cluster VII with 1,1,1,1 and 1 genotypes respectively. Genetic drift and selection forces under diverse environments could cause greater diversity than geographical distance Kole *et al.,* (2013). Genotype from different geographical regions were also grouped in the same cluster indicating no relationship between geographical distribution and genetic divergence, similar results were also reported by Meena *et al.,* (2010) and Meena *et al.,* (2014)

A personal of results on intra cluster and inter cluster distance (Table 2) revealed very interesting trend of genetic diversity. Intra-cluster (D^2) values of various clusters were found to be relatively high indicating thereby the presence of substantial genetic diversity even within a cluster. The minimum inter cluster distance (6.51) was observed between clusters I and II followed by clusters V and VI (7.13). Shalini *et al.,* (2000) and Verma and Sachan (2000) also reported considerable diversity in Indian mustard and Meena *et al.,* (2010) are reported in fennel. In heterosis breeding, genotypes of diverse clusters are likely to play an important role as potential parents as when genotypes from different clusters are intercrossed they are likely to produce heterotic combinations.

Table.1 Distribution of 19 fennel varieties in clusters based on D^2 values

Cluster No	Number of genotypes	Name of the genotypes
Cluster I	6	RF-178, RF-281, GF-2, RF-143, RF-145, RF-125
Cluster II	8	GF-11, RF-157, RAJENDRA SAURBH, RF-205,AZAD SAUNF-1, CO-1, RF-101, GF-12
Cluster III	1	AF-2
Cluster IV	1	GF-1
Cluster V	1	AF-1
Cluster VI	1	HISAR SWARUP
Cluster VII	1	PANT MADURIKA

Table.2 Intra (bold) and Inter cluster distance assessed in fennel genotypes

Clusters	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7
Cluster 1	**5.70**	7.82	7.56	7.96	8.64	8.00	11.24
Cluster 2		**4.91**	7.69	9.93	10.48	12.30	9.30
Cluster 3			**0.00**	7.84	12.98	11.17	13.46
Cluster 4				**0.00**	12.75	10.79	14.58
Cluster 5					**0.00**	7.13	6.51
Cluster 6						**0.00**	11.94
Cluster 7							**0.00**

Table.3 Contribution of various characters to divergence in fennel

S.NO.	Characters	Time Ranked 1st	Contribution %
1.	Days to germination	6	3.51%
2.	King umbel anthesis	2	1.17%
3.	50% flowering	2	1.17%
4.	King umbel diameter (cm)	0	0.00%
5.	Plant height (cm)	2	1.17%
6.	Number of primary branches	5	2.92%
7.	Number of secondary branches	7	4.09%
8.	Number of umbels per plant	51	29.82%
9.	Number ofumbellets per umbel	3	1.75%
10.	Number of Seeds per umbellets	0	0.00%
11.	Test weight (g)	3	1.75%
12.	Seed yield per plot (kg)	84	49.12%
13.	Essential oil %	6	3.51%

Table.4 Cluster means for various characters in fennel genotypes

Traits / Clusters	No of Genotypes in	Days to germination	King umbel anthesis	Days to 50% flowering	King umbel diameter (cm)	Plant height (cm)	Number of primary	Number of secondary branches	Number of umbesper plant	Number of umbellets per umbel	Number of Seeds per umbellet	Test weight (g)	Seed yield Per plot (kg)	Essential oil (%)
Cluster 1	6	8.17	25.44	84.33	14.66	150.83	9.01	28.20	47.13	21.20	24.68	7.19	1.08	2.00
Cluster 2	8	8.25	25.44	84.46	15.34	149.19	7.97	26.10	48.94	23.66	25.35	7.17	1.45	2.08
Cluster 3	1	7.33	27.67	93.00	16.93	153.67	8.20	28.07	37.30	23.60	27.87	6.65	1.29	2.22
Cluster 4	1	7.00	24.67	76.67	15.13	138.00	6.19	12.13	32.33	21.93	25.07	6.46	0.86	1.83
Cluster 5	1	7.33	24.67	93.00	15.73	167.33	9.07	28.33	74.33	23.00	28.93	7.17	0.90	1.77
Cluster 6	1	8.67	25.00	99.00	16.47	165.00	9.33	29.00	57.00	26.47	26.60	6.98	0.70	2.16
Cluster 7	1	7.00	24.67	96.00	18.93	165.00	8.20	24.33	81.00	26.67	30.73	6.92	1.28	1.94

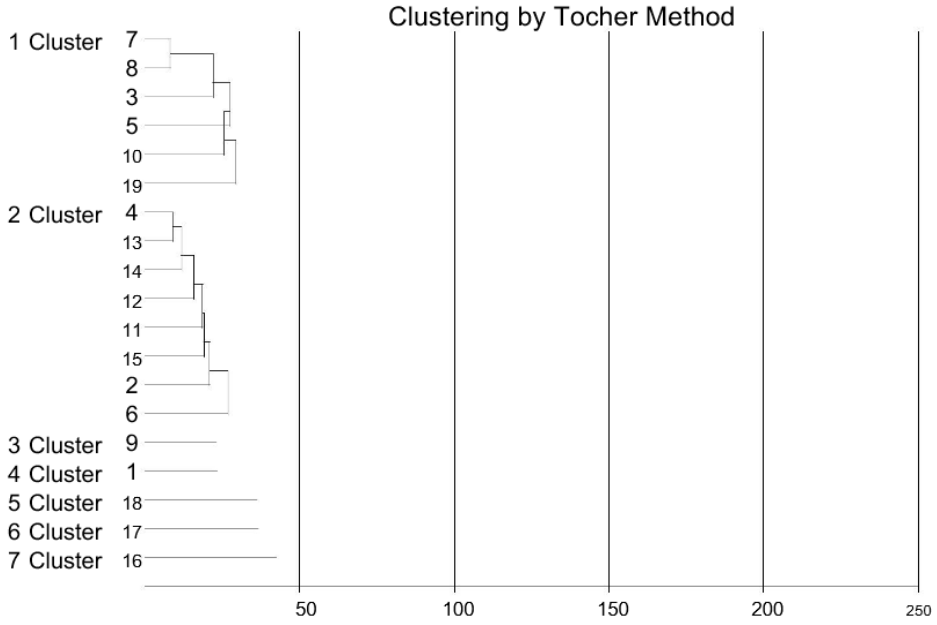

Figure 10. Clustering of fennel varities by Tocher's method. 1. GF-1, 2. RF-101, 3.GF-2, 4. GF-11, 5. RF-143, 6. GF-12, 7. RF-178, 8. RF-281, 9. AF-2, 10. RF-145, 11. Azad Saunf 1, 12.RF-205, 13.RF-157, 14. Rajendra Saurabha, 15. Co-1, 16. Pant Madhurika, 17. Hisar Swarup, 18.AF-1, 19.RF-125.

The contribution of individual characters to the divergence was worked out in terms of number of times it appeared first (Table 3) seed yield per plot (1.08) contributed maximum towards genetic divergence, followed by number of umbels per plant, number of secondary branches, days to germination and essential oil. Selection of parents from diverse clusters in breeding programmes has been suggested by many workers in pulse crop Kumar *et al.*, (1998) for exploiting non-additive gene action.

In the present study (Table 4), revealed that cluster I showed the highest mean value for plant height (150.83), days to 50% flowering (84.33), number of umbels per plant (47.13), number of seeds per umbellet (24.68), number of umbellets per umbel (21.20), number of primary branches (9.01), test weight (7.19) and the lowest mean value for seed yield per plot (1.08). Cluster VI had the smallest mean value for seed yield per plot (0.70), essential oil (2.16), test weight (6.98), number of primary branches (9.33), number of seeds per umbellet (26.60), number of umbellets per umbel (26.47), number of secondary branches (29.00), number of umbels per plant (57.00) and plant height (165).

The clustering pattern could be utilized in choosing the parents or making cross combinations which may generate high variability for various traits. Selection based on cluster means and inter cluster distances may be effective.

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 *et al.,* (1990) and Meena *et al.,* (2017) 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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