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# Assessment of Genetic Divergence in Fennel Germplasms

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## Abstract

Thirty genotypes of fennel were evaluated to assess the genetic diversity and variability present in fennel genotypes for different agronomic traits. The field experiment was conducted in augmented block design at CCS Haryana Agricultural University, Hisar during the Rabi season 2020-2021. The Euclidean cluster analysis divided all the thirtygenotypes under study into six differentclusters. The clustering patternrevealed that cluster I was having maximum number of genotypes that was nine followed bycluster II with eight number of genotypes, clusterIII was having two genotypes,clusterIVcontains three genotypes, clusterVwithfive number ofgenotypes and the last cluster, cluster VI was having three genotypes. The highest intra-cluster distance is reported for cluster III followed by cluster II, cluster I, cluster VI, cluster V and lowest in cluster IV. The highest divergence occurred between cluster VI and I followed by cluster VI and IV, cluster VI and III, cluster V and IV, cluster III and I, cluster II and I, cluster IV and III, cluster IV and I, cluster IV and III, cluster V and II, cluster III and II and lowest in cluster IV and V.Clustering pattern of genotypes was not related to geographical differentiation and it suggests that selection of these traits could be effective in improving yield potential of fennel genotype and selection of diverse parents for purposeful hybridization will lead to the achievement of a breeding goal. As a result, superior parents can be chosen from these divergent clusters for crosses, and a hybridization programme can be developed to obtain superior segregants.

***Key words :*** *Cluster analysis, genetic diversity, fennel.*

## Introduction

The fennel (*Foeniculum vulgare* Mill.) also known as *'Saunf'* is an important seed spice belonging to family Apiaceae (Umbelliferae). It is a diploid species, having somatic chromosome number, 2n = 22 and is native of European and Meditarrean region of the world (Meena *et al.,* 2019). Being a hardyplant it can be grown in a wide range of agro-climatic conditions of the world *viz.,* India, Japan, China, Italy, Bulgaria, Morocco, Spain Argentina and Turkey.India ranks first in fennel production with having a production of about 128 thousand MT from area of 75 thousand ha during 2019-2020 (1). Among seed spices fennel is contributed about 17.47% of total seed spices production of India (2). In India, it is mainly grown in the states of Rajasthan, Maharashtra, Gujarat and Haryana and also in some parts of Punjab, Uttar Pradesh, Madhya Pradesh, Haryana and Andhra Pradesh. In Haryana, fennel isgrown in an area of about 0.27 thousand hectares with the production of 0.17 thousand metric ton (3). Fennel is a cross pollinated crop owing to self-incompatibility, which result in a high degree of variation within each population and this offers the breeder to undertake screening and selection of plants to improve the population for the desired traits (4, 5). The importance of fennel based on its medicinal value and export potential as spices was recognized long back but it remained neglected for a long time from scientific attention for its improvement in its productivity as well as its quality. Though many improved varieties of fennel have been released in the country, there is still ample scope for crop improvement by traditional and advanced methods of breeding to increase its production. Genetic manipulation in fennel breeding has been restricted up to selection of distinct genotype based on morphological characters and seed yield. As crop improvement program for improving yield associated agronomic traits depends mainly on the existence of high magnitude of genetic variability and its efficientutilization, thus there is an acute need to examine the genetic variation for various traits of different genotypes/accessions in order to understand genotypic association and contribution of various yield components for crop improvement.

Genetic divergence analysis estimates the extent of diversity present among the studied genotypes and these studies could help the plant breeder in selecting the diverse parents for purposeful hybridization. The understanding of genetic divergence gives a scientific foundation for selecting genotypes for use in hybridization programmes in the future. Selecting parents based on a number of characters with the greatest divergence is required to improve yield and yield attributing features. $D^2$ analysis, as described by (6), was used to examine genetic divergence between any two genotypes, resulting in the genotypes being divided into various clusters using Ward's minimum variance method. The current study of genetic divergence is based on the classification of genotypes into six groups based on their relative D2 values. Genetic divergence analysis estimates the extent

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**Table-1 : Cluster membership profile of different genotypes of fennel.**

| Clusters | Genotypes | No. of genotypes |
|---|---|---|
| I | HF-197, HF-198, HF-200, HF-201, HF-199, HF-205, HF-203, HF-206, HF-202 | 9 |
| II | HF-207, HF-213, HF-209, HF-219, HF-220, HF-226, HF-231, HF-233 | 8 |
| III | HF-223, HF-232 | 2 |
| IV | HF-228, HF-229, HF-230 | 3 |
| V | HF-208, HF-212, HF-211, HF-222, HF-224 | 5 |
| VI | HF-210, HF-225, HF-214 | 3 |

**Table-2 : Estimates of inter and intra cluster distances in different fennel genotypes.**

| | ClusterI | Cluster II | ClusterIII | Cluster IV | Cluster V | Cluster VI |
|---|---|---|---|---|---|---|
| ClusterI | 3.219 | 5.363 | 6.151 | 5.234 | 7.624 | 9.077 |
| Cluster II | | 3.288 | 4.496 | 4.191 | 4.764 | 5.858 |
| Cluster III | | | 4.015 | 5.238 | 5.160 | 7.252 |
| Cluster IV | | | | 2.229 | 6.832 | 8.061 |
| Cluster V | | | | | 3.022 | 4.102 |
| Cluster VI | | | | | | 3.168 |

Diagonal : Intra-cluster distancesOff diagonal : Inter-cluster distances.

of diversity present among the studied genotypes and these studies could help the plant breeder in selecting the diverse parents for purposeful hybridization. Hence, the study was conducted to assess the genetic divergence and inter-relationship among the thirty genotypes of fennel for different yield attributes.

## Materials and Methods

The present experiment was carried out during *Rabi* season 2020-21 at Chaudhary Charan Singh Haryana Agricultural University, Hisar. The field experimental site was located at Vegetable Science farm, Hisar that is between 29.15°N latitude 75.69°E longitudes with a mean altitude of 215 m above msl. The present investigation was carried out with 30 fennel genotypes along with two checks **(**Hisar Saurab and GF-2). These diverse genotypes were sown (30th October 2020) with Augmented block design having four blocks with fifteen entries in each block and having plot size of 3.0 m × 1.0 m with spacing of 50 cm × 20 cm. All recommended agronomic practices were followed timely for successful raising the crop. Randomly five competitive plants were taken to record observation on quantitative characters namely plant height (cm), primary branches per plant, secondary branches per plant, umbels per plant, umbellate per plant, seeds per umbellate, seeds per umbel and seed yield/plant(g). Euclidean cluster analyses (7) have been applied to assess genetic diversity and grouping of genotypes was done on the basis of minimum genetic distance using (8) minimum method.

## Results and Discussion

By using the Euclidean cluster analysis, all the thirtygenotypes under study were divided into six differentclusters. These clusters of fennel genotypes under study are shown in the (Table-1). The clustering patternrevealed that cluster I was having maximum number of genotypes that was nine namely HF-197, HF-198, HF-199, HF-200, HF-201, HF-202, HF-203, HF-205 and HF-206 followed bycluster II with eight number of genotypes namely HF-207, HF-209, HF-213, HF-219, HF-220, HF-226, HF-231 and HF-233, clusterVwithfive number ofgenotypes namely, HF-208, HF-211, HF-212, HF-222 and HF-224, cluster IV contains three genotypes namely HF-228, HF-229 and HF-230 andcluster VI was also having three genotypes namely, HF-210, HF-214 and HF-225 and the last clusterIII was having two genotypes being HF-223 and HF-232. Diversity analysis of different fennel genotypes resulted in greater inter cluster distances in comparison to the intra cluster distances. The Mahalonobis' Euclidean distances are shown in the Fig-2. These findings revealed that there is a greater range of diversity among genotypes or between six different clusters than there is within a cluster. The results revealed that inter-cluster distances were greater than intra-cluster distances, indicating that fennel genotypes have a vast genetic diversity. The highest intra-cluster distance is reported for cluster III (4.015) followed by cluster II (3.288), cluster I (3.219), cluster VI (3.168), cluster V (3.022) and cluster IV (2.229). The intra and inter cluster distances are shown in (Table-2) which helps in measuring the range of diversity present in intra and inter clusters. The highest inter-cluster distance was reported in cluster VI and I (9.077) followed by cluster VI and IV (8.061), cluster VI and III (7.252), cluster V and IV (6.832), cluster III and I (6.151), cluster II and I (5.363), cluster IV and III (5.238), cluster IV and I (5.234), cluster IV

**Table-3 : Mean performance of clusters for yield and its contributing traits in different fennel genotypes.**

| Cluster | Plant Height (cm) | Primary branches/Plant | Secondary branches/Plant | Days to 50% flowering | Umbels/plant | Umbellets/ Plant | Seeds/umbellet | Seeds/umbel |
|---|---|---|---|---|---|---|---|---|
| I | 166.763 | 8.141 | 8.344 | 99.719 | 44.315 | 21.233 | 15.052 | 403.215 |
| II | 155.679 | 8.604 | 8.692 | 107.512 | 55.558 | 30.133 | 18.129 | 494.888 |
| III | 167.067 | 8.417 | 8.633 | 108.100 | 57.450 | 31.067 | 19.050 | 524.683 |
| IV | 129.022 | 8.433 | 8.311 | 110.500 | 47.400 | 30.267 | 17.444 | 407.133 |
| V | 164.540 | 11.113 | 11.200 | 106.087 | 62.967 | 34.813 | 20.267 | 587.867 |
| VI | 166.778 | 11.667 | 11.867 | 107.600 | 66.322 | 36.200 | 21.022 | 590.678 |

***Table-3 : Contd……***

| Cluster | Days to maturity | Seed yield/plant (g) | Test weight (g) | Standard germination (%) | Seedling length (cm) | Seedling dry weight (g) | Seed Vigour Index-I | Seed Vigour Index-II |
|---|---|---|---|---|---|---|---|---|
| I | 190.607 | 41.119 | 4.031 | 85.352 | 13.826 | 2.961 | 1180.123 | 252.915 |
| II | 216.104 | 49.625 | 4.786 | 86.840 | 15.050 | 3.224 | 1306.945 | 279.996 |
| III | 217.067 | 54.317 | 5.487 | 86.997 | 14.320 | 2.203 | 1245.482 | 191.695 |
| IV | 225.667 | 42.356 | 3.572 | 86.160 | 13.323 | 3.018 | 1147.976 | 260.068 |
| V | 212.947 | 57.953 | 5.276 | 88.232 | 16.372 | 2.947 | 1444.243 | 259.988 |
| VI | 216.711 | 59.356 | 6.113 | 89.512 | 16.082 | 3.832 | 1440.277 | 342.942 |

and III (5.160), cluster V and II (4.764) and cluster III and II (4.496) and cluster VI and II (4.191).

The cluster mean values of all the six clusters for 30 fennel genotypes under investigation is represented in the (Table-3). The analyzed data showed that the cluster mean for plant height was observed highest in cluster III (167.067) followed by cluster VI (166.778) and cluster I (166.763) (99.819) and lowest in the cluster IV (129.022). The trait primary branches per plant was observed highest in the cluster VI (11.667) followed by cluster V (11.113) and cluster II (8.604) and lowest in the cluster I (8.141). Secondary branches per plant were recorded highest in the cluster VI (11.867) followed by cluster V (11.200) and cluster II (8.311) and lowest in cluster IV (8.311). The cluster mean for the character days to 50% flowering for the genotypes taking less days to flower were grouped into cluster I (99.719) followed by cluster II (106.087) and cluster VI (107.512). The mean for the traitumbels perplantwas noted highest in the cluster VI (66.322) followed by cluster V (62.967) and cluster II I(57.450) and lowest in the cluster I (44.315).The mean values for the character umbellets per umbel were grouped in the cluster VI (36.200) followed bycluster V (34.813) and cluster III (31.067) and lowest in cluster I (21.233). The cluster mean for the character seeds per umbellet was noted highest in the cluster VI (21.022) followed by cluster V (20.267) and cluster III (19.050) and lowest in the cluster I (15.052). The cluster VI (590.678) followed by cluster V (587.867) and cluster III (524.683) were grouped byhighest mean for the trait seeds per umbeland lowest in the cluster I (403.215). The earliest maturing genotypes were grouped in the cluster I (190.607) followed by cluster V (212.947) and cluster II (216.104) and the late maturing genotypes were grouped in the cluster IV (225.667) and in cluster III (217.067). The mean for character test weight was observed highest in the cluster VI (6.113) followed by cluster III (5.487) and in cluster V (5.276) and lowest in the cluster I (4.031). The genotypes with highest seed yield plant were grouped in cluster VI (59.356) followed by cluster V (57.953) and cluster III (54.317) and lowest in the cluster I (41.119). The character standard germination reported highest mean value in the cluster VI (89.512) followed by the cluster V (88.232) and in cluster III (86.997) and lowest in the cluster I (85.352). Seedling length was recorded highest in the cluster V (16.372) followed by cluster VI (16.082) and cluster II (15.050) and lowest in the cluster IV (13.323). The data for the trait seed vigour index-I has resulted in highest mean performance of the cluster V (1444.243) followedby cluster VI (1440.277) and cluster II (1306.945) and lowest in the cluster IV (1147.976). The highest mean for seed vigour index-II was categorized in the cluster VI (342.942) followed by cluster II (279.996) and cluster IV (260.068) and lowest in the cluster III (191.695).

Similar results were confirmed by (9) in fenugreek and the cluster analysis suggested that there was considerable diversity among the germplasms and there is a very good scope to bring about improvement through hybridization and selection by crossing germplasms from different clusters. Similar results were reported by (10, 11, 12) in fennel and observed that the genetic diversity is not related to geographical variations necessarily. (4) studied the clustering pattern of the fennel accessions based on agro morphological data using UPGMA and the accessions were grouped into four clusters based on 2011 data and three clusters for 2012 data. In the first year grouping, cluster 1, included four accessions of

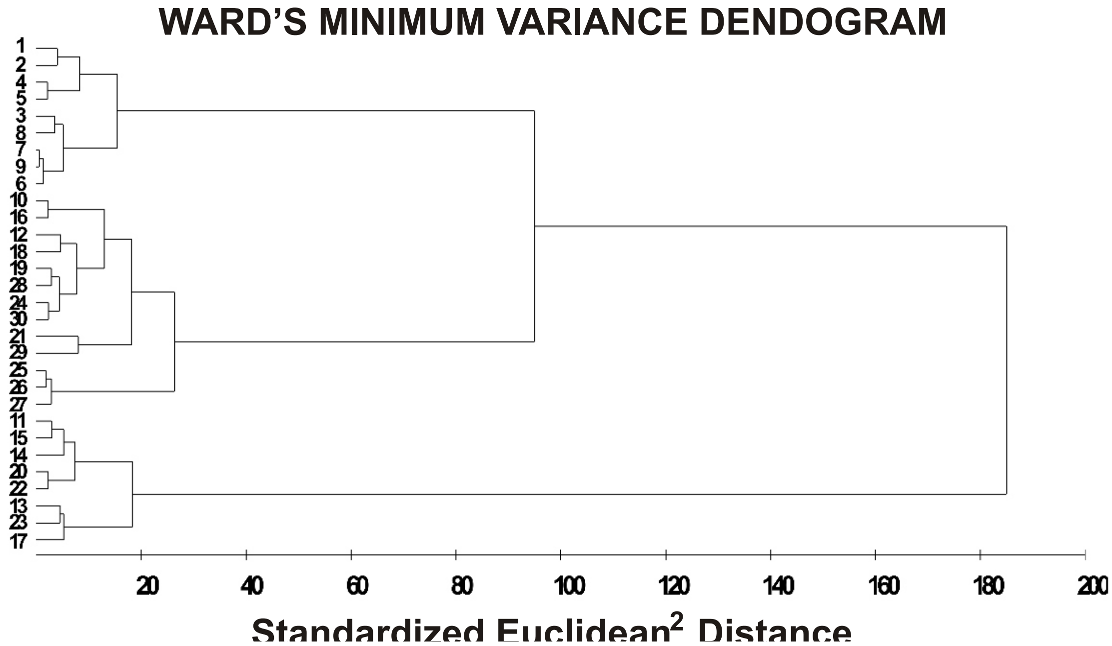

**Fig-1 : Dendrogram showing the clustering pattern of different genotypes of fennel.**

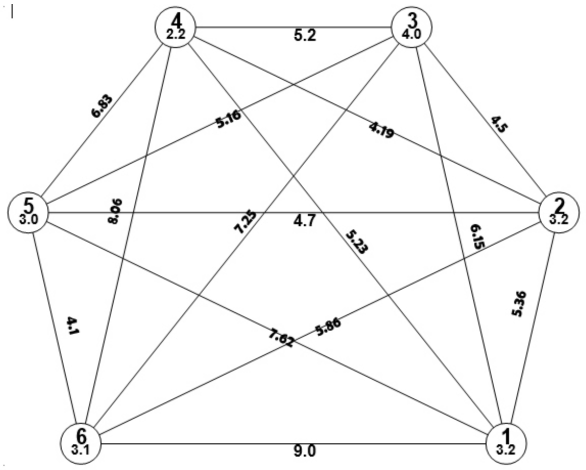

**Fig-2 : Mahalonobis' Euclidean distances among six clusters of different fennel genotype.**

Kashan, Yazd I, Yazd II, and European II and cluster 2 consisted of eight accessions of Tehran, European I, Hamadan, Shiravan, Esfahan I, Shiraz, Bushehr and Ebnesina. In the second year grouping, accessions of these two clusters combined together to form a single cluster. These accessions were characterized by moderate to late maturity, the tallest plant height, high fresh and dry weights, and the highest essential oil percentage.

The study of genetic divergence in sixty genotypes of fennel by (13, 14) revealed that total eight clusters were formed with estimated range of intra cluster distance from 1.420-3.213 with largest intra cluster distance in Cluster VI and smallest intra cluster distance in VIII. Among the VIII clusters, maximum inter-cluster distance was shown by cluster VIII with two clusters namely; cluster VI (8.827) followed by cluster V (7.381). This shows that genotypes (Fig.-1) in cluster VII were more divergent than other clusters. Cluster II having highest number of genotypes followed by cluster VII and V. (15) confirmed in the study of fennel genotypes that the high level of diversity and genetic distance beneficial for breeding proposes.

In conclusion, results of cluster analysis showed that there is no concordance between geographical resemblance and genetic diversity as the genotypes developed from different geographical region were included in the same clusters. The analysis suggested that there was considerable diversity among the germplasms. There is a very good scope to bring about improvement through hybridization and selection by crossing germplasms from different clusters. Present study suggests that selection of these traits could be effective in improving yield potential of fennel genotype and selection of diverse parents for purposeful hybridization will lead to the achievement of a breeding goal.

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