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Diversity Analysis Based Upon Yield and its Contributing Traits in Fennel (*Foeniculum vulgare* L.)

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A B S T R A C T

Sixty 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 2016-2017. Divergence study among the genotypes revealed that sixty genotypes were grouped in VIII clusters. Cluster II having highest number of genotypes followed by cluster VII and V. Based on Euclidean cluster analysis sixty genotypes were grouped into VIII distinct clusters. The distances were significant difference which helps for maximum genetic segregation and genetic recombination for crosses as well as obtaining heterotic response in breeding program for improving yield and yield related traits. 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.

Introduction

Fennel (Sauf) belongs to the family Umbelliferae (Apiaceae) grown as seed crop in North Indian plains and it is a medicinal plant used as anti-spasmodic, appetite stimulant, stomatic, diuretic, anti inflammatory, anti diarrheic, against colic and as a lactation promoter (Neamatollahi *et al.,* 2009). Availability of sufficient germplasm is a basic requirement for the genetic improvement of a crop. Germplasm has a pool of desirable traits in respect to yield, quality, biotic and abiotic stress resistance. 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 the adaptability and productivity of the crop.

Since most of the characters are quantitatively inherited and highly influenced by environment, it is difficult to judge whether the observation variability is heritable or not. Genetic diversity studies offers prospects for improvement of individual plant traits.

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. Hence, the study was conducted to assess the genetic divergence and inter-relationship among the sixty genotypes of fennel for different yield attributes.

Materials and Methods

The present experiment was carried out during *Rabi* season 2016-17 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. Sixty genotypes of fennel seeds were collected from different locations of India (Gujarat, Haryana and Rajasthan).These diverse genotypes were sown (13 November 2016) 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 eight 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 (Spark, 1973) have been applied to assess genetic diversity and grouping of genotypes was done on the basis of minimum genetic distance using Wards (1963) minimum method.

Results and Discussion

Cluster analysis is the most basic method for estimating similarities and the objective of cluster analysis is to group the variables in to clusters such that elements within a analysis have a high degree of natural association among themselves while the cluster are relatively distinct from each other. The magnitude of D² value suggested that there was considerable diversity in the genotypes of fennel. The range of variation allowed for grouping of sixty genotypes into VIII clusters based on data of yield and yield attributes (Table 1). The analysis of genetic diversity of fennel genotypes through the cluster analysis based on Euclidean distance (Ward, 1963) showed considerable amount of genetic diversity in the material. On the basis of relative magnitude of distances, 60 fennel genotypes were grouped into VIII clusters in such a way that the genotypes within the cluster had more similarity than the genotypes belonging to different clusters (Fig. 2). In general intra-cluster distances were relatively lower than inter-cluster distances showing that genotypes included within a cluster were genetically closer to each other than the genotypes included in different clusters (Table 2). Cluster VIII had smallest intra-cluster distance (1.420) while cluster VI had largest intra-cluster distance (3.213). Maximum intra-cluster distance (Fig. 1) was shown by cluster VII (3.213) followed by cluster II (2.788) followed by cluster IV (2.475), cluster VII (2.417), cluster I (2.384), cluster III (2.337), cluster V (2.283) and cluster I (1.420).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. In cluster VIII, genotypes showed higher yield per plant and cluster VI is characterized by having most of the agronomic traits such as primary branches per plant, umbellate per plant, seeds per umbellate, seeds per umbel and seed yield/plant (Table 3). Constellation of genotypes into different clusters based on yield and yield attributes was completely randomly at random and no relationship was observed between geographical origin and genetic diversity as the genotypes developed from different geographical region were included in the same clusters (Table 1).

Table.1 Number of genotypes fallen in different clusters

Clusters	No. of Genotypes	Genotypes
I	4	HF-101,HF-103, HF-104, HF-105
II	18	HF-102,HF-118, HF-123, HF-124,HF-196,HF-120,HF-129,HF-125,HF-130, HF-126,HF-127,HF-197,HF-121,HF-198,HF-199, HF-200
III	3	HF-229,GF-2,Raj.Saurab
IV	5	HF-122,HF-223, HF-207, HF-208,HF-209
V	7	HF-210,HF-222, HF-211, HF-220,HF-212,HF-225,HF-213
VI	4	HF-219,HF-226, HF-214, HF-228
VII	16	HF-106,HF-108, HF-113, HF-114,HF-116,HF-115,HF-201,HF-202,PF-35, HF-107,HF-112,HF-203,HF-207
VIII	3	HF-109,HF-110, HF-111

Table.2 Percent contribution of each trait toward divergence

Traits	Times ranked first	Percent contribution toward divergence
Plant Height(cm)	450	25.42
Number of primary branches per plant	8	0.45
Number of secondary branches per plant	38	2.15
Number of umbels per plants	562	31.75
Number of umbellate per plant	101	5.71
Number of seeds per umbellate	4	0.23
Number of Seeds per umbel	28	1.58
Seed yield/plant(g)	579	32.71

Table.3 Average inter and intra clusters D² values

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	2.384	3.432	4.643	4.172	4.686	6.197	3.619	4.196
Cluster II		2.788	3.727	3.489	3.490	4.849	3.894	5.843
Cluster III			2.337	4.765	5.033	5.770	3.889	5.960
Cluster IV				2.475	3.296	4.206	4.830	7.072
Cluster V					2.283	3.608	5.168	7.381
Cluster VI						3.213	6.649	8.827
Cluster VII							2.417	3.893
Cluster VIII								1.420

Table.4 Cluster mean for different traits of fennel

Clusters	Plant Height (cm)	Primary branches	Secondary branches	Umbels per plant	Umbellate /Umbel	Seeds per umbellate	Seeds per umbel	Seed yield(g)
Cluster I	149.375	5.591	21.184	56.725	28.119	18.211	428.628	56.296
Cluster II	158.529	8.699	27.306	63.316	31.118	17.444	447.443	63.282
Cluster III	179.968	9.410	28.727	49.308	31.786	13.763	396.333	51.333
Cluster IV	176.217	11.370	22.251	65.265	34.843	20.679	539.913	63.085
Cluster V	153.554	10.559	31.354	65.940	32.238	21.218	602.280	69.940
Cluster VI	162.022	11.554	27.188	65.457	35.964	23.354	639.438	78.693
Cluster VII	142.010	10.224	24.086	46.965	23.915	14.663	396.735	49.138
Cluster VIII	106.309	4.884	18.640	35.572	20.660	13.710	353.566	41.517

Fig.1 Cluster diagram showing genetic divergence among the 8 clusters based on inter and intra clusters D² values
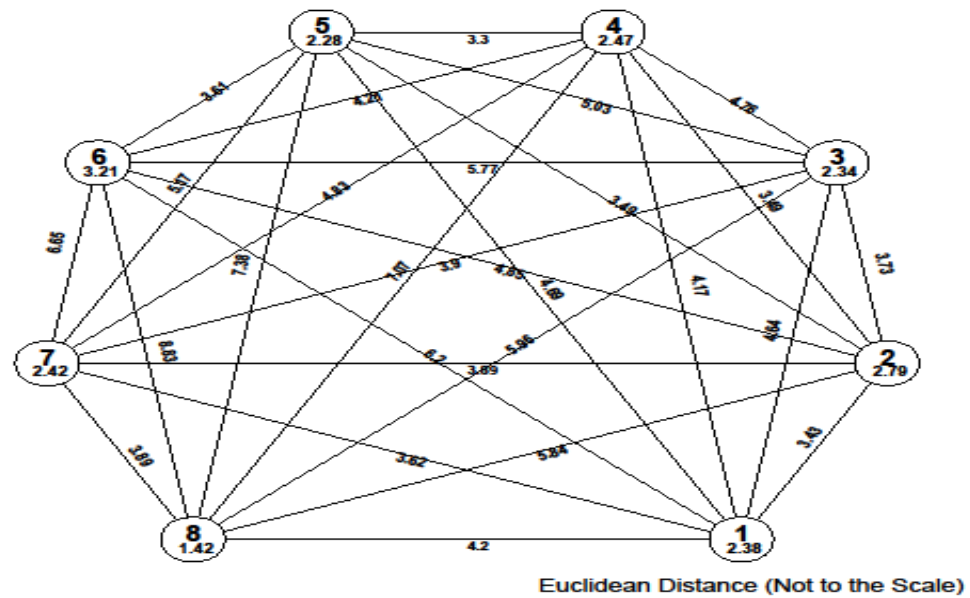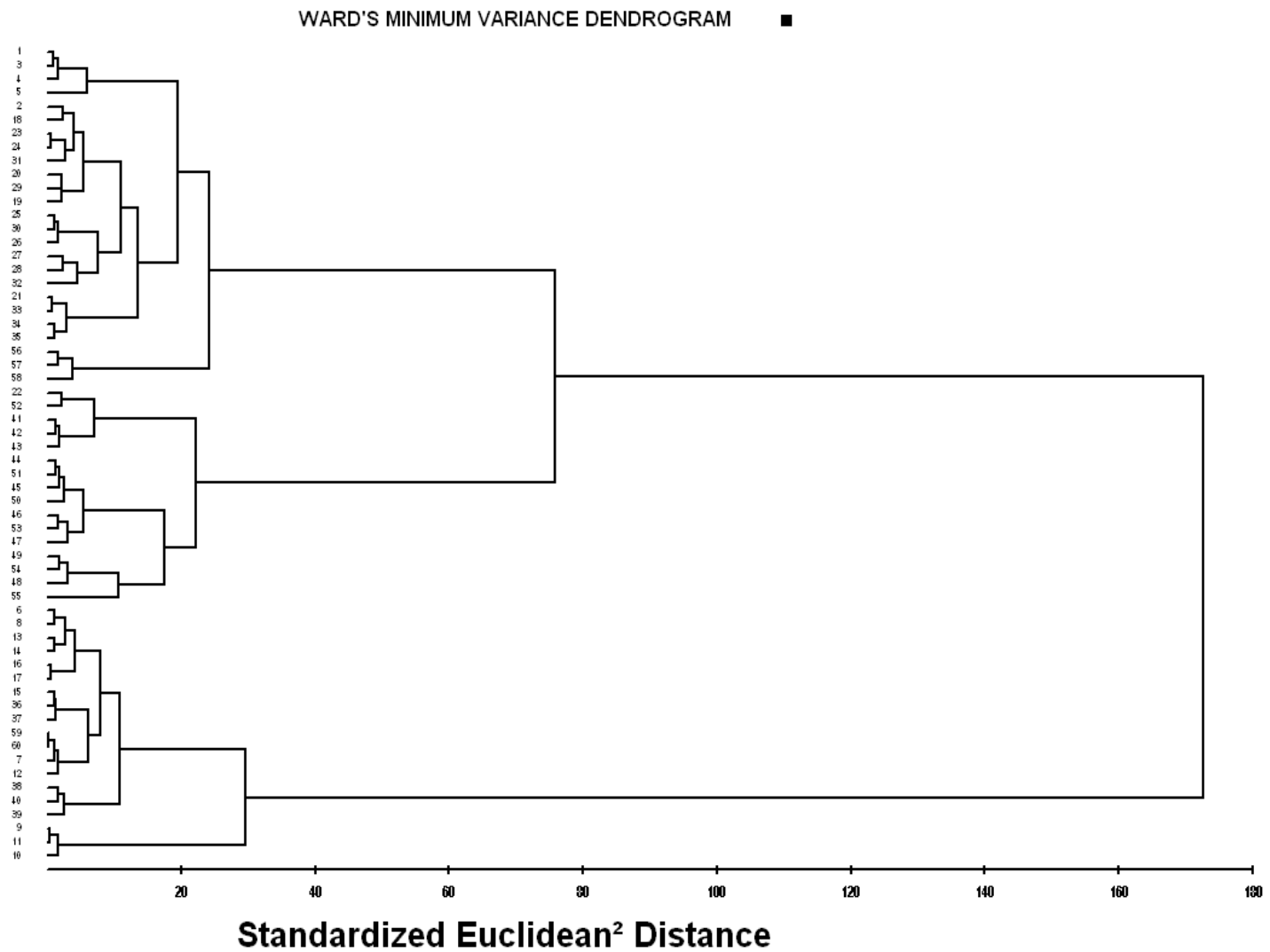

Euclidean Distance (Not to the Scale)

Fig.2 Dendrogram of 60 genotypes of Fennel based on Euclidean distance

Similar results were reported by Zahid *et al.,* (2008), Meena *et al.,* (2010), Sefidan *et al.,* (2014) in fennel and observed that the genetic diversity is not related to geographical variations necessarily. Similar results were confirmed by Wojo *et al.,* (2015) 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. The number of times each of the eight characters appeared in first rank and its respective per cent contribution towards diversity is presented in table 3. Among all the characters studied, seed yield contributed maximum(32.71 %) to diversity by taking first rank 574 times, followed by number of umbels per plant (31.75 %) ranking 562 times first, plant height (25.42 %) 450 ranking times first, umbellate per plant (5.75) with ranking 101 times first, number of secondary branches per plant (2.15 %) with ranking 38 times first, seeds per umbels (1.58 %) with ranking 28 times first, number of primary branches per plant (0.45 %) with ranking 8 times first and seeds per umbellate (0.25 %) with 4 ranking times first. Cluster means together information on the traits that contribute maximum towards divergence would help in selection of parents (Table 4). Among the genotypes of fennel, variability is high for seed yield, umbels per plant and plant height. Diversity of umbels per plant, umbellate per plant and plant height can be exploited for getting high yield and increase the yield level further. Salami *et al.,* (2017) 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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