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ESTIMATION OF THE GENETIC DIVERGENCE FOR THE SEED YIELD AND ITS COMPONENT TRAITS IN FENNEL (*FOENICULUM VULGARE* MILL.)

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ABSTRACT

A total 78 genotypes with three checks of fennel (*Foeniculum vulgare* Mill.) were evaluated for genetic divergence for the seed yield during *Rabi* season of 2020-2021 at the Main Experiment Station, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (U. P.), India. Utilizing Beale and Spark D², the genetic divergence was calculated, and the genotypes were arranged into clusters using Ward's non-hierarchical. The maximum intra cluster & inter cluster distance ranged cluster III (17.33) to cluster I (13.57), between cluster IV, V (28.37) cluster I, V (20.41), respectively. Cluster V (16) had highest number of genotypes followed by cluster VI (15), cluster I (14), cluster II (13), cluster IV (11) cluster III (9). The highest cluster mean for number of branches per plant in cluster V (9.88), number of umbels per plant in cluster I (74.89), number of umbellate per umbel in cluster V (34.88), number of fruit per umbel in cluster V (35.64), umbel diameter in cluster I (17.03), plant height in cluster V (131.00), nodes per plant in cluster V (8.67), days to maturity in cluster I (167.41), 1000 – seed weight in cluster III (7.07), seed yield per plant in cluster VI (43.57).

Key words : Cluster mean, Inter & intra cluster distance, Clusters of genotype.

Introduction

India is the land of spices and also known as home of spices which play significant role in Indian spice economy. International organization for Standardization defined “Spices and condiments as such natural material or plant or vegetative products used as pouring flavor, aroma and piquancy for food”.

Fennel (*Foeniculum vulgare* Mill.), chromosome number (2n = 22) belong to family Apiaceae, is one of the important seed spices & cultivated temperate & subtropical region of the world due to its aromatic seeds, which is used as culinary purpose in food industry. In India, it is mostly cultivated in Gujarat, Rajasthan and some extent in Uttar Pradesh, Bihar, MP, Punjab and Haryana (Meena *et al.*, 2010). Origin place of fennel is Southern Europe and Mediterranean region. Gujarat is

the leading state in production of fennel (98.40 tonnes) and Uttar Pradesh is the fifth leading state with production of about (0.64 tonnes) (NHB, 2019). In India, the total cultivated area is 83,000 ha, production is 140, 000 MT. Thus, productivity is 1.63 metric tonnes per ha (NHB, 2019).

It is an annual, biennial or perennial aromatic herb, depending on the variety and essential oil of fennel fruits was used for flavouring purpose, cosmetic and pharmaceutical products (Bilia *et al.*, 2000).

The genetic diversity within the population helps in selecting suitable parents for the hybridization programme. Beale and Spark D² statistic is employed to assess genetic diversity and select potential parents for hybridization in breeding programme. Average linkage tends to twelve clusters with small variance and is slightly biased towards

producing clusters with the some variance (Johnson and Wichern, 1996).

Materials and Methods

The study was carried out during *Rabi* season 2020 to 2021 at the Main Experiment Station Department of Vegetable Science Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (U. P.), India; latitude 24.47° to 26.56° N and longitudes 83.98° E at an altitude of 113 m above the mean sea level. 75 germplasm & Check varieties like- Rajendra Fennel (RF-101), Rajendra Fennel (205) and Narendra Fennel (NDF-1) was grown in sandy loam soil, pH 8.5 in augmented block design. Observation recorded during field work was Plant height (cm), Number of primary branches per plant, Nodes per plant, Days to maturity, Inter nodal length (cm), Days to 50% flowering, Number of umbels per plant, Number of umbellate per umbel, Number of seed per umbellate, Umbel diameter (cm), 1000- seed weight (g), Seed yield per plant (g). The genetic divergence D^2 was estimated by using non - hierarchical Euclidean cluster analysis Beale & Spark.

Table 1 : Clustering pattern of seventy five genotypes of fennel.

| Cluster number | Number of genotypes | Genotypes |
|----------------|---------------------|--|
| I | 14 | NDF-24, NDF-25, NDF-49, NDF-192, NDF-44, NDF-47, NDF-188, NDF-27, NDF-50, NDF-16, NDF-28, NDF-8, NDF-6, NDF-48 |
| II | 13 | NDF-31, NDF-22, NDF-41, NDF-15, NDF-35, NDF-36, NDF-38, NDF-18, NDF-39, NDF-21, NDF-30, NDF-40, NDF-52 |
| III | 9 | NDF-198, NDF-37, NDF-202, NDF-43, NDF-203, NDF-184, NDF-55, NDF-187, NDF-1 |
| IV | 11 | NDF-54, NDF-12, NDF-7, NDF-201, NDF-194, NDF-195, NDF-29, NDF-32, NDF-197, NDF-190, NDF-200 |
| V | 16 | NDF-19, NDF-193, NDF-191, NDF-23, NDF-42, NDF-9, NDF-26, NDF-17, NDF-196, NDF-51, NDF-45, NDF-46, NDF-10, NDF-199, NDF-11, NDF-183 |
| VI | 15 | NDF-5, NDF-53, NDF-185, NDF-2, NDF-14, NDF-20, NDF-3, NDF-4, NDF-34, NDF-33, NDF-189, NDF-13, NDF-186, RF-205, RF-101 |

Table 2 : Intra and inter clusters D^2 values of six clusters in fennel genotypes.

| Cluster number | I | II | III | IV | V | VI |
|----------------|--------------|--------------|---------------|--------------|--------------|--------------|
| I | 13.57 | 20.82 | 27.15 | 27.80 | 20.41 | 26.22 |
| II | | 13.71 | 22.156 | 21.38 | 25.76 | 21.79 |
| III | | | 17.331 | 23.29 | 25.65 | 28.09 |
| IV | | | | 15.43 | 28.37 | 27.44 |
| V | | | | | 14.60 | 25.17 |
| VI | | | | | | 17.05 |

*Bold diagonal values indicate intra-cluster distance; the remainder of values indicates the inter-cluster distances.

Results and Discussion

The study of genetic divergence among the seventy five genotypes of fennel was carried out by using D^2 statistics (Spark and Beale). All the genotypes grouped into six cluster presented in Table-1. Cluster V (16) had highest number of genotypes followed by cluster VI (15), cluster I (14), cluster II (13), cluster IV (11) cluster III (9). Number of genotypes, which are grouped into different cluster that indicate genetic divergence present in genotypes. The estimates of intra and inter – cluster distant represented by D^2 values given in Table 2. The maximum intra cluster distance observed in the case cluster III (17.33) and minimum cluster I (13.57).

The maximum inter cluster distance value observed between cluster IV and V (28.37) revealed that these two cluster are genetically more diverse to each other. The minimum cluster distance value was recorded in cluster I and V (20.41) the lower inter cluster values between the clusters showed that there are not much genetically diverse from each other.

The inter clusters mean for twelve characters in fennel had given in Table 3. It showed that cluster mean for different characters had considerable difference among the clusters for all the characters under study. The highest cluster mean for 50% flowering in cluster I (107.41), number of branches per plant in cluster V (9.88) inter nodal length in cluster V (16.67) number of umbels per plant in cluster I (74.89) number of umbellate per umbel in cluster V (34.88), number of fruit per umbel in cluster V (35.64), umbel diameter in cluster I (17.03), plant height in cluster V (131.00), nodes per plant in cluster V (8.67), days to maturity in cluster I (167.41), 1000 – seed weight in cluster III (7.07), seed yield per plant in cluster VI

Table 3 : Cluster mean for twelve characters in fennel.

| Characters Cluster No. | Days to 50 % flowering | Number of branches per plant | Inter nodal length (cm) | Number of umbels per plant | Number of umbellate per umbel | Number of fruit per umbellate | Umbel diameter (cm) | Plant height (cm) | Nodes per plant | Days to maturity | 1000-seed weight(g) | Seed yield per plant (g) |
|------------------------|------------------------|------------------------------|-------------------------|----------------------------|-------------------------------|-------------------------------|---------------------|-------------------|-----------------|------------------|---------------------|--------------------------|
| I | 107.41 | 9.11 | 15.51 | 74.89 | 29.44 | 30.22 | 17.03 | 124.83 | 7.69 | 167.41 | 6.70 | 39.03 |
| II | 100.70 | 8.05 | 14.87 | 54.65 | 24.99 | 30.25 | 15.40 | 109.74 | 7.07 | 160.70 | 5.79 | 40.19 |
| III | 93.38 | 8.73 | 16.30 | 52.65 | 30.88 | 26.18 | 14.53 | 110.81 | 8.67 | 153.38 | 7.07 | 43.35 |
| IV | 86.95 | 8.38 | 14.62 | 56.99 | 30.42 | 33.55 | 15.09 | 122.41 | 7.28 | 146.95 | 6.19 | 37.61 |
| V | 105.60 | 9.88 | 16.67 | 55.67 | 34.88 | 35.64 | 14.83 | 131.00 | 8.03 | 165.60 | 6.95 | 43.18 |
| VI | 102.66 | 9.87 | 12.15 | 55.83 | 32.95 | 28.63 | 13.00 | 119.11 | 6.54 | 162.66 | 5.64 | 43.57 |

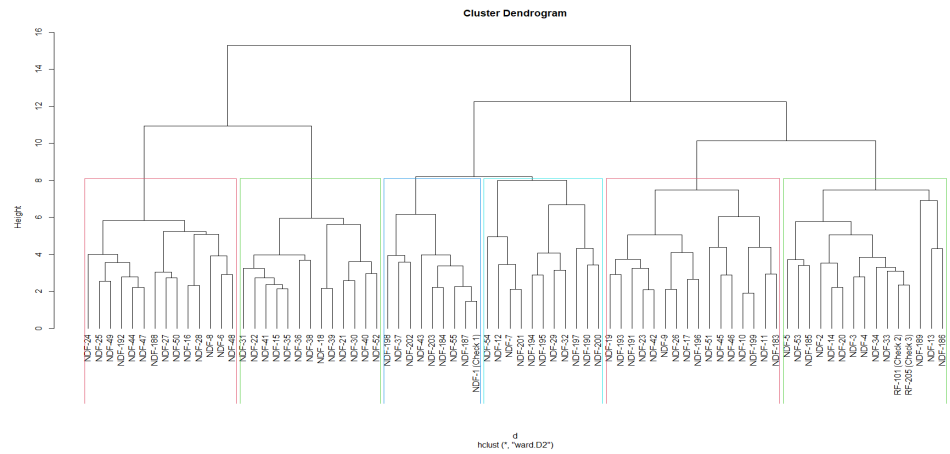


Fig. 1 : Dendrogram of 75 genotypes with three checks of fennel following Ward's method.

(43.57). The lowest cluster mean for days to 50% flowering number in cluster IV (86.95), number branches per plant in I cluster (8.05), inter nodal length in cluster VI (12.15), number of umbels per plant in cluster III (52.65), number of umbellate per umbel in cluster II (24.99), number of fruit per umbellate in cluster III (26.18), umbel diameter in cluster VI (13.00), plant height in cluster II (109.74), nodes per plant in cluster VI (6.54), days to maturity in cluster IV (146.95), 1000 – seed weight in cluster VI (5.64), seed yield per plant in cluster IV (37.61). 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 mean and inter cluster distances may be effective. Similar report also given by Dhakar *et al.* (2018).

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