

Genetic Diversity in Fennel (*Foeniculum Vulgare* Mill)



Agriculture

KEYWORDS :

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ABSTRACT

Fennel is an important seed spice crop, having high market value. The present productivity of the country is quite low seeing the per unit time and area it takes as it's a long duration crop having high biomass. Therefore to increase the present productivity levels there is need to identify and develop high yielding genotypes. Hence the present study was done to know the extent of diversity present among twelve varieties of fennel and their sixty six F1's for eight component traits. The extent of variability observed for each trait was considerable, but the extent of vigour expected in F1's as compared with the parents was not too high, which shows lack of diverse alleles in the genotypes selected. There is an immense need to collect geographically diverse genotypes of fennel to strengthen the ongoing improvement programmes on fennel.

Introduction

Fennel (*Foeniculum vulgare* Mill.) well known as Raziyan in Persian is considered as one of the oldest herbs and possesses very good medicinal value, it belongs to the family Apiaceae and is native to Mediterranean regions (Hornok, 1992). In India it is mainly cultivated in the south western parts of Rajasthan and Northern Gujarat, though scattered areas also exist in the states of Uttar Pradesh, Madhya Pradesh, Punjab, Haryana etc. But significant production comes from the Gujarat and Rajasthan. In India fennel is cultivated in an area of about 61,680 ha giving a production of about 1,05,320 tonnes, hence the annual productivity is about 17.07 q/ha (Annual Report, 2013).

Fennel is a major seed spice crop having high potential it is used as food and is also used in cosmetic, and medical industries. Fennel essential oil has possess valuable antioxidant, and has antibacterial, anticancer and antifungal activity (Lucinewton et al., 2005; El-Awadi & Esmat, 2010). With time the demand of fennel has increased in the food processing industries due to its high use in food processing and value addition. Being a long duration crop the potential yield of the crop is still low and there is an immense need to increase the present yield level. Therefore, to execute a strong fennel varietal improvement programme the prime necessity is to know the extent of variability available in hand. The variability may be from the natural variants available in nature or it may be created by means of hybridization or mutation. In the present study a set of twelve promising varieties were taken and crosses among them were made in a diallel fashion. The aim of the present study was to broaden the genetic base of fennel by recombining the genome of two parents. Morphological observation for yield and yield contributing traits were taken. The set of 78 genotypes including parents were evaluated for the extent of diversity present among them for the traits studied.

Material and Methods

A set of twelve parents viz., 1) RF-143, 2) RF-178, 3) AF-1, 4) RF-125, 5) RF-101, 6) Co-1, 7) GF-2, 8) AS-1, 9) GF-1, 10) Pant Madurika, 11) Hisar Sugandha, 12) Rajendra Sugand were selected to undertake present study. These twelve parents were crossed in a diallel fashion excluding reciprocals and sixty six F1's were generated. These F1's and 12 parents were evaluated together to know the extent of genetic diversity present among each other for traits viz., primary branches per plant, secondary branches per plant, umbel per plant, umbellate per umbel, seed per umbel, plant height, test weight and yield per plot (Single row plot of 3 m; plant to plant distance was kept 50 cm). Observation was recorded on randomly selected plants. Based on the mean value of eight traits genetic diversity was estimated among 78 genotypes using the NTSys PC ver. 2.01e software (Rohlf, 2005). Euclidean distance matrix was created and further using the SHAN sub-programme the UPGMA based dendrogram was generated.

Results and Discussion:

Based on the observation recorded for the eight traits, both

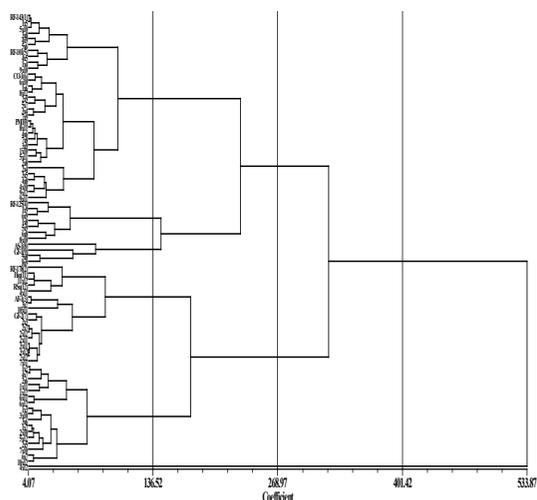
for the parents and the F1's generated showed that there is an ample amount of variation present in fennel and a significant amount of variability was created by recombination. The range of variation observed for yield per plot was maximum (parents: 806.77; F1's: 935.75 g), followed by plant height (parents: 50.80; F1's: 57.34 cm), seed per umbel (parents: 9.18; F1's: 16.04). In other traits also significant amount of variation was observed. The mean performance of the F1's was higher than the parents, showing the effect of heterosis, but the difference was not too high, suggesting occurrence of heterosis at a very low extent. The coefficient of variation for each trait was also high, in parents the maximum CV of 29.57 was observed for yield per plot (g), followed by umbels per plant (13.05). In F1's the similar results were observed as the CV was high for yield per plot (19.29), followed by umbels per plant (9.86). In fennel significant amount of variability exists as reported earlier by (Bhandari and Gupta, 1991; Piccaglia and Marotti 2000; Singh and Mittal, 2003; Rawat et al. 2013)

The extent of diversity was also estimated among the 78 genotypes (12 parents and their 66 F1's). Based on the Euclidean distance matrix, the coefficient of dissimilarity ranged from 4.07 to 533.87 on the scale. Two major clusters were formed at the coefficient value 268.97, further the cluster -1 partitioned into two sub-clusters, similarly the second major cluster also partitioned into two sub-clusters. The minimum distance of 4.06 was observed between (3 (AF-1) x 12 (R Su) and 4 (RF-125) x 12 (R Su)). The dendrogram presented in the Fig 1 depicts that the clustering of genotypes is irrespective of the parentage. The performance of the parents is not much diverse and the traits observed are governed by polygenes, hence the distribution pattern observed may be due to absence of diverse alleles in the parental population selected. This shows that in fennel there is need to broaden the genetic base by introduction of diverse genotypes from other geographical locations. The recombination of diverse alleles will contribute much to the heterotic vigour of the first filial generation. The present finding suggest that there is an ample amount of variability present in the fennel genotypes but the diversity is not of much importance to exploit heterosis. The set of data will be further subjected for calculation of heterosis to know the exact amount of vigour obtained by recombination.

In fennel very low attempts of recombination breeding have been done in past. The new landraces from Iran can be introduced in the country as it may happen that the geographical diversity may contribute to the accumulation of diverse alleles in the Indian landraces. The present era of biotechnology has opened up new horizons to identify diverse genotypes in fennel, studies are going on using RAPD and ISSR markers in fennel (Bahmani et al., 2012). Hence considering the importance of fennel and the future need to boost the present yield levels, it very much required to strengthen the available gene pool of the fennel by introducing and inducing more variability for development of high yielding genotypes.

Table 1. Extent of variation observed among the set of genotypes evaluated (parents and F1's)

Traits/Parameters	No. of Primary branches per plant	No. of Secondary branches per plant	No. of Umbels per plant	No. of Umbellates per plant	No. of Seed per umbel	Plant height (cm)	Yield per plot (g)	Test weight (g)
Parents								
Mean	5.74	20.75	23.86	27.76	34.70	129.90	956.91	9.72
Minimum	4.80	17.26	18.94	23.73	29.66	106.40	502.08	6.70
Maximum	6.87	24.26	27.89	31.07	38.84	157.20	1308.85	11.48
CV	11.16	11.14	13.05	9.20	9.20	10.51	29.57	12.97
F1's								
Mean	5.94	21.50	25.85	29.78	36.50	132.02	970.05	9.89
Minimum	4.52	17.20	17.97	23.81	24.73	103.31	558.37	7.71
Maximum	6.61	23.75	29.85	31.53	40.77	160.65	1494.12	11.39
CV	8.36	7.47	9.86	6.73	7.27	9.28	19.29	8.45

**Fig 1. Euclidian distance based dendrogram depicting the extent of dissimilarity among the fennel genotypes**

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