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Genetic Variability Analysis of Inbred Lines of Fennel (*Foeniculum vulgare* Mill.)

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Abstract

Genetic variability, correlation coefficients and path coefficients analysis were estimated in a set of 120 accessions of *Foeniculum vulgare* Mill. grown in an augmented complete block design with six blocks and five checks during rabi 2018-19. Analysis of variance indicated significant difference among accessions and significant variability with respect to all the characters namely days to 50 per cent flowering, days to maturity, plant height, branches per plant, umbels per plant, umbellets per umbel, seeds per umbellet, 1000- seed weight and seed yield per plant. The high estimates of heritability and genetic advance were found for the characters seed yield per plant and seeds per umbellet where it was low for days to maturity. The highest percentage of PCV and GCV was observed for seed yield per plant.

Key words : *Fennel, variability, gcv, pcv, umbellets and augmented design.*

Introduction

Fennel (*Foeniculum vulgare* Mill. 2n=22) belonging to the family *Apiaceae* is an allogamous crop with 82.2 to 95.4% cross-pollination (1) and native of Europe and Mediterranean region (2).

It is a 100–180 cm tall, sturdy, scented annual plant with a smooth, branching stem that grows hollow and has prominent veins as it matures. The leaves are sheathed, alternating, and decompound. The terminal flower bears a compound umbel that is surrounded by bract involucres. Flowers are pentamerous, complete, complete, hermaphrodite, and tiny. The fruit, also called the seed, is actually a schizocarp made up of two mericarps that are joined by a splitting carpophore. A fruit can grow to a length of 4 to 8 mm. The stage of harvesting determines the fruit's size and color. The entire plant, including the leaves, stalks, bulbs, and seeds, has a lovely perfume. The leaves that resemble fish strings are prized for their flavor garnish and diuretic qualities. The seeds are also chewed and masticated in India, either by themselves or in conjunction with betel leaves. (3).

About 9.5% protein, 2.0% fat, 42.3% carbs, 18.5% crude fiber, and 13.4% minerals are found in the seeds. Depending on the genotypes or botanical categories, the volatile oil content of the seeds ranges from 0.7% to 6.0%. Anethole and fenchone are the primary components in fennel oil. Alpha-pinene, camphene, alpha-phellandrene, and dipentene are the additional ingredients. To smell soaps and flavor cakes, volatile oil from seeds is extracted (4,5).

It is generally acknowledged that fennel originated in Southern Europe. It is mostly grown in nations like India, Romania, Russia, Hungary, Germany, France, Italy, Sri Lanka, Malaysia, Japan, Argentina, and the United States, although it is grown all over the temperate and subtropical regions of the world. As a cold-weather crop, it is mostly grown in Gujarat and Rajasthan, as well as to lesser extent in Uttar Pradesh, Karnataka, Andhra Pradesh, Punjab, Madhya Pradesh, Bihar, Haryana, and Jammu & Kashmir. Total area under the crop in India is about 0.91 lakh hectares with production of 1.53 lakh tonnes (6).

In Rajasthan, it occupies an area of 0.31 lakh hectares with an annual production of 0.35 lakh tonnes. (7). It is mainly cultivated in the districts of Sirohi, Jodhpur, Nagour, Tonk, Dausa and Pali and to a limited extent in Bharatpur, Kota and Ajmer. Though the crop has a potential as a cash crop in Rajasthan, limited work has been done as far as its genetic improvement is concerned.

Inbreds were traditionally developed through continued selfing in selected plants. Recently however, production of dihaploids through either anther or pollen culture is also used. As a matter of fact, a patent on the method of dihaploid production was awarded to (8). In the present investigation, inbreds produced through traditional continuous selfing method have been used for evaluation.

Fennel is a cross pollinated crop with high heterozygosity prevailing in the natural population (1). Genetic variability is prerequisite for any crop improvement in a crop. The success of any crop improvement programme depends on the magnitude of

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genetic variability and extent to which desirable characters are heritable.

The knowledge of the magnitude and direction of interrelationship between yield and its component characters has great importance in breeding programme for the selection of desirable types, when correlation studies involve many characters then it becomes difficult to determine the importance of each of the factors. In such cases path coefficient analysis provides an effective clue for this entangling direct as well as indirect effects of characters on dependable characters like seed yield.

Materials and Methods

In the present investigation, 120 accessions were evaluated in augmented randomized complete block design with 5 checks. These lines were obtained from "All India Coordinated Research Project on Spices" at S.K.N. College of Agriculture, Jobner. Jobner is located in the semi-arid tropic zone of Rajasthan. Geographically Jobner is situated at a latitude of $20^{0}5'$ N and longitude of $75^{0}20'$ E at an altitude of 427 m above the sea mean level.

The inbreds were evaluated during *Rabi* season 2018-19 at Research Farm of S.K.N. College of Agriculture, Jobner in augmented design in six blocks with five checks viz., RF-101, RF-125, RF-143, RF-157 and RF-205 assigned randomly to each block. Each inbred and check were sown in a plot of single row of 3 meter length. The row to row and plant to plant distance was maintained 50 cm and 20 cm, respectively by thinning at 25th day after sowing. Non-experimental rows were planted as border rows in each block to eliminate the border effect if any. All the agronomical practices were followed to raise a good and healthy crop. Five plants were randomly selected and tagged before flowering from each line in each block to record the data. Data on days to 50 per cent flowering, days to maturity and test weight were recorded on whole plot basis. Various offline and online softwares (at IASRI website etc.) were used for required calculations.

Results and Discussion

The overall mean, range, genotypic and phenotypic coefficients of variation, genotypic variance, phenotypic variance, heritability (broad sense) and genetic advance as percentage of mean for different characters are given in table-1

Days to 50% flowering varied between 115 and 127 days (ILF-52) with a mean of 120.49 days. In comparison to the matching genotypic variance (2.64) and genotypic coefficient of variation (1.35), the phenotypic variance (9.54) and phenotypic coefficient of variation (2.56) were higher. The genetic advance stated as a percentage of mean corresponded to the broad sense heritability, which was 27.67 per cent, and was 1.46 per cent.

Days to maturity varied between 168 and 174 days (ILF-35 to RF-205) with a mean of 170 days. The coefficients of variation for genotype and phenotype were 0.48 and 0.93 percent, respectively. Variances due to genotype and phenotype are 0.66 and 2.53, respectively. The genetic advance expressed as a percentage of mean was 0.50 percent, and the broad sense heritability was 26.09 percent in magnitude.

Plant height ranged from 100 cm (ILF-105) to 164 cm (ILF-108) with an overall mean of 133.80 cm. The genotypic and phenotypic coefficient of variation was 2.67 and 4.43 per cent, respectively. The genotypic and phenotypic variance was observed as 12.80 and 35.10, respectively. The magnitude of broad sense heritability was 36.47 per cent with corresponding genetic advance expressed as percentage of mean being 0.50 per cent.

With a mean of 6.14, the number of branches per plant varied from 6.20 in ILF-04 to 12.60 in ILF-93. The coefficients of variation for genotype and phenotype were 8.94 and 13.78%, respectively. The variances due to genotype and phenotype are 0.57 and 21.37, respectively. The genetic advance represented as a percentage of the mean was 11.95%, and the broad sense heritability was 42.08 percent.

The range of umbels per plant was 7.20 (ILF-44) to 26.20 (ILF-32) with a mean of 15.34. The coefficients of variance for genotype and phenotype were 24.47 and 25.62 percent, respectively. There were 14.90 and 15.45 respectively in the genotypic and phenotypic variance. The genetic advance stated as a percentage of mean corresponded to the broad sense heritability, which was 91.20 percent, and was 48.14 percent.

The average number of umbellets per umbel ranged from 27.44 (ILF-74) to 14 (ILF-73) to 46 (ILF-57). The coefficients of variance for genotype and phenotype were 21.96 and 24.09 percent, respectively. 36.30 and 43.70 were the genotypic and phenotypic variances, respectively. The genetic advance stated as a percentage of mean corresponded to the broad sense heritability, which was 83.07 percent, and was 41.22 percent.

The average number of seeds per umbellet was 23.36, ranging from 9 (ILF-123) to 46 (ILF-42). The coefficients of variance for genotype and phenotype were 32.69 and 33.05 percent, respectively. There were 58.30 and 59.60 respectively in the genotypic and phenotypic variance. The genetic advance stated as a percentage of mean corresponded to the broad sense heritability, which was 77.14 percent, and was 31.88 percent.

With a mean of 5.92, the 1000-seed weight (g)

Table-1 : Mean sum of squares (ANOVA) for different characters in fennel.

Source of Variation	d.f.	Days to 50 % flowering	Days to maturity	Plant height (cm)	Branches per plant	Umbels per plant	Umbellets per umbel	Seeds per umbellet	1000-Seed weight (g)	Seed Yield per plant (g)
Blocks (b-1)	5	12.45	7.63*	35.30	0.511	2.47	9.01	4.40*	0.29*	1.06*
Entries(c+g)-1	124	9.96	2.72	137.70**	1.435	21.80**	43.70**	57.90**	0.58**	15.13**
Checks (c-1)	4	7.28	6.47*	32.00	2.665*	8.77**	43.00**	19.80	1.15	1.29*
Accessions(g-1)	119	9.54	2.53	135.10	1.376	15.45	43.70	59.60	0.55	15.56**
Accessionsvs Checks	1	70.73**	9.88*	864	3.527	829.79	48.70*	11.80**	1.40**	18.90
Error (b-1) (c-1)	20	6.90	1.87	22.3	0.797	1.36	7.40	1.30	0.102	0.39

* Significant at p = 0.05 and ** significant at = 0.01

Table-2 : General mean, range, variance, genotypic and phenotypic coefficients of variation, heritability (broad sense) and genetic advance as percentage of mean for different characters in fennel.

S. No.	Characters	Mean	Range	Vg	Vp	GCV	PCV	h^2 (bs)	GA (%)
1.	Days to 50% flowering	120.49	115-127	2.64	9.54	1.35	2.56	27.67	1.46
2.	Days to maturity	170.25	168-174	0.66	2.53	0.48	0.93	26.09	0.50
3.	Plant height (cm)	133.80	100-164	12.80	35.10	2.67	4.43	36.47	3.33
4.	Branches per plant	8.51	6.20-12.60	0.57	1.37	8.94	13.78	42.08	11.95
5.	Umbels per plant	15.34	7.20-26.20	14.09	15.45	24.47	25.62	91.20	48.14
6.	Umbellets per umbel	27.44	14-46	36.30	43.70	21.96	24.09	83.07	41.22
7.	Seeds per umbellet	23.36	9-46	58.30	59.60	32.69	33.05	97.82	66.59
8.	1000-seed weight (g)	5.92	4.32-7.80	0.44	0.55	11.31	12.53	81.45	21.02
9.	Seed yield per plant (g)	9.96	3.80-23.80	15.17	15.56	39.11	39.60	97.49	79.54

Vg = Genotypic variance
Vp = Phenotypic variance
h^2(bs) = Heritability (broad sense)
GCV = Genetic coefficients of variation
PCV = Phenotypic coefficients of variation
GA (%) = Genetic advance as percentage of mean

ranged from 4.32 (ILF-17) to 7.80 (ILF-20). The coefficients of variance for genotype and phenotype were 11.31 and 12.53 percent, respectively. The variances for genotype and phenotype were 0.44 and 0.55, respectively. The genetic advance stated as a percentage of the mean corresponded to the broad sense heritability, which was 81.45 percent, and was 21.02 percent.

The average seed yield per plant was 9.96 g, with individual plant averages ranging from 3.80 g (ILF-26) to 23.80 g (ILF-55). The coefficients of variation for genotype and phenotype were 39.11 and 39.60%, respectively. 15.17 and 15.56 were the genotypic and phenotypic variances, respectively. The proportion of broad sense heritability was 97.49%, and the genetic progress expressed as a percentage of mean was correspondingly 79.54%.

The data were analyzed, and analysis of variance showed that all of the characters had significant differences among the entries, with the exception of days to 50% flowering, days to maturity, and branches per plant, indicating that there was variation among the entries (accessions + checks) for the characters under study, whereas blocks had significant differences for days to maturity, seeds per umbellet, 1000-seed weight, and seed yield per plant. Plant height, branches per plant, umbels per plant, and seed output per plant were the only features for which checks v/s accessions were not highly significant. This was revealed by partitioning the entries sum of squares into distinct components. With the exception of seed output per plant, accessions did not significantly differ for the most of the characteristics.

These are in agreement with the earlier reports of (9,10,11,12). The block effect was significant for the characters indicating the sensitivity of accession to the environment. The checks showed significant differences for most of the characters, it indicated that checks themselves were diverse.

Estimates of genotypic and phenotypic variations revealed that phenotypic variances were typically higher than genotypic variances, showing the influence of environmental influences on the manifestation of character. On the basis of the coefficient of variation, the variances of different characters were compared. Higher GCV (genotypic coefficient of variation) and PCV (phenotypic coefficient of variation) were recorded for seed yield per plant, seeds per umbellet, umbellets per umbel and umbels per plant. Such results were also reported by (13,14,15,16,17). The GCV and PCV were moderate for branches per plant, test weight and, whereas low for plant height, days to maturity and days to 50 per cent flowering, which are in agreement with the earlier (14). On the contrary, (18) observed high value of GCV and PCV for plant height and days to 50 per cent flowering. The results revealed that the differences between genotypic and phenotypic coefficient of variations were low and this is expected in augmented design. In an augmented design, the error component used is based on checks which are repeated in blocks. This often is very limited; hence the difference is very limited. The closeness of the estimates of genotypic and phenotypic coefficient of variation indicated that these characters were least affected by the environment.

The estimates of heritability were higher (>60 per cent) for most of the traits viz. seed yield per plant, umbels per plant, umbellets per umbel and test weight indicating that these characters were less affected by environment and direct selection for these yield contributing traits would be effective for future improvement in yield. Such results were also reported by (19). While it had moderate for seeds per umbellet, which are in agreement with the earlier report of (20).

In the present investigation, genetic advance as percentage of mean was also estimated in order to determine the relative merits of different characters that can be further utilized in selection programme.

The expected genetic advance expressed as percentage of mean was observed to be high for seed yield per plant, seeds per umbellet, umbels per plant, which are in accordance with the earlier reports of (9,14,21,22). In the present study, low genetic advance was observed for days to 50 per cent flowering, plant height and days to maturity, (23). Moderate genetic advance was observed for umbellets per umbel, branches per plant and 1000- seed weight.

High heritability (broad sense) coupled with high genetic advance as percentage of mean was observed for the characters viz. seed yield per plant, seeds per umbellet and umbels per plant, which is in agreement with earlier reports of (10,11,24), while umbellets per umbel and 1000- seed weight showed high heritability with moderate genetic advance. The moderate heritability and low genetic advance were recorded for days to 50 per cent flowering, plant height, branches per plant and days to maturity, which is in agreement with earlier reports of (25).

Conclusions

With the exception of the days to 50% flowering, the days to maturity, and the number of branches per plant, the analysis of variance revealed significant differences across entries for all the characters, but blocks varied significantly for the days to maturity, seeds per umbellet, 1000-seed weight, and seed yield per plant. With the exception of plant height, branches per plant, umbels per plant, and seed yield per plant, partitioning the entries sum of squares into different components revealed that checks v/s accessions were highly significant for all of the traits, while accessions differed non-significantly for the majority of the traits. For seed yield per plant, seeds per umbellet, and umbels per plant, the GCV and PCV were higher. Most of the time, the estimates of heritability (in the broad sense) were high.

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