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Variability Studies on Yield and Yield Attributing Characters in Fennel (Foeniculum vulgare Mill.) Genotypes

Ravi Kumar Telugu^{1*}, Tehlan, S.K.¹, Mukesh K.² and Mamtha N.C.¹

¹Department of Vegetable Science, ²Department of Genetics and Plant Breeding, Chaudhary Charan Singh Haryana Agricultural University, Hisar-124004 (Haryana) *Corresponding Author E-mail: ravikumar.horti@gmail.com

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ABSTRACT

The experimental material comprised of fifty genotypes of fennel (Foeniculum vulgare Mill.) and evaluated at Vegetable Research Farm of the Department of Vegetable Science, Chaudhary Charan Singh Haryana Agricultural University, Hisar (Haryana), during the Rabi seasons of 2015-16 and 2016-17 in a randomized block design with three replications. The analysis of variance indicated high significant differences among the genotypes for all thirteen traits evaluated. This revealed prevalence of sufficient amount of variation in genotypes of fennel. Overall mean and range values indicated ample variability for most of the characters evaluated. The phenotypic coefficient of variation (PCV) was higher than corresponding genotypic coefficient of variation (GCV) were observed for characters like plant height, primary branches per plant, secondary branches per plant, days to 50% flowering, umbels per plant, Umbellates per umbel, seeds per umbellate, seeds per umbel, seed yield per plant (g), seed yield per ha (Q), harvest index (%) and test weight (g). High heritability coupled with moderate to high genetic advance as per cent of mean were observed for characters plant height (cm), primary branches per plant, secondary branches per plant, umbels per plant, Umbellates per umbel, seeds per umbellate, seeds per umbel, seed yield per plant (g), seed yield per ha (Q), harvest index (%) and test weight (g). This indicates the attributing characters among the genotypes evaluated and will be improved by selecting for yield and attributing characters.

Key words: Fennel, Variabilty, PCV, GCV and Heritability.

INTRODUCTION

Fennel, commonly known as 'saunf', an open pollinated spice crop of temperate and subtropical regions belongs to the family Umbelliferae (Apiaceae), has originated from Mediterranean region, where its high degree of genetic variability persists⁹. *Foeniculum vulgare* has two commercially important

types: bitter fennel (*F.vulgare* Mill. subsp. *vulgare var. vulgare*) and sweet fennel (*F. vulgare* Mill. subsp. *vulgare var. dulce*). It is a diploid species with chromosome number 2n = 22. Several fennel parts are edible viz., leaves, stalks, bulbs and fruits (seeds). Their inflated leaf bases are eaten as a vegetable, both raw and cooked.

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The fennel seeds are aromatic, stimulant and carminative, used in diseases of cholera, bile disturbances, nervous disorders, constipation and dysentery and also used for control of diseases attacking lungs, chest, spleen and kidney stones, menopausal problems^{10,20}.

Fennel fruits produced in India are largely consumed within the country; however there is a great scope of export to U.K., U.S.A., Malaysia and Sri Lanka. By virtue of its finest quality and high vitamin content, demand of export of its high quality seed is increasing. In India, the fennel growing states are Gujarat, Rajasthan, Haryana, Punjab, Utter Pradesh, Bihar, West Bengal, Orissa, Madhya Pradesh, Andhra Pradesh and Maharashtra. Fennel is considered as one of the minor spices, since its quantity and value is much smaller compared to other spices. In India, it occupies an area of 0.91 lakh hectares and produces 1.53 Lack MT with productivity of 1.7 MT per hectare².

Germplasm is a vital source for generating new genotypes having desirable traits that help in increasing the crop production along with quality and thus improves the level of human nutrition and health. Very few efforts have been made to improve fennel through genetic manipulation. Since most of the yield attributing characters quantitatively are inherited and highly affected by environment, it is difficult to judge whether the observed variability is heritable or not. Genetic variability estimates including genotype mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as per cent mean. Therefore, the present study was undertaken to obtain information on the nature and magnitude of variability present in fennel for yield and its yield attributing characters.

MATERIAL AND METHODS

The study was conducted at Vegetable Research Farm of the Department of Vegetable Science, Chaudhary Charan Singh Haryana Agricultural University, Hisar (Haryana), during the *Rabi* seasons of 2015-16 and 2016-17. The experimental material

50 fennel consisted of genotypes randomized block design with three replications. Each genotype is planted at a spacing of 50 cm x 20 cm (single row of 3.0 m length for each genotype). The observations were recorded on 5 randomly selected plants for 13 characters namely, plant height (cm), branches per plant, secondary primary branches per plant, days to 50% flowering, umbels per plant, Umbellates per umbel, seeds per umbellate, seeds per umbel, seed yield per plant (g), seed yield per ha (Q), harvest index (%) and test weight (g). The pooled means of two years data were statistically analysed to study the ANNOVA was worked out as per the procedure given by Panse and Sukhatme¹¹, the phenotypic and genotypic coefficient of variation (PCV& GCV) were calculated using the formula given by Burton³, Heritability (h²b) in board sense was calculated according to the method suggested by Burton and Devane et al. and the formula given by Johnson et al. was used to compute genetic advance as per cent of mean (GAM).

RESULTS AND DISCUSSION

The analysis of variance for 13 characters is presented in Table 1. The mean of sum of squares due to genotypes showed highly significant differences for all the characters, indicating sufficient amount of genetic variation in the genotypes assessed, suggesting that the breeder could proceed for further crop improvement programme using present material. Similar results have been reported by Singh and Mittal¹⁸, Rajput *et al.*¹³, Patel *et al.*¹², Meena *et al.*⁸, Sengupta *et al.*¹⁵ in fennel.

The pooled means of two years data pertaining to genetic parameters are presented in Table 2. Plant height at peak harvest stage showed that there was a significant difference among the genotypes which varied from 118.07 cm (JF-406) to 184.90 cm (HF-173) with an overall mean of plant height recorded for all genotypes was 149.28 cm. Plant height had moderate phenotypic and genotypic coefficients of variation were observed, indicating that there was a broad genetic variability for this character. Plant height

exhibited high heritability and moderate genetic advance as percent of mean, indicating that the selection of genotype for plant height in early generations would be effective. These results have also been reported by Singh *et al.* ¹⁷ and Yogi *et al.* ¹⁹.

Primary branches per plant ranged from 5.08 (JF-12) to 12.70 (HF-167) with an overall mean 9.11. Moderate phenotypic and genotypic coefficients of variation were recorded, indicating moderate amount of variability for primary branches per plant. High heritability and high genetic advance as per cent of mean suggested additive gene action for this character, thus, for improving this trait, the selection could be effective in early generations. Similar results have also been reported by Singh and Mittal¹⁸, Patel *et al.*¹² and Rawat *et al.*¹⁴.

The maximum number of secondary branches per plant was recorded in genotype H-168 (24.60), while minimum number of secondary branches per plant was recorded in genotype JF-12 (10.74) with an overall mean 17.00. Moderate phenotypic and genotypic coefficients of variation were recorded, indicating moderate amount of variability for secondary branches per plant. High heritability and high genetic advance as per cent of mean suggested additive gene action for this character, thus, for improving this trait, the selection could be effective in early generations. Similar results have also been reported by Singh and Mittal¹⁸, Patel et al.¹², Rawat et al. 14 and Sengupta et al. 15.

Significant difference among the genotypes for days to 50% flowering exhibited in the population and it ranged from 107.03 to 125.80 days with the overall mean of 115.88. Low phenotypic and genotypic coefficients of variation were observed, indicating that there was a very low genetic variability for this trait. High heritability and low genetic advance as per cent of mean were observed for days to 50% flowering, indicating that this trait could be improved through heterosis breeding since direct selection is not effective. These results are in confirmation with the findings of Rajput *et al.* ¹³ and Choudhary *et al.* ⁵.

Umbels per plant ranged from 23.67 to 71.40 with an overall mean of 44.74. Umbels

per plant were found to have high phenotypic and genotypic coefficients of variation, indicating that there was a broad genetic variability for this character. High heritability and high genetic advance as percent of mean suggested additive gene action for this character, thus, for improving this trait, the selection could be effective in early generations. These results are in confirmation with the findings of Singh and Mittal¹⁸, Singh *et al.*¹⁷ and Meena *et al.*⁸.

The data pertaining to umbellates per umbel, which ranged from 17.93 to 33.37 with an average of 25.26, showed significant differences among the genotypes. Umbellates per umbel had moderate phenotypic and genotypic coefficients of variation, with high heritability and high genetic advance as percent of mean were observed, indicating the existence of moderate genetic diversity and prevalence of additive gene action. This trait could be improved through direct selection. The results confirm the findings of Rawat *et al.* ¹⁴, Yadav *et al.*, Yogi *et al.* ¹⁹ and Sengupta *et al.* ¹⁵.

The character seeds per umbellate ranged from 14.93 to 25.60, with an overall mean of 19.52. Moderate phenotypic and genotypic coefficients of variation, with high heritability and moderate genetic advance as per cent of mean were observed for seeds per umbellate, indicating the existence of moderate genetic diversity and prevalence of additive gene action. This trait could be improved through direct selection. The results confirm the findings of Sharma *et al.*¹⁶.

The character seeds per umbel ranged from 268.90 to 851.83, with an overall mean of 501.60. High phenotypic and genotypic coefficients of variation were observed seeds per umbel, indicating that there was a broad genetic base for this trait. High heritability and high genetic advance as percent of mean were observed for seeds per umbel indicating a possible role of additive gene effect for the genotypic variance for this character. The results are in agreement with the findings of Singh *et al.* ¹⁷ and Meena *et al* ⁸.

There was a significant difference among the genotypes for seed yield per plant, which ranged from 19.04 g to 73.17 g, with an

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overall mean of 42.77 g. Seed yield per plant had high phenotypic and genotypic coefficients of variation, with high heritability coupled with high genetic advance as per cent of mean, indicating that there was a broad genetic variability for this character and selection for seed yield per plant in early generations would be effective. These results are in agreement with the results of Agnihotri *et al.*¹, Patel *et al.*¹², Meena *et al.*⁸, Sengupta *et al.*¹⁵ and Choudhary *et al.*⁵.

There was a significant difference among the genotypes for seed yield per ha, which ranged from 17.13 Q to 65.85 Q, with an overall mean of 39.07 Q. High phenotypic and genotypic coefficients of variation, with high heritability and high genetic advance as percent of mean were observed, which indicated that higher response for selection to high yields as these characters are governed by additive gene actions. These results are in agreement with the results of Agnihotri *et al.*¹, Patel *et al.*¹² and Choudhary *et al*⁵.

The character biological yield per plant (g) ranged from 210.71 g to 311.95 g, with an overall mean of 256.11 g. Low phenotypic and genotypic coefficients of variation, indicating that there was a low genetic variability for this trait. High heritability and moderate genetic advance as per cent of mean were observed for this trait, suggesting that minimum

improvement could be achieved through direct selection. These result corroborate the finding of Meena $et\ al^8$.

There was a significant difference among the genotypes for harvest index was observed, which ranged from 9.06 per cent to 24.16 per cent and the overall mean value was calculated to be 16.70 per cent. High phenotypic and genotypic coefficients of variation were recorded, indicating that there was a broad genetic variability for this character. High heritability coupled with high genetic advance as per cent of mean, indicating a possible role of additive gene effect for the genotypic variance for this trait. These results are in confirmation with the findings of Rajput *et al.*¹³, Yogi *et al.*¹⁹ and Ghanshyam *et al*⁶.

Significant difference among the genotypes for test weight (g) exhibited and it ranged from 3.47 g to 9.51 g and the overall mean of 6.05 g. Moderate phenotypic and genotypic coefficients of variation was observed, indicating that there was a moderate amount of genetic variability for this character. High heritability coupled with high genetic advance as per cent of mean, suggesting that phenotypic selection for this trait would be effective. Similar results have also been reported by Patel *et al*¹².

Table 1: Analysis of Variance for different characters of 50 fennel genotypes in pooled means of two years

S.	Character	Mean Sum of Squares				
No.	Character	Replications (2)	Treatments (49)	Error (98)		
1.	Plant height (cm)	293.23	729.25**	44.18		
2.	Primary branches per plant	2.78	8.53**	0.18		
3.	Secondary branches per plant	11.31	15.27**	0.55		
4.	Days to 50% flowering	40.31	51.71**	3.52		
5.	Umbels per plant	250.51	324.14**	4.60		
6.	Umbellates per umbel	26.81	31.54**	0.94		
7.	Seeds per umbellate	8.88	14.47**	1.50		
8.	Seeds per umbel	11196.79	44597.47**	337.32		
9.	Seed yield per plant (g)	290.86	425.38**	13.49		
10.	Seed yield per ha (Q)	223.21	345.31**	4.45		
11.	Biological yield per plant (g)	621.11	953.57**	117.73		
12.	Harvest index (%)	36.29	44.04**	1.96		
13.	Test weight (g)	0.09	4.83**	0.05		

^{*, **} significant at P=0.05 and 0.01, respectively

Table 2: Genetic parameters for different characters in 50 fennel genotypes in pooled means of two years

S.	Character	Overall Mean	Range	Coefficient of Variation		Heritability	Genetic advance	Genetic advance
No.				Genotypic	Phenotypic	(Broad sense)	(GA)	as per cent of
						(%)		mean (%)
1.	Plant height (cm)	149.28	118.07 - 184.90	10.123	11.059	83.8	28.497	19.089
2.	Primary branches per plant	9.11	5.08 - 12.70	18.309	18.883	94.0	3.333	36.571
3.	Secondary branches per plant	17.00	10.74 - 24.60	13.049	13.766	89.9	4.322	25.481
4.	Days to 50% flowering	115.88	107.03 - 125.80	3.458	3.819	82.0	7.477	6.452
5.	Umbels per plant	44.74	23.67 - 71.40	23.065	23.558	95.9	20.815	46.519
6.	Umbellates per umbel	25.26	17.93 - 33.37	12.337	13.799	79.9	5.740	22.720
7.	Seeds per umbellate	19.52	14.93 - 25.60	10.649	12.362	74.2	3.690	18.899
8.	Seeds per umbel	501.60	268.90 - 851.83	24.215	24.490	97.8	247.403	49.322
9.	Seed yield per plant (g)	42.77	19.04 - 73.17	28.916	31.719	83.1	21.406	54.303
10.	Seed yield per ha (Q)	39.07	17.13 - 65.85	22.791	25.967	77.1	18.004	52.821
11.	Biological yield per plant (g)	256.11	210.71 - 311.95	6.517	7.773	70.3	28.830	11.257
12.	Harvest index (%)	16.70	9.06 – 24.16	22.344	23.946	87.0	7.173	45.950
13.	Test weight (g)	6.05	3.47 - 9.51	17.694	19.186	85.1	3.169	33.615

CONCLUSION

From the present study it was concluded that there is a sufficient variability for different yield and its attributing characters in 50 genotypes of fennel evaluated under field conditions, which can be utilized in further crop improvement programme.

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