

## VARIABILITY STUDIES ON YIELD AND YIELD ATTRIBUTING CHARACTERS IN FENNEL (*FOENICULUM VULGARE* MILL.) GENOTYPES

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**Abstract** – The experimental material consisted of fifty genotypes of fennel (*Foeniculum vulgare* Mill.) that were evaluated in a randomised block design with three replications at the Department of Vegetable Science, Chaudhary Charan Singh Haryana Agricultural University, Hisar (Haryana), during the Rabi seasons of 2015-16 and 2016-17. For all thirteen traits studied, the analysis of variance revealed substantial variations across genotypes. This demonstrated that fennel genotypes have a substantial level of variety. For majority of the traits studied, the overall mean and range values suggested plenty of variation. 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, harvest index (%) and test weight (g) the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) (Q). 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 all had high heritability and moderate to high genetic advance as a percent of mean (g). This shows that among the genotypes studied, the attributing traits will be improved by selecting for yield and attributing traits.

### INTRODUCTION

Fennel, often known as 'saunf,' is a temperate and subtropical open pollinated spice crop that belongs to the Umbelliferae (Apiaceae) family. It originated in the Mediterranean region, where it retains a high degree of genetic variety (Miranldi, 1999). *Bitter fennel* (*F.vulgare* Mill. subsp. *vulgare* var. *vulgare*) and *sweet fennel* (*F.vulgare* Mill. subsp. *vulgare* var. *vulgare*) are two commercially important varieties of *Foeniculum vulgare* (*F. vulgare* Mill. subsp. *vulgare* var. *dulce*). It is a diploid species with  $2n = 22$  chromosomes. The leaves, stalks, bulbs, and fruits of the fennel plant are all edible (seeds). Their swollen leaf bases are consumed raw or cooked as a vegetable. Fennel seeds are fragrant, stimulating, and carminative, and are used to treat cholera, bile irregularities, mental disorders, constipation, and dysentery, as well as ailments of the lungs, chest, spleen, and kidney stones, and menopausal issues (Mohamed and Abdu, 2004; Zahid *et al.*, 2009).

Fennel fruits grown in India are mostly consumed within the country, but there is a lot of potential for export to the United Kingdom, the United States of America, Malaysia, and Sri Lanka. The demand for its high-quality seed is increasing as a result of its superior quality and high vitamin content. Gujarat, Rajasthan, Haryana, Punjab, Uttar Pradesh, Bihar, West Bengal, Orissa, Madhya Pradesh, Andhra Pradesh, and Maharashtra are the fennel-growing states in India. Fennel is classified as a minor spice since its amount and value are insignificant in comparison to other spices. It covers 0.91 lakh hectares in India and produces 1.53 million tonnes per hectare, with a yield of 1.7 tonnes per hectare (Anonymous, 2017).

Germplasm is an important source for developing novel genotypes with desired features that aid in boosting crop production while also improving food quality, hence improving human nutrition and health. There have been few attempts to improve fennel through genetic manipulation. It's

difficult to say whether the observed variability is heritable or not because most yield-attributing traits are quantitatively inherited and heavily influenced by the environment. Estimates of genetic variability, including genotype mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, and genetic progress as a percentage of the population. As a result, the purpose of this study was to learn more about the nature and amount of variability in fennel production and yield-attributing features.

### MATERIALS 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 consisted of 50 fennel genotypes in 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), 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). 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 Sukhatme

(1967), the phenotypic and genotypic coefficient of variation (PCV & GCV) were calculated using the formula given by Burton (1952), Heritability ( $h^2b$ ) in board sense was calculated according to the method suggested by Burton and Devane *et al.* (1953) and the formula given by Johnson *et al.* (1955) 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 Mittal (2002), Rajput *et al.* (2004); Patel *et al.* (2008); Meena *et al.* (2013); Sengupta *et al.* (2014) 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

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

S. No.	Character	Mean Sum of Squares		
		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

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.* (2004) and Yogi *et al.* (2013).

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 Mittal (2002), Patel *et al.* (2008) and Rawat *et al.* (2013). This shows that among the genotypes studied, the attributing traits will be improved by selecting for yield and attributing traits.

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 Mittal (2002); Patel *et al.* (2008); Rawat *et al.* (2013) and Sengupta *et al.* (2014).

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.* (2004) and Choudhary *et al.* (2017).

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 Mittal (2002), Singh *et al.* (2004) and Meena *et al.* (2013).

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

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

S. No.	Character	Overall Mean	Range	Coefficient of Variation		Heritability (Broad sense) (%)	Genetic advance (GA)	Genetic advances per cent of mean (%)
				Genotypic	Phenotypic			
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

prevalence of additive gene action. This trait could be improved through direct selection. The results confirm the findings of Rawat *et al.* (2013); Yadav *et al.* (2013); Yogi *et al.* (2013) and Sengupta *et al.* (2014).

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.* (2015).

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 per cent 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.* (2004) and Meena *et al.* (2013)

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 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.* (1997); Patel *et al.* (2008); Meena *et al.* (2013); Sengupta *et al.* (2014) and Choudhary *et al.* (2017).

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.* (1997); Patel *et al.* (2008) and Choudhary *et al.* (2017).

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.* (2013).

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.* (2004); Yogi *et al.* (2013) and Ghanshyam *et al.* (2015).

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.* (2008) and Yadav *et al.* (2013).

## 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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