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Variability studies on yield and yield governing traits in fennel (*Foeniculum vulgare* Mill.) genotypes

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Abstract

Genetic variability was studied in a set of 40 genotypes of fennel (*Foeniculum vulgare* Miller) grown at department of Seed Technology, Sardarkrushinagar Dantiwada Agriculture University, Sardarkrushinagar. The experiment was conducted during *Rabi* 2019-2020 in Randomized Block Design with three replications. Observation on five randomly selected plants were recorded for days to flowering, days to maturity, plant height, number of branches per plant, number of umbels per plant, number of umbellets per main umbel, number of seeds per main umbel, 1000-seed weight and volatile oil content in seed. Analysis of variance revealed highly significant genotypic difference among 40 genotypes for all the characters under study. Indicating the presence of wide range of variation in the material. High genotypic variances were observed for days to flowering, days to maturity, plant height, number of umbels per plant, number of umbellets per main umbel, seeds per main umbel and seed yield per plant. The genotypic coefficient of variation was highest for number of umbels per plant followed by number of umbellets per main umbel, seeds per main umbel, volatile oil content in seed (%) and seed yield per plant (g). Heritability estimates were high for Seed oil content followed by seed yield per plant, seeds per umbel, 1000-seed weight, Number of umbels per plant, number of umbellets per main umbel, number of branches per plant, plant height and days to flowering. High genetic advance as per cent of mean was recorded for seed yield per plant followed by seeds per umbel, volatile oil content, number of umbellets per main umbel, number of umbels per plant, 1000-seed weight and number of branches per plant.

Keywords: Variability, GCV, PCV, heritability, genetic advance, fennel

Introduction

Fennel (*Foeniculum vulgare* Mill.) belonging to the family Apiaceae, is a cross pollinated crop and a diploid species with chromosome number $2n=22$. It is a native of Europe and the Mediterranean region. Fennel is an annual, aromatic herb of 100-180 cm height having a slender, branched, smooth stem which becomes hollow at maturity with distinct veins. Leaves are alternate, de compound and have sheathed petiole. The inflorescence is terminal bearing compound umbel subtended by involucre of bracts. Flowers are small, hermaphrodite, complete, regular and pentamerous. The fruit commonly known as a seed is a schizocarp of two mericarps attached to dividing carpophores. A fully-grown fruit is 4 to 8 mm long. The size and the colour of the fruit depending on the stage of harvesting. The fish-string like leaves is valued as a source of flavour to garnish and also possess diuretic properties. The root is regarded as a purgative. Fennel fruits are used in diseases like cholera, bile disturbances, nervous disorders, constipation and dysentery and also used for control of diseases attacking the chest, lungs and kidney and in colic pain. In India, these seeds are also used for mastication and chewing either alone or with betel leaves.

The seeds contain about 9.5% protein, 10.0% fat, 42.3% carbohydrate, 18.5% crude fibre and 13.4% minerals. The seeds contain about 0.7 to 6.0% volatile oil depending upon genotype and botanical types. A 100 grams portion of fennel seeds provides 345kilo calories energy and a rich source of protein, dietary fibre, vitamins and several dietary minerals like calcium, magnesium, manganese, all of which exceeds 100% DV. The main constituent of the fennel oil is anethole and fenchone. The volatile oil is primarily beneficial for the digestive system and also exhibits Vermicidal, antispasmodic and anti-flatulence properties.

Fennel is a cross pollinated crop with high heterozygosity prevailing in the natural population (Ramanujam *et al.*, 1964)^[13]. Genetic variability is a prerequisite in any crop for crop improvement programme depends on the magnitude of genetic variability and extent to which desirable characters are heritable. The collection, maintenance and evaluation of germplasm are the most crucial and primary steps in any crop improvement programme. For formulating a successful breeding programme, a better understanding of the nature and magnitude of genetic variability present in the breeding material is important. Yield is a complex character governed by several other yields attributing characters. Since most of the yield attributing characters are quantitatively inherited and highly affected by the environment, it is difficult to judge whether the observed variability is heritable or not. The primary parameters like genotypic and phenotypic variances, genetic advance, genetic gain and heritability are useful in understanding the nature of inheritance of different traits.

Materials and Methods

The study was conducted at Department of Seed Technology Farm of Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Dantiwada (Gujarat), during Rabi season of 2019-20. The experimental material consisted of 40 genotypes in Randomized Block Design with three replications. Each genotype was planted at a spacing of 90 x 60 cm (single row of 6.0 m length for each genotype). The observations were recorded on 5 randomly selected plants for ten characters namely, days to flowering, days to maturity, plant height, number of branches per plant, number of umbels per plant, number of umbellates per main umbel, seeds per main umbel, 1000-seed weight, volatile oil content in seeds and seed yield per plant. The mean data were statistically analysed to study the ANOVA as per the procedure given by Panse and Sukhatme, the phenotypic and genotypic coefficient of variations (PCV & GCV) were calculated using the formula given by Burton, Heritability (h^2b) in broad sense was calculated according to the method suggested by Burton and Devan *et al.* and the formula given by Johnson *et al.* was used to compute genetic advance as per cent of mean (GAM).

Result and Discussion

The analysis of variance for 10 characters is given in Table 1. The mean sum of squares due to genotypes showed highly significant differences for all the characters, indicating the sufficient amount of genetic variation among the genotypes assessed, suggesting that the breeder could proceed for further crop improvement programme using present material. A similar results were showed by Agnihotri (1990)^[1], Sharma (1994)^[15], Patel (1995)^[11], Agnihotri *et al.* (1997)^[2], Kalra *et al.* (2002)^[7], Shukla *et al.* (2003)^[16], Singh (2003)^[19], Rajput *et al.* (2004)^[12], Lal (2006)^[9], Lal (2007)^[10], Sengupta *et al.* (2011)^[14], Chaudhry *et al.* (2012)^[3], Yogi *et al.* (2013)^[21], Jeeterwal (2015)^[5], Telugu *et al.* (2017)^[20], Dhakar *et al.* (2017)^[4], Kumar *et al.* (2017)^[8]. The mean data pertaining to genetic parameters are presented in Table 2.

The range of phenotypic variability for days to flowering was varied from 74 (JF-637) to 110.33 days (JF-680) with general mean being 88.90 days. The genotypic, phenotypic and environmental variances for trait were 35.09, 54.48 and 19.38 respectively. While the genotypic and phenotypic coefficient of variation was 6.66 and 8.30 per cent, respectively. The earliest flowering was observed in JF-637 followed by JF-530 and JF-625. Days to flowering exhibited high heritability coupled with high genetic advance as per cent of mean. The

same results have also been reported by Singh *et al.* and Patel *et al.* Days to maturity recorded a general mean of 231.67 days and it ranged from 217.66 (JF-530) to 252.33 days (JF-498). The earliest maturity was observed in JF-530 at 217.66 days followed by JF-637 and JF-311 with 218.67 and 218.84 mean, respectively. The genotypic, phenotypic and environmental variances for trait were 54.05, 145.33 and 91.28 and the genotypic and phenotypic coefficient was 3.17 and 5.20 per cent, respectively. 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 Patel *et al.* and Singh and Mittal.

The range for phenotypic variability for plant height varied from 124 (JF-412) to 181.70 cm (JF-530) with general mean of 160.06 cm. The desirable plant height was observed in JF-412 (124 cm) and eighteen genotypes were recorded short in plant height than general mean. The genotypic, phenotypic and environmental variances for trait were 147.49, 225.18 and 77.68 respectively, while genotypic and phenotypic coefficient of variation were 7.58 and 9.37 per cent. High heritability with high genetic advance as per cent of mean was recorded for plant height indicating the additive gene action, thus for improving this trait, the selection could be effective in early generations. Similar results were observed by Jindal and Allah-Rang.

The highest numbers of branches per plant were recorded in JF-391 (15.56), while the minimum number of branches per plant was recorded in JF-332 (9.33) with an overall mean of 11.60. Moderate genotypic and phenotypic coefficient of variation indicate moderate amount of variability for number of branches per plant. High heritability with 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 were observed by Singh and Mittal, Patel *et al.* and Sengupta *et al.* Significant difference was recorded for number of umbels per plant which was ranged from (16.93) JF-391 to (45.43) JF-192 with overall mean of 29.68. High genotypic and phenotypic coefficient of variation indicating that there was broad genetic variability for this character. High heritability with 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. These results are in confirmation with the findings of Jindal and Allah-Rang, Agnihotri, Agnihotri *et al.*, Shukla *et al.*, Rajput *et al.* and Kumar *et al.*

The character umbellates per main umbel ranged from 22.80 (JF-192) to 78.33 (JF-484) with general mean of 49.27. High genotypic and phenotypic coefficient of variations were indicating the presence of broad genetic variability. High heritability with 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. These results are in confirmation with the findings of Jindal and Allah-Rang, Patel, Shukla *et al.* and Kumar *et al.*

The character number of seeds per main umbel ranged from 644.08 to 2486.81 with general mean of 1146.31. Genotypes JF-484 (2486) was recorded highest seeds per main umbel. High genotypic and phenotypic coefficient of variations was indicating the presence of broad genetic variability. High heritability with high genetic advance as per cent of mean indicating a possible role of additive gene effect for the

genotypic variance for this character. The results are in agreement with Patel, Singh, Jeeterwal *et al.* and Kumar *et al.* There was a significant difference among the genotypes for 1000-seed weight ranged from JF-412 (4.84g) to JF-484 (10.47g) with overall mean of 7.57 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. These

findings are in confirmation with Agnihotri *et al.* and Kumar *et al.*

The character volatile oil content ranged from 0.47 to 2.17 per cent with mean oil content 1.37 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 Patel.

Table 1: Analysis of variance for different characters in fennel

Sr. No.	Character	Mean sum of square		
		Replication	Treatment	Error
	Degree of freedom	2	39	78
1	Days to flowering	8.108	124.666**	19.382
2	Days to maturity	33.658	253.419**	91.282
3	Plant height	6.676	520.168**	77.687
4	Number of branches per plant	1.203	7.889**	0.423
5	Number of umbels per plant	4.531	135.525**	5.788
6	Number of umbellets per main umbel	39.515	465.739**	21.088
7	Number of seeds per main umbel	3,659.578	492,591.190**	9,940.131
8	Test weight	0.155	5.352**	0.154
9	Volatile oil content	0.000	0.309**	0.001
10	Yield per plant	80.721	4,257.208**	63.797

*, ** Significant at 5% and 1% respectively

Table 2: Range, mean, genotypic, phenotypic and environmental variances, GCV, PCV, H² (broad sense), GA and GA as per cent of Mean for different characters in fennel

Characters	Range	Mean	Genotypic variance (σ_g^2)	Phenotypic variance (σ_p^2)	Environmental Variance (σ_e^2)	GCV (%)	PCV (%)	H ² (%)	GA	GA as % of Mean
Days to flowering	74 - 110.33	88.90	35.09	54.48	19.38	6.66	8.30	64.42	9.79	11.02
Days to maturity	217.66 - 252.33	231.67	54.05	145.33	91.28	3.17	5.20	37.18	9.23	3.99
Plant height (cm)	124 - 181.70	160.06	147.49	225.18	77.68	7.58	9.37	65.50	20.24	12.65
Number of branches per plant	9.33 - 15.56	11.60	2.49	2.91	0.42	13.60	14.71	85.46	3.00	25.91
Number of umbels per plant	16.93 - 45.43	29.68	43.25	49.03	5.78	22.2	23.59	88.19	12.72	42.86
Number of umbellets per main umbel	22.80 - 78.33	49.27	148.22	169.30	21.09	24.70	26.41	87.55	23.46	47.62
Seeds per umbel	644.08 - 2486.81	1,146.31	160883.99	170823.92	9939.93	34.99	36.06	94.18	801.87	69.95
1000-seed weight (g)	4.84 - 10.47	7.57	1.73	1.88	0.15	17.39	18.14	91.88	2.59	34.32
Volatile Oil content (%)	0.47 - 2.17	1.37	0.10	0.10	0.0003	23.34	23.41	99.72	0.66	47.93
Seed yield per plant (g)	36.94 - 165.33	107.55	1397.89	1461.70	63.81	34.76	35.55	95.64	75.32	70.02

Conclusion

From the present study it was concluded that there is a sufficient variability for different yield and its attributing characters in 40 genotypes of fennel evaluated under field conditions, which can be utilized in further crop improvement programme.

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