Original Research Article

Analysis of Genetic variability and Character association in Fennel (*Foeniculumvulgare*Mill.) Germplasm

Abstract

Two hundred sixteen germplasms with six check varieties of fennel (*Foeniculumvulgare*Mill.) were evaluated in augmented randomized complete block design in four blocks during Rabi 2016-17 at Research Farm, SKN college of agriculture, Jobner to determine nature of variability, character association. Analysis of variance revealed significant differences among the genotypes and checks for all the characters except days to 50 per cent flowering in genotypes. The highest PCV and GCV expressed as percentage was observed for seed yield per plant followed by seeds per umbel, umbels per plant, branches per plant, umbellets per umbel, test weight, plant height, days to maturity and days to 50 per cent flowering. The high estimates of heritability and genetic advance were found for seed yield per plant, seeds per umbel, umbels per plant and branches per plant whereas it was low for days to 50 per cent flowering and days to maturity. Correlation studies revealed that seed yield per plant was significantly and positively correlated with test weight, seeds per umbel, umbellets per umbel and umbels per umbel.

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Keywords: Genetic variability, Character association,Heritability, Genetic advance

Introduction

Fennel (*Foeniculumvulgare*Mill) belonging to family Apiaceae, is a cross pollinated crop and a diploid species with chromosome number, 2n =22. It is native of Europe and Meditarean region.The seeds contain about 9.5% protein, 10.0% fat, 42.3% carbohydrates, 18.5% crude fibre and 13.4% minerals. The seeds contain about 0.7 to 6.0% volatile oil depending on the genotype or botanical types. A 100-gram portion of fennel seeds provides 345 kilo calories energy and rich source of protein, dietary fibre, vitamins and several dietary minerals like calcium, iron, magnesium, maganease, all of which exceed 100% DV. The main constituents of the fennel oil are anethole and fenchone. The volatile oil is primarily beneficial for digestive system and also exhibits vermicidal, antispasmodic and anti-flatulence properties. In India, it is mainly grown in the states of Gujarat and Rajasthan and to some extent in U.P., Karnataka, A.P., Punjab, M.P., Bihar, Haryana and J & K. Total area under the crop in India is about 94070 hectares with production of 135930 tonnes (Anonymous, 2013-14). The productivity of fennel in India is 1444.98 kg/ha. In Rajasthan, it occupies an area of 25587 hectares with an annual production of 30717 tonnes (Anonymous, 2015-16). It is mainly cultivated in the districts of Sirohi, Jodhpur, Nagour, Tonk, Dausa and

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Pali and to a limited extent in Bharatpur, Kota and Ajmer. The productivity of fennel in Rajasthan is 1200.49 kg/ha. Genetic variability is prerequisite for any crop improvement in a crop. The survey of genetic variability with the help of suitable genetic parameters like genotypic and phenotypic coefficients of variations, heritability estimates and genetic advance as percentage of mean are indispensable in breeding programmes aimed at improvement of seed yield. Correlation measures the extent of association between yield and their components.

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Material and methods

The experimental material for the present investigation consisted of 216 germplasms obtained from germplasm collection of AICRP on Spices, S.K.N. College of Agriculture, Jobner, and six checks viz. RF-101, RF-125, RF-143, RF-157, RF-205, RF-281. The germplasm lines were evaluated during *Rabi* 2016-17 at Research Farm of S.K.N. College of Agriculture, Jobner in augumentedrandomized complete block design in four blocks with six checks *viz.*, RF-101, RF-125, RF-143, RF-157, RF-205, RF-281 and plot size of 3.0 x 1.0 m^2.The row to row and plant to plant distance was maintained 50 cm and 20 cm respectively. Recommended cultural practices were followed to raise a healthy crop during the crop season. Each genotype was sown in a plot of two row of 3m length.

Result and Discussions

Two hundred sixteen genotypes of fennel along with six checks *viz*., RF-101, RF-125, RF-143, RF-157, RF-205 and RF-281 were evaluated in an augmented complete randomized block design in *Rabi* 2016-17 to estimate the genetic variability, heritability, genetic advance as percentage of mean, association among different morphological characters with each other and with seed yield.

Mean seed yield per plant ranged from 2.30 g (UF-243) to 29.57 g (UF-23) with an overall mean of 12.26 g. The genotypic and phenotypic coefficient of variation was 46.29 and 46.83 per cent, respectively. The magnitude of broad sense heritability was 97.68 per cent with corresponding genetic advance expressed as percentage of mean being 94.24 per cent.

A wide range of variability present in any crop always provides the better chance to select desired types because selection, which is the base to every breeding programme, operates only on variation, which is of genetic nature. The data were analysed and analysis of variance revealed that there was significant difference among blocks, entries and checks for all the characters *viz*. days to 50 per cent flowering, days to maturity, plant height, branches per plant, umbels per plant, umbellets per umbel, seeds per umbel, test weight and seed yield per plant. These are in agreement with the earlier reports of Agnihotri *et al*. (1997), Meena *et al*. (2009), Kumawat (2010), Jeeterwal*et al*. (2015) and Kumar *et al.* (2017). The block effect was significant for all the characters indicating the sensitivity of accession to the environment. The check showed significant differences for all the characters, it indicated that checks themselves were diverse.

Estimates of genotypic and phenotypic variance indicated that in general the phenotypic variances were higher than genotypic variance indicating the role of environmental factors on the character expression. The variances of various characters were compared on the basis of coefficient of variation. Higher GCV (genotypic coefficient of variation) and PCV (phenotypic coefficient of variation) were recorded for seed yield per plant, seeds per umbel and umbels per plant. Such results were also reported by Bhargava *et al.* (1971), Menon *et al*. (1973), Lal (2007), Meena *et al.* (2010), Dashora and Sastry (2011) andSengupta *et al.* (2014). The GCV and PCV were moderate for branches per plant, test weight and umbellets per umbel, whereas low for plant height, days to maturityand days to 50 per cent flowering, which are in agreement with the earlier report of Lal (2007). On the contrary, Yogi *et al.* (2014) 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 genotypic coefficient of variations and phenotypic coefficient of variation alone would not be sufficient to indicate the proportion of total heritable part of variation. The estimates of heritability were used to estimate genetic advance.

The broad sense heritability estimates along with genetic advance were also determined. Since in augmented design only the error variance of check varieties could be subtracted from the variance of accessions, a portion of it may be confounded with the genotypic variance used for calculating the heritability. Therefore, caution should be exercised in interpreting the estimates of heritability values as they represent only the upper limit of heritability. The estimates of heritability were higher (>60 per cent) for all the traits *viz*. plant height, seed yield per plant, umbels per plant, seeds per umbel, branches per plant, umbellets per umbel, days to maturity, test weight and days to 50 per cent flowering indicating that these characters were less influenced by environment and direct selection for these yield contributing traits would be effective for future improvement in yield. Such results were also reported by Robinson *et al*. (1949).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 umbel, umbel per plant and branches per plant which is in agreement withearlier reports of Meena *et al*. (2010), Rawat *et al*. (2013), Sengupta *et al*. (2014), Jeeterwal*et al*. (2015) and Kumar *et al*. (2017), while umbellets per umbel, test weight and plant height showed high heritability with moderate genetic advance.The high heritability and low genetic advance was recorded for days to 50 per cent flowering and days to maturity.

The expected genetic advance expressed as percentage of mean was observed to be high for seed yield, seeds per umbel, umbels per plant, branches per plant, which are in accordance with the earlier reports of Johnson (1955), Agnihotri (1997), Singh *et al*. (2006), Lal (2007) and Meena *et al*. (2010). In the present study, low genetic advance was observed for days to 50 per cent flowering, days to maturity. Moderate genetic advance was observed for umbellets per umbel, plant height and test weight.

In the present study seed yield was positively and significantly correlated with most of the morphological characters. The seed yield per plant was significantly and positively correlated with test weight, umbellets per umbel, seeds per umbel and umbels per plant. Similar results were reported by Kathiria *et al*. (1980), Agnihotri *et al*. (1997) andPareek *et al*. (2009)for these character with seed yield per plant.The association of seed yield per plant with plant height, branches per plant, days to maturity and days to 50 per cent flowering was negative and significant. Similar findings were reported earlier by Agnihotri *et al*. (1997) for days to 50 percent flowering with seed yield. Contradictory to this Rajput *et al*.(2004), Cosge*et al.* (2009), and Jeeterwal*et al.* (2015) reported positive and significant correlation for plant height and branches with seed yield per plant, whereas Yadav *et al*. (2013) reported positive and significant correlation of days to 50 per cent flowering, branches and plant height with seed yield.

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Table 1 General mean, range, genotypic and phenotypic coefficient of variation, heritability (broad sense) and genetic advance as percentage of mean for different characters in fennel

S.No.	Characters	Range	Mean	Genotypic coefficient of variation (GCV)	Phenotypic coefficient of variation (PCV)	Heritability in broad sense (%)	Genetic advance	Genetic advance as percentage of mean
1	Days to 50% flowering	114.54-121.87	116.82	0.98	1.22	64.42	1.89	1.62
2	Days to maturity	178.92-196.75	185.98	1.78	2.02	77.77	6.03	3.23
3	Plant height (cm)	98.84-154.54	127.57	6.56	6.63	97.78	16.90	13.35
4	Branches per plant	5.20-10.20	7.53	11.29	12.07	87.61	1.62	21.77
5	Umbels per plant	17.56-38.85	27.22	17.16	17.52	95.98	9.62	34.64
6	Umbellets per umbel	17.64-28.44	21.90	10.39	11.22	85.88	4.29	19.84
7	Seeds per umbel	206.50-617.73	330.87	20.51	21.54	90.62	136.38	40.21
8	Test weight (g)	3.77-6.66	5.33	11.07	13.32	69.14	0.99	18.96
9	Seed yield per plant (g)	2.30-29.57	12.27	46.29	46.83	97.68	12.19	94.24

Table 2 Genotypic and phenotypic correlation coefficients between different characters in fennel

Character	Correla-tion	Days to maturity	Plant height	Branches per plant	Umbels per plant	Umbellets per umbel	Seeds per	Test weight (g)	Seed yield per

			(cm)				umbel		plant (g)
Days to 50% flowering	r_g	0.4155**	0.5026**	-0.1516*	-0.8563**	-0.8182**	-0.7982**	-0.4730**	-0.5107**
	r_p	0.5664**	0.6018**	0.0185	-0.9391**	-0.8972**	-0.883**	-0.5970**	-0.5775**
Days to maturity	r_g		0.9299**	0.3537**	-0.4841**	0.5370**	0.5091**	0.8017**	-0.8300**
	r_p		0.9353**	0.3624**	-0.5841**	-0.5843**	-0.572**	-0.8441**	-0.8409**
Plant height (cm)	r_g			0.4081**	-0.5898**	-0.6331**	-0.6318**	-0.7834**	-0.8898**
	r_p			0.4433**	-0.6218**	-0.6185**	-0.625**	-0.8735**	-0.9007**
Branches per plant	r_g				0.0568	-0.0091	-0.0376	-0.3561**	-0.4126**
	r_p				-0.0854	-0.1190	-0.1628*	-0.3401**	-0.4438**
Umbels per plant	r_g					0.9745**	0.9667**	0.4960**	0.5925**
	r_p					0.9874**	0.9776**	0.6240**	0.6363**
Umbellets per umbel	r_g						0.9835**	0.5138**	0.6419**
	r_p						0.9846**	0.6265**	0.6445**
Seeds per umbel	r_g							0.4761**	0.6360**
	r_p							0.6019**	0.6526**
Test weight (g)	r_g								0.9106**
	r_p								0.9586**

*and** refers to significant at P = 0.05 and P = 0.01, respectively and r_g= Genotypic correlation r_p=Phenotypic correlation

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