



Variability Studies in Fennel (*Foeniculum vulgare* Mill.)

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ABSTRACT: Thirty genotypes of fennel were tested to access the extent of genetic variability, heritability and genetic advance. The analysis of variance revealed significant mean sum of square values for all the thirteen traits studied suggesting a sufficient amount of variability present among them. The values of phenotypic coefficient of variation (PCV) were observed slightly higher than genotypic coefficient of variation (GCV) for all thirteen characters indicating minor influence of environmental factors. In addition to this, high heritability coupled with high genetic advance as % mean was exhibited by days to 50 % lowering, plant height, tillers plant, secondary branches plant, umbels per plant, umbellates per umbel, seed width, seed yield plant and test weight showed the role of additive gene action in these traits and therefore improvement by direct phenotypic selection over the genotypes would be worth it.

Keywords: Fennel, genetic variability, heritability, genetic advance.

INTRODUCTION

India is known as home of spices. Spices play a very important role in the economy of our country as some of them are exported to earn foreign exchange. Seed spices occupy a prominent place in the total basket of spices of the country and play a significant role in the Indian economy. Seed spices include all those annuals whose dried seeds are used as spices viz., fennel, fenugreek, coriander, cumin, ajwain, dill and nigella. Among them, fennel (*Foeniculum vulgare* Mill) is a cross-pollinated species having diploid chromosome number $2n = 22$ belongs to Apiaceae family. Being an aromatic plant, it is commercially cultivated as an annual herb, the seeds of which are used for flavoring purposes. Fennel seeds are used to cure diseases like cholera, bile disturbances, nervous disorders, constipation, dysentery and diarrhea and are also used for control of diseases attacking the chest, lungs, spleen, kidney and in colic pain (Girija, 1952).

Being a cross-pollinated crop, high heterozygosity is prevailing in the natural population (Ramanujam *et al.*, 1964). Genetic variability is a prerequisite for any crop improvement program. The success of any crop improvement programme depends on the magnitude of genetic variability and the extent to which desirable characters are heritable. The ultimate goal of any breeding programme is to improve the characteristics of plants so they become more desirable agronomically and economically. 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 a %age of mean are indispensable in breeding programmes aimed

at improvement of seed yield. The heritability measures the contribution of genetic variability to the total variability i.e. phenotypic variability observed for any quantitative trait. The estimated heritability can be utilized for the estimation of genetic gain expected for the selection of the top 5 % of individuals. Such studies enable the breeders to have a maximum selection response of the variance exhibited by population which is largely due to additive gene effects. Keeping these views, the present study was carried out to estimate genetic variability, heritability and genetic advance in various fennel genotypes.

MATERIALS AND METHODS

Initially nursery was prepared by sowing the seeds of thirty genotypes. Thirty days old seedlings were transplanted on actual experimental plot in randomized block design with three replications with 45 cm × 30 cm row to plant spacing during Rabi-2023-24 at Research Farm, Department of Genetics and Plant Breeding, N.M. College of Agriculture, Navsari Agricultural University, Navsari, Gujarat. The recommended package of practices was followed to raise a healthy crop. The crop was regularly irrigated at regular periods to maintain optimum moisture level throughout the experimental season. For observations, five competitive plants were marked with labels in each plot. Observations were recorded 13 various seed yield and yield parameters. The characters like days to 50 % flowering, days to maturity and test weight, observations were recorded on a plot basis while for remaining traits, data were recorded on individual plants basis and their averages were used in the

statistical analysis. The data obtained on various characters were subjected to statistical analysis as per randomized block design. The mean data were statistically analyzed for analysis of variance (Panse and Sukhatme 1978). To compare the genotypes, GCV, PCV, heritability (h^2) and genetic advance (GA) were calculated for each character by using standard statistical procedures (Burton, 1952).

RESULTS AND DISCUSSION

The analysis of variance was performed to test the differences among genotypes for all the thirteen characters and presented here in Table 1. The results revealed that the mean sum of square due to genotypes were highly significant for all the quantitative characters viz., days to 50 % flowering, plant height (cm), tillers per plant, primary branches per plant, secondary branches per plant, umbels per plant, umbellates per umbel, seeds per umbellate, seed length (mm), seed width (mm), seed yield per plant (g), test weight (g) and days to maturity which indicated that presence of considerable amount of variability among genotypes for various characters. This shows that there is ample scope to generate early and high yielding materials by applying a judicious selection pressure for specific traits. All thirteen characters under study had shown a wide range of phenotypic variation. Similar results for all characters were also reported by Seet *et al.* (2020); Patel *et al.* (2021); Rajput *et al.* (2022); Deshwal *et al.* (2023); Rajneetha *et al.* (2021) also reported similar kinds of result in Ajwain.

Earliness is a desirable trait as it provides the opportunity to take more number of cropping cycle per year from unit area. The earliest genotype (FNL 9) flowered at 49.33 days and matured in 108.00 days whereas, the late genotype (FNL 16) flowered at 89.00 days and matured in 147.33 days (Table 2). FNL 20 and FNL 21 even matured late in 153.33 days after sowing. The genotypic, phenotypic and environmental variances were 119.40, 125.74 and 6.34, respectively. The GCV was 16.30 % and the PCV was 16.73 %, showing the moderate genetic variation among the genotypes for this trait. The present result was at par with findings of Patel *et al.* (2008); Sabzi *et al.* (2014) for having moderate GCV and PCV. The GCV for days to maturity was 9.60 % and PCV was 9.98 %, showing the low genetic variation among the genotypes for this trait (Table 3). The present results was at par with findings of Hadli *et al.* (2021); Patel *et al.* (2021); Deshwal *et al.* (2023) having low GCV and PCV.

Significant variability was recorded for plant height in present study. The genotype FNL 21 recorded highest plant height of 145.27 cm followed by FNL 14 (130.93cm), FNL 15 (130.67cm), while lowest plant height was reported by the genotype FNL 10 (71.20 cm). Moderate value of GCV and PCV for this trait indicated presence of moderate variation for plant height. These results are in accordance with Hadli *et al.* (2021); Deshwal *et al.* (2023).

Tillers per plant is an important yield contributing characters in fennel and significant variability was reported in the genotypes under study. FNL 25 (6.97)

possessed the maximum number of tillers per plant followed by FNL 16 (4.73) and FNL 24 (4.73), while genotype FNL12 (0.53) possessed minimum number of tillers per plant. The high values of GCV (37.90) and the PCV (40.19) revealing high role of inherent variation among the genotypes for this trait.

Highest number of umbels per plant was exhibited by FNL 11 (52.93) followed by FNL 13 (51.13), FNL 23 (49.53) and FNL 22 (48.27), while that of lowest reported in FNL 10 (19.63). The high values of GCV was 22.17 % and the PCV was 24.27 %. The results was in agreement with the findings of Seet *et al.* (2020); Patel *et al.* (2021); Rajput *et al.* (2022) having high value of GCV and high value of PCV.

Seeds per umbellate was highest in the genotype FNL 2 (31.53) followed by FNL 4 (30.67) and FNL 26 (28.53) and lowest being reported in FNL 3 (20.20). The GCV and PCV for this trait was 8.51 and 15.35 % respectively, showing the low genetic variation among the genotypes for this trait. These results were found similar with Yogi *et al.* (2013) having low values of GCV and moderate values of PCV.

The genotype under study exhibited great variability in test weight and it ranged from 2.47 to 7.15g. The genotype FNL 24 produced bold seed size (7.15) followed by FNL 11 (6.91) and FNL 30 (6.76), while the genotype FNL 8 (2.47) produced smaller seed size. The high value of genotypic and phenotypic coefficient of variation were 26.22 % and 26.99 %, respectively. The results were opposite to the findings of Kumar *et al.* (2017); Seet *et al.* (2020); Jat and Choudhary (2022) having low GCV and PCV.

Genotypes tested under present investigation showed greater diversity for seed yield per plant which was proved by exhibiting highest yield by the genotype FNL 30 (44.85g) which was followed by FNL 6 (40.56g), FNL 7 (40.01g), while that of lowest being produced by FNL 8 (7.85g). The components of variance recorded due to genotypes, phenotypes and environments were 79.57, 88.64 and 9.06, respectively. The moderate value of GCV was 37.19 % and PCV was 39.25 %. The present results were on accordance with findings of Sengupta *et al.* (2014); Jeeterwal *et al.* (2015); Patel *et al.* (2018); Deshwal *et al.* (2023) having high values for GCV and PCV.

The presence of genotypic variation alone cannot give idea of improvement obtained through selection. The estimation of heritability of the trait shows the relative % of heritable variability allowing for efficient selection. High heritability was observed for most of the characters including days to 50 % flowering (94.96 %), plant height (74.53 %), tillers per plant (89.14 %), secondary branches per plant (79.42 %), umbels per plant (83.00 %), umbellates per umbel (80.39 %), seed width (83.38 %), seed yield per plant (89.77 %), test weight (94.36 %) and days to maturity (92.51 %) (Table 3). High heritability for these traits are worth beneficial to breeders in identifying superior genotypes by selection as it is less influenced by the environment. Similar results were reported by Seet *et al.* (2020); Hadli *et al.* (2021); Patel *et al.* (2021); Rajput *et al.* (2022); Deshwal *et al.* (2023).

It is worth to estimate the genetic advance along with heritability which would be more successful in predicting the effectiveness of selecting the best individuals. Higher heritability coupled with high genetic advance as % mean was observed for days to 50 % flowering, plant height, tillers per plant, secondary branches per plant, umbels per plant, umbellates per umbel, seed width, seed yield per plant and test weight. This confirmed a role of additive gene action and thus improvement in these traits could be brought about by direct phenotypic selection over the genotypes. These findings were similar to results of Sengupta *et al.* (2014); Madam (2021); Jat and Choudhary (2022); Deshwal *et al.* (2023). Higher heritability with medium

genetic advance as % mean was observed in days to maturity indicating the effect of non-additive gene action and there is a limited scope of improvement through direct phenotypic selection for this trait. These findings were opposite to the results of Yadav *et al.* (2013); Seet *et al.* (2020); Deshwal *et al.* (2023) having high heritability with low genetic advance as % of mean for days to maturity. Moderate heritability with low genetic advance as % mean was observed in seeds per umbellate indicating the high influence of environmental effect and selection would be non-effective. These findings were opposite to the results of Patel *et al.* (2008) having moderate heritability with medium genetic advance.

Table 1: Analysis of variance of experimental design for yield and yield contributing characters.

Source	df	Mean sum of square						
		Days to 50 % flowering	Plant height (cm)	Tillers per plant	Primary branches per plant	Secondary branches per plant	Umbels per plant	Umbellates per umbel
Replication	2	9.24	275.48	0.33	5.17	4.64	9.11	8.88
Genotypes	29	364.55**	828.03**	4.50**	2.37**	77.61**	202.44**	70.69**
Error	58	6.33	84.68	0.18	0.56	6.17	12.94	5.32
Source	df	Mean sum of square						
		Seeds per umbellate	Seed length (mm)	Seed width (mm)	Seed yield per plant (g)	Test weight (g)	Days to maturity	
Replication	2	11.36	0.07	0.01	18.51	0.13	29.20	
Genotypes	29	23.90**	0.64**	0.09**	247.78**	5.32**	457.87**	
Error	58	10.26	0.12	0.01	9.06	0.10	12.04	

Table 2: Mean values of thirteen characters in thirty fennel genotypes.

Genotypes	DF	PH	TPP	PBPP	SBPP	UPP	UPU	SPU	SL	SW	SYPP	TW	DM
FNL 1	61.00	101.47	3.20	5.27	18.27	29.60	23.07	27.33	5.23	1.15	24.33	5.30	120.67
FNL 2	59.33	117.80	4.70	5.73	18.80	30.27	36.43	31.53	4.61	1.06	22.75	4.47	117.33
FNL 3	51.67	82.27	2.33	4.93	17.73	32.80	17.40	20.20	4.66	0.88	21.66	5.87	108.67
FNL 4	61.67	117.00	2.90	6.20	20.33	33.00	33.67	30.67	5.14	1.11	24.94	6.26	120.33
FNL 5	57.00	97.40	2.20	5.73	16.27	26.53	22.73	24.33	5.15	1.05	33.15	6.47	120.33
FNL 6	56.67	92.27	2.33	6.73	17.47	30.53	27.40	26.60	5.10	1.03	40.56	5.55	113.33
FNL 7	54.00	101.93	1.87	6.87	12.60	19.93	31.93	28.13	4.95	1.10	40.01	6.13	116.00
FNL 8	63.00	85.20	3.03	8.60	23.00	33.13	29.73	21.47	4.73	0.75	7.85	2.47	121.33
FNL 9	49.33	104.00	2.87	5.73	18.20	33.33	21.67	21.67	5.25	1.09	31.03	5.25	108.00
FNL 10	77.00	71.20	2.67	4.27	11.07	19.63	25.47	20.67	6.20	1.24	11.38	5.83	138.00
FNL 11	56.00	111.40	1.40	7.33	27.53	52.93	19.40	23.93	5.11	0.95	16.76	6.91	115.00
FNL 12	56.00	123.80	0.53	6.93	22.27	39.33	24.53	24.87	5.06	1.06	30.55	4.49	113.33
FNL 13	87.33	125.67	3.20	7.13	27.00	51.13	25.07	24.20	4.94	0.93	23.20	4.25	150.33
FNL 14	86.00	130.93	3.90	5.53	26.13	37.40	25.60	25.87	4.95	0.68	20.81	2.50	134.67
FNL 15	82.33	130.67	3.40	7.53	23.27	29.87	28.07	27.13	4.39	0.78	12.17	5.00	140.00
FNL 16	89.00	127.93	4.73	7.07	19.53	25.00	27.87	27.53	4.31	0.59	9.59	2.85	147.33
FNL 17	67.00	97.87	2.67	6.13	25.47	38.40	21.93	22.80	4.89	1.03	22.80	6.05	124.33
FNL 18	64.67	118.80	3.07	6.20	25.20	39.27	30.47	25.93	5.33	1.04	27.21	6.18	126.00
FNL 19	71.00	126.53	4.27	6.47	27.20	35.33	25.47	26.07	4.21	0.64	14.97	4.63	126.00
FNL 20	81.67	129.27	2.87	5.53	21.33	33.53	28.07	25.87	5.30	0.73	23.55	4.37	153.33
FNL 21	83.00	145.27	3.80	6.33	28.93	43.33	33.53	27.53	4.54	0.73	24.40	3.24	153.33
FNL 22	66.00	100.00	4.33	7.00	33.20	48.27	19.87	21.40	5.03	1.00	25.87	5.74	127.67
FNL 23	67.67	94.13	3.93	5.80	28.07	49.53	20.33	22.93	4.48	0.89	14.49	4.70	128.33
FNL 24	68.67	122.07	4.73	7.53	31.27	43.13	29.07	23.80	5.72	0.91	23.25	7.15	129.33
FNL 25	73.67	110.60	6.97	6.40	24.27	36.47	17.47	22.00	5.17	0.90	24.54	4.53	133.67
FNL 26	66.00	117.93	2.67	5.60	21.40	35.20	25.87	28.53	5.74	1.28	28.28	5.55	127.67
FNL 27	59.67	103.67	1.73	6.07	21.07	33.73	22.13	23.20	5.40	0.99	20.12	4.19	128.33
FNL 28	67.00	113.60	3.33	7.00	23.00	39.93	31.67	26.07	4.75	1.04	18.01	2.48	124.67
FNL 29	65.67	114.33	2.80	6.13	23.27	41.73	24.87	24.27	5.29	0.96	36.54	5.69	125.00
FNL 30	61.67	107.80	2.60	5.80	21.60	36.27	26.13	25.33	5.84	1.07	44.85	6.76	118.67
S.Em ±	1.45	5.31	0.24	0.43	1.43	2.08	1.33	1.85	0.20	0.04	1.74	0.19	2.00
C.D. (5%)	4.11	15.04	0.68	1.22	4.06	5.88	3.77	5.24	0.57	0.12	4.92	0.53	5.67
C.V %	3.76	8.31	13.22	11.84	11.04	10.00	8.90	12.78	6.93	7.81	12.55	6.41	2.73

Table 3: Measures of variability parameters of thirteen characters.

Characters	Range	Mean	Genotypic variance (σ^2_g)	Phenotypic variance (σ^2_p)	Environmental Variance (σ^2_e)	GCV (%)	PCV (%)	H ² b (%)	GA	GA as % of Mean
Days to 50% flowering	49.33 - 89.00	67.02	119.40	125.74	6.34	16.30	16.73	94.96	21.93	32.73
Plant height (cm)	71.20 - 145.27	110.76	247.78	332.47	84.68	14.21	16.46	74.53	27.99	25.27
Tillers per plant	0.53 - 6.97	3.18	1.44	1.62	0.18	37.90	40.19	89.14	2.33	73.71
Primary branches per plant	4.27 - 8.60	6.32	0.60	1.16	0.56	12.30	17.07	51.88	1.15	18.24
Secondary branches per plant	11.07 - 33.20	22.49	23.81	29.98	6.17	21.70	24.34	79.42	8.96	39.83
Umbels per plant	19.63 - 52.93	35.95	63.17	76.11	12.94	22.17	24.27	83.00	14.92	41.49
Umbellates per umbel	17.40 - 36.43	25.90	21.79	27.11	5.32	18.03	20.10	80.39	8.62	33.29
Seeds per umbellate	20.20 - 31.53	25.06	4.55	14.81	10.26	8.51	15.35	30.71	2.43	9.72
Seed length (mm)	4.21 - 6.20	5.05	0.17	0.29	0.12	8.20	10.74	58.29	0.65	12.90
Seed width (mm)	0.59 - 1.28	0.96	0.03	0.03	0.01	17.39	19.05	83.38	0.31	32.71
Seed yield per plant (g)	7.85 - 44.85	23.99	79.57	88.64	9.06	37.19	39.25	89.77	17.41	72.58
Test weight (g)	2.47 - 7.15	5.03	1.74	1.84	0.10	26.22	26.99	94.36	2.64	52.47
Days to maturity	108.00 - 153.33	127.03	148.61	160.65	12.04	9.60	9.98	92.51	24.15	19.01

DFF = Days to 50% flowering; PH = Plant height (cm); TPP = Tillers per plant; PBPP = Primary branches per plant; SBPP = Secondary branches per plant; UPP = Umbels per plant ; UPU = Umbellates per umbel ; SPU = Seeds per umbellate ; SL = Seed length (mm); SW = Seed width (mm); TW = Test weight (g); DM = Days to maturity; SYPP = Seed yield per plant (g)

CONCLUSION

In present study, large phenotypic differences were observed for all the thirteen characters under study. The wide range of variation obtained may be due to inclusion of divergent genotypes in the present study. Highly significant mean sum of squares due to genotypes for all thirteen characters indicated the presence of sufficient genetic variability in the materials under study. The higher and closer values of phenotypic coefficient of variation (PCV) than the respective genotypic coefficient of variation (GCV) for all the thirteen traits indicated the inherent connection between genotypic and phenotypic expression of these traits. Results indicated that these parameters are very important for selecting a suitable genotype because if the heritability of a character is high, selection for such traits would be quite effective. This is because there would be a close correspondence between genotypic and phenotypic variation due to a relatively smaller contribution of the environment to the phenotype. The genotype FNL 30 performed better for seed yield per plant along with plant height, primary branches per plant, umbels per plant, umbellates per umbel and test

weight. Therefore, this genotype should be widely utilized in further fennel improvement programme.

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