

Genetic variability, character associations, path coefficient and divergence analysis in inbreds of fennel (*Foeniculum vulgare* Mill.)

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Abstract

One hundred seven inbred lines of fennel (*Foeniculum vulgare* Mill.) were evaluated in Augmented Design with four blocks for genetic variability, correlation, path coefficient and genetic divergence at Agriculture Research Farm, S.K.N. College of Agriculture, Jobner. Significant amount of variability among the inbred lines was recorded for the characters studied viz. plant height, branches plant⁻¹, umbels plant⁻¹, umbellets umbel⁻¹, seeds umbel⁻¹ and seed yield plant⁻¹. High phenotypic and genotypic coefficient of variation coupled with high heritability and genetic advance expressed as percentage of mean were observed for seed yield plant⁻¹ and seeds umbel⁻¹. Seed yield plant⁻¹ was significantly and positively correlated with branches plant⁻¹ and plant height. Path coefficient analysis revealed that traits like branches plant⁻¹, plant height and 1000-seed weight revealed highly positive and direct effect as well as positive correlation with seed yield plant⁻¹. Diversity among the clusters with regard to distribution of inbred lines was noted. The diversity is however not limited to the diversity among the parental lines.

Key words: Fennel, genetic variability, correlation, path coefficient, diversity analysis

Introduction

Fennel (*Foeniculum vulgare* Mill, 2n=22) is an important seed spice crop, mainly grown for its seeds in the Rajasthan and Gujarat. Among all the seed spices, fennel has potential as cash crop in the state of Rajasthan. A simple and effective technique for hybridization in fennel has been developed by the centre. (Singh *et al.*, 11). Using this technique hybridization has been carried out and diallels have been developed to study the genetics of seed yield and yield contributing characters (Dashora *et al.*, 2). Since fennel is a cross pollinated plant, hybridization has been limited to the development of population hybrids which are good for the study of inheritance, particularly the inheritance of heterosis (Dashora *et al.*, 3). The hybridization can be extended to develop hybrids in fennel. This requires development of inbreds initially and their evaluation as a second step to select compatible inbred lines for development of hybrids. Therefore, an extensive programme for development of inbreds was initiated at S K N Agriculture University, Jobner as part of AICRP on Spices. The inbreds are now in S₇ generation and have mostly stabilized. The present study is a preliminary one to estimate the genetic variation *vis-à-vis* the divergence among the inbred lines so that suitable lines may be selected for the study of combining ability to exploit heterosis..

Materials and methods

One hundred seven inbreds randomly selected from a pool of inbred lines developed from various open pollinated lines were evaluated during *Rabi* at Research Farm of S.K.N. College of Agriculture, Jobner in augmented design in four blocks. Each block had five checks viz., RF 101, RF 125, RF 143, RF 205 and a Local variety. Each line/check was sown in a plot size of 3.0 x 2.5 m² accommodating one row spaced 30 cm apart with intra row spacing of 20 cm maintained by thinning at 25th days after sowing. Non-experimental rows were planted as border rows in each bed to eliminate the border effect if any. All the agronomical practices were followed to raise a good and healthy crop. Observations were recorded for plant height (cm), branches plant⁻¹, umbels plant⁻¹, umbellets umbel⁻¹, seeds umbel⁻¹, 1000- seed weight (g), seed yield per plant (g) and days to 50% flowering reporting as an average based on random sample of five plants per line/check in each block while days to 50% flowering was reported on whole plot basis.

Analysis of variance was carried out as per the procedure suggested by Federer (5). The expected genetic advance was calculated by following the formula as suggested by Johnson *et al.*, (7). Heritability in broad sense was calculated by the formula given by Hanson *et al.*, (6). The pairwise characters association were

estimated using the Pearson's product-moment correlation method. The estimates of direct and indirect effects were calculated by the path coefficient analysis as suggested by Wright (15) and elaborated by Dewey and Lu (6) both at phenotypic and genotypic levels. The clustering analysis using the adjusted means was done using Ward's minimum variance method with SPSS software version 12.0.

Results and discussion

The analysis of variance revealed that significant amount of variability was present among the inbred lines for the morphological traits studied (Table 1). Estimates of genotypic and phenotypic variances indicated that in general phenotypic variances were higher than genotypic variances for all the characters studied indicating the role of environmental factors on the character expression. The variability of characters was compared on the basis of coefficient of variation (Table 2). The range and coefficient of variation indicated that the variability was high for seed yield plant⁻¹ (g), umbels plant⁻¹, seeds umbel⁻¹, umbellets umbel⁻¹ and moderate for branches plant⁻¹ and plant height (cm). These results are in line with the report of Sharma *et al.*, (12). The variability was low for 1000-seed weight (g) and days to 50% flowering, which in turn, indicated that simple selection of inbred lines on the basis of seed yield plant⁻¹ (g), umbels plant⁻¹, seeds umbel⁻¹ and umbellets umbel⁻¹ might be advantageous as compared to other characters under study. In the present investigation, broad sense heritability was observed to be high for seeds yield plant⁻¹ and seeds umbel⁻¹. Genetic advance as percentage of mean for the characters ranged from 0.71% (days to 50% flowering) to 42.10% (seed yield per plant (g)). High

magnitude of genetic advance as percentage of mean was estimated for seed yield per plant (g). The umbels plant⁻¹, branches plant⁻¹, seed yield plant⁻¹(g) and seeds per umbel had higher magnitude of heritability and genetic advance as percentage of mean. The umbels plant⁻¹, branches plant⁻¹, seed yield plant⁻¹ (g) and seeds umbel⁻¹ had higher magnitude of heritability and genetic advance as percentage of mean (Table 2).

The association analysis revealed that the genotypic correlation coefficients were generally higher than their respective phenotypic correlation coefficients (Table 3). Low phenotypic correlations may result from the modifying effect of environment on the association of characters at the genetic level. seed yield per plant had significant positive correlation with branches per plant (0.2560) and plant height (0.1987) whereas, it had non significant positive correlation with umbels per plant (0.1328) and 1000-seed weight (0.0498) and its association with days to 50% flowering (-0.1559), umbellets per umbel (-0.0621) and seeds per umbel (-0.0874) was non significant and negative. Positive and significant correlation of seed yield per plant with branches per plant and plant height are in agreement with earlier reports of Agnihotri *et al.*, (1), Singh and Sastry (12), Meena *et al.*, (8) and Pareek *et al.*, (9).

Very few interrelationships among different morphological combinations showed to be statistically significant. The correlation among the characters *inter se* showed that days to 50% flowering had positive and non significant association with plant height, branches plant⁻¹, umbellets umbel⁻¹ and seeds umbel⁻¹. While, plant height had positive significant association with umbellets umbel⁻¹, seeds umbel⁻¹ and 1000-seed weight Umbellets

Table 1: Analysis of variance (ANOVA) for seed yield and its component traits in fennel.

Characters	Mean sum of squares					
	Blocks (3)	Treatments (111)	Inbreds (106)	Checks (4)	Inbreds vs checks(1)	Error (12)
Days to 50% flowering	5.650	4.356	4.147	6.181*	1.884	1.900
Plant height (cm)	97.697	144.878*	142.816*	203.725*	47.155	44.136
Branches plant ⁻¹	2.034	3.002**	3.097**	0.952	0.021	0.628
Umbels plant ⁻¹	4.333	24.568**	25.420**	9.388	4.269	4.167
Umbellets umbel ⁻¹	8.850	11.381	11.650	1.777	2.612	11.350
Seeds umbel ⁻¹	1030.800	12539.426**	12558.197**	12487.797**	8401.345*	1566.717
1000- seed weight (g)	0.490	0.486	0.499	0.121	0.122	0.579
Seed yield plant ⁻¹ (g)	5.721	35.364**	35.513**	21.805**	1.824	2.143

* Significant at p = 0.05 and ** significant at = 0.01; Figures in parenthesis indicate degrees of freedom.

Table 2: Mean, range and genetic parameters for different characters in fennel.

Characters	Range	Mean SEm ±	Coefficient of variation (%)		Heritability (Broad sense) %	Genetic advance as % of mean
			Genotypic	Phenotypic		
Days to 50% flowering	98.65-108.65	103.228 ±0.689	0.726	1.520	22.82	0.71
Plant height (cm)	92.07-170.95	134.713 ±3.322	3.687	6.158	35.85	4.55
Branches per plant	4.22-14.02	8.230 ±0.396	9.545	13.558	49.57	13.84
Umbels per plant	9.90-39.30	19.815 ±1.020	11.633	15.539	56.05	17.94
Umbellets per umbel	16.65-33.85	22.733 ±1.684	1.205	14.869	0.66	0.20
Seeds per umbel	201.20-734.20	439.157 ±19.79	11.937	14.957	63.69	19.62
1000- seed weight (g)	4.59-8.01	6.382 ±0.380	-	-	-	-
Seed yield per plant (g)	1.06-35.54	12.606 ±0.732	22.912	25.687	79.56	42.10

Table 3: Genotypic and phenotypic correlation coefficient between different characters in fennel

Characters	G/P	Days to 50% flowering	Plant height (cm)	Branches plant ⁻¹	Umbels plant ⁻¹	Umbellets umbel ⁻¹	Seeds umbel ⁻¹	1000-seed weight (g)	Seed yield plant ⁻¹ (g)
Days to 50% flowering	G	1.00	0.0066	0.1414	-0.1164	-0.0368	-0.0323	-0.0928	-0.0976
	P	1.00	0.1836	0.0588	-0.0151	0.0583	0.0501	-0.0436	-0.1559
Plant height (cm)	G		1.00	0.0192	0.1076	0.1088	0.2898**	0.3143**	0.1914*
	P		1.00	0.0820	0.1028	0.3144**	0.3219**	0.2217*	0.1987*
Branches plant ⁻¹	G			1.00	0.6059**	-0.1308	-0.1840	-0.0506	0.2799**
	P			1.00	0.7466**	-0.0175	-0.0972	-0.1206	0.2560**
Umbels plant ⁻¹	G				1.00	0.0383	-0.0202	-0.0235	0.0979
	P				1.00	0.0351	-0.0117	-0.0553	0.1328
Umbellets umbel ⁻¹	G					1.00	0.5417**	0.0205	-0.1497
	P					1.00	0.6153**	0.1402	-0.0621
Seeds umbel ⁻¹	G						1.00	0.2208*	-0.1193
	P						1.00	0.2079*	-0.0874
1000- seed weight (g)	G							1.00	0.0627
	P							1.00	0.0498
Seed yield plant ⁻¹ (g)	G								1.00
	P								1.00

* Significant at p = 0.05 and ** significant at = 0.01

The phenotypic correlations represent simple correlations estimated using unadjusted values while genotypic correlations represented the correlations using adjusted values between any two characters.

umbel⁻¹ had significant positive association with seeds umbel⁻¹ while its association with 1000- seed weight (g) non significant and positive. The association of seeds per umbel with 1000- seed weight had significant and positive. It is also noticed that character which exhibited positive association with seed yield per plant have also

exhibited positive association among themselves. Thus, these characters could be simultaneously improved to increase the seed yield (Table 3).

Path analysis revealed that the direct effects were stronger than indirect effects and the change in either direction between the genotypic and phenotypic path

coefficients were seldom noted. Path coefficient analysis based on phenotypic correlations indicated that maximum direct contribution to seed yield plant⁻¹ was through branches plant⁻¹ which had highest positive and significant correlation with seed yield. The plant height also had high direct effect on seed yield plant⁻¹ and had also high positive correlation with seed yield. Magnitude of the correlation coefficient between a causal factor and the effect is almost equal to its direct effect. Hence, correlations explained the true interrelationship and suggested that a direct selection of these traits will be effective (Table 4). Important information which emerged from the correlation and path analysis studies is that umbels plant⁻¹, seeds umbel⁻¹, branches plant⁻¹, umbellets umbel⁻¹ and 1000- seed weight are the most important component characters for seed yield plant⁻¹ and these were also found to be responsible for the observed relationship of different morphological characters with seed yield plant⁻¹. Hence, due emphasis should be given to umbels plant⁻¹, seeds umbel⁻¹ and branches plant⁻¹ in yield improvement.

The knowledge of genetic divergence provides us a sound scientific basis for selection of genotypes to be used in hybridization programme for further improvement. Ward method was carried out to estimate genetic divergence among the 112 genotypes (107 inbred lines+ 5 check varieties) of fennel. The generalized ward values were calculated for each pair of genotypes in all possible combination. All the genotypes were grouped into ten clusters. Maximum numbers of genotypes were twenty which were included in cluster I. clusters IX and X, both had 16 genotypes and cluster IV had 15 genotypes while clusters V, VIII and II had 11, 10 and 9 genotypes respectively and the clusters III and VI both had 4 genotypes each (Table 5).

Perusal of the clustering indicates that the clusters included inbred lines of diverse origin, indicating diversity among the inbred lines which is not related to their parentage alone. Perusal of Table 6 indicates that cluster VIII had the highest mean for seed yield among all the clusters, it also had the lowest mean for days to flowering which is desirable, had higher branches plant⁻¹ and umbels plant⁻¹. The cluster with next higher mean for seed yield was cluster IV, although the difference between the mean seed yields of clusters VIII and IV was high, however this cluster did not exhibit higher means for other characters.

An ideal genotype in fennel would be one which is dwarf, has more branches per plant as they are expected to carry more umbels. The umbels are expected to have more of seeds thus resulting in higher yield. Fennel is a

long duration crop, hence genotypes which mature early will fit well into different crop rotations. Hence for developing hybrids, selection of inbreds should be made so that they exhibit good combining ability for the above traits. It appears that entries in cluster VIII are very ideal as the average seed yield of this cluster was high besides the cluster also had higher mean values for 1000 seed weight, branches plant⁻¹, umbels plant⁻¹ and days to 50% flowering, besides being ideal even for seeds umbel⁻¹ and umbellets umbel⁻¹ (Table 6). In other words the entries in this cluster appear to be good for almost all the traits. The other clusters which appear to be important are cluster VI for days to 50% flowering and umbels plant⁻¹; cluster IX for umbellets umbel⁻¹ and seeds umbel⁻¹. Thus lines from cluster VIII, VI and IX may be tested for combining ability to isolate highly heterotic crosses for seed yield and its components.

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Table 4: Direct (diagonal) and indirect effects of different characters on seed yield per plant in fennel at genotypic and phenotypic level

Characters	G/P	Days to 50% flowering	Plant height (cm)	Branches plant ⁻¹	Umbels plant ⁻¹	Umbellets umbel ⁻¹	Seeds per umbel	1000-seed weight (g)	Correlation with seed yield plant ⁻¹ (g)
Days to 50% flowering	G	-0.1792	0.0016	0.0543	0.0209	0.0029	0.0028	-0.0007	-0.0976
	P	-0.2186	0.0493	0.0216	0.0026	-0.0040	-0.0048	-0.0020	-0.1559
Plant height (cm)	G	-0.0012	0.2354	0.0074	-0.0193	-0.0086	-0.0247	0.0024	0.1914*
	P	-0.0401	0.2685	0.0302	-0.0174	-0.0215	-0.0310	0.0101	0.1987*
Branches plant ⁻¹	G	-0.0253	0.0045	0.3838	-0.1087	0.0103	0.0157	-0.0004	0.2799**
	P	-0.0129	0.0220	0.3679	-0.1262	0.0012	0.0094	-0.0055	0.2560**
Umbels plant ⁻¹	G	0.0209	0.0253	0.2325	-0.1793	-0.0030	0.0017	-0.0002	0.0979
	P	0.0033	0.0276	0.2747	-0.1690	-0.0024	0.0011	-0.0025	0.1328
Umbellets umbel ⁻¹	G	0.0066	0.0256	-0.0502	-0.0069	-0.0788	-0.0462	0.0002	-0.1497
	P	-0.0127	0.0844	-0.0064	-0.0059	-0.0684	-0.0593	0.0064	-0.0621
Seeds umbel ⁻¹	G	0.0058	0.0682	-0.0706	0.0036	-0.0427	-0.0854	0.0017	-0.1193
	P	-0.0110	0.0864	-0.0358	0.0020	-0.0421	-0.0964	0.0094	-0.0874
1000 - seed weight (g)	G	0.0166	0.0740	-0.0194	0.0042	-0.0016	-0.0188	0.0078	0.0627
	P	0.0095	0.0595	-0.0444	0.0093	-0.0096	-0.0200	0.0454	0.0498

Residual effect: Genotypic = 0. , Phenotypic = 0. , * significant at p = 0.05 and ** significant at = 0.01.

Table 5: Number of clusters along with the included genotypes formed for the inbred lines of fennel.

Clusters	Number of lines	Genotypes
I	20	ILF-1, ILF- 41, ILF-119, ILF-143, ILF-137, RF-125, ILF-2, RF-205, ILF-138, ILF-50, ILF-87, ILF-21, ILF-69, ILF-85, ILF-12
II	9	ILF-101, ILF-102, ILF-44, ILF-99, ILF-50, RF-59, ILF-94, ILF-95, ILF-97
III	4	ILF-39, ILF-83, ILF-82, ILF-91
IV	15	ILF-10, ILF-104, ILF-51, ILF-79, ILF-118, ILF-6, ILF-61, ILF-113, ILF-63, ILF-132, ILF-14, ILF-135, ILF-41, ILF-56, ILF-5
V	11	ILF-110, ILF-117, ILF-45, ILF-54, ILF-112, ILF-128, ILF-116, ILF-127, ILF-64, ILF-38, ILF-70
VI	4	ILF-109, ILF-35, ILF-28, ILF-29
VII	7	ILF-122, ILF-37, ILF-34, ILF-74, ILF-53, ILF-71, ILF-32
VIII	10	ILF-129, ILF-142, ILF-144, ILF-80, Local, ILF-48, ILF-75, ILF-46, ILF-67, ILF-68
IX	16	ILF-103, ILF-49, ILF-86, ILF-20, ILF-30, ILF-23, ILF-4, RF-101, RF-143, ILF-11, ILF-138, ILF-18, ILF-62, ILF-66, ILF-134, ILF-140
X	16	ILF-106, ILF-93, ILF-98, ILF-136, ILF-19, ILF-27, ILF-31, ILF-90, ILF-96, ILF-107, ILF-26, ILF-7, ILF-43, ILF-76, ILF-78, ILF-89

Table 6: Mean and ranking of different clusters for various morphological traits and seed yield

Cluster No.	Days to 50% flowering	Plant height (cm)	Branches plant ⁻¹	Umbels plant ⁻¹	Umbellets umbel ⁻¹	Seeds per umbel	1000 seed weight (g)	Seed yield plant ⁻¹ (g)								
									Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank
Cluster I	101.43	2.00	130.19	3.00	7.27	8.00	17.45	8.00	21.05	8.00	384.85	8.00	6.33	5.00	12.27	4.00
Cluster II	105.63	10.00	127.66	2.00	8.56	5.00	17.01	10.00	21.07	7.00	294.82	9.00	6.36	4.00	7.81	9.00
Cluster III	103.00	5.00	112.08	1.00	8.66	4.00	17.50	7.00	17.40	10.00	259.20	10.00	4.86	10.00	11.30	5.00
Cluster IV	105.57	9.00	146.65	10.00	7.99	7.00	17.26	9.00	22.26	4.00	408.27	6.00	6.17	7.00	15.99	2.00
Cluster V	103.87	6.00	138.96	8.00	8.83	3.00	20.46	4.00	20.20	9.00	468.84	3.00	7.02	1.00	10.95	6.00
Cluster VI	100.25	1.00	132.55	5.00	8.41	6.00	30.70	1.00	23.95	3.00	464.20	4.00	6.27	6.00	9.61	8.00
Cluster VII	104.99	8.00	133.61	6.00	11.67	1.00	28.24	2.00	22.02	5.00	387.11	7.00	5.88	8.00	12.50	3.00
Cluster VIII	101.46	3.00	141.64	9.00	10.22	2.00	22.88	3.00	21.89	6.00	409.96	5.00	6.50	3.00	23.01	1.00
Cluster IX	102.26	4.00	138.04	7.00	7.08	10.00	17.86	6.00	25.96	1.00	561.93	1.00	6.93	2.00	10.85	7.00
Cluster X	104.20	7.00	131.10	4.00	7.26	9.00	18.03	5.00	25.76	2.00	514.55	2.00	5.77	9.00	7.21	10.00

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