

Mass, full and half sib-selection for genetic improvement in fennel (*Foeniculum vulgare* Mill.)

V V Singh & E V Divakara Sastry

Department of Plant Breeding & Genetics
S.K.N. College of Agriculture
Rajasthan Agricultural University
Jobner 303329, Rajasthan, India

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Abstract

A study was conducted to estimate genetic variances and heritability for yield and yield attributes in fennel UF-143 population using North Carolina Design-I. The dominance component was high for days to 50% flowering, branches per plant, umbels per plant, seeds per umbel, seed yield, harvest index and test weight. Preponderance of additive gene action was observed for plant height, umbellets per umbel and biological yield. The heritability in narrow sense was high for biological yield. Among the various methods for which theoretical responses were calculated, mass selection appeared suitable for the improvement of biological yield, harvest index, test weight, seed yield, umbellets per umbel, umbels per plant and branches per plant.

Key words: *Foeniculum vulgare*, genetic variance, heritability

Fennel is a cross pollinated crop and is an important seed spice. The production of fennel is basically limited due to non-availability of high yielding varieties and poor stability in performance. A survey of literature clearly indicated that limited work has been done on genetic improvement in fennel (Agrawal *et al.* 2001). Before an efficient breeding methodology can be formulated for improvement in yield and other traits of interest, it is essential to resolve the genetic architecture of the elite base populations. Quantitative genetics provides the methodology for the estimation of genetic parameters like additive genetic effects and dominance deviation. The ultimate aim of estimating components of genetic variance is to predict expected genetic advance in different selection programmes. The present investigation

was therefore carried out to estimate genetic architecture of a random mating fennel population, UF-143.

The experimental material consisted of full sib and half sib progenies developed according to North Carolina Design-I (Comstock & Robinson 1948) from the population UF-143. The plants of UF-143 are of medium maturity, medium tall with long grains and was developed through five cycles of half sib recurrent selection from a local collection of sarwad (Ajmer). For this, 25 male plants were randomly selected from the population of UF-143 and each male plant was crossed with four randomly selected female plants (different from the selected male plants). The progeny of each female x male plant consisted a full sib family and the progenies of

all the 4 females with a common male plant were designated as one male group. All the 100 full sib families of the 25 male groups were divided into 5 sets of 5 male groups each. The sets were evaluated in Randomized Block Design with 3 replications during rabi season of 2001-2002 at S. K. N. College of Agriculture, Jobner, Rajasthan. The sets were first randomized in each replication. The males in each set followed by the full sib families of each male were also randomized afresh in each replication. The progeny of each full sib family was sown in single row of 3.0 m length spaced at 45 cm. The plant to plant spacing was adjusted by thinning at 3 to 4 leaf stage. Observations were recorded on days to 50 per cent flowering, plant height, branches per plant, umbels per plant, umbellets per umbel, seeds per umbel, biological yield per plant, seed yield per plant, harvest index and test weight on 10 randomly selected plants. The data were analysed according to Design-I of Comstock & Robinson (1948) and Robinson *et al.* (1949). The estimates of additive (σ_A^2) and dominance (σ_D^2) variances obtained from design-I were also used to calculate heritability in narrow sense (h_{ns}^2) and theoretical responses to different selection schemes according to Pandey (1970). The formulae used for the estimation of responses (R) in various selection schemes are given below-

$$\text{Mass selection: } R = \frac{i\sigma_A^2}{\sqrt{\sigma_m^2 + \sigma_f^2 + \sigma_e^2}} \quad (1)$$

$$\text{Full sib selection: } R = \frac{i\frac{1}{2}\sigma_A^2}{\sqrt{\sigma_m^2 + \sigma_f^2 + (\sigma_e^2/r)}} \quad (2)$$

Half sib family selection : Selection based on half sib family means and deriving the offspring by inter crosses from a bulked sample of the remnant seed of selected families:

$$R = \frac{i\frac{1}{4}\sigma_A^2}{\sqrt{\sigma_m^2 + (\sigma_f^2/f) + (\sigma_e^2/rf)}}$$

Where R = response to selection, I = selection intensity-(2.06 at 5% intensity), σ_A^2 = additive

variance, σ_f^2 = variance due to females, = σ_m^2 variance due to males, r = No. of replications and f = No. of females in a male.

The results of analysis of variance are presented in Table 1 for characters based on individual values and for characters based on plot means. Perusal of both the tables indicated significant differences among sets for all the characters studied. This indicates the existence of significant inherent variability for all the characters. Partitioning of the progenies mean squares into males/sets and females/males/sets also indicates that the male groups representing half sibs and females in males representing full sibs exhibited significant differences for all the characters. A perusal of Table 2 shows that plant height, umbellets per umbel and biological yield per plant were controlled by additive variance, while the remaining characters exhibited preponderance of dominance. This is also clear from the σ_A^2 / σ_D^2 ratio which tilted more towards the dominance side. Negative estimates of was observed for plant height. Theoretically, the variances are never negative. The negative estimates, most probably, resulted from sampling error around mean value zero or very low.

The population has shown high variation for umbels per plant, seeds per umbel and harvest index. The variation for other traits were lower. The differences between genotypic (GCV) and phenotypic (PCV) variances are very low for days to 50 per cent flowering, seeds per umbel, biological yield per plant, harvest index and test weight, indicating that these are least affected by environment. For other traits, the differences are much inflated, indicating a positive role of environment on the expression of genotypes.

The narrow sense heritability (h_{ns}^2) estimate was highest for biological yield per plant. For other characters, the estimates were considerably lower, umbels per plant and seeds per umbel exhibited lowest heritability. The results are thus in general agreement with the earlier reports of Kathiria (1980).

Table 1. Mean sum of squares of different characters in the biparental progenies of UF-143

Source of variation	df	Mean sum of squares based on individual plants				
		Plant height	Branches plant ⁻¹	Umbels plant ⁻¹	Umbellets umbel ⁻¹	Seeds umbel ⁻¹
Sets	4	3394.89**	93.24**	2002.72**	105.46**	23920.29**
R/S	10	59.70	8.12	102.89**	11.82	12981.42**
M/S	20	822.31**	26.16**	172.66**	43.00**	5199.81**
F/M/S	75	587.71**	19.80**	140.86**	28.36**	4984.03**
Rep. x fem.	190	575.53**	15.09**	110.38**	23.95**	470.00
Error	2700	128.78	8.22	25.42	12.72	2716.59

	df	Mean sum of squares based on plot means				
		Days to 50% flowering	Biological yield	Seed yield	Harvest index	Test weight
Sets	4	53.19**	111.85**	22.58**	438.74**	0.82**
R/S	10	4.15	504.91**	33.70**	28.26	0.04
Progenies	95	5.04**	75.01**	6.32**	225.08**	0.53**
M/S	20	6.46**	152.91**	8.68**	297.72**	0.85**
F/M/S	75	4.66**	54.23**	5.69**	205.71**	0.44**
Remainder	190	2.67	5.59	3.93	20.70	0.05

Table 2. Estimates of additive (σ_A^2) and dominance variances, genotypic (GCV) and phenotypic (PCV) coefficients of variation and heritability in narrow sense (h_{ns}^2)

Character	σ_A^2	σ_D^2	σ_A^2 / σ_D^2	GCV	PCV	h_{ns}^2
Days to flowering	0.60	2.05	0.29	1.44	2.04	11.27
Plant height	78.20	-61.90	(-)*	4.42	26.39	13.51
Branches plant ⁻¹	2.12	4.16	0.51	35.60	64.39	10.32
Umbels plant ⁻¹	10.60	30.04	0.35	45.44	86.85	7.14
Umbellets umbel ⁻¹	4.88	1.00	4.88	15.44	34.02	17.09
Seeds umbel ⁻¹	71.93	5946.7	0.01	42.19	42.88	1.16
Biological yield	32.89	31.96	1.03	34.15	35.59	46.65
Seed yield	1.00	1.35	0.74	24.12	39.45	15.88
Harvest index	30.67	216.01	0.14	56.68	59.01	11.47
Test weight	0.14	0.39	0.35	11.62	12.11	23.92

* σ_A^2 / σ_D^2 not calculated σ_D^2 is negative.

Genetic advance at 5% selection intensity was higher for biological yield per plant while for other traits it was low to medium. Negligible values of genetic advance were observed for days to 50% flowering and seeds per umbel (Table 3). The estimates of responses in different selection schemes (Table 3) do not lead to any general conclusion. Among the different traits, the biological yield per plant showed maximum response with all the selection schemes while days to 50 per cent flowering gave minimum response which may be due to non additive gene action. The trait days to 50%

flowering can be improved through hybridization with unlike parents. Among the three different schemes, the responses obtained with mass selection were very high in comparison to the other two schemes. The responses with half sib selection were the lowest.

Since non-additive genetic variance appeared to be in considerable portion, this population can further be improved by appropriate selection scheme operating on non-additive genetic variance. In female biological yield is a major yield component, therefore selection based on

Table 3. Estimates of genetic advance and response to selection in different selection schemes

Character	GA _(ns)	Mass selection	Full sib selection	Half sib selection
Days to flowering	0.54 [0.47]	0.66 [0.58]	0.47 [0.42]	0.42 [0.37]
Plant height	6.69 [7.34]	6.65 [7.30]	5.54 [6.08]	4.90 [5.38]
Branches plant ⁻¹	0.96 [13.68]	1.08 [15.33]	0.83 [11.85]	0.75 [10.67]
Umbels plant ⁻¹	1.79 [12.77]	1.99 [14.17]	1.56 [11.14]	1.45 [10.33]
Umbellets umbel ⁻¹	1.88 [11.97]	2.00 [12.71]	1.57 [9.99]	1.34 [8.58]
Seeds umbel ⁻¹	1.88 [1.02]	3.57 [1.94]	1.86 [1.01]	1.83 [0.99]
Biological yield	8.07 [34.24]	12.36 [52.44]	6.61 [28.02]	4.74 [20.12]
Seed yield	0.82 [12.91]	0.94 [14.81]	0.70 [11.04]	0.61 [9.50]
Harvest index	3.86 [13.94]	6.65 [24.02]	3.61 [13.05]	3.17 [11.44]
Test weight	0.37 [5.97]	0.61 [9.81]	0.33 [5.30]	0.27 [4.24]

Figures in parentheses indicate percentage

this character using mass selection may be used for improving seed yield of fennel.

References

- Agrawal S, Sastry E V D & Sharma R K 2001 Seed Spices-Production, Quality and Export. Pointer Publishers, Jaipur.
- Comstock R E & Robinson H F 1948 The components of genetic variance in population of biparental progenies and their use in estimating average degree of dominance. *Biometrics* 4 : 254-266.
- Kathiria K B 1980 Variability and correlation in a selected and unselected bulk of fennel. M. Sc. Thesis, University of Udaipur, Campus Jobner.
- Pandey R S 1970 Inheritance of leaf morphological characters in three open-pollinated populations of *Zea mays* L. Ph. D. Thesis, University of Guelph, Canada.
- Robinson H G, Comstock R E & Harvey P H 1949 Estimates of heritability and degree of dominance in corn. *Agron. J.* 41: 353-359.