Short Communication

Genetic variance and expected selection response in fennel (*Foeniculum vulgare* Miller)

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Fennel (*Foeniculum vulgare* Miller) is an important allogamous spice crop, grown in many parts of the world, which received little attentions from the breeders. Hence, most of the varieties grown are basically land races. The genetics of most of the traits in fennel is not yet known. A few varieties have been developed through mass selection. North Carolina mating Design offer an opportunity to estimate the quantitative genetic parameters of a character from such populations. Selection within a population is effective if gene action is additive, while preponderance of dominance suggests the development of a hybrid. Thus, comparison of the estimates of genetic variation provides a measure for a breeding strategy to be adopted in the fennel improvement programme.

The experimental material used in the present study consisted of full-sib and half-sib progenies developed according to North Carolina mating Design-I [1] from the population RF-125. This population was developed through recurrent selection based on individual plant progeny (half-sibs) performance in EC-243380 from Italy. 25 male plants were randomly selected from this population during growing season 2000-2001. Each such selected plant was used to pollinate it with four randomly selected plants. This constituted 25 half-sib families and 100 full-sib progenies. Further, these 25 male groups were divided into 5 sets consisting of 5 half-sib families in each set. In the following year (2001-02) these sets were evaluated in a randomized block design with three replications. The sets were first randomized in each replication. The half-sib families in each set followed by the full-sib families within each male were also randomized afresh in each replication. Each full-sib family was sown in a 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 as listed in table 1 were recorded on 10 randomly selected plants. The data were analysed according to Comstock and Robinson [1] and Robinson *et al.*, [2]. The estimates of additive (σ^2_A) and dominance (σ^2_D) variance obtained from design-I were used to calculate heritability in narrow sense (h^2_{ns}) and expected responses to different selection schemes according to Pandey [3].

The results of analysis of variance indicated presence of significant variability for most of the characters. Partitioning of the progenies mean squares into half-sibs (males/sets) and full-sibs (females/males/sets) exhibited significant differences for most of the characters. A perusal of Table 1 indicates that the magnitude of σ^2_f was higher than σ^2_m for most of the traits. A higher σ^2_f over σ^2_m indicates preponderance of both additive and dominance components as σ^2_f consists of 1/4 σ^2_A and 1/4 σ^2_D. Perusal of Table 1 further showed preponderance of dominance variance for plant height, umbels/plant, umbellets/plant and seeds/umbel. This is also clear from the value of σ^2_A / σ^2_D. Negative estimates of σ^2_D were observed for branches per plant, biological yield and harvest index, while σ^2_A was negative for test weight. Theoretically, variances are not negative. Negative estimates, most probably resulted from sampling error around a low mean value [4].

The narrow sense heritability (h^2_{ns}) estimate was highest for branches per plant. For other traits, the estimates were moderate to low. Seeds per umbel and plant height exhibited the lowest heritability. The results are in accordance with earlier reports of Kathiria [5]. Genetic advance at 5 per cent selection intensity was highest for branches per plant, while for other traits it was low to medium.

Negligible values of genetic advance were observed for days to 50 per cent flowering and seeds per umbel (Table 2). The estimates of responses at different selection schemes indicates that branches per plant showed the maximum expected response for all

Table 1. Estimates of components of variation and heritability in narrow sense (as percent) in fennel

Characters	σ^2_f	σ^2_m	σ^2_e	σ^2_A	σ^2_D	σ^2_A / σ^2_D	h^2 (ns)
Days to flowering	0.62	0.33	4.55	1.31	1.17	1.11	18.59
Plant height (cm)	156.67	8.34	576.30	33.28	593.31	0.06	2.77
Branches/plant	0.23	1.32	9.92	5.29	−4.37	-	48.81
Umbels/plant	21.28	6.65	124.42	26.61	58.51	0.45	12.70
Umbellets/plant	4.57	0.60	25.93	2.41	15.89	0.15	5.44
Seeds/umbel	977.51	51.61	19289.35	206.43	3703.61	0.06	0.89
Biological yield/plant (g)	6.62	9.19	80.51	36.76	−10.28	-	34.36
Seed yield/plant (g)	0.98	0.94	7.12	3.74	0.19	19.70	33.87
Harvest index (%)	−2.66	1.69	125.02	6.77	−17.40	-	5.92
Test weight (g)	0.14	−0.08	1.21	−0.31	0.88	-	-

When σ^2_A and σ^2_D were negative, the ratio σ^2_A / σ^2_D was not estimated. Ns = narrow sense

Table 2. Estimates of genetic advance and response to selection (as percentage of mean) for different selection schemes for the characters studied in fennel

Character	Genetic advance (%)	Mass selection (%)	Full-sib selection (%)	Half-sib selection (%)
Days to flowering	0.89	1.01	0.76	0.64
Plant height (cm)	2.24	2.86	2.06	1.99
Branches/plant	51.00	49.58	38.09	28.25
Umbels/plant	30.32	35.56	26.34	23.21
Umbellets/plant	5.05	6.02	4.51	4.24
Seeds/umbel	1.34	1.43	1.18	1.16
Biological yield/ plant (g)	31.05	32.72	24.58	19.16
Seed yield/ plant (g)	36.53	40.39	29.31	22.78
Harvest index (%)	4.71	4.52	3.94	3.72

the selection schemes, while days to 50 per cent flowering gave the minimum expected response. 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.

Thus, in present study, it was observed that additive as well as non-additive components of variance were playing important role in this population. So, this population can further be improved by appropriate selection scheme operating on additive and non-additive genetic variance.

References

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