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Assessment of S_1 progenies in two diverse populations of fennel (*Foeniculum vulgare* Mill.)

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Abstract

An investigation was conducted at Jobner (Rajasthan) to estimate variability, heritability and expected selection gain among S_1 progenies generated from RF-125 and UF-143 populations of fennel (*Foeniculum vulgare*). The inter-family variance was higher in comparison to intra-family variance in both the populations for most of the characters studied. The estimates of heritability (narrow sense) were high only for plant height in RF-125. For rest of the characters, the heritability was medium to low. The expected genetic gain was medium to low in both the populations and was highest in umbels·plant^{-1} in RF-125. The study suggests that significant inter family variance is still present in these populations which can be exploited.

Key words: expected genetic gain, fennel, *Foeniculum vulgare*, heritability, S_1 progenies.

Fennel (*Foeniculum vulgare* Mill.) is a highly cross pollinated crop with 82.2% to 91.4% cross pollination (Ramanujam *et al.* 1964) and to improve such crops, population improvement is the recommended method. Commonly used methods for population improvement are mass (individual phenotypic) selection, full sib, half-sib and S_1 progeny selection. Further, selfing through which S_1 progenies are produced, provides a chance to unravel the hidden variability through the breakdown of heterozygosity or epistasis, which can be exploited. The present investigation was carried out at Research Farm, SKN College of Agriculture, Jobner (Rajasthan) in two populations of fennel namely, RF-125 and UF-143. Both these populations were developed through half-sib recurrent selection. RF-125 was developed from exotic collection EC-243380 originating from Italy while UF-143 was developed from local collection of Sarwad (Ajmer). In each population, 100 plants were randomly tagged before initiation of flowering. Each plant was selfed and the seed obtained through selfing was harvested separately from each plant. In the succeeding *rabi* season, 50 single plants forming the S_1 families from each population were evaluated in a randomized block design with three replications. Each family was sown in a single row plot of 3 m length spaced 45 cm apart with plant to plant spacing of 20 cm. Data were recorded on 10 randomly selected plants for plant height, branches plant^{-1}, umbels plant^{-1}, umbellets umbel^{-1}, seeds umbel^{-1} and biological yield plant^{-1}. Data of days to 50% flowering, seed yield plant^{-1}, test weight and harvest index were recorded on mean basis. The analysis of variance was done as per Hallauer & Miranda (1988) for characters based on individual values, while rest of the characters were analysed as per Panse & Sukhatme (1978).

Analysis of variance indicated the existence of significant differences between families for all the traits in both the populations (Table 1). The family mean square of these characters was significant when tested against within mean sum of squares, indicating that inter family variance was higher in comparison to intra family variance. In such cases, the between family selection is supposed to be more effective to within family selection. The analysis of variance based on family means indicated existence of significant differences between families for seed yield plant^{-1} in both the populations while days to 50% flowering and test weight were significant in RF-125 and UF-143, respectively. In progenies resulting from selfing, such type of results are expected because selfing exposes the hidden variability through breakdown of heterozygosity. Significant differences between S_1 families have also been reported by Kumhar (1999) in pearl millet.

The differences between σ^2_A and σ^2_p estimates of plant height in RF-125 was low, indicating the importance of additive variance in the inheritance of this character (Table 2). The heritability (narrow sense) was high for plant height in RF-125 indicating effectiveness of selection for this character. For rest of the characters, the heritability was medium except branches plant^{-1} where low heritability was observed in both the populations. The expected genetic gain was low to medium in all the characters and it was highest in umbels plant^{-1} in RF-125 followed by biological yield plant^{-1} in both the populations.

Table 1. Mean sum of squares of different characters of S_1 progenies of fennel

Source	DF	Plant height	Branches plant^{-1}	Umbels plant^{-1}	Umbellets plant^{-1}	Seeds umbel^{-1}	Biological yield
				(Based on individual plants)			
RF-125							
Between families	149	375.44**	5.32**	38.34**	11.95**	5449.49**	143.44**
Replications	2	53.12	4.52	62.90**	10.56**	6274.08**	398.01**
M_1 families	49	1077.41**	8.83**	96.64**	31.10**	14354.75**	368.55**
M_2 error	98	31.03	3.58	8.69	2.41	1082.07	25.69
M_3 within families	1350	9.06	2.55	5.14	2.15	521.32	13.22
UF-143							
Between families	149	309.91**	2.57*	6.19**	5.35**	919.93**	91.69**
Replications	2	124.21	5.66	6.06*	5.01	5836.03**	5.00
M_1 families	49	809.41**	3.73*	14.94**	12.24**	2139.86**	239.01**
M_2 error	98	63.95	1.93	1.82	1.91	209.64	19.81
M_3 within families	1350	14.80	2.79	1.01	1.33	168.39	11.16

Source	DF	Days to 50% flowering	Seed yield plant^{-1}	Harvest index	Test weight
		(Based on plot means)			
RF-125					
Replications	2	3.08	9.82**	93.11	1.32
Families	49	6.07*	3.97**	43.45	0.97
Error	98	2.54	0.49	48.23	0.92
UF-143					
Replications	2	7.08	0.91**	56.03	0.96
Families	49	7.02	0.58**	33.13	0.75**
Error	98	9.19	0.07	35.40	0.47

* Significant at P= 0.05; ** Significant at P=0.01

Table 2. Estimates of additive and phenotypic variance, heritability (narrow sense) and genetic advance in S_1 populations of fennel (based on individual plant data)

Character	σ^2_S	σ^2_A	σ^2_P	h^2 (ns) as % of mean	GA as % of mean
RF-125					
Plant height	5.99	69.76	100.79	69.21	14.49
Branches plant^{-1}	0.54	0.35	3.93	8.90	12.38
Umbels plant^{-1}	1.79	5.88	14.57	40.36	41.37
Umbellets umbel^{-1}	1.02	1.91	4.32	44.21	14.52
Seeds umbel^{-1}	21.87	884.84	1966.91	44.98	22.96
Biological yield plant^{-1}	3.50	22.86	48.55	47.08	34.06
UF-143					
Plant height	5.19	49.68	113.63	43.72	10.39
Branches plant^{-1}	0.35	0.12	2.05	5.85	6.23
Umbels plant^{-1}	0.71	0.87	2.69	32.49	7.77
Umbellets umbel^{-1}	0.64	0.69	2.59	26.56	6.01
Seeds umbel^{-1}	8.45	128.68	337.92	38.08	9.60
Biological yield plant^{-1}	2.82	14.61	34.42	42.45	36.25

From the mean squares of M_1, M_2 and M_3 of Table 1, σ^2_A, σ^2_P, σ^2_S, h^2 (ns) were estimated as per the following formulae (Hallauer & Miranda 1988).

The family variance = $\sigma^2_f = \dfrac{M_1 - M_2}{nr}$

The variance due to selfed family means = $\sigma^2_S = \sqrt{\dfrac{M_1}{nr}}$

The additive variance = $\sigma^2_A = 2\,\sigma^2_f$

The phenotypic variance = $\sigma^2_P = \sigma^2_A + M_3$

The estimated GA= $\left[\dfrac{\Delta G\,K.1/2\;\sigma^2_A}{\frac{\sigma^2_S}{X}}\right]$

Where, $\overline{X}$, is the general mean of the character; n=number of plants/family; r=number of replications

Table 3. Estimates of genotypic and phenotypic variance, their coefficients, heritability (broad sense) and genetic advance in S_1 families of fennel (based on plot means)

Character	σ^2_g	GCV	σ^2_P	PCV	h^2 (bs) as % of mean	GA among families as % of mean
RF-125						
Days to 50% flowering	1.17	0.97	3.71	1.72	31.54	1.12
Seed yield plant^{-1}	1.16	23.21	1.65	27.68	70.30	40.09
UF-143						
Seed yield plant^{-1}	0.51	47.92	0.58	51.11	87.93	92.62
Test weight	0.09	6.65	0.56	16.59	16.07	5.48

In characters where mean data were available, the estimates of GCV and PCV were low except seed yield plant^{-1} in both the populations (Table 3). The heritability (broad sense) was also high for seed yield plant^{-1} in both the populations while expected genetic gain was high only for seed yield plant^{-1} in UF-143.

Thus the study indicated that significant inter family variance for major yield components is still present in both the populations of fennel which can be exploited for further refinement of these populations.

References

Hallauer A R & Miranda J B 1988 Quantitative Genetics in Maize Breeding. 2nd Edn. Iowa State University Press, Iowa.

Kumhar J P 1999 Comparative study of half-sib and selfed progenies of the composite UUJ-1 of fodder bajra [*Pennisetum glaucum* (L.) R.Br.]. MSc (Ag) Thesis, Rajasthan Agricultural University, Bikaner.

Panse V C & Sukhatme P V 1978 Statistical Methods for Agricultural Workers. 3rd Edn. Indian Council of Agricultural Research, New Delhi.

Ramanujam S, Joshi B S & Saxena M B L 1964 Extent and randomness of cross pollination in some umbelliferous spices of India. Indian J. Gen. 24 : 62–67.