Comparison of full sib, half sib and S$_1$ progenies in fennel (*Foeniculum vulgare* Mill.)

V V Singh, E V Divakara Sastry & D L Singhania

Department of Plant Breeding and Genetics
SKN College of Agriculture
Jobner – 303 329, Rajasthan, India

Abstract

A field experiment was conducted at Jobner (Rajasthan), to compare different population improvement methods in a fennel *(Foeniculum vulgare)* population namely, UF-143. Estimates of genotypic coefficient of variation and phenotypic coefficient of variation were higher in full sib than S$_1$ and half sib progenies for most of the traits. Heritability estimate was higher in full sib progenies for days to 50% flowering, seeds umbel^{-1} and test weight, while half sib showed maximum heritability for branches plant^{-1}, umbels plant^{-1} and umbelletes umbel^{-1}. S$_1$ progenies recorded maximum heritability and genetic gain for seed yield plant^{-1}. For most of the traits, full sib progenies recorded maximum genetic gain except plant height, umbellets umbel^{-1} and seed yield plant^{-1}.

Key words: fennel, *Foeniculum vulgare*, full sib, half sib, S$_1$ progenies.

In cross pollinated crops, selection schemes using full sib, half sib and S$_1$ progenies have been very effective in exposing the hidden variability, so that selection can be made effective. Knowledge regarding comparative efficiency of different population improvement methods in generating variability is limited in fennel (*Foeniculum vulgare* Mill.). Hence, the present investigation was carried out at the Research Farm of SKN College of Agriculture, Jobner (Rajasthan), to generate information on these aspects in a fennel population, namely, UF–143.

The fennel (UF–143) population was developed through five cycles of half sib recurrent selection from a local collection of Sarwad (Ajmer). Fifty plants were randomly tagged in the fennel population before initiation of flowering. Each plant was selfed and allowed to open pollinate simultaneously. This constituted S$_1$ and half sib progenies, respectively. Further, five sets of five plants each were selected randomly and constituted the male plants. Each male plant in each set was crossed with a set of four randomly selected plants from the population using them as females. Thus, a total of 100 crosses was made to develop bi-parental progenies (full sib) as per North Carolina Design-I (Comstock & Robinson 1948). All the three types of progenies namely, S$_1$, half sib and full sib were evaluated in a randomized block design with three replications. Each progeny was sown in a single row plot of 3 m length spaced 45 cm apart with plant to plant spacing of 20 cm. Data for days to 50% flowering were recorded at the time of flowering on whole plot basis while data for plant height, branches plant^{-1},

umbels plant[-1], umbelletes umbel[-1], seeds umbel[-1], seed yield plant[-1] and test weight were recorded at harvest during *rabi* 2001-02 on 10 randomly selected plants plot[-1] in each replication. To compare these progenies, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h[2]) and genetic advance (GA) were calculated for each character in each type of progenies by using standard statistical procedures (Burton & De Vane 1953).

The analysis of variance indicated significant differences for all the characters in the three types of progenies except days to 50% flowering in S_1 (Table 1). This indicated the presence of significant inherent variability in the population for almost all the characters. The mean was greater in bi-parental progenies than in S_1 and half-sib progenies for all the characters. PCV was higher than GCV for all the characters in the three types of progenies indicating positive influence of the environment on character expression. GCV and PCV in bi-paren-

tal progenies were higher than in corresponding S_1 and half sib progenies for most of the traits, which might be due to breakage of undesirable linkages and appearance of new gene combination.

Heritability expresses the proportion of the total variance that is attributable to the average effect of genes and determines the degree of resemblance between relatives (Falconer & Mackay 1996). Broad sense heritability estimate for all the characters revealed that full sib progenies had higher estimate of heritability for days to 50% flowering, seeds umbel[-1] and test weight while half sib population showed higher values of heritability for branches plant[-1], umbels plant[-1] and umbelletes umbel[-1]. S_1 progenies recorded higher heritability estimates for plant height and seed yield plant[-1]. The estimate of GA expressed as per cent of mean showed that bi-parental progenies had higher GA for most of the traits except plant height, umbelletes umbel[-1] and seed yield plant[-1]. For seed yield plant[-1],

Table 1. Mean, genotypic and phenotypic coefficient of variation, heritability (broad sense) and genetic advance in full sib, half sib and S_1 progenies of fennel population UF-143

Character/ Parameter	Days to 50% flowering	Plant height (cm)	Branches plant[-1]	Umbels plant[-1]	Umbellets plant[-1]	Seeds umbel[-1]	Seed yield plant[-1] (g)	Test weight (g)
Full sib								
Mean	116.16	91.17	7.04	14.03	15.71	183.87	3.74	5.52
GCV	1.44	4.42	35.60	45.44	15.44	42.19	24.12	11.62
PCV	2.04	26.39	64.39	86.85	34.02	42.88	39.45	12.11
H (%)	49.84	2.81	30.56	27.37	20.59	96.81	37.39	91.95
GA as % of mean	2.09	1.52	40.54	48.97	14.43	85.52	30.39	22.94
Half sib								
Mean	108.16	91.67	5.69	15.87	17.43	160.31	1.65	4.65
GCV	0.79	15.61	15.32	15.37	13.84	17.20	46.94	7.13
PCV	1.66	17.99	25.10	17.72	16.37	19.15	62.98	16.69
H (%)	22.43	75.27	37.25	75.22	71.50	80.70	55.55	18.24
GA as % of mean	0.76	27.80	19.13	27.38	23.94	31.95	72.01	6.27
S_1								
Mean	104.64	94.79	5.63	16.34	18.12	163.28	1.49	4.51
GCV	-	16.63	13.76	12.79	10.23	15.53	47.92	6.55
PCV	-	18.65	28.25	15.23	12.76	17.89	51.11	16.59
H (%)	-	79.53	23.71	70.60	64.30	75.42	87.93	16.07
GA as % of mean	-	30.35	13.97	22.27	16.83	27.64	92.62	5.48

GCV=genotypic coefficient of variation; PCV=phenotypic coefficient of variation; H=heritability (broad sense); GA=genetic advance as % of mean

S_1 showed maximum genetic gain which was also accompanied by high heritability. For some characters, higher magnitude of heritability was not accompanied by high GA. This inconsistency may be attributed to low magnitude of phenotypic standard deviation which was an important component of GA. In maize, El-Sheikh (1999) reported that half sib method gave high estimates of heritability as compared to full sib and S_1 methods, which might be due to differences in genetic material used. Hence, it can be concluded that bi-parental mating (full sib) can substantially supplement fennel breeding programmes by way of improving the mean performance and creating more genetic variability because of accumulation of favourable genes in the fennel population and thus improving the efficiency of selection.

References

Burton G W & De Vane E W 1953 Estimating heritability in tall fescue (*Festuca areendinacea*) from replicated material. Agron. J. 4 : 78–81.

Comstock R E & Robinson H F 1948 The components of genetic variability in population of bi-parental progenies and their use in estimating the average degree of dominance. Biometrics 4 : 254–266.

El-Sheikh M H 1999 Advances from half sib and full sib family selection within two maize populations. Alexandria J. Agric. Res. 44 : 195–208

Falconer D S & Mackay T F C 1996 Introduction to Quantitative Genetics (4th Edn.). Longman, England.