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Stability of seed yield and its component traits in fennel (*Foeniculum vulgare*)

PREETI VERMA[1] and R K SOLANKI[2]

Agricultural Research Station, Kota, Rajasthan

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ABSTRACT

Stability of eleven genotypes of fennel (*Foeniculum vulgare* M) was assessed for yield and component traits based on three years consecutive experimentation, i.e. 2009-2011. Mean square due to environment + (variety × environment) was significant for all the traits except number of umbellets per umbel indicating the existence of genotype × environment interaction. Based on the mean performance, regression coefficient and deviation from regression values, it was found that the stability of yield is imparted in the genotypes, viz. UF 281, AF 1, GF 11, JF 586 2/5, HF 131 and NDF 16 through the stable performance of major yield contributing traits like primary and secondary branches, number of umbels and umbellets, number of seeds/plant and test weight. These genotypes may be useful genetic resources for development of high yielding, stable varieties in fennel.

Key words: Fennel, Seed yield, Stability, Traits

Fennel (*Foeniculum vulgare* Miller) is well known for its aromatic seeds which are used in flavoring food and other value added products. Besides, it has high medicinal application both in Ayurveda and Unani medicine as an abortifacient, carminative, cardiotonic, stimulant, vermicide, and lactagogue. Fennel seeds are popular as aromatic carminative, emmenagogue, and stimulant and also used as a stomachic (Lal 2014).

Though it is a native of Southern Europe and Mediterranean region, it is cultivated in Germany, Spain, France, Hungary, India and China. In India, Gujarat, Rajasthan represents 95% of the total area and the average productivity of the country is 13-15 q/ha (Spices Board 2014a). The earning from export of fennel is reported to be around ₹ 10 Crore during the year 2012-13 (Spices Board 2014b). In the last five years, nearly 60 percent increase has been achieved in export value, due to increasing demand of the Indian spices in the world. Looking to the opportunity available in the international market, seed spice crops needs due attention in term of intensive research and development.

Although several high yielding varieties of fennel have been developed, but basic genetic information on genotype performance under varied environmental conditions is very meager (Mangat 1986, Lal 2014, Drazic *et al.* 2014). Past reports suggests that in these seed spices crops like fennel, coriander, celery, anise; high amount of environmental interaction exists for yield and yield contributing traits (Drazic *et al.* 2014, Verma *et al.* 2014). Suitability of a variety/genotype for any agro ecological zones depends upon its adaptability to the particular soil and climatic conditions and uniform performance over and across the period. In the scenario of climate change, it is also essential to evaluate promising genotypes for its stability, as high stability will make the variety/genotype sustain in the region of adoption. Considering the above facts and figures, genotype × environmental interaction was carried to identify the suitable and stable genotypes for fennel genetic improvement.

MATERIALS AND METHODS

A set of 11 genotypes of fennel (Table 1) comprising of 10 test entries contributed from different coordinating centres of AICRP on Spices, IISR, Calicut and one national check was evaluated in randomized block design with three replications for three consecutive years during *rabi* 2009-

Table 1 Genotypes evaluated in the experiment

Entry	Contributing centre
AF 1	Ajmer (Rajasthan.)
JF 586 2/5	Jagudan (Gujarat.)
RF 21	Dholi (Bihar)
RF 31	
HF 131	Hisar (Haryana)
HF 143	
UF 281	Jobner (Rajasthan.)
UF 282	
NDF 16	Kumarganj (Uttar Pradesh)
NDF 24	
GF 11	National check

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[1]e mail: preetiarskota2005@hotmail.com; [2]e mail: rksolanki.ars@gmail.com, National Research Centre on Seed Spices, Tabiji, Ajmer, Rajasthan

10 to 2011-12 at Agricultural Research Station, Kota to study the stability performance. Each genotype was accommodated in eight rows of 4m length with row to row and plant to plant spacing of 30 cm and 10 cm, respectively. All the recommended cultural practices were followed to raise a good crop. Observations were recorded on five randomly selected competitive plants from each genotype in each replication for 10 characters, viz. plant height, number of primary branches, number of secondary branches, number of umbels, number of umbellets per umbel, number of seeds per plant, test weight, seed yield while days to 50% flowering and days to maturity were recorded on plot basis in all the environments. The data were subjected to stability analysis as per the model of Eberhart and Russel (1966), as this model is easy to understand and is very familiar and authentic for consideration by plant breeders.

RESULTS AND DISCUSSION

Pooled analysis of variance (Table 2) for stability performance of different genotypes showed significant difference for only three characters, viz. days to 50% flowering, days to maturity and seed yield. Thus, the genotypes were not significantly different for most of the traits except the above said three. However, the mean squares of environments were significant for all the characters indicating that the environments were significantly diverse from one another.

Mean square due to variety × environment interaction was non-significant for all the traits except seed yield when tested against pooled error. It revealed the non significant differential response of the varieties to the changing environments. But the performance of the genotypes for seed yield was predictable across the environments. Whereas, mean square due to environment + (variety × environment) was significant for all the traits except number of umbellets indicating the existence of genotype × environment interaction. The environment linear component was also significant for all the traits which indicated the difference among all the environments and their considerable influence on all the traits under study. The genotype × environment (linear) mean squares were found to be non–significant for most of the traits except the major yield attributes like number of secondary branches, number of umbellets, number of seeds per plant and seed yield indicating lack of differences in the regression of the genotype on environment for most of the traits. This implies that the tested genotypes showed similar response to the different environments for the expression of most of the characters except number of secondary branches, number of umbellets, number of seeds per plant and seed yield. It indicates significant differences among the regression coefficients implying that the prediction of the genotypes will be feasible across the environments for these important traits.

The mean squares due to pooled deviations were significant for all the characters except days to maturity suggesting genotypic differences in the non – linear regression for all the traits. It indicates the importance of

Table 2 Pooled analysis of variance for different characters in fennel

Source	df	DF	PH	NPB	NSB	NUm	NUmb	NSP	DM	TW	SY
Rep within Env.	6	0.485	14.793	0.124	0.072	0.955	227.788	716.621	2.209	0.204	2388.380
Varieties	10	42.141**	75.639	0.722	3.329	4.199	758.115	14972.310	11.281*	0.953	99455.200**
Env. + (Var.* Env.)	22	226.606**	287.161*	2.045**	9.446**	6.226*	1428.568	1877690.00**	319.800**	4.779**	138082.100**
Enviroments	2	2416.043**	2368.868**	14.256**	74.024**	32.082**	8719.690**	510470.00***	3482.402**	44.327**	797007.700**
Var.* Env.	20	7.662	78.991	0.824	2.988	3.641	699.456	14411.940	3.540	0.824	72189.560**
Environments (Lin.)	1	4832.086**	4737.737**	28.511**	148.048**	64.164**	17439.3804**	1020950.000**	6964.804**	88.654**	1594015.000**
Var.* Env. (Lin.)	10	8.453	60.343	1.141	4.316*	5.469*	109.994	21060.090*	3.057	0.959	130572.000**
Pooled deviation	11	6.247**	88.762**	0.460**	1.510**	1.648**	1171.744**	7057.988**	3.657	0.626**	12551.950**
Pooled error	60	0.477	27.496	0.054	0.055	0.170	104.050	1121.625	2.049	0.039	2186.595
Total	32	168.961	221.061	1.631	7.534	5.593	1219.052	1295591.000	223.388	3.583	126011.200

**, * Significant at P=0.01and P=0.05 respectively. DF: Days to flowering; PH: Plant height (cm); NPB:No of primary branches; NSB:No of secondary branches NUm: No. of Umbels; NSP: No of seed per umbel; DM: Days to maturity; TW: Test weight (g); SY: Seed yield (kg/ha)

Table 4 Estimation of mean and stability parameters for number of umbellets, number of seeds/plant, days to maturity, test weight and seed yield

Genotypes	No of umbellets			No of seeds per plant			Days to maturity			Test weight (g)			Seed yield (kg/ha)		
	μ	b_i	S^2d_i	μ	b_i	S^2d_i	μ	b_i	S^2d_i	μ	b_i	S^2d_i	μ	b_i	S^2d_i
AF 1	181.589	1.19	5267.91	1186.045	0.93	12481	154.889	0.88	-1.37	4.812	1.22	-0.05	1052.662	-0.38	37859
JF 586–2/5	184.233	1.14	3682.59	1309.400	1.02	7124	153.556	0.89	5.30	5.101	1.23	0.12	993.056	0.91	75845.64
RF 21	129.856	0.60	712.38	1139.245	1.00	3015	155.556	0.95	0.87	4.414	1.32	0.06	949.074	1.11	86118.28
RF 31	158.289	1.06	20.18	1122.956	0.93	693	157.667	1.04	-1.86	4.114	0.28	2.10	813.658	0.29	1902.75
HF 131	166.700	1.30	46.13	1226.556	1.05	-171	153.833	0.98	2.82	5.473	1.31	1.17	849.537	1.52	-11.66
HF 143	160.000	1.16	162.60	1097.222	0.89	11979	153.500	1.08	-1.89	4.900	1.39	0.42	1074.074	2.75	17669
UF 281	169.244	1.23	1356.22	1225.644	1.13	455	154.022	1.04	1.40	5.776	0.95	0.67	1359.954	0.94	28639
UF 282	153.056	0.92	-50.48	1084.778	0.92	11283	153.800	1.03	2.31	5.394	0.94	0.05	914.352	0.00	-1981.31
NDF 16	168.733	1.12	-102.08	1161.733	1.07	13426	154.933	0.99	1.08	4.344	0.89	0.57	887.732	1.00	-198.83
NDF 24	147.511	0.55	150.57	1135.556	1.06	-1081	153.833	1.05	-1.33	4.187	0.58	0.55	641.204	0.36	-684.03
GF 11	147.533	0.72	374.88	1256.422	1.00	6500	149.567	1.08	10.18	5.247	0.89	0.62	1038.774	2.35	2465
Population mean		160.613			1176.869			154.105			4.888			961.280	

Table 3 Estimation of mean and stability parameters for days to 50% flowering, plant height, number of primary branches, number of secondary branches and number of umbels

Genotypes	Days to flowering			Plant height (cm)			No of primary branches			No of secondary branches			No of umbels		
	μ	b_i	S^2d_i	μ	b_i	S^2d_i	μ	b_i	S^2d_i	μ	b_i	S^2d_i	μ	b_i	S^2d_i
AF 1	92.667	0.79	34.39	132.056	1.02	-5.53	5.378	0.23	0.58	8.653	0.30	0.84	12.356	-0.77	0.44
JF 586 2/5	89.556	0.97	-0.35	132.189	1.13	321.97	5.667	0.68	0.19	8.998	0.75	2.33	12.478	0.33	-0.22
RF 21	100.556	1.00	14.32	136.533	1.10	3.58	4.521	1.64	0.40	7.889	1.52	2.86	10.367	2.17	1.90
RF 31	98.00	1.21	-0.11	133.333	1.07	0.69	4.833	1.27	0.91	7.143	0.95	3.37	10.922	1.71	0.10
HF 131	98.333	0.95	2.51	137.122	1.38	180.20	5.300	0.98	0.08	9.788	1.03	0.46	13.722	0.55	-0.03
HF 143	96.667	1.23	6.68	141.878	1.65	-8.97	5.978	2.00	0.42	10.599	1.90	0.80	13.733	2.08	1.94
UF 281	94.333	0.93	3.22	125.211	0.61	-23.80	5.389	1.80	0.08	9.510	1.81	1.67	12.867	1.38	5.22
UF 282	96.000	0.80	-0.48	132.900	0.77	6.14	4.811	1.09	0.19	7.477	0.81	1.41	11.500	1.18	-0.18
NDF 16	99.333	1.00	0.53	129.600	0.77	92.93	5.933	-0.01	0.75	9.322	0.28	0.66	14.022	-0.41	4.07
NDF 24	97.667	1.08	-0.34	136.811	1.20	2.64	5.567	0.27	-0.06	8.333	0.44	-0.02	11.733	1.21	1.03
GF 11	89.556	1.03	3.09	125.556	0.29	116.77	5.889	1.05	0.85	9.522	1.21	1.62	12.600	1.58	1.22
Population mean		95.697			133.017			5.388			8.839			12.391	

non linear component accounting for total genotype x environment interaction for all these characters. Therefore, the prediction of the response of the genotypes on the basis of regression analysis for these traits might not be reliable. Similar results were reported by Mangat (1986). The higher magnitude of linear component, i.e. environment (linear) and variety × environment (linear) than the non-linear component (pooled deviation) indicated that the prediction of stability or performance of the genotypes could be made reliably to some extent.

In a stability analysis, both linear (b_i) and non – linear (S^2d_i) components of g × e interactions should be considered for measuring the stability of genotypes (Eberhart and Russell 1966). Linear regression could be regarded as a measure of response of a particular genotype, whereas the deviation from regression (S^2d_i) as the measure of stability. Thus, the genotype with lowest deviation around the regression line ($S^2d_i = 0$) was considered to be the most stable and vice – versa. The estimates of the three stability parameters, mean performance, regression coefficient and deviation from regression for different traits are presented in Table 3 and 4. The highest mean value for seed yield was shown by the genotype UF – 281 with b_i value below unity and non significant S^2d_i value and, therefore, can be said to be the most stable genotype followed by genotype AF 1.

For days to 50 % flowering, genotypes JF 586 2/5, AF 1 and for days to maturity, genotypes GF 11, JF 586 2/5 and HF 143 with lowest mean were found to be the stable genotypes owing to their mean lower than the population mean (desirable for earliness), b_i less than unity and non significant S^2d_i value indicating above average stability (uniform performance even under poor environments).

The genotypes HF 143, HF 131 and NDF 24 with high mean, b_i above unity and non – significant deviation from regression showed below average stability for plant height (good performance in favourable environments only). While genotypes UF 281 and GF 11 with mean lower than the population mean (desirable for developing dwarf / semi dwarf varieties), b_i less than unity and non significant deviation showed above average stability (uniform performance even under poor environments).

HF 143 had the highest mean for number of primary and secondary branches and non – significant deviation from regression, but due to b_i above unity, it has below average stability. While for the same trait, the genotypes JF 586 2/5, HF 131, NDF 16 and GF 11 showed above average stability due to b_i either near to or less than unity. For number of umbels, genotypes NDF 16 and HF 131 indicated above average stability owing to their high mean values, b_i less than unity and non–significant S^2d_i values. For number of umbellets, average stability was indicated by the genotypes JF 586 2/5, AF 1 and UF 281 due to their highest mean, b_i near to unity and non – significant S^2d_i. With high mean values, near to unity regression and non – significant deviation from regression, genotypes JF 586 2/5, GF 11, HF 131 and UF 281 were found to be highly stable for number of seeds per plant. The genotypes UF 281, UF 282 and GF 11 indicated above average stability for test weight.

The information generated from the present investigation suggests that in fennel considerable amount of genetic stability with respect to environmental interactions do exists. Based on the mean performance, regression coefficient and deviation from regression values, it can be concluded that the stability of yield is imparted in the genotypes UF 281, AF 1, GF 11, JF 586 2/5, HF 131 and NDF 16 through the stability of major yield contributing traits like primary and secondary branches, number of umbels and umbellets, number of seeds per plant and test weight. These genotypes are useful genetic resources for development of high yielding and stable varieties in fennel.

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