

Variability and character association studies in dill (*Anethum graveolens* L., & *Anethum sowa*)

Manoj Choudhary¹, R. K. Kakani², R. S. Meena³ and Taslima Gauhar¹

¹MJRP College of Agriculture & Research (Mahatma Jyoti Rao Phoole University, Jaipur - 302 001 (Rajasthan)

²Plant Breeding Unit ICAR-Central Arid Zone Research Institute, Jodhpur, Rajasthan

³ICAR - National Research Centre of Seed Spices, Tabiji, Ajmer

Abstract

One hundred twenty germplasm of dill (*Anethum graveolens* L., & *A. sowa*) were evaluated with four checks namely AD-1, AD-2, Gene Pool, and AD-S-44 using Augmented Block Design in twelve blocks during *Rabi* season 2016-2017 at research farm of National Research Centre on Seed Spices, to estimate variability and character association among seed yield and its contributing traits. Analysis of variance revealed significant variability for most of the traits studied. High estimates of phenotypic coefficient of variance along with genotypic coefficient of variance as well as broad sense heritability, genetic advance and genetic advance as percentage of mean were observed for plant height up to top of the plant, umbel plant⁻¹, umbellate umbel⁻¹, plant height up to main umbel, primary branches plant⁻¹, test weight, seeds umbel⁻¹ and seed yield plant⁻¹. The association analysis at both genotypic and phenotypic level revealed that the seed yield plant⁻¹ were significantly and positively correlated with plant height up to main umbel, secondary branches plant⁻¹ and test weight. While the associations of seed yield plant⁻¹ with plant height up to top of the plant, primary branches plant⁻¹, days to 50% flowering, days to maturity and umbel plant⁻¹ were also positive but found non-significant.

Key words : *Anethum graveolens* L., *A. sowa*, character association, heritability, genetic advance, variability.

Introduction

Dill (*Anethum graveolens* L. *Anethum sowa* 2n = 20) is a seed spice crop and an important aromatic herb which is used for flavouring, tea, pickles and confectionery. Dill leaves are rich in minerals and fibers. The seeds are mainly used for spice, culinary and medicinal purposes. It is also used as a vegetable and an aromatic herb (Sharma 2004). The aroma volatiles of seed and herb of dill have been identified along with several therapeutic properties and the antimicrobial activities of carvone (terpenoid found naturally in many essential oils) isolated from dill seed oil has been reported (Aggarwal *et al.*, 2002). Dill contains carotenoids, vitamin C and polyphenols, the contents of which vary during different stage of its growth. Dill is probably native to South-West Asia or South-East Europe and also has been cultivated since ancient times. In India dill is grown with the name of sowa (*Anethum sowa*) also known as Indian dill, in the states of Rajasthan, Gujarat, Maharashtra, Andhra Pradesh and Madhya Pradesh for its seed. Dill is primarily a summer crop of the temperate region but it has also adapted to grow in warmer areas. In the Northern Indian plains, it is grown during the *Rabi*

season. Yield is a complex character governed by several other yield attributing characters. Since, most of the yield attributing characters are quantitatively inherited and highly affected by environment, it is difficult to judge whether the observed variability is heritable or not. Correlation studies are helpful in determining the components of complex traits like yield. The present study was undertaken to estimate the variability present in active germplasm of dill and to evaluate the extent of association among yield and yield contributing traits.

Material and methods

The experimental material for the present studies consisted of 120 germplasm lines and four checks *viz.*, (AD-1, AD-2, Gene Pool, AD-S-44). The experiment was laid out in an augmented design with 12 blocks having 10 test entries and 4 checks in each block. The plot size was 3 × 2m with row to row spacing of 60 cm and plant to plant spacing 20 cm. Observations were recorded on different morphological characters and seed yield per plant. Five plants were randomly selected and tagged from each plot before flowering to record the data on plant height, primary branches plant⁻¹, secondary branches plant⁻¹,

umbels plant⁻¹, umbellate umbel⁻¹, seeds umbel⁻¹, 1000-seed weight, seed yield plant⁻¹, while data on days to 50% flowering and days to maturity was recorded on whole plot basis. These quantitative characters were used to estimate phenotypic and genotypic coefficient of variation, broad sense heritability, expected genetic advance at 5 per cent selection intensity and correlation coefficient following the standard statistical methods (Singh and Choudhary, 1979).

Results and discussion

The analysis of variance revealed that significant amount of variability was present in germplasm lines for almost all morphological traits studied (plant height up to main umbel, plant height up to top of the plant, primary branches plant-1, secondary branches plant-1, days to 50% flowering, days to maturity, umbel plant-1, umbellate umbel-1, seeds umbel-1, test weight and seed yield plant-1 (Table 1). The present findings confirm the earlier reports on variability in characters suitable for selection in fenugreek (Jain *et al.*, 2013), fennel (Jeeterwal *et al.*, 2015) and coriander (Ameta *et al.*, 2016).

Higher GCV (Genotypic coefficient of variation) was recorded for plant height up to top of the plant (71.73), seed yield plant-1 (54.88), umbel plant-1 (24.80), umbellate umbel-1 (18.89), secondary branches plant-1 (16.84), plant height up to main umbel (16.45), primary branches plant-1 (13.53), test weight (12.91), seeds umbel-1 (11.72). It expresses the true genetic potential which indicated the presence of high amount of genetic variability for these characters thus selection may be more effective for these characters because the response to selection is directly proportional to the component of variability. Similarly, Higher PCV (phenotypic coefficient of variation) was recorded for plant height up to top of the plant (72.13), seed yield plant-1 (57.57), umbel plant-1 (28.41), umbellate umbel-1 (22.52), test weight (21.01), plant height up to main umbel (19.91), secondary branches plant-1 (17.79), seeds umbel-1 (16.11), primary branches plant-1 (15.65), (Table 2). The result revealed that the differences between genotypic and phenotypic variation were low and effective for selection and this is expected in augmented design. In an augmented design, the error component used is based on checks which are repeated in blocks. This often is very limited, hence the differences are very limited. The closeness of the estimates of genotypic and phenotypic coefficient of variation indicates that these traits are least affected by the environment. The present finding confirms the earlier reports in dill (Solanki and Dodiya, 2014) in fennel (Jeeterwal *et al.*, 2015 and Kumar *et al.*, 2017).

Table 1. Analysis of variance for different characters (Dill)

Sources of variation	d.f.	Plant height up to main umbel	Plant height up to top of the plant	Primary branches plant ⁻¹	Secondary branches plant ⁻¹	Days to 50% flowering	Days to maturity	Umbel plant ⁻¹	Umbellate umbel ⁻¹	Seeds umbel ⁻¹	Test weight	Seed yield plant ⁻¹
Block (Eliminating check + Var.)	11	108.480	230.044	0.850**	5.932**	0.546	0.183	205.759**	42.330**	75.172**	0.130	24.315
Entries (Ignoring Block)	120	527.619**	13807.319**	1.415**	7.567	23.970**	10.169**	349.722**	36.611**	19.173**	0.735**	204.04**
Checks	3	890.498**	572.114**	0.071	0.507	0.722	0.056	20.875	5.132	18.734	1.512**	304.98**
Germplasm	119	380.763**	14241.820**	1.378**	7.807**	23.725**	9.469**	261.121**	36.405**	19.345**	0.512*	180.26**
Checks vs. germplasm	1	16542.850**	5495.646**	9.772**	0.069	123.771**	123.771**	11879.770**	155.660**	0.059	24.900**	2829.38**
Error	33	100.612	120.471	0.282	0.655	0.449	0.298	50.205	8.846	7.822	0.285	12.817

* = Significant at 5 % and ** = significant at 1% level of significance

Table 2. Overall mean values of genotypes, their ranges, genotypic and phenotypic coefficient of variation, heritability in broad sense, genetic advance and genetic advance as % of mean for different characters in dill.

Characters	Mean	Range (min-max)	Genotypic coefficient of variation (GCV%)	Phenotypic coefficient of variation (PCV%)	Heritability in broad sense (%)	Genetic Advance	Genetic advance as % of mean
Plant height up to main umbel	69.33	23.29 – 143.96	16.45	19.91	66.22	25.00	27.99
Plant height up to top of the plant	144.66	70.50 – 1421.69	71.73	72.13	98.89	212.61	146.95
Primary branches per plant	6.75	4.03 – 10.87	13.534	15.65	74.75	1.62	24.10
Secondary branches per plant	13.88	8.14 – 22.81	16.84	17.79	89.59	4.56	32.84
Days to 50% flowering	74.36	65.50 – 81.75	5.66	5.739	97.53	8.57	11.52
Days to maturity	167.10	162.75 – 170.25	1.58	1.61	95.91	5.33	3.19
Umbel per plant	51.13	15.77 – 99.72	24.80	28.41	76.21	22.81	44.61
Umbellate per umbel	24.26	6.90 – 45.54	18.89	22.52	70.38	7.92	32.65
Seeds per umbel	25.29	9.97 – 41.90	11.72	16.11	52.91	4.44	17.56
Test weight	3.22	1.43 – 5.26	12.91	21.01	37.78	0.52	16.36
Seed yield per plant	20.59	1.30 – 83.45	54.88	57.57	90.88	22.19	107.78

In the present investigation, the estimates of heritability expressed in percentage was high for the characters viz., plant height up to top of the plant, days to 50% flowering, days to maturity, seed yield plant⁻¹, secondary branches plant⁻¹, umbels plant⁻¹, primary branches plant⁻¹ and umbellates umbel⁻¹, indicating that these characters are less influenced by environment and direct selection for these yield contributing traits would be effective for future improvement in yield. Similar result was also found by Yadav *et al.*, 2013, Sengupta *et al.*, 2014 and Sharma *et al.*, 2015 in fennel, Ameta *et al.*, 2016 in coriander, Meena *et al.*, 2016 in cumin.

Genetic advance as percentage of mean for the characters ranged from 3.19 (days to maturity) to 146.95 (plant height up to top of the plant). High magnitude of genetic advance as percentage of mean was estimated for plant height up to top of the plant, seed yield plant⁻¹, umbel plant⁻¹, secondary branches plant⁻¹ and umbellate umbel⁻¹.

The phenotypic correlation coefficient was higher than their genotypic correlation coefficient counterparts in most of the characters. This implies that the non genetic causes affect the values of genotypic correlation because of the influence of the environmental factors.

The association analysis at both genotypic and phenotypic level revealed that the seed yield plant⁻¹ was significantly and positive correlated with plant height up to main umbel, secondary branches plant⁻¹ and test weight. While the associations of seed yield plant⁻¹ with plant height up to top of the plant, primary branches plant⁻¹, days to 50% flowering, days to maturity, umbel plant⁻¹ were found positive but non-significant (Table 3). Similar results were reported by Dashora and Sastry, 2011 in fennel, Kassahun *et al.*, 2013 in Ethiopian coriander, Tripathi *et al.*, 2000 in coriander and Jain *et al.*, 2003 in coriander.

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Table 3. Phenotypic and genotypic correlation coefficient between different characters in dill

characters	level	Plant height up to main umbel	Plant height top of the plant	Primary branches plant ⁻¹	Secondary branches plant ⁻¹	Days to 50% flowering	Days to maturity	Umbel plant ⁻¹	Umbellate umbel ⁻¹	Seeds umbel ⁻¹	Test weight	Seed yield plant ⁻¹
Plant height up to main umbel	P	1	0.113	-0.024	0.009	0.584**	0.595**	-0.188*	0.424**	0.327**	0.402**	0.304**
	G	1	0.146	0.094	0.166	0.584**	0.614**	-0.119	0.523**	0.235**	0.425**	0.289**
Plant height top of the plant	P		1	0.071	0.061	0.187*	0.167*	0.178*	0.111	0.240**	0.234**	0.130
	G		1	0.098	0.117	0.192*	0.189*	0.126	0.141	0.166*	0.190*	0.098
Primary branches plant ⁻¹	P			1	0.84**	0.017	-0.096	0.315**	0.138*	0.136	-0.053	0.104
	G			1	0.804**	0.074	0.091	0.115	0.168*	0.135	-0.041	0.068
Secondary branches plant ⁻¹	P				1	0.043	-0.095	0.378**	0.219*	0.206*	0.031	0.181*
	G				1	0.143	0.120	0.154	0.207*	0.243**	0.057	0.229*
Days to 50% flowering	P					1	0.654**	-0.181*	0.501**	0.397**	0.471**	0.092
	G					1	0.654**	-0.125	0.491**	0.169	0.423**	0.068
Days to maturity	P						1	-0.297**	0.405**	0.346**	0.488**	0.122
	G						1	-0.204*	0.422**	0.068	0.477**	0.106
Umbel plant ⁻¹	P							1	-0.189*	-0.041	-0.257**	0.141
	G							1	-0.153	-0.080	-0.263**	0.147
Umbellate umbel ⁻¹	P								1	0.636**	0.446**	0.168
	G								1	0.617**	0.522**	0.306**
Seeds umbel ⁻¹	P									1	0.399**	0.219*
	G									1	0.354**	0.157
Test weight	P										1	0.339**
	G										1	0.415**
Seed yield plant ⁻¹	P											1
	G											1

*G- Genotype *P- Phenotype $d f = n-2$ (124 - 2= 122) Test of significant at 0.05% 0.176
0.01% 0.230

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