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Assessment of Genetic Variability and Character Association in Fenugreek (*Trigonella foenum-graecum* L.) Genotypes

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ABSTRACT

An experiment was conducted during rabi 2016-17 at Agronomy Farm, S.K.N. College of Agriculture, Jobner with 48 genotypes of fenugreek in randomized block design with three replications to estimate the genetic variability, heritability, genetic advance and character association for nine quantitative characters. The analysis of variance showed mean squares due to genotypes were highly significant for all the characters indicated that considerable amount of genetic variability was present in the experimental material. In general, the PCV were higher than the corresponding GCV for all the characters studied, which indicated effect of environments on the character expression. High estimates of GCV and PCV were observed for pods per plant, seed yield per plant and plant height. The estimates of broad sense heritability were high for seeds per pod followed by plant height, pods per plant, pod length, days to maturity and seed yield per plant. Genetic advance as percentage of mean was high for pods per plant and seed yield per plant. High estimates of PCV, GCV, heritability and genetic advance were found for pods per plant and seed yield per plant indicating additive gene action in the inheritance of these characters. The association analysis revealed that seed yield per plant was positively and significantly correlated with plant height, pods per plant and 1000-seed weight. On the basis of the present study, it is suggested that in breeding programmes major emphasis should be given during selection for pods per plant and 1000-seed weight as these had good positive correlation with seed yield per plant.

Key word: *Variability, Heritability, Genetic advance, Character association, Fenugreek.*

INTRODUCTION

Fenugreek (*Trigonella foenum-graecum* L.) is an annual self-pollinated diploid species[3] popularly grown by its vernacular name "methi", belonging to the sub-family "Papilionaceae" of the family "Fabaceae". The place of origin of fenugreek supposed to between Iran and North India[20]. India is a leading producer and consumer of fenugreek for its culinary uses and medicinal application.

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In India, it is mainly cultivated in Rajasthan, Gujarat, Tamil Nadu, Andhra Pradesh, Uttar Pradesh, Himachal Pradesh and Haryana with total area of 123000 hectares and production of 131000 metric tonnes[1]. Fenugreek seed contains carbohydrates (48%), proteins (25.5%), mucilaginous matter (20.0%), fats (7.9%) and saponins (4.8%)[13]. Fenugreek seeds are generally found in most blends of curry powder, spice mixes, meat products and also serves as a soil renovating crop. The fenugreek seeds are bitter in taste due to presence of an alkaloid "Trigonellin" and potential use of fenugreek is for extraction of diosgenin, which has importance to the pharmaceutical industry. Diosgenin is a steroid precursor, which is used as a basic material in the synthesis of sex hormones and contraceptives. It is used in certain Ayurvedic medicines to treat flatulence, dysentery, enlargement of lever span, gout, headache, deafness, baldness, leucorrhoea, mouth ulcer, abdominal pain, kidney problem, chapped lips, diabetes, colic, dropsy, spleen, heart disease and obesity etc. Seeds are considered to be a restorative, used for relief in joints pains particularly of old age, promote milk flow and have aphrodisiacal properties. Fenugreek can be grown under wide range of climatic conditions. The productivity of the crop is low due to many limiting factors such as its cultivation on marginal lands with poor fertility, lack of superior genotypes or improved cultivars for use in breeding programme to develop potential hybrids. So, there is need for development of new varieties with high productivity. A study on variability available in the material is the prerequisite for initiating a varietal development programme. Improvement in any crop is proportional to the magnitude of its genetic variability present in germplasm. Greater the variability in a population, the greater chance for effective selection for desirable types[21]. 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. Heritability is a suitable measure for assessing the magnitude of genetic portion of total variability and genetic advance aids to make improvement in crop by selection for various characters. Thus, the estimation of heritability accompanied with genetic advance is generally more useful than heritability alone in prediction of the resultant effect for selecting the best individuals[5]. Hence, analyzing the nature and magnitude of the heritable genetic variation present in the material is necessary. Understanding of the association of different component characters towards yield forms the basic requirement for any selection programme. The genotypic correlation provides the association for the heritable part and shows the true picture of effective selection. Therefore, the present research study was conducted to find out the genetic variability, heritability, genetic advance and character association between different pairs of characters for developing high yielding fenugreek genotypes.

MATERIALS AND METHODS

The experiment was carried out with 48 genotypes of fenugreek selected from the germplasm collection of AICRP on Spices at Agronomy Farm, S.K.N. College of Agriculture, Jobner (20º 6' N, 75º 25' E and 420 m above sea level) raised in a randomized block design with three replications. In each replication, each genotype was sown in a single row plot of 3 m length. The row to row and plant to plant distance was maintained 30 cm and 10 cm, respectively. Five plants were randomly selected and tagged before flowering from each plot to record the observations on plant height (cm), branches per plant, pods per plant, pod length (cm), seeds per pod, 1000-seed weight (g) and seed yield per plant (g). Data on days to 50% flowering and days to maturity were however, recorded on whole plot basis. The crop was raised as per the recommended package of practices. The analysis of variance was carried out as per the procedure given by Panse and Sukhatme[10]. Genotypic and phenotypic correlation coefficients of variation were estimated according to the Burton[2] and Johnson *et al.*[5] by using the following formulae:

using the following formulae:

$$\text{GCV} = \frac{\sqrt{\sigma^2_g}}{\overline{X}} \times 100$$

$$\text{PCV} = \frac{\sqrt{\sigma^2_p}}{\overline{X}} \times 100$$

Where, σ^2_g = genotypic variance, σ^2_p = phenotypic variance, $\overline{X}$ = character mean

Heritability in broad sense was estimated as per the following formula given by Johnson *et al.*[5].

$$\text{Heritability } (h^2_{bs}) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where, σ^2_g = genotypic variance, σ^2_p = phenotypic variance

The expected genetic advance for each character was calculated according to the following formulae suggested by Johnson *et al.*[5].

$$\text{Genetic advance (GA)} = h^2.k.\sigma_P$$

$$\text{Genetic advance as percentage of mean} = \frac{\text{GA}}{\overline{X}} \times 100$$

Where, h^2 = heritability in broad sense, k = intensity of selection at 5% (k = 2.06), σ_P = phenotypic standard deviation and $\overline{X}$ = general mean of character

The character association between different pairs of characters at the phenotypic and genotypic levels was calculated from the phenotypic, genotypic and environmental components of variances and co-variances as described by Singh and Chaudhary[19] as per formulae given by Johnson *et al*.[5].

Phenotypic correlation coefficient (r_P) between character x and y

$$r_P = \frac{\text{Cov}_{xy(p)}}{\sqrt{\text{Var}_{x(p)} \times \text{Var}_{y(p)}}}$$

Genotypic correlation coefficient (r_G) between character x and y

$$r_G = \frac{\text{Cov}_{xy(g)}}{\sqrt{\text{Var}_{x(g)} \times \text{Var}_{y(g)}}}$$

$\text{Cov}_{xy(p)}$ and $\text{Cov}_{xy(g)}$ denote genotypic and phenotypic co-variances between characters x and y, respectively. $\text{Var}_{x(p)}$ and $\text{Var}_{x(g)}$ denote phenotypic and genotypic variances for character x and $\text{Var}_{y(p)}$ and $\text{Var}_{y(g)}$ denote phenotypic and genotypic variance for character y, respectively.

The significance of correlation coefficient was tested using the "r" table. The calculated value of r were compared with tabulated value of "r" at n-2 degree of freedom at p = 0.05 and 0.01 levels, where n = number of genotypes.

RESULTS AND DISCUSSION

The analysis of variance revealed significant difference among the genotypes for all the characters (Table 1). This suggested that the material had adequate variability and response to selection may be accepted in the breeding programme for seed yield or any of its supporting characters. These results are in agreement with the findings of Singh and Kaur[18], Verma and Ali[22], Yadav *et al.*[24], Kole *et al.*[6], Sharma *et al.*[16] and Singh and Naula[17]. The mean, range and coefficient of variation (CV) for yield and yield attributing characters are presented in Table 2. The range was wider for pods per plant followed by plant height and days to maturity. High estimates of coefficients of variation were observed for seed yield per plant, pods per plant, branches per plant and 1000-seed weight. Thus, selection might be more effective for these characters because the response to selection is directly proportional to the variability present in the experimental material.

The genotypic and phenotypic coefficients of variation (GCV and PCV), broad sense heritability (%) and genetic advance as percentage of mean for yield and yield attributing characters are presented in Table 3. GCV and PCV parameters are useful in detecting the amount of variability present in the available genotypes. The PCV were found higher than the corresponding GCV for all the characters studied, which indicated that effect of environments on the character expression. The GCV and PCV were highest for pods per plant and seed yield per plant therefore, selection might be more effective for these characters. Whereas, they were moderate for characters like plant height, 1000-seed weight and branches per plant. The lowest GCV and PCV were recorded for seeds per pod, pod length, days to 50% flowering and days to maturity, which indicated that selection might not be effective for these characters. Similar results were also reported by Sarada *et al.*[15], Prajapati *et al.*[12], Kumari *et al.*[7] and Sharma *et al.*[16].

Heritability and genetic advance help in determining the influences of environment on expression of the characters and extent to which improvement is possible after selection. Estimates of heritability provide a useful guide to the breeder. The breeder is able to appreciate the proportion of variation that is due to the genotype (broad sense heritability) or additive (narrow sense heritability) effects i.e. the heritable portion of variation of the first case and the portion of genotypic variation that is fixable in pure lines in the later case. If heritability of a character is high (> 60%), selection for such a characters should be fairly easy. This is because there would be close correspondence between genotypic and phenotypic variation due to a relatively smaller contribution of environment to the phenotype, but for a character with a low heritability (< 40%), selection may be considerably difficult or virtually impractical due to masking effect of environment on the genotypic effect[5]. In present investigation, broad sense heritability was observed to be high for seeds per pod followed by plant height, pods per plant, pod length, days to maturity and seed yield per plant, which is in close agreement with earlier reports of Sarada *et al.*[15], Naik *et al.*[9], Sharma *et al.*[16] and Wojo *et al*[23]. The high estimate of genetic advance as percentage of mean was obtained for pods per plant and seed yield per plant and lower for branches per plant, pod length, days to 50% flowering and days to maturity. Johnson *et al.*[5] has pointed out that heritability estimates along with genetic advance were more useful than heritability estimates alone in predicting the response to selection. Therefore, high heritability (> 60%) coupled with high genetic advance as percentage of mean (> 20%) was more reliable to determine the relative merits of different characters that can be further utilized in the selection programme. In the present study, high heritability coupled with high genetic advance as percentage of mean were observed for pods per plant and seed yield per plant which indicated that these characters might be under the control of additive gene action and selection for these characters might be effective. Pod length, branches per plant, days to 50% flowering and days to maturity had moderate to low heritability and low genetic advance as percentage of mean. These findings are in agreement with earlier reports of Sarada *et al.*[14], Naik *et al.*[9], Patahk *et al.*[11] and Sharma *et al.*[16].

Depending upon the variability, heritability and genetic advance estimates, it could be predicted that improvement by direct selection was possible in fenugreek for pods per plant and seed yield per plant.

Success of any breeding programme depends upon the efficiency of the selection. Selection cannot be applied on the basis of single character because most of the characters are polygenic in nature and are influenced by each other. The values of all possible correlation coefficients among morphological characters at phenotypic and genotypic levels were calculated and are presented in Table 4. The direction of phenotypic and genotypic correlation coefficients was similar for most of the character combinations. Genetic correlation provides information about degree and direction of association between two or more than two variables. It may result due to genetic causes, such as pleiotropic effect or linkage or it may also be due to environmental causes. The magnitude and direction of correlation coefficient varies with the genetic material being evaluated. The phenotypic correlations in general were stronger as compared to genotypic correlations, this indicated the strong effect of environment on the expression of characters. Significance was tested at phenotypic level only. The associations at phenotypic level are generally considered, as there is no tangible test for knowing the statistical significance of correlation at genotypic level[18]. The seed yield per plant had positive and significant association with plant height (0.219), pods per plant (0.783) and 1000-seed weight (0.341), whereas days to maturity (-0.166) and seeds per pod (-0.173) expressed negative and significant association with seed yield per plant. Reports of Mahey *et al.*[8], Singh and Kaur[18], Sarada *et al.*[15], Jain *et al.*[4] and Kumari *et al.*[7] supported the above findings.

On the basis of the present study, it is suggested that in breeding programmes major emphasis should be given during selection for pods per plant and 1000-seed weight as these had good positive correlation with seed yield per plant.

Table 1: Mean sum of squares for different characters in fenugreek

S. No.	Source of variation	d.f.	Days to 50% flowering	Days to maturity	Plant height (cm)	Branches per plant	Pods per plant	Pod length (cm)	Seeds per pod	1000-seed weight (g)	Seed yield per plant (g)
1	Replications	2	2.80	7.92	2.18	0.19	39.74	0.01	0.06	1.17	0.87
2	Genotypes	47	8.92**	19.08**	75.80**	0.42**	112.47**	0.59**	2.46**	1.79**	3.74**
3	Error	94	1.86	2.87	8.10	0.16	13.86	0.08	0.23	0.48	0.61

** represents significant at 1% level of significance

Table 2: Grand mean, range and coefficient of variation (CV %) for yield and its attributes in fenugreek

S. No.	Character	Mean	Range		CV %
			Minimum	Maximum	
1	Days to 50% flowering	47.74	45.00	56.00	2.86
2	Days to maturity	102.53	98.00	111.00	1.65
3	Plant height (cm)	62.98	48.60	72.00	4.52
4	Branches per plant	4.96	4.27	6.27	8.06
5	Pods per plant	37.73	24.53	51.40	9.58
6	Pod length (cm)	10.33	9.40	11.47	2.75
7	Seeds per pod	16.05	13.37	18.40	2.99
8	1000-seed weight (g)	10.96	9.48	12.79	6.34
9	Seed yield per plant (g)	6.71	4.84	9.69	11.65

Table 3: Genotypic and Phenotypic coefficients of variation (GCV and PCV), heritability (broad sense) and genetic advance as percentage of mean for yield and its attributes in fenugreek

S. No.	Character	GCV	PCV	h^2_{bs} (%)	GA as % of mean
1	Days to 50% flowering	3.21	4.30	55.82	4.94
2	Days to maturity	2.27	2.80	65.30	3.77
3	Plant height (cm)	7.54	8.79	73.59	13.34
4	Branches per plant	6.04	10.07	36.00	7.45
5	Pods per plant	15.87	18.53	73.30	27.99
6	Pod length (cm)	3.99	4.84	68.00	6.78
7	Seeds per pod	5.36	6.14	76.29	9.66
8	1000-seed weight (g)	6.05	8.75	47.83	8.67
9	Seed yield per plant (g)	15.19	19.13	63.03	24.88

Table 4: Genotypic and phenotypic correlation coefficients between different characters in fenugreek

Character	Correlation	Days to maturity	Plant height (cm)	Branches per plant	Pods per plant	Pod length (cm)	Seeds per pod	1000-seed weight (g)	Seed yield per plant (g)
Days to 50% flowering	G	0.797	-0.619	0.120	-0.262	-0.197	-0.196	0.145	-0.235
	P	0.539**	-0.441**	0.044	-0.144	-0.126	-0.135	0.096	-0.133
Days to maturity	G		-0.576	0.155	-0.275	-0.123	-0.131	-0.021	-0.175
	P		-0.404**	0.027	-0.239**	-0.158	-0.108	-0.056	-0.166*
Plant height (cm)	G			-0.326	0.274	-0.111	0.004	0.131	0.272
	P			-0.160	0.249**	-0.109	0.005	0.055	0.219**
Branches per plant	G				0.088	-0.367	-0.332	0.244	-0.018
	P				0.096	-0.134	-0.172*	0.245**	0.108
Pods per plant	G					-0.104	-0.396	0.137	0.833
	P					-0.054	-0.279**	0.116	0.783**
Pod length (cm)	G						0.580	-0.042	0.061
	P						0.404**	-0.055	0.066
Seeds per pod	G							-0.256	-0.294
	P							-0.156	-0.173*
1000-seed weight (g)	G								0.464
	P								0.341**

*and** refers to significant at P = 0.05 and P = 0.01, respectively and G= Genotypic correlation, P=Phenotypic correlation

CONCLUSION

Based on the present investigation on genetic variability, it may be concluded that there were highly significant differences among fenugreek genotypes for all the characters studied. This suggested that the material had adequate variability and response to selection may be accepted in the breeding programmes for seed yield or any of its supporting characters. The characters like pods per plant and seed yield per plant showed high amount of genetic variability along with heritability and genetic advance indicating that most likely the heritability is due to additive gene effects and selection may be effective in early generations for these characters. This reveals that there is a greater scope for improving these characters by simple phenotypic selection. Correlation studies provide information on the nature and extent of association between any two pairs of metric characters. Thus, it could be possible to bring about genetic upgradation in one character by selection of the other character. In present study, it is suggested that in breeding programmes, major emphasis should be given to selection of pods per plant and 1000-seed weight as these had good correlation with seed yield per plant. The genotypes showed variability at phenotypic level and some of them also showed suitable agronomic performance and can be used to broaden the genetic base of breeding programmes.

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