Studies on genetic variability and selection criteria in F_3 generation of a cross in fenugreek (*Trigonella foenum - graecum* L.)

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Abstract

Thirty F_3 families of the cross UM - 305 X UM - 117 in fenugreek were evaluated for seed yield and other component characters. Substantial amount of genetic variability was observed at inter as well as intra-family levels for all the observed characters. Plant height and number of pods per plant, having true positive association with seed yield per plant, were mainly under the control of additive gene action and thus, direct selection for these characters would be effective for the improvement of seed yield per plant. Genetic variability at the intra-family level could be exploited by further selection for plant height and number of pods per plant. Superior families with respect to high mean performance for seed yield and its components were also identified. These families will be useful in developing high yielding fenugreek genotypes.

Key words: fenugreek, genetic variation, selection criteria, *Trigonella foenum - graecum*

Introduction

Fenugreek (*Trigonella foenum-graecum* L.) is an annual autogamous crop (Levandovskii *et al.* 1979) grown as seed spice crop in India and it occupies a prime position among the seed spices grown in Rajasthan. Inspite of the importance of this crop, attempts to improve its genetic potential are limited due to narrow range of genetic variability particularly for seed yield and various seed yield components (Shukla & Sharma 1978). Therefore, hybridization programme among genetically diverse parents was undertaken to generate genetic variability in fenugreek.

Evaluation of genetic potential of a cross can be done in early segregating generations such as F2 and F3 generations (Yonezawa & Yamagata 1981) in order to use the available resources in an efficient manner and to isolate the superior segregants. Shebeski (1967) also advocated early generation evaluation. The present investigation was therefore carried out to assess the amount of genetic variability in F_3 generation of cross UM - 305 X UM - 117 in fenugreek and also to identify superior families for seed yield and its components.

Materials and methods

In the present investigation thirty randomly selected F_3 families of a fenugreek cross UM - 305 X UM - 117, the two parents viz. UM - 305 (P_1) and UM - 117 (P_2) and the commercial check variety (RMt-1) were studied in RBD with three replications of single row plots (3

m length) for seed yield per plant and its component characters. The experiment was conducted during *rabi* season 1999-2000 at Agricultural Research Farm of S.K.N. College of Agriculture, Jobner. The row to row and plant to plant distance were 30 cm and 10 cm, respectively. In each replication additional single rows of the parent 1, parent 2 and the check variety were grown after every ten rows for comparison of morphology/plant type between plants of F_3 families and the plants of parents and the check variety. Data from these additional rows were not collected and included in statistical analysis. In each replication, observations were recorded on five randomly selected plants in each of the 33 treatments (i.e. in each family, parent and the check variety) for seed yield per plant and various seed yield components.

Analysis of variance (ANOVA) was carried out by modifying the method of Hallauer & Miranda (1988) (Table 1). The modification was made to accommodate parents and check in addition to F_3 families. No two plants in F_3 generation are supposed to be genetically identical and hence, in the present investigation the total sum of squares was partitioned into sum of squares due to "between treatment" and "within treatments". The latter includes the intra family variance. Ideally significant "between treatment" variance over "within treatment" variance will indicate the importance of "between treatment" variance. The "between treatment" sum of squares was partitioned as per the procedure detailed by Haullauer & Miranda (1988). Significance of variance was carried out first for "between treatment" variance which was tested against the "within treatment" variance. Further, the error variance was tested against "within treatment" variance. If the error variance was significant against the "within treatment" variance, error variance was used to test the significance of variance due to "replications" and also variance due to components of treatment variance i.e. "family + parent", "families", "parents family vs. parent" and "family + parent vs. check". For the

characters recorded on the plot basis, analysis of variance was carried out in a similar manner, except in this case "within treatment" variance was not estimated due to the absence of individual plant observations. In this case variance due to replications, treatments and other variances were tested against error variance.

Mean, range, coefficient of variation (CV) and range of CV were estimated by following standard procedure for each family, each parent and the check variety by using 15 individual plant observations for all the characters, except days to 50% flowering and days to maturity. Range of CV of F_3 families for all characters except days to 50% flowering and days to maturity, was also computed. Family means for all the characters were compared with parent means and the check means by using the CD values to identify superior families.

Mean, range and CV were also computed for the population of F_3 generation plants and were termed as population mean, population range and population CV. Phenotypic, genotypic and the environmental variances were estimated only for the F_3 generation for all the characters based on individual plant observation by using the following formulae.

Genotypic variance (σ^2g) = (variance due to family - error variance) / nr
= $[(n\sigma^2e + \sigma^2w + rn\sigma^2g) - (\sigma^2w + n\sigma^2e)]$ / nr
Environmental variance (σ^2e) = (error variance - within treatment variance) / n
= $[(\sigma^2w + n\sigma^2e) - (\sigma^2w)]$ / n
Phenotypic variance (σ^2p) = $\sigma^2g + \sigma^2e$

For the characters, days to 50% flowering and days to maturity, phenotypic, genotypic and environmental variances were estimated by using the following formulae.

Genotypic variance ($\acute{o}^2g$) = (variance due to family - error variance)/r
$[(\acute{o}^2e + r\,\acute{o}^2g) - \acute{o}^2e]$ / r
Environmental variance ($\acute{o}^2e$) = error variance
Phenotypic variance ($\acute{o}^2p$) = $\acute{o}^2g + \acute{o}^2e$

Heritability (Hanson *et al.* 1956), coefficient of variation (Burton 1952), genetic advance

Table 1. Analysis of variance for different characters of fenugreek

Sources of variation	df	MSS						
		Plant height (cm)	No. of primary branches per plant	No. of pods per plant	Pod length (cm)	Seeds per pod	100-seed weight (g)	Seed yield per plant (g)
Between treatment	98	403.25++	5.26*	674.11++	8.84++	55.78++	0.190++	7.36**
Replications	2	1778.86**	25.64**	2230.87**	9.05	39.45	0.285*	1.63
Treatments	32	838.72**	7.67**	1324.81**	16.42**	123.28**	0.337**	12.47**
Family + parent	31	848.29**	6.82**	1249.52**	16.63**	122.80**	0.333**	12.58**
Family	29	808.50**	6.63*	1080.76**	17.22**	124.55**	0.338**	12.11**
Parent	1	982.69**	2.13	70.55	3.46	2.70	0.042	2.90
Family Vs. parent	1	1868.03**	17.11*	7322.51**	12.70	192.08**	0.468*	36.09**
(Family + parent) Vs. Check	1	541.95	34.10**	3658.93**	10.03	138.28*	0.467*	8.82
Error	64	142.53**	3.42**	300.11*	5.04**	22.54**	0.113	4.98
Within treatment	396	52.59	1.88	215.74	2.57	13.03	0.086	4.03

* Significant at 5% level of significance against error variance
** Significant at 1% level of significance against error variance
++ Significant at 1% level against with family variance

(Johnson *et al.* 1955) and genetic advance as percentage of mean were estimated for all the observed characters in the F_3 generation. Correlation coefficients (Miller *et al.* 1958) were estimated for the F_3 generation. Path coefficient analysis (Dewey & Lu 1959) was carried out for the F_3 generation by taking seed yield per plant as dependent variable and other characters as independent variable to identify true relationship among various characters and seed yield per plant.

Results and discussion

Analysis of variance for the characters recorded on individual plant basis indicated that "between treatment" variance was significant against "within treatment" variance for all the characters (Table 1) which indicated that families, parents and check differed significantly for all the characters. It also indicated higher relative amount of "between family" variance than the "within family" variance for all the characters. Significance of variance due to replications (Table 1) for the characters plant height, number of primary branches per plant, number of pods per plant and 100 seed weight indicated that genotypes differed significantly from each other over the replications. This was justified because the genotypes in the three replications were not genetically identical as they belonged to F_3 generation, which is an early segregating generation. There was significant variance due to treatments, "family + parent" and "family" for all the observed characters (Table 1). First, the families, parents and check differed significantly from each other for all the observed characters. Second, there was substantial amount of variability in "family + parent" as a group. Third, the families differed significantly from each other with respect to all the observed characters. However, the parents differed significantly from each other for plant height alone.

Significance of variance due to "family vs parents" was observed for all the characters except days to 50% flowering and pod length which indicated that families differed

Table 2. Mean, range and coefficient of variation of parents, families and check for various characters of fenugreek

Character	Parent 1			Parent 2			F₃ Families				Check (RMt-1)		
	Mean	Range	CV¹	Mean	Range	CV¹	mean²	Range	CV¹	Range of CV¹	Mean	Range	CV¹
Days to 50% flowering	61.33	61-62	0.94	62.00	61-63	1.61	62.16	59.33-64.66	1.26	0.91-4.41	61.66	60-63	2.47
Days to maturity	123.00	121-124	1.40	122.66	119-126	2.86	125.70	120.00-129.66	2.53	0.44-3.24	125.33	124-127	1.21
Plant height (cm)	24.33	19.6-29.4	15.52	35.78	33.74-38.60	10.90	37.88	24.33-52.53	29.25	8.96-35.59	43.80	42.8-45.4	10.81
No. of primary branches per plant	5.40	4.4-6.2	9.05	5.93	5.6-6.4	14.71	6.35	5.33-7.53	24.70	12.11-36.32	4.86	4.6-5.0	29.94
No. of pods per plant	28.26	19.2-38.8	6.28	31.33	27.4-37.6	15.80	44.44	31.73-63.13	38.12	17.17-57.94	29.06	27.0-31.8	24.55
Pod length (cm)	9.60	8.9-10.7	19.68	8.92	8.0-9.56	18.29	8.65	6.73-10.78	22.86	9.53-31.94	9.46	8.2-10.24	18.52
Seeds per pod	14.00	12.2-17.4	28.23	14.60	13-16.2	14.79	11.94	6.40-16.33	39.98	13.44-65.67	14.93	12.6-16.4	21.2
100-seed weight (g)	1.329	1.156-1.583	14.743	1.254	1.329-1.290	14.303	1.406	1.137-1.665	23.382	13.652-30.240	1.233	1.206-1.259	15.494
Seed yield per plant (g)	3.813	3.71-4.56	19.323	4.436	4.19-3.54	7.477	5.162	3.423-7.130	42.264	22.593-62.015	4.407	3.98-4.82	26.030

1- population CV; 2 - population mean

significantly from parents for these characters. Significance of variance due to "(family + parent) vs check" for the characters number of primary branches per plant, number of pods per plant, number of seeds per pod and 100 seed weight indicated that "family + parent" as a group differed significantly from the check for these characters. Analysis of variance indicated that generated variability was substantial for seed yield and its components, which can be further exploited through selection. Significant amount of genetic variability for the characters, number of primary branches per plant, pods per plant and seed yield per plant was reported by Pant et al. (1983), Mehta et al. (1992) and Arora & Lodhi (1993).

The mean, range and coefficient of variation of F₃ population were compared with that of P₁, P₂ and check variety (Table 2) to judge the superiority of F₃ generation over P₁, P₂ and the check. F₃ population mean was greater than mean of P₁ and P₂ for the characters viz. plant height, number of primary branches per plant, number of pods per plant, 100 seed weight

Table 3. Genetic parameters of variation for seed yield and its components in F_3 generation of fenugreek.

Character	Mean	Range of means of families	$\sigma^2 p$	$\sigma^2 g$	PCV	GCV	h^2(B)	GA	GA as per cent of mean
Days to 50% flowering	62.16	59.33-64.66	2.25	0.89	2.41	1.52	39.72	1.21	1.96
Days to maturity	125.70	120.00-129.66	8.52	5.01	2.32	1.78	58.80	3.53	2.81
Plant height (cm)	37.88	24.33-52.33	62.38	44.39	20.85	17.58	71.16	11.58	30.56
No. of primary branches per plant	6.35	5.33-7.53	0.52	0.21	11.37	7.27	40.92	0.61	9.59
No. of pods per plant	44.44	31.73-63.13	68.91	52.04	18.67	16.23	75.51	12.90	29.05
Pod length (cm)	8.65	6.73-10.78	1.30	0.81	13.20	10.41	62.20	1.46	16.91
Seeds per pod	11.94	6.40-16.33	8.70	6.80	24.63	21.83	78.15	4.75	39.76
100-seed weight (g)	1.406	1.137-1.665	2.032	1.500	10.134	8.710	73.87	0.22	15.423
Seed yield per plant (g)	5.162	3.423-7.130	0.666	0.472	15.797	13.35	71.43	1.19	23.247

and seed yield per plant. A comparison of range of mean values of families with those in parents and check (Table 2) indicated that variability was greater in families. Similarly, CV and range of CV of F_3 population was higher than CVs of parents and check for the characters viz. plant height, number of pods per plant, pod length, number of seeds per pod, hundred seed weight and seed yield per plant. This again indicated that the variation in F_3 generation for these characters was very high as compared to that in parents and check.

Genetic parameters of variation were estimated for all the characters in the population of F_3 generation plants (Table 3) in order to assess the possibility of improvement in seed yield per plant and also to determine selection criteria for improvement of seed yield per plant in the segregating generation. The estimates of phenotypic variances were greater than the corresponding genotypic variances for all the characters. However, for plant height, number of pods per plant and seeds per pod the differences between the estimates of phenotypic and genotypic variance were low which indicated that these characters were relatively less influenced by the environment. Similar finding was reported by Mehta *et al.* (1992) and Arora & Lodhi (1993). Similarly, the estimates of PCV were higher than the corresponding estimates of GCV, which indicated the influence of environment on the character expression. High estimates of PCV and GCV were recorded for the characters plant height, number of pods per plant, seeds per pod and seed yield per plant, which indicated that selection for these characters may be effective. Similar findings were also reported in fenugreek for plant height (Kohli *et al.* 1988), pods per plant (Mehta *et al.* 1992; Arora & Lodhi 1993) and seed yield per plant (Kohli *et al.* 1988 ; Arora & Lodhi 1993). High heritability estimates along with high genetic advance as percentage of mean were recorded for plant height, number of pods per plant and seeds per pod. This indicated that these characters were mainly under the

Table 4. Phenotypic (P) and genotypic (G) correlation coefficients among various characters in F_3 generation of fenugreek

Character		Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches per plant	Pods per plant	Pod length (cm)	Seeds per pod	100-seed weight (g)	Seed yield per Plant (g)
Days to 50% flowering	P	1	0.118	0.030	-0.089	0.076	-0.108	0.004	-0.008	0.003
	G	1	0.226	0.314	-0.007	0.248	-0.388	-0.069	-0.067	-0.192
Days to maturity	P		1	0.457*	0.417*	0.564**	-0.524**	-0.541**	0.472**	0.124
	G		1	0.735	1.041	0.933	-1.113	-0.951	0.762	-0.041
Plant height (cm)	P			1	0.068	0.337	-0.280	-0.171	0.071	0.357*
	G			1	0.216	0.430	-0.533	-0.323	0.248	0.595
No. of primary branches per plant	P				1	0.568**	-0.302	-0.478**	0.293	0.117
	G				1	1.078	-1.036	-1.075	1.156	-0.380
No. of pods per plant	P					1	-0.572**	-0.594**	0.387*	0.268
	G					1	-0.958	-1.001	0.792	-0.105
Pod length (cm)	P						1	0.874*	-0.551**	0.233
	G						1	0.974	-0.977	0.293
Seeds per pod	P							1	-0.635**	0.305
	G							1	-0.991	0.325
100-seed weight (g)	P								1	-0.141
	G								1	-0.528
Seed yield per plant (g)	P									1
	G									1

* Significant at 5% PL
** Significant at 1% PL

control of additive gene action and therefore, selection for these characters in the segregating generation will be highly responsive was reported by Mehta *et al.* (1992) & Arora & Lodhi (1993) for pods per plant. Characters like 100 seed weight and seed yield per plant had high heritability but they had moderate genetic advance as percentage of mean. This indicated that these characters were mainly under the control of non-additive gene action. Other characters had moderate to low heritability estimates along with moderate to low genetic advance as percentage of mean.

Correlation analysis (Table 4) indicated that seed yield per plant had positive and significant correlation with plant height at phenotypic level and had positive correlation with pods per plant at genotypic level. Shukla & Sharma (1978) and Mehta *et al.* (1992) too obtained similar findings. Other characters showing positive correlation with seed yield per plant were pod length and seeds per pod at genotypic and phenotypic levels. Primary branches per plant and 100-seed weight had negative correlation at both genotypic and phenotypic levels. Thus, correlation analysis revealed that seed yield per pant had positive correlation with plant height, pods per plant, pod length and seeds per pod at genotypic level.

Path coefficient analysis revealed that plant height, pods per plant and pod length had positive direct effects at genotypic and phenotypic levels on seed yield per plant (Table 5). Plant height in addition to its very high positive direct effect, also had positive indirect effects via pods per plant at genotypic and phenotypic levels on seed yield per plant and via seeds per pod on seed yield per plant at genotypic level. Thus plant height had true positive association with seed yield per plant

Table 5. Phenotypic (P) and genotypic (G) path coefficients for various characters on seed yield per plant in F_3 generation of fenugreek

Character		Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches per plant	Pod per plant	Pod length (cm)	Seeds per pod	100-seed weight (g)	Seed yield per plant (g)
Days to 50% flowering	P	-0.034	0.005	0.009	-0.012	0.039	-0.006	0.003	-0.001	0.003
	G	-0.362	0.003	0.286	0.006	0.107	-0.407	0.118	0.058	-0.192
Days to maturity	P	-0.004	0.044	0.134	0.056	0.293	-0.031	-0.410	0.043	0.124
	G	-0.082	0.013	0.669	-0.835	0.401	-1.167	1.617	-0.658	-0.041
Plant height (cm)	P	-0.001	0.020	0.293	0.009	0.175	-0.017	-0.129	0.006	0.357*
	G	-0.114	0.009	0.911	-0.173	0.185	-0.559	0.550	-0.214	0.595
Primary branches per plant	P	0.003	0.018	0.020	0.134	0.295	-0.018	-0.362	0.026	0.117
	G	0.003	0.013	0.197	-0.802	0.463	-1.086	1.829	-0.997	-0.380
Pods per plant	P	-0.003	0.025	0.099	0.076	0.520	-0.034	-0.450	0.035	0.268
	G	-0.090	0.012	0.392	-0.865	0.430	1.004	1.703	-0.683	-0.105
Pod length (cm)	P	0.004	-0.023	-0.082	-0.040	-0.297	0.060	0.662	-0.050	0.233
	G	0.141	-0.014	-0.486	0.831	-0.412	1.048	-1.657	0.843	0.293
Seeds per pod	P	0.000	-0.024	-0.050	-0.064	-0.309	0.052	0.757	-0.058	0.305
	G	0.025	-0.012	-0.294	0.862	-0.430	1.021	-1.700	0.855	0.325
100-seed weight (g)	P	0.000	0.021	0.021	0.039	0.201	-0.033	-0.481	0.091	-0.141
	G	0.024	0.010	0.226	-0.927	0.341	-1.024	1.685	-0.863	-0.528

Residual effect G= -0.0793
              P= 0.5025
* Significant at 5% PL

Table 6. Families having significantly higher mean values than either of the parents and check with low, moderate and high coefficient of variation

Character	Group I	Group II	Group III	Mean			CD
	Families with significantly higher mean values than mean of P_1, P_2 and check with low CV	Families with significantly higher mean values than mean of P_1, P_2 and check with higher CV	Families with significantly higher mean values than mean of P_1, P_2 and check with moderate CV	P_1	P_2	Check	
Days to 50% flowering	Nil	Nil	22*(59.33)	61.33	62.00	61.66	1.90
Days to maturity	Nil	Nil	Nil	123.00	122.66	125.33	3.06
Plant height (cm)	22 (44.60)	18 (52.53)	15 (49.20)	24.33	35.78	43.80	8.71
No. of primary branches per plant	27 (7.40), 5 (7.33)	Nil	1 (7.533)	5.40	5.93	4.86	1.35
No. of pods per plant	18 (56.40), 13 (55.86) 3(52.66), 20 (51.13) 11 (50.13), 5 (48.86), 1(49.00)	15 (55.86), 27 (59.00) 7 (49.0), 16 (46.73) 21 (44.73), 6 (47.86)	2 (63.66), 8 (54.33), 4 (47.13) 22 (46.46) 10(54.46)	28.26	31.33	29.06	12.65
Pod length (cm)	Nil	Nil	Nil	9.60	8.92	9.46	1.63
No. of seed per pod	Nil	Nil	Nil	14.00	14.6	14.93	3.46
100 seed weight (g)	16 (1.647), 15 (1.592), 8 (1.591)	Nil	20 (1.665)	1.329	1.254	1.233	0.245
Seed yield per plant (g)	25 (6.233), 2 (6.183)	28 (6.141), 18(7.130)	30 (7.05), 29 (6.205)	3.81	4.43	4.40	1.63

* Significantly smaller than mean of P_1, P_2 and check

and selection for higher values of plant height will be effective in improving seed yield per plant. Like plant height pods per plant also had positive direct effect on seed yield per plant, via seeds per pod and plant height at genotypic level. However, pods per plant had high negative indirect effect via primary branches per plant, pod length and 100 seed weight at genotypic level. Thus, direct positive effect of pods per plant was nullified by its high indirect negative effects. This indicated that while selecting for higher values of pods per plant, selection should also be carried out for lower values for primary branches per plant, pod length and 100 seed weight.

Pod length had high positive direct effect along with positive indirect effect via primary branches per plant and 100 seed weight at genotypic level whereas, negative indirect effect via plant height, pods per plant and seeds per pod. Days to 50% flowering, primary branches per plant, seeds per pods and 100 seed weight had negative direct effect on seed yield per plant. Seeds per pod had negative indirect effect too via plant height and pods per plant at genotypic and phenotypic levels. Primary branches per plant and 100 seed weight had high negative indirect effects via pod length. They had high negative indirect effects via each other on seed yield per plant. The residual effect was of a very low magnitude at genotypic level which indicated that variables included were sufficient to explain the variation in seed yield per plant.

Thus path coefficient analysis revealed that direct selection for plant height along with pods per plant will be effective for improvement in seed yield per plant. Similar findings, although in non-segregating generations, were reported for plant height (Pant et al. 1983) and for pods per plant (Mehta et al. 1992; Sade et al. 1996) in fenugreek. Analysis of genetic parameters of variation in the present investigation indicated that the above two characters having true positive association with seed

yield per plant, were mainly under the control of additive gene action.

On the basis of mean performance and CV of various families estimated by using the observations recorded on 15 sampled plants (five plants in each replication) of each F_3 family, parent and check, 22 superior families with significantly higher mean value than the parents and check in desired direction but with varying CVs for the characters days to 50% flowering, plant height, number of primary branches per plant, number of pods per plant, 100-seed weight and seed yield per plant were identified (Table 6). Consideration of mean and CV values for seed yield per plant and main seed yield components indicated the possibility of further improvement within the families by carrying out selection for plant height and pods per plant. Indirect selection for these two characters within the F_3 families will be effective for improvement of seed yield per plant as these characters showed true positive association with seed yield per plant along with high heritability and high genetic advance as percentage of mean in the present investigation.

Out of these above mentioned superior families, six families viz. family no. 2, 18, 25, 29 and 30 had significantly higher mean seed yield per plant than that of parents and check (Table 7). These six families showed superior performance for one or more component characters. Family no. 2, 25 and 18 showed superior performance for plant height, pods per plant and primary branches per plant. Family no. 28 and 30 showed superior performance for plant height, pods per plant and seeds per pod, while family no. 29 showed superior performance for plant height and pods per plant.

On the basis of present investigation it can be concluded that substantial amount of genetic variability was present at the interfamily as well as intra-family level for seed yield per plant and its components. Analysis of genetic parameters of variation indicated that plant height and pods per plant were mainly under the control of additive gene action. Correlation and path-coefficient analysis indicated that plant height and pods per plant had true positive association with seed yield per plant. Thus, the generated genetic variability can be exploited by carrying out selection for plant height and

Table 7. Performance of superior families (with respect to seed yield per plant) for various characters of fenugreek

Family No.	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches per plant	No. of pods per plant	Pod length (cm)	No. of seeds per pod	100 seed weight (g)	Seed yield per plant (g)
18	61.33	128.00	52.53	7.00	56.40	7.75	9.40	1.440	7.130
30	62.33	124.66	42.86	5.93	39.73	9.98	16.33	1.289	7.051
25	60.00	124.66	40.26	6.33	36.80	10.36	15.00	1.412	6.233
29	62.66	124.33	39.73	5.46	38.06	9.56	14.26	1.217	6.205
2	62.66	126.00	44.33	7.26	63.13	7.89	9.06	1.464	6.183
28	61.00	124.00	43.40	5.66	37.60	9.76	15.26	1.323	6.141
P_1 mean	61.33	123.00	24.33	5.40	28.26	9.60	14.00	1.329	3.81
P_2 mean	62.00	122.66	35.78	5.93	31.33	8.92	14.60	1.254	4.43
Check mean	61.66	125.33	43.80	4.86	29.06	9.46	14.93	1.233	4.40
CD	1.90	3.06	8.71	1.35	12.65	1.63	3.46	0.245	1.63

O = Significantly higher than P_1 mean
* = Significantly higher than P_2 mean
a = Significantly higher than check mean

pods per plant, particularly within the families viz. family no. 18, 28, 29 and 30. Some families such as family no. 2 and 25 with high mean seed yield per plant should be further verified for within family variation and should be advanced, as these are having low CV for seed yield per plant. These identified superior families will be very useful in developing high yielding fenugreek genotypes.

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