



Half diallel analysis in indigenous genotypes of fenugreek (*Trigonella foenum-graecum* L.)

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Abstract

To study the nature of gene action and its components, six genotypes of fenugreek were crossed in a half diallel mating design during Rabi 2017-18, resulting in fifteen one-way F₁ hybrids which were evaluated in the experimental field of the Indira Gandhi Krishi Vishwavidyalaya, All India Coordinated Research Project on Spices, College of Agriculture and Research Station (CARS), Raigarh, Chhattisgarh with two checks during *rabi* season, 2018–19 in a randomized complete block design with three replications. Diallel analysis of indigenous landraces of fenugreek was conducted to identify and develop elite 'pure lines' for subsequent use in fenugreek breeding programmes. Crosses with high SCA effects were arranged in the order of their per se performance, general combining ability of the parents of these crosses and per cent superiority over standard check RMT 305 and Hisar Sonali. Best GCA effects and high mean performance parents were observed between high × high, high × low or low × low general combiners for different traits. The best recombinants were observed for IFHyb-4, IFHyb-11, IFHyb-7, and IFHyb-9 which were best for days to 50 % flowering, primary branches, secondary branches, and seed yield respectively, which belonged to high × low combining parents, indicating non additive × additive effects and additive × additive effects. This suggests that single plant selection would be desirable in their segregating generations. High heritability coupled with low genetic advance was recorded for days to 50 % flowering, secondary branches per plant, pod length, and seed yield (q/ha) which were regulated by non-additive gene action and presence of high genotype × environment interaction.

Keywords: GCA, SCA, gene action, heritability, genetic advance

Introduction

The commonly used methi *Trigonella foenum-graecum*, also known as fenugreek, is a self pollinated clistogamous important annual diploid crop having chromosome number $2n = 16$. It can be grown all round the year and is used as a good flavoring agent in certain culinary preparations for making delicious food items, as well as a commonly used as green leafy vegetable throughout the year (Ahmad *et al.*, 1999; Mc Cormick *et al.*, 2006). Morphologically, it is an erect, aromatic annual crop. The stem is long and cylindrical (30–60 cm long) and green in color; whereas its roots are massive finger-like structures (Moradi kor and Zadeh, 2013). Fenugreek seed is a rich source of vitamins *viz.* choline, vitamin A, B1, B2, C, nicotinic acid, and niacin and is used for human consumption in diverse ways (Leela and Shafeekh, 2008; Srinivasan, 2006).

For seed purposes, it is cultivated in mild winter and cool summer (Mc Cormick *et al.*, 2006). The narrow range of available genetics stocks in fenugreek limits transfer of its useful genes to desirable cultivars. The knowledge of combining ability helps in identifying superior parents and specific cross combinations, which can be exploited for different breeding purposes. As limited data on this aspect are available, an experiment was conducted to study the combining ability effects for yield and other important characters of fenugreek. The superiority of recombinants over indigenous landraces in terms of uniformity, autogamy, productivity, yield stability, and field tolerance to pest and diseases shifted the

breeding emphasis from pure line selection to recombinant breeding. Diallel analysis of indigenous landraces can help to identify and develop elite high yielding pure lines which later can be used in fenugreek breeding programmes. The diallel mating design is an efficient method for the study of combining ability as well as the gene action involved. The analysis of combining ability of Griffing (1956 b), method II, model 1 was employed in the present investigation to get an overview of genetic architecture of yield and its components. Six diverse indigenous genotypes were used for the synthesis of 15 single crosses with an objective to generate new gene combination and high yielding segregants. The knowledge on combining ability and type of gene action responsible for the regulation of expression of different traits would certainly help in planning appropriate breeding strategies. The general combining ability and the specific combining ability estimates can be translated into measures of additive and dominance components of genetic variation, respectively, in a given population (Griffing, 1956). The aim of the present study was to increase the seed yield by considering yield attributing traits and to identify vegetable purpose materials for general cultivation.

Materials and methods

First year: Griffing's Breeding Method II with Model I half diallel design

Knowledge of combining ability is essential for selection of suitable parents for hybridization and identification of promising hybrids in breeding programme. The study material consisted of 15 F_1 s with two checks from six diverse lines of

fenugreek (IFGS-04, IFGS-07, IFGS-09, IFGS-11, IFGS-12 and Gujarat-2). For crossing programme of fenugreek the sowing was done in four splits with one-week intervals, to obtain the plants for the emasculation and pollination. During rabi 2017-18 crossing programme was attempted among six parents in a half diallel fashion (Table 6) to obtain 15 F_1 's (excluding reciprocals) and evaluated during rabi 2018-19 for yield and yield attributing traits along with parents and checks at the experimental field of All India Coordinated Research Project on Spices, College of Agriculture and Research Station, Raigarh, Indira Gandhi Krishi Vishwavidyalaya, Chhattisgarh. Each genotype sown in two rows of two-meter lengths was kept for the emasculation of the flower and for making crosses in the emasculated flower. Another row of 2 m length was kept for collection of pollen grain. For emasculation, unopened immature buds were selected from each female parent. Forceps were cleaned by dipping in ethyl alcohol. Hand emasculation was done before the opening of the flower by removing the anther with the help of forceps from 4 pm to 5 pm every day and separate coloured threads were used for each emasculated line. The next day early morning between 7.00 am to 8.00 am pollen grains were collected from male parental block and pollinated with the help of fine pointed brush on the respective emasculated line.

Second year evaluation of single crosses

The complete set of experimental materials comprised of 23 genotypes *i.e.* six parents, 15 crosses, and two checks were sown in

randomized block design with three replications in rabi 2018-19 with each replication accommodating 30 plants. Each genotype was sown in 3 rows, each of three meter length. Spacing between two lines was 30 cm and between plants was 10 cm. The total plot size was 0.9 m x 3 m and single plant per hill was maintained. A fertilizer dose of 80 kg N, 60 kg P_2O_5 , and 60 kg K_2O was applied through ammonium sulphate, single super phosphate, and muriate of potash. Nitrogen was given in two equal splits, half as basal dose and the remaining half after one month of sowing. All the recommended cultural and plant protection measures were undertaken during the crop growth period. Five competitive plants were randomly selected from each genotype per replication for recording the observations. Observations were recorded on days to 50 % flowering, days to maturity, plant height (cm), primary branches $plant^{-1}$, secondary branches $plant^{-1}$, pod length (cm), no of seeds pod^{-1} , and seed yield ($q ha^{-1}$). Yield data were recorded on 24 central plants leaving one plant on either side of the row. The wilt and powdery mildew disease reaction of genotypes was scored on the scale as follows 0–10% -resistant (R), 10–30% -moderately resistant (MR), 30–70% -susceptible (S), and 70–100% -highly susceptible (HS). Further, the percent disease incidence (PDI) was measured as the (number of infected plants/total number of plants) \times 100.

Statistical analysis

Variance resulting from various causes was estimated according to Panse and Sukhatme (1967). The diallel analysis was carried out

as per Griffing (1956). The significance was tested by applying the F test. Using Method II and Model I of Griffing, 1956 a and b, the combining ability analysis based on mean values over replication was performed for all eight characters. The genotypic and the phenotypic coefficients of variation were calculated as per Burton (1951) and heritability in broad sense and genetic advance as percent of mean were computed following the methods of Allard (1960) and Johnson *et al.* (1955) respectively.

Results and discussion

The present investigation was undertaken to obtain information on gene action and genetic architecture of economic traits through diallel analysis in fenugreek. The analysis of variance was worked out to assess the variations in selected fenugreek genotypes and crosses for eight characters. The analysis of variance for eight characters consisting of replication mean squares, treatment mean squares, error mean squares, standard error, and critical difference at 5 percent and 1 percent is given in Table 1. The analysis of variance showed that differences among the treatments concerning all the characters were significant at both 5 percent and 1 percent levels except for seeds /pod. This demonstrated that there is a notable degree of diversity among the treatments for yield and contributing characters. Further portioning of treatment variance into components *viz.* parents, hybrids, and parents vs hybrids also differed significantly among them for all the characters except for seeds per pod.

Per se performance of parents

The parents' range for days to 50% flowering was between 31 to 42 days, and the range for single crosses was between 35 to 41 days (Table 2). For seed production purpose, early flowering is preferred, while late flowering is preferred for green vegetable purpose. The parents IFGS 9 (31 days), IFGS 4 (34 days), and IFGS 07 (34 days) recorded the earliest days to 50% flowering, ideal for seed purpose. On the other hand, IFGS 11 (42 days), IFGS-12, and Gujarat Methi-2 each took 37 days to flower, indicating delayed flowering which is beneficial for leafy uses. Early maturity is a favorable trait in fenugreek. It took less days for the parent Gujarat methi 2 (102 days) to mature followed by IFGS-12 (106 days). The higher plant height exhibited by Gujarat Methi-2 (75.6 cm) over Hisar Sonali (70.2 cm) was at par with the mean plant height (75.3 cm). The highest primary and secondary branches were recorded by IFGS-07 (5.1 and 14.5 respectively) followed by IFGS -04 (5.1 and 14.3 respectively). It was observed that IFGS-12 recorded the highest seed yield (17.1 q/ha) followed by IFGS-4 (16.5 q/ha) and IFGS-9 (15.4 q/ha) over the best check RMT 305 (14.6 q/ha).

Per se performance of single crosses

If parents show variation for certain loci at specific recombination sites, high vigor and high yielding combinations are typically obtained. Different compatible group of gene interactions revealed both favorable and unfavorable forms of pairings. Days from sowing to 50% flowering ranged from

31 to 42 DAS with an average of 37 DAS. The two hybrids IFHyb-10 and IFHyb-15 were significantly earlier (35 days) to flower while IFHyb-4 and IFHy-14 required 36 days which is at par with the mean of days to 50% flowering of hybrids. Days to maturity ranged from 85 to 105 days. Ten hybrids showed superiority for days to maturity over the mean of all the hybrids. The hybrid IFHyb-7 (85 days) was the earliest to mature followed by hybrid IFHyb-6 and IFHyb-13 (88 days). The

maximum plant height was recorded by hybrid IFHyb-11 (95.4 cm), highest primary branches plant⁻¹ by IFHyb-10 (4.7 cm), maximum secondary branches plant⁻¹ by IFHyb-4 (24.3 cm), while maximum pod length by IFHyb-14 (17.4 cm) and maximum number of seeds/pod by IFHyb-7 (14.5) over the mean of all the hybrids. IFHyb-11 (21.6 q/ha) recorded the highest seed yield followed by hybrid IFHyb-9 (19.9 q/ha) and IFHyb-15 (19.5 q/ha) over the mean seed yield of all the hybrids.

Table 1. Analysis of variance for experimental design

Source of variation	DF	Mean Squares							
		Days to 50 % flowering	Days to maturity	Plant ht. (cm)	Prim. bran. /plant	Sec. bran./ plant	Pod length (cm)	No. of seeds/ pod	Seed yield /plot
		1	2	3	4	5	6	7	8
Replication	2	0.034	0.090	1.915	0.271	1.003	1.179	31331.3	0.4
Treatment	20	3591.7**	3360.9**	3174.2**	4049.7**	2664.2**	3937.4**	27826.4	2952.2**
Parents	5	29.2**	33.6**	34.2**	32.5**	32.2**	35.4**	34.1	678.6**
Hybrids	14	150.2**	172.9**	176.1**	167.1**	165.5**	182.2**	175.5	3489.9**
Parents vs. Hybrids	1	220.3**	253.6**	258.3**	245.1**	242.8**	267.2**	257.4	5118.5**
Error	40	0.5500	0.2990	0.5650	0.3020	0.2550	0.3760	15883.9	0.4880

Table 2. Mean performance of parents, crosses and checks of fenugreek for yield and yield attributing traits (2018-19)

S. N.	Entry	Gene ration	Days to 50 % flowering	Days to maturity	Plant ht. (cm)	Prim. bran. /plant	Sec. bran/plant	Pod length (cm)	No. of seeds/pod	Seed yield (q/ha)	Disease reaction	
											Wilt	P.M.
	Parents											
1	IFGS-12	P1	37	106	63.4	3.3	8.9	11.21	10.8	17.1	MR	MR
2	IFGS-4	P2	34	109	62.5	5.1	14.3	11.61	11.4	16.5	MR	MR
3	IFGS-9	P3	31	115	65.6	3.9	14	9.92	9.5	15.4	MR	MR
4	IFGS-11	P4	42	114	65	3.3	12.3	9.82	9.6	14	MR	MR
5	IFGS-07	P5	34	108	53.6	5.1	14.5	11.55	11.1	13.7	MR	MR
6	Gujarat methi -2	P6	37	102	75.6	3.2	14.6	11.74	11.3	12.9	MR	MR
	Mean		35.8	109.0	64.3	4.0	13.1	11.0	10.6	14.9		
	Crosses											
7	IFHyb-1	F1	38	89.9	76.2	4.2	12.4	12.6	12.3	13.9	MR	MR
8	IFHyb-2	F1	37	98.5	76.3	4.3	10.9	12.01	11.6	12	MS	MR
9	IFHyb-3	F1	37	91.4	85.1	4.3	10.4	12.51	12.3	14.6	MR	MR
10	IFHyb-4	F1	36	94.9	84.1	5	24.3	11.62	11.2	11.4	MS	MR
11	IFHyb-5	F1	41	103.5	75.6	4	19.7	14.42	14.2	16	MR	MR
12	IFHyb-6	F1	39	87.9	80.3	4	13.3	10.75	10.3	18.7	MR	MR
13	IFHyb-7	F1	37	84.5	70.2	4.3	10.3	14.94	14.5	16.7	MR	MR
14	IFHyb-8	F1	41	111.4	76.5	4.3	10.7	14.6	14.3	9.6	S	MR
15	IFHyb-9	F1	38	104.9	81.3	3	10.8	13.61	13.2	19.9	MR	MR
16	IFHyb10	F1	35	91.5	75.1	4.7	10.9	9.11	8.9	13.6	MS	MR
17	IFHyb-11	F1	36	96.9	95.4	3	9.3	14.72	14.3	21.6	MR	MR

18	IFHyb-12	F1	39	91.5	92.6	4.2	10.8	14.42	14.2	17.5	MR	MR
19	IFHyb-13	F1	37	88.4	75.6	4.3	6.9	13.35	12.9	19	MR	MR
20	IFHyb-14	F1	36	97.4	80.3	4.1	8.3	17.44	17	16.8	MR	MR
21	IFHyb-15	F1	35	109	70.2	2.9	9.4	10.4	10.1	19.5	MR	MR
	Mean		37.5	96.1	79.7	4.0	11.9	13.1	12.8	16.1		
22	RMT 305 (C1)	C1	42	102	80.3	5.6	15.2	11.01	10.6	14.6	MR	MR
23	Hisar Sonali (C2)	C2	39	103	70.2	5.1	16.3	12.61	12.2	13.2	MR	MR
	SEm±		0.428	0.316	0.434	0.317	0.297	0.354	0.72	0.407		
	CD 5%		1.229	0.905	1.244	0.910	0.837	1.016	0.231	1.157		
	CV %		2.03	1.588	2.388	1.492	1.617	1.757	2.38	2.588		

Analysis of combining ability

The analyses of variance for combining ability for eight characters (Table 3) revealed that the mean sum of squares due to general combining ability was highly significant only for seed yield, suggesting that additive gene effects are important for seed yield. On the other hand mean sum of squares due to specific combining ability was highly significant for all the traits except for plant height indicating the importance of non-additive gene effects in expression of these characters. Singh and Raghuvanshi (1986) showed the importance of both additive and non-additive types of gene effects in fenugreek. The magnitude of specific combining ability variances was higher than general combining ability

variances for all characters except for seed yield indicating predominance of non-additive gene action for days to 50 % flowering, days to maturity, plant height (cm), primary branches plant⁻¹, secondary branches plant⁻¹, pod length (cm), no of seeds pod⁻¹, and additive gene action for seed yield⁻¹.

GCA effects of parents

Table 4 reveals the GCA effects of parental genotypes for all the studied characteristics. For days to 50% flowering, GCA effects varied from -5.86 for IFGS-4 to 6.478 for IFGS-12. The highest positive GCA effects for days to maturity were observed in IFGS-9 (3.332) while negative GCA effects for Gujarat methi -2 (-3.731). IFGS-4 recorded the highest

significant positive GCA effects for plant height (6.161) and primary branches plant⁻¹ (8.147) while for secondary branches plant⁻¹ and pod length both positive and negative GCA effects were found. The estimation of GCA effects for number of seeds /pod varied from -2.719 for IFGS-4 to 7.014 for IFGS-07. Significant GCA effects for seed yield were found in IFGS-

12 (77.569) while, IFGS-4, IFGS-9, IFGS-11, IFGS-07, and Gujarat Methi-2 showed negative GCA effects for seed yield. The high GCA effects of single cross IFGS 12 for seed yield is due to positive significant GCA effects for days to 50 % flowering.

Table 3. Analysis of variance for combining ability in 6 x 6 diallel design

Source of variation	DF	Mean sum of squares							
		Days to 50 % flowering	Days to maturity	Plant ht. (cm)	Prim. bran. /plant	Sec. bra./ plant	Pod length (cm)	No. of seeds/ pod	Seed yield (q/ha)
GCA	5	532.158	179.777	537.442	968.579	283.569	140.196	332.524	35,241.4**
SCA	15	2,004.3**	2,050.9**	1,645.032	2,107.2**	1,910.9**	1,988.3**	2,103.4**	15,258.7**
Error	40	841.334	968.161	986.273	935.979	926.953	1,020.337	982.793	19,54.2

Table 4. Estimates of GCA effects of parents

S.N.	Parent	Days to 50 % flower	Days to maturity	Plant ht. (cm)	Prim. Bran. /plant	Sec. Bra./ plant	Pod Length (cm)	No. of seeds/ pod	Seed yield (q/ha)
1	IFGS-12	6.478**	0.136	-3.256	-3.703	-3.613	-4	-0.365	77.569*
2	IFGS-4	-5.86*	2.032	6.161*	8.147*	1.733	-1.538	-2.719	-21.239
3	IFGS-9	1.457	3.332	-0.047	-6.011*	-2.108	2.325	0.901	-15.385
4	IFGS-11	1.344	0.949	-4.047	0.285	3.413	1.762	-2.224	-16.418
5	IFGS-07	1.811	-2.718	-4.218	-5.865*	-3.371	-0.075	7.014	-6.485
6	GUJARAT -2	-5.231	-3.731	5.407	7.147*	3.946	1.525	-2.607*	-18.043
	SE (m) (gi)	5.405	5.798	5.852	5.701	5.673	5.952	5.842	26.050
	SE (m) (gi-gj)	8.373	8.982	9.066	8.832	8.789	9.221	9.050	40.356

SCA effects of hybrids

The specific combining ability (SCA) effects investigated for all the eight traits studied is presented in Table 5. The results showed that for days to 50% flowering the highest significant positive SCA effects were recorded for IFHyb-7 (42.2) while IFHyb-15 (30.8) had the lowest positive significant SCA effects. The minimum SCA effects for days to maturity were registered by IFHyb-6 (-28.0) while highest SCA effects were recorded by IFHyb-15 (40.7). The two hybrids IFHyb-12 (37.3) and IFHyb-15 (18.6) exhibited significant positive SCA effects for days to maturity while significant negative SCA effects was exhibited by IFHyb-9 (-32.4) and IFHyb-6 (-30.0). The results showed that highest significant positive SCA effects were exhibited by IFHyb-4 for primary branches per plant (39.3) and secondary branches plant⁻¹ (47.0). For pod length, IFHyb-6 (37.8) recorded the highest SCA effects while IFHyb-9 (44.0) showed the highest SCA effects for number of seeds pod⁻¹. The SCA effects for seed yield varied from -108.9 for IFHyb-4 to 45.0 for IFHyb-11. The highest significant positive SCA effects were exhibited by IFHyb-11 (45.0) followed by IFHyb-7 (44.1) and IFHyb-9 (42.6) respectively for seed yield.

The range of variation was high for days to maturity (85 to 115 days), plant height (53.6 to 95.4 cm), pod length (17.4 to 9.11 cm) and

seed yield (21.6 to 9.6 q/ha) as observed by Dashora *et al.*, (2011) and Mishra *et al.*, (2021). The estimation of different genetic parameters revealed high magnitude of heritability for days to 50 % flowering (95.2 %), plant height (99.2 %), primary branches per plant, pod length, no of seeds per pod and seed yield (Table 7) indicating selection of diverse parents for crossing programme and presence of dominance x dominance type of gene interaction. Less heritability was recorded for days to maturity (3.5 %), and primary branches per plant (47.5 %) (Raje *et al.*, 2003, Dashora *et al.*, 2011 and Mishra *et al.* 2021). The estimates of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the traits studied which is an indicator of additive effect of the environment on the expression of the trait. The highest genotypic and phenotypic coefficient of variation was observed for secondary branches per plant followed by days to maturity and seed yield (q/ha). The estimates of genetic advance was highest for plant height (20.6%). The highest magnitude of genetic gain was recorded for secondary branches per plant (50 %) and seed yield (39.3 %). Pod length and number of seeds per pod also showed good genetic gain. It clearly showed that seed yield in fenugreek is directly depending on its yield attributing traits. Similar results have been recorded by Mishra *et al.*, (2021).

Table 5. Estimates of SCA effects of crosses

S. N.	Crosses		Days to 50 % flowering	Days to maturity	Plant ht. (cm)	Prim. bran. /plant	Sec. bra./ plant	Pod length (cm)	No. of seeds/ pod	Seed yield (q/ha)
1	IFHyb-1	IFGS 12* IFGS 4	-23.8	-3.7	21.7	35.9**	18.1	-3.9	-15.6	-94.6
2	IFHyb-2	IFGS 12* IFGS 9	-19.8	-25.6	-19.1	-15.4	6.9	29.3	36.2**	-53.5
3	IFHyb-3	IFGS 12* IFGS 11	16.0	35.9**	22.4	-7.5	-17.7	-16.3	-19.0	-82.2
4	IFHyb-4	IFGS 12* IFGS 07	-28.9**	-21.8	6.6	39.3**	47.0**	20.1	-18.0	-108.9**
5	IFHyb-5	IFGS 12* Gujarat-2	12.4	-11.6	-22.7	-25.0	-25.2	0.4	29.4	-42.7
6	IFHyb-6	IFHyb-4* IFGS-9	-15.5	-28.0**	-30.0**	-4.2	27.1	37.8**	22.7	7.4**
7	IFHyb-7	IFHyb-4* IFGS-11	42.2**	9.1	-13.4	-26.9	-26.7	-25.4	-0.1	44.1**
8	IFHyb-8	IFHyb-4* IFGS-07	-19.8	0.7	18.0	30.8	15.8	-9.9	-23.3	-8.2
9	IFHyb-9	IFHyb-4* Gujarat-2	-2.0	-21.8	-32.4**	-41.3**	-4.6	27.9	44.0**	42.6**
10	IFHyb-10	IFGS-9* IFGS-11	-24.6	-26.3	-1.1	27.8	31.1	17.9	-12.3	-4.3
11	IFHyb-11	IFGS-9* IFGS-07	13.6	-11.9	-15.0	-13.0	-20.9	-7.1	21.5	45.0**
12	IFHyb-12	IFGS-9* Gujarat-2	0.7	27.3**	37.3**	11.1	-13.8	-23.4	-19.0	-5.3
13	IFHyb-13	IFGS-11* IFGS-07	34.9**	21.2	-4.1	-18.4	-23.7	-26.6	-7.6	35.1
14	IFHyb-14	IFGS-11* Gujarat-2	-20.0	1.2	27.6	34.3**	6.5	-14.4	-15.4	-1.4
15	IFHyb-15	IFGS-07* Gujarat-2	30.8**	40.7**	18.6**	-11.6	-19.9	-24.0	-27.9	7.2
	SE (m) (Sij)		12.3	13.1	13.3	15.7	15.6	16.3	16.0	71.5
	SE (m) (Sij-Sik)		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	SE (m) (Sij-Skl)		20.510	22.02	22.21	21.63	21.53	22.58	22.16	98.85

Table 6. Half diallel crossing plan of fenugreek

M/F	IFGS-12	IFGS-4	IFGS-9	IFGS-11	IFGS-07	Gujarat -2
IFGS-12		IFGS 12*IFGS 4	IFGS 12*IFGS 9	IFGS 12*IFGS 11	IFGS 12 *IFGS 07	IFGS 12*Gujarat-2
IFGS-4			IFHyb-4* IFGS-9	IFHyb-4* IFGS-11	IFHyb-4* IFGS-07	IFHyb-4* Gujarat-2
IFGS-9				IFGS-9*IFGS-11	IFGS-9* IFGS-07	IFGS-9*Gujarat-2
IFGS-11					IFGS-11*IFGS-07	IFGS-11*Gujarat-2
IFGS-07						IFGS-07*Gujarat-2
Gujarat -2						

M= Male parent; F=Female parent

Table 7. Estimates of different genetic parameters for yield and yield attributing traits

Particulars	Days to 50 % flowering	Days to maturity	Plant ht. (cm)	Prim. bran. /plant	Sec. bra./ plant	Pod length (cm)	No. of seeds/ pod	Seed yield (q/ha)
Mean	37.5	96.1	79.7	4	11.9	13.1	12.8	16.1
Range (max. to min.)	42 to 31	115 to 85	95.4 to 53.6	5.6 to 2.9	24.3 to 6.9	17.4 to 9.11	17 to 8.9	21.6 to 9.6
Heritability (h^2)	95.2	3.5	99.2	47.5	99.7	95.5	98.5	99.4
GCV %	6.8	20.7	13.3	9.7	24.3	16.3	17.4	19.1
PCV %	6.9	110.7	13.4	14.0	240.4	16.7	17.5	19.2
Genetic advance	5.0	9.2	20.6	0.5	5.9	4.1	4.3	6.2
Genetic gain % of mean	13.6	8.0	27.4	13.7	50.0	32.9	35.5	39.3
Standard error	0.5	102.9	0.7	0.3	0.1	0.4	0.2	0.2

In the present study, heritability showed positive correlation with genetic advance for the traits secondary branches per plant (99.7 % & 5.9 %), plant height (99.2 % & 20.6 %) and seed yield (99.4 % & 6.2 %). Less heritability for days to maturity (20.7 %) showed high value of genetic advance (9.2 %). Overall, in present study highest genetic gain was recorded for secondary branches per plant (50 %) followed by seed yield (39.3 %) and no. of seeds/pod (35.5 %). The results are in agreement with Narolia *et al.*, (2017). High heritability coupled with low genetic advance has been recorded for days to 50 % flowering, secondary branches per plant, pod length, and seed yield (q/ha), regulated by non-additive gene action and presence of high genotype x environment interaction. Low heritability as well as genetic advance was observed for the traits days to maturity and primary branches per plant. Similar results have been recorded by Panwar *et al.*, (2018), Singh *et al.*, (2019), and Upadhyay *et al.*, (2020).

The manner of manifestation of gene action determines the breeding strategy to be

adopted for improving the genetic and morphological characteristics of the crop. Finding better parents with significant high general combining ability (GCA) effects and superior cross combinations with high specific combining ability (SCA) effects is made easier with the use of combining ability analysis. In the present study the most significant negative SCA effects for seed yield were seen in IFHyb-4 parents with high x low GCA effects, suggesting its superiority in luxury growth and usefulness for leafy purpose genotype selection. For IFHyb-11, the combination of the greatest yielding and lowest yielding parents produces low x low GCA effects. IFHyb-7 and IFHyb-9 crosses, on the other hand, displayed the highest SCA effects for seed yield. The research finding indicates that potential female parents having good vigour used in the crossing program contribute desirable traits to its F_1 progenies. Non-additive x non-additive types of gene action of parents lead to the development of superior combinations. Additive and non-additive gene actions in the parents estimated through combining ability may be

useful in commercial exploitation of heterosis and isolation of pure lines among the progenies of the heterotic combinations. In conclusion, parents IFGS-7, IFGS-9 and IFGS 12 of hybrid IFHyb-11, and IFHyb-4 are good general combiners for seed yield which can be used in the future for the development of superior transgressive segregants. Present study showed that non-additive gene action plays important role in inheritance process through combination breeding and selection of genotypes in F3 and F4 generation will be useful in fenugreek. The breeding methods like pure line selection and pedigree breeding will be useful for the selection of homozygous pure line.

References

- Ahmad FSN, Acharya Z Mir & Mir S 1999 Localization and activity of rRNA genes on fenugreek chromosomes by fluorescent in situ hybridization and silver staining. *Theoretical Appl. Genet.* 98: 179-185.
- Allard R W 1960 *Principles of Plant Breeding*. John W. & Sons, New York, USA pp.83-108
- Baker R J 1968 Issues in diallel analysis. *Crop Sci.* 18: 533-536
- Burton G W 1951 Quantitative inheritance in pearl millet (*Pennisetum glaucum*). *Agronomy Journal.* 43: 409-17.
- Dashora A, Maloo SR, Dashora LK 2011. Variability, correlation and path coefficient analysis in fenugreek (*Trigonella foenum-grae cum* L.) under water limited conditions. *Journal of Spices and Aromatic crops.* 20(1): 38-42.
- Griffing B 1956 A generalized treatment of the use of diallel cross in quantitative inheritance. *Heredity.* 10: 31-50.
- Griffing B 1956 Concept of general and specific combining ability in relation to diallel crossing systems. *Aust. J. Biol. Sci.* 9: 463-493.
- Johnson H W, Robinson H F & Comstock R E 1955 Estimates of genetic and environment variability in soyabean. *Agronomy Journal.* 47: 314-8.
- Leela N K & Shafeekh K 2008 *Fenugreek In: Chemistry of Spices* CAB International, Pondicherry, India.
- McCormick K, Norton R & Eagles H A 2006 Fenugreek has a role in south-eastern Australian farming systems. In: *Proceedings of "Groundbreaking stuff". 13th Annual Agronomy Conference, Perth, Australia, 639p.*
- Mishra A, Dodiya N S, Dashora A, Meena B S, Deora N S & Dave M 2021 Assessment of genetic variability, heritability and genetic advance in fenugreek (*Trigonella foenum-graecum* L.). *The Pharma Innovation Journal.* 10(9): 1038-1040.
- Moradi K Z & Zadeh J B 2013 Fenugreek (*Trigonella foenum-graecum* L.) As a Valuable Medicinal Plant. *Int. J. Adv. Biol. Biomed. Res.* 1(8): 922-931.
- Narolia S L, Meena M L, Atal M K & Verma N 2017 Genetic variability,

- heritability and genetic advance in fenugreek (*Trigonella foenum-graecum* L.) genotypes. *Int. J. Pure App. Biosci.* 5 (6): 452-458.
- Panse V G & Sukhatme P V 1967 *Statistical Methods for Agricultural Workers*. Indian Council of Agricultural Research, New Delhi, 381p.
- Panwar A, Sharma Y K, Meena R S, Solanki R K & Aishwath O P 2018 Genetic variability, association studies and genetic divergence in Indian fenugreek (*Trigonella foenum-graecum* L.) varieties. *Legume Research-An International Journal* 41(6): 816-821
- Raje R S, Singhania D L, Singh D 2003 Evaluation of early generation progenies (F₂) of fenugreek (*Trigonella foenum-graecum* L.) crosses for seed yield and yield related characters. *Journal of Spices and Aromatic Crops.* 12: 127-134.
- Singh A, Pandey V P, Singh A P, Singh A K, Yadav S, Verma M 2019 To estimate genetic variability analysis among different characters in germplasm of fenugreek [*Trigonella foenum-graecum* L.]. *Journal of Pharmacognosy and Phytochemistry.* 8(1): 1073- 1076.
- Singh J, Singh A K & Raghuvanshi S S 1986 Vigor and fertility spectra in autotetraploid fenugreek. *Indian Journal of Horticulture.* 43 (3-4): 278-280.
- Srinivasan K 2006 Fenugreek (*Trigonella foenum-graecum*): a review of health beneficial physiological effects. *Food review international.* 2: 203-226.
- Upadhyay R, Naidu A K & Dhakhariya T 2020 Studies on genetic variability among yield attributing traits of fenugreek genotypes. *International Journal of Chemical Studies.* 8(4): 1821-1825.
- Zahra Moradi kor & J B Zadeh 2013 Fenugreek (*Trigonella foenum-graecum* L.) As a Valuable Medicinal Plant. *International Journal of Advanced Biological and Biomedical Research.* 1(8): 922-931.