



Genotype and phenotype variability studies in fenugreek (*Trigonella foenum-graecum* L.) accessions in Kaffa Zone, South West Ethiopia

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Abstract

The present investigation was conducted on 36 geographically diverse Ethiopian accessions of fenugreek with an objective to study the extent of genetic and phenotypic variation among yield and its related traits. The accessions differed significantly for most of the characters and exhibited a relatively wide range. These characters indicated existence of variation among the tested accessions. High GCV was only observed in number of secondary branches per plant. High PCV were observed in number of primary and secondary branches per plant, number of seeds per pod, and 1000-seeds weight. High heritability values were observed in the number of seed per pod (63.1%), plant height (65.3%), biological yield per plot (80.1%), seed yield per plot (89.0%), day to maturity (80.8%), and day to flowering (71.4%). High genetic advance was observed for days to maturity, number of pod per plant, number of secondary branches per plant, biological yield and seed yield per plot. Seed yield per plot had positive and significant genotypic correlations with all traits except days to 50% flowering and plant height. Seed yield per plot had positive and significant phenotypic association with number of primary branches and plant height at maturity. This study revealed that there is good scope of concurrent improvement in yield by exploiting the Ethiopian germplasm of fenugreek.

Keywords: coefficient, fenugreek, heterosis, variability

Introduction

Fenugreek (*Trigonella foenum-graecum* L.) is an annual herb, self-pollinating with diploid ($2n=16$) chromosome numbers. It originated from the countries bordering on the eastern shores of the Mediterranean and is widely cultivated in China, India, Egypt, Ethiopia, Morocco, Ukraine, Greece, Turkey, etc. (Polhil & Raven 1981; Petropoulos 2002; Acharya *et al.* 2006; Davoud *et al.* 2010). Ethiopia is also known

as the original homeland of fenugreek subspecies Mediterranean, ecotype Abyssinians with its distribution extending to Eritrea and Somalia (Sinskaya 1950). In Ethiopia, fenugreek-growing regions are the high plateaus (1800-2300 m.a.s.l.) characterized by subtropical climate of wet and dry seasons. According to Central Statistics Agency (2009/10), the total area under production was 21,183 ha and production was estimated to be over 271,220 q. Although

the production scale makes it rank the 6th among the highland pulses, fenugreek stands at number one in generating cash. Thus, improving this crop means opening a new vista of the market opportunity in the face of the ever expanding world trade for the country in general and for the resource-poor farmer in particular (Rathore 2001).

Despite its extraordinary economic importance, the yield of fenugreek under farmers' conditions is very low (12.80 q h⁻¹). This is much less than the attainable yield under good management practices (52 q h⁻¹). The wide gap in yield is attributed to lack of improved varieties for different agro-ecological zones of Ethiopia (including south west Ethiopia), poor agronomic practices, poor soil fertility, diseases (powdery mildew) and insect pests (borer), etc. (Soori & Mohammadi-Nejad 2012).

In Ethiopia, fenugreek breeding is at its infant stage. Seed stocks that are grown landraces of the specific agro-ecological conditions (Mustefa 2006). Variety trial for high seed yield has been recorded from Sinana and Debreziet Agricultural Research Centers in the country (DZARC 2004; SARC 2005). Thus, efforts have been undertaken to improve the productivity of the fenugreek and in the past decade some better performing cultivars (such as *Challa*) were identified and released. Hence, in Ethiopia there have simply been inadequate research efforts up to this time. Consequently, fenugreek takes a considerably low research priority in the national agricultural research system. As the understanding of the other seed spice crops has improved, it is appropriate that a more thorough and systematic evaluation of fenugreek genetic resources be conducted in Ethiopia conditions (Mustefa 2006).

Currently, under Ethiopian fenugreek improvement project, large numbers of fenugreek accessions are collected from different major fenugreek growing regions of Ethiopia by the Institute of Biodiversity Conservation (IBC). As far as the genotypic and phenotypic variability and association among characters in these accessions are concerned little or no sufficient information is available.

Therefore, the objectives of this study were (i) to study the extent of genetic and phenotypic variability and heritability among 36 accessions of fenugreek collected from different region of Ethiopia and (ii) to estimate the extent of association between pairs of characters at phenotypic and genotypic levels and thereby compare the direct and indirect effects of the characters on yield.

Material and methods

Study area

The experiment was conducted at Deka town in Danito Yeri development project highland site, in Gesha Woreda, Kefa Zone of South Nation and Nationality People Region (NNPR) in 2013 main cropping season. The soils of the area are characterised by Nitisols. It lies at 6.2408.13' N and 35.480 36.78' E. The site is situated at an altitude of 2200 m.a.s.l. The mean annual rainfall is 2200 mm, while the mean annual minimum and maximum temperatures were 10.1 and 27.5°C, respectively (Ayele 2004).

Experimental materials and design

Thirty five random samples of fenugreek accessions along with one local check were considered in this study. The majority of the accessions represent the national collection from major growing regions of the Ethiopia (Table 1). The experiment was laid out in a 6 × 6 simple lattice design with 2 m long and 1 m wide plot size. Each plot has four rows spaced 20 cm apart with 10 cm inter-plant spacing. Weeding and other cultural practices were performed as per the recommendations (Fikreselassie *et al.* 2012).

Data and analysis

Data on the following eleven quantitative characters were recorded on five randomly selected plants from the two middle rows of each plot: Days to flowering (DF), Days to maturity (Provorov *et al.* 1996), Plant height at maturity (PHM), Number of primary branches (NPBP), Number of secondary branches (NSBP), Pod number (NPP), Seed number (NSP) Thousand kernel weight (TKW), Biomass yield plant⁻¹ (BIMYPt), Harvest index plant⁻¹ (HI) Seed yield plant⁻¹ (SYP). The relevant statistical analyses

Table 1. List of fenugreek accessions passport data

Accession No.	Regional areas					
	Regions	Zones	Districts	Longitude	Latitude	Altitude(m)
53008	Amhara	South-Gonder	Tach-gayint	08-07-00N	40-12-00E	2480
53009	Amhara	South-gonder	Este	08-26-00N	32-15-00E	2330
53012	Amhara	South-wollo	Wereilu	06-19-00N	27-45-00E	2240
53013	Amhara	South-wollo	Wereilu	-	-	NA
53014	Amhara	South-wollo	Legambo	12-02-00N	41-32-00E	2300
53026	Amhara	East-gojam	Enarg-enawg	-	-	2115
53055	Amhara	East-gojam	Shebel-benta	-	-	2045
53059	Amhara	East-Gojam	Shebel-benta	-	-	NA
239065	Amhara	Bahrdar	Bahir dar	16-05-00N	26-08-00E	2000
239066	Amhara	West-Gojam	Merawi	10-06-00N	28-12-00E	2050
239068	Amhara	West-Gojam	Around-Bahirdar	11-39-18N	37-13-41E	1930
215261	Amhara	North-Wello	Guba-lafto	11-48-00N	39-33-00E	1910
215731	Amhara	South-Wello	Werebabu	08-44-00N	41-16-00E	2050
53060	Amhara	East-Gojam	Shebel-beret	-	-	1845
53063	Amhara	Agawui	Danigla	09-23-00N	32-14-00E	NA
53056	Amhara	East-Gojam	Shebel-bere	-	-	1950
53057	Amhara	East-Gojam	Shebel-bere	-	-	2115
53066	Benshangul	Metekel	Dangur	-	-	2000
53006	Oromia	Arsi	Gedeb	-	-	NA
53016	Oromia	East-Hararge	Tullo	09-07-00N	41-01-00E	2400
51012	Oromia	Harerghe	Deder	09-28-00N	28-12-00E	2410
53020	Oromia	Bale	Goro	09-32-00N	42-16-00E	2560
53022	Oromia	East-Wollega	Amuru-garte	-	-	NA
237984	Oromia	Balle	Gasserana	-	-	2330
230536	Oromia	East-Hararge	Gursum	09-24-00N	42-1700E	2200
237982	Oromia	West-Shewa	Decho	-	-	2110
53072	Oromia	Arsi	Chole	08-22-00N	39-53-00E	2520
53074	Oromia	Arsi	Chole	08-40-00N	39-50-00E	2660
53064	Oromia	Bale	Agrfa	07-17-00N	39-50-00E	2450
53030	Oromia	Harerghe	Girawa	-	-	2420
53032	SNNP	Kaffa	Telo	-	-	2010
Local	SNNP	Kaffa	Gesha	-	-	NA
238247	Tigray	Mehaklegnaw	Lalay-maychew	14-05-00N	39-06-00E	1990
234033	Tigray	Mehaklegnaw	Naederadet	14-03-00N	38-44-00E	2120
234034	Tigray	Mehaklegnaw	Lalay-maychew	14-04-00N	38-43-00E	2120
53065	Tigray	Adwa	Adwa	-	-	NA

Source: Ethiopian Institute of Biodiversity Conservation (2012); NA=information is not available

were done using SAS version 9.2 (SAS Institute 2008).

Results and discussion

Variability assessments

Significant differences among genotypes ($P < 0.05$) were observed for all traits except the number of secondary branches plant⁻¹ and biological yield plot⁻¹ (Table 2). Davoud *et al.* (2010) reported significant differences among different Fenugreek accessions for day to flowering, day to maturity, plant height at maturity, number of primary branches, number of pod plant⁻¹, number of seed plant⁻¹, thousand seed weight, harvest index and seed yield plant⁻¹. The maximum seed yield plot⁻¹ (255.0 g) was recorded for the germplasm 237982 and the minimum (144.5 g) for the germplasm 53072. The over-all mean seed yield plant⁻¹ was 203.15 g. Around forty two percentages of germplasm accessions gave above the grand mean. The result of this investigation is in agreement with previous reports of Mustefa (2006) and Fikreselassie *et al.* (2012).

When accessions were grouped on the basis of number of days to flowering, 44.44% were early (42.5-47.14 days) and 55.56% were late flowering (47.5-52.5 days) with baseline of 50% flowering days. This result is in general agreement to Sade *et al.* (1996). Thus, the variability that has been exhibited by these accessions can offer great flexibility for the development of suitable varieties for the various agro-ecological zones in Ethiopia. The results from these investigations are in agreement with earlier findings (Rathore 2001; Mustefa 2006). There was also a wide variability for days to maturity with the late flowering genotype requiring 162 days to mature and the early flowering requiring 123 days to mature. Out of the top the total accessions, 50% were early maturing (123-141 days) and 50% were late maturing (142-162 days).

Variance components and coefficients of variations

Deshmukh *et al.* (1999) classified phenotypic coefficients variation (PCV) and genotypic coefficient of variation (GCV) values as high (>20%), medium (10-20%) and low (<10%).

Accordingly, high GCV was only observed in number of secondary branches plant⁻¹. High PCV were observed in number of primary and secondary branches plant⁻¹, number of seeds pod⁻¹, and 1000-seeds weight (Table 3). Medium GCV was observed in number of primary branches plant⁻¹, number of pods plant⁻¹, number of seeds pod⁻¹ and 1000-seeds weight. It indicated that selection may be effective based on these characters which showed medium and high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values. The rests of the characters, which recorded low scores (10%) of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) offered less scope of selection. Similarly, Raghuvanshi & Singh (1984) reported high genetic coefficients of variation for number of pods and number of branches, while Sade *et al.* (1996) and Mustefa (2006) reported high estimates of genotypic coefficient of variation (GCV) for seed yield plant⁻¹, number of pods and number of secondary branches. In addition, similar results were reported by Mathur & Lal (1994) who found high estimates of phenotypic coefficient of variation (PCV) for number of secondary branches. Seed yield plot⁻¹ was showed low GCV and PCV. In contrast, Sade *et al.* (1996) reported a high estimate of phenotypic coefficient of variation (PCV) for seed yields plant⁻¹, and number of pods. Generally, the estimates for phenotypic coefficient of variation (PCV) were greater than genotypic coefficient of variation (GCV) for the corresponding traits. This was in agreement with the finding of Sharma *et al.* (1986).

Heritability and genetic advance

Heritability values are useful in predicting the expected progress to achieve through the process of selection (Wright 1921). According to Robinson *et al.* (1949), heritability value is classified as high (>60%), moderate (30-60%) and low (<30%). Genotypic coefficients of variation along with heritability estimate provide a reliable estimate of the amount of genetic advance to expect through phenotypic selection. High heritability values were observed in number of seeds pod⁻¹, plant height at maturity,

Table 2. Mean performance of fenugreek genotypes with respect to various characters

Gen.	DF	DM	PH	NPB	NSB	NPP	SNP	TSW	BY	SYP
53008	47.0	144.0	49.0	5.0	6.5	20.0	8.3	14.2	785.3	201.5
53009	42.5	139.5	48.0	4.5	5.0	18.45	8.2	14.4	758.8	197.5
53012	50.0	150.0	52.5	5.0	6.0	18.2	9.8	13.6	749.3	181.0
53013	48.0	128.5	56.0	5.0	4.5	21.5	11.0	14.4	723.8	186.5
53014	46.0	127.5	43.0	4.0	4.0	20.3	10.8	14.8	812.8	241.5
53026	48.5	135.0	50.5	5.0	5.5	18.45	8.5	15.4	742.3	202.0
53055	47.5	133.0	46.0	4.5	4.5	19.9	9.1	15.0	755.3	213.0
53059	45.5	141.0	45.5	4.0	5.0	19.75	11.4	15.4	807.8	219.0
239065	47.0	137.0	41.5	5.0	8.0	21.0	10.6	14.8	756.8	204.5
239066	47.0	137.0	41.5	5.0	8.0	21.0	10.8	14.8	781.8	225.0
239068	47.5	151.5	52.5	4.0	4.5	21.0	12.9	15.2	816.4	235.0
215261	50.0	149.0	41.5	4.0	5.0	21.9	9.3	13.7	820.3	214.0
215731	49.5	140.5	51.0	4.0	5.0	17.1	9.9	11.8	742.83	189.5
53060	47.5	130.0	50.5	5.5	6.0	16.45	11.2	12.2	829.5	247.0
53063	47.5	141.0	54.0	5.5	7.0	17.65	10.7	15.2	766.3	175.5
53056	45.0	142.0	57.0	3.5	3.5	16.7	7.6	13.6	775.3	164.5
53057	46.0	157.5	48.0	5.0	5.5	22.6	13.5	18.2	829.3	245.0
53066	47.5	143.5	49.0	3.5	4.5	21.5	11.4	14.4	789.3	214.0
53006	46.5	162.0	50.5	5.0	5.5	22.3	10.2	15.4	737.3	203.0
53016	52.5	161.0	55.0	4.5	5.5	22.0	12.6	16.6	811.8	240.0
51012	47.5	137.5	52.0	3.5	4.0	16.35	8.8	11.4	758.3	160.0
53020	47.0	152.0	48.0	4.5	5.5	17.65	7.6	12.6	738.3	199.0
53022	46.0	128.5	53.5	4.0	4.5	17.85	10.9	14.2	724.6	197.5
237984	49.5	143.5	47.5	4.0	5.0	22.5	10.1	15.4	713.33	191.5
230536	49.0	147.0	46.0	3.5	4.0	19.35	11.8	12.6	719.8	174.0
237982	45.5	126.0	47.0	5.5	7.0	19.35	12.1	13.6	865.7	255.0
53072	46.5	123.5	52.0	4.0	5.0	20.45	9.5	13.7	670.7	144.5
53074	48.0	153.5	45.0	4.0	4.0	19.05	9.7	12.4	794.3	198.0
53064	47.5	159.0	50.5	4.0	4.5	22.35	13.4	18.6	813.1	215.0
53030	44.0	143.0	51.5	5.0	6.0	21.95	9.2	18.2	779.6	250.0
53032	47.5	137.0	47.0	3.5	3.5	18.50	10.6	13.1	732.8	202.0
Local	49.0	143.0	45.5	4.0	5.0	19.3	7.4	13.6	739.6	158.0
238247	43.0	154.5	50.0	4.0	5.5	19.1	9.9	14.6	728.83	172.5
234033	48.0	148.0	56.5	5.5	6.0	18.05	8.9	13.2	749.4	197.5
234034	46.0	129.0	55.0	5.5	4.5	18.15	8.0	15.0	791.3	213.0
53065	44.5	127.5	48.0	4.0	5.0	19.5	8.4	14.8	721.8	187.0
LSD (5%)	2.2	3.3	3.7	8.1	NS	3.88	2.6*	1.8	NS	1.92
CV (%)	2.7	12.0	5.4	15.9	14.2	15.9	13.7	12.9	200.2	21.1

(*Significant level; NS=not significant)

DF=days to 50% flowering; DM=days to maturity; PH=Plant height at maturity (9 cm); NPB=Number of primary branch plant⁻¹; NSB=Number of secondary branch plant⁻¹; NPP=Number of pod plant⁻¹; SNP=Number of seed pod⁻¹; TSW=Thousand seed weight; BY=Biological yield plot⁻¹ (g); SYP=Seed yield plant⁻¹ (g)

Table 3. Estimates of ranges, mean, genetic components of variances and coefficient of variation at phenotypic (σ^2_p), genotypic (σ^2_g) levels, heritability in broad sense, genetic advance and genetic advance expressed as percentage of mean for 10 traits fenugreek landraces.

Traits	Range	Mean±SE	σ^2_p	σ^2_g	GCV(%)	PCV(%)	h2(%)	GA	GAM(%)
DF	42.5-52.5	47.1±0.4	12.7	9.1	6.4	7.6	71.4	13.1	4.7
DM	123.5-162	141.8±1.7	138.9	112.0	7.5	8.3	80.8	209.2	23.0
PH	41.5-57.0	49.4±0.6	26.3	17.2	8.4	10.4	65.3	129.7	15.2
NPBP	3.5-5.5	4.4±0.1	2.0	0.6	18.2	31.7	32.8	28.0	13.4
NSBP	3.5-8.0	5.3±0.2	6.0	2.5	30.0	46.3	41.8	12.2	23.1
NPP	16.4-22.6	19.6±0.3	6.3	4.0	10.2	12.8	63.1	40.1	24.7
NSP	7.4-13.5	10.1±0.3	6.4	2.4	15.4	24.9	38.4	194.1	6.2
TSW (g)	11.4-18.6	14.4±0.2	15.2	6.7	17.9	26.9	44.3	273.3	13.7
BM (g)	670.8-865.3	767.6±7.1	2453.5	1964.8	5.8	6.4	80.1	6.9	30.8
SYP (g)	144.5-255.0	203.2±4.6	240.5	214.1	7.2	7.6	89.0	4.4	28.8

DF=days to flowering, DM=days to maturity, PH=Plant height at maturity (cm), NPBP=Number of primary branch plant⁻¹, NSBP=Number of secondary branch plant⁻¹, NPP=Number of pod plant⁻¹, NSP=Number of seed pod⁻¹, TSW=Thousand seed weight (g), BY=Biological yield plot⁻¹ (g), SYP =Seed yield plot⁻¹ (g)

biological yield plot⁻¹, seed yield plot⁻¹, day to maturity, and day to flowering (Table 3). This result also similar to the findings of Dashora *et al.* (2011). Moderate heritability values were found in number of primary and secondary branches plant⁻¹, number of seeds pod⁻¹ and 1000-seeds weight. These traits, therefore, may respond effectively to selection pressure. This study agreed with the study of Rakesh & Korla (2003).

Genetic advance as percent mean ranged from 4.67% for days to 50% flowering to 30.83% for biological yield plot⁻¹ (Table 3). Falconer & Mackay (1996) classified genetic advance as percent of mean as low (0-10%), moderate (10-20%) and high (20% and above). Based on this, high genetic advance expressed as percentage of mean was observed for days to maturity, number of pod plant⁻¹, number of secondary branches plant⁻¹, biological yield and seed yield plot⁻¹. Moderate genetic advance as a percentage of mean was observed for plant height, number of primary branches plant⁻¹ and 1000-seeds weight. Selection based on those traits with high genetic advance as percent mean will result in the improvement of performance of germplasm accessions for the traits. Mustefa (2006) reported that the expected genetic advance for days to flowering, day to maturity and thousand seed

weight which were in partial agreement with the present investigation. Mathur & Sharma (1992) also reported high expected genetic advance as a percentage of mean for secondary branches per plant, which was in agreement with this study. Rakesh & Korla (2003) reported that high genetic advance for biological and yield plot⁻¹. They also observed moderate genetic advance for plant height. Dashora *et al.* (2011) also reported that high genetic advance for number pods plant⁻¹, biological and seeds yield plot⁻¹.

Correlation of seed yield and yield related traits

The phenotypic and genotypic correlation among the yield and yield components in fenugreek are presented in Table 4. Seed yield plot⁻¹ had positive and significant genotypic correlations with all traits except days to 50% flowering and plant height.

Seed yield per plot had positive and significant phenotypic association with number of primary branches and plant height at maturity. It had negative and significant phenotypic association with biological yield plot⁻¹, number of seed pod⁻¹ and day to flowering.

The positive and significant correlation observed between seed yield and number of primary and secondary branches indicated that

Table 4. Estimates of Correlation coefficients at Genotypic (above diagonal) and Phenotypic (below diagonal) levels of 10 characters in fenugreek landraces studied at Deka 2013.

	DF	DM	PH	NPB	NSB	NPP	NSP	TSW	BY	SYP
DF										
DM	0.46**									
PHM	-0.241*	0.661**								
NPB	0.071	0.05	0.137*							
NSB	0.021	0.343**	0.161*	0.372**						
NPP	0.481**	0.573**	0.258**	0.223*	0.362**					
NSP	0.112	0.188*	0.573**	0.258**	0.223*	0.362**				
TSW	0.58**	0.211*	0.357**	0.034	0.501**	0.148	0.551**			
BY	0.098*	-0.042	-0.167*	-0.079	0.021	-0.132	0.006	-0.13	0.088	0.153*
SYP	-0.093	0.054	0.153*	0.268*	0.054	0.069	-0.173*	0.092	-0.158*	0.678**

*, ** Significant and highly significant 0.05 and 0.01 at probability level respectively.
 DF=days to flowering; DM=days to maturity; PH=Plant height at maturity (cm); NPB=Number of primary branch plant⁻¹; NSB=Number of secondary branch plant⁻¹; NPP=Number of pod plant⁻¹; NSP=Number of seed pod⁻¹; TSW=Thousand seed weight (g); BY=Biological yield plot⁻¹ (g); SYP=Seed yield plot⁻¹ (g)

a lot of branches of plants supporting many leaves could be partitioned to reproductive organ. Pods plant⁻¹ exhibited a positive association with seed yield plant⁻¹. This is an indication that plants bearing more number of pods plant⁻¹ produce more seed yield. Thus, selection for pods number alone will bring about a definite improvement in seed yield. Numbers of primary and secondary branches were found to be positively and highly significantly correlated with seed yield plot⁻¹. This suggested that more prolific accessions are likely to bear more pods than less branching ones. The positive significant correlations observed between seed yield plot⁻¹ with number of branches and numbers of pods are in agreement with the results reported by Sohoo & Bhardwaj (1987), Provorov *et al.* (1996), McCormic (2004) and Fikreselassie *et al.* (2012) and similar to the present results, Mustefa (2006) reported that the associations between seed yield plot⁻¹ and plant height at maturity was negative insignificant level only.

The present result also agreed with the work of Jian *et al.* (2013) and Miheretu Fufa (2013) who reported a significant and positive correlation of seed yield with plant height, number of pods on the main axis and the total number of pods plant⁻¹. They also mentioned non-significant and positive correlation of seed yield plant⁻¹ with secondary branches plant⁻¹ and number of seeds pod⁻¹. Generally, this study revealed the importance of focusing on the number of branches plant⁻¹, pods plant⁻¹ and seeds pod⁻¹ while selecting for seed yield. In case where fenugreek is grown for its forage, concentrating on biomass yield plant⁻¹ is crucial.

Path coefficient analysis

The path analysis at genotypic level revealed that, number of primary branches plant⁻¹, number of secondary branches and thousand seed weight contributed major positive direct effects (Table 5). These traits showed positive and significant genotypic correlations with seed yield (Table 4). As a result, these characters can be considered as core components for selection in a breeding program for higher seed yield. These positive direct effects indicated that by

Table 5. Estimates of direct (bold-and under line diagonal) and indirect effects (off-diagonal) at genotypic levels of 10 traits on seed yield plot⁻¹ in fenugreek landraces.

	DF	DM	PH	NPB	NSB	NPP	NSP	TSW	BY	Rg
DF	-0.18	0.09	-0.11	0.4	-0.29	0.09	0.18	-0.15	-0.01	0.02
DM	0.03	-0.2	0.21	0.94	-0.28	-0.3	-0.09	0.07	0.03	0.41
PH	0.09	0.09	-0.28	-0.31	0.19	0.12	0.07	0.11	0.07	0.15
NPB	-0.14	-0.08	-0.23	2.29	-0.95	-0.36	0.51	-0.1	-0.19	0.75
NSB	-0.14	-0.14	0.42	0.93	1.13	-0.92	-0.4	-0.18	-0.18	0.52
NPP	0.14	-0.06	-0.31	0.1	-0.14	0.65	-0.02	0.1	-0.07	0.39
NSP	0.03	0.09	-0.11	0.04	0.09	-0.1	0.10	0.23	-0.54	-0.17
TSW	-0.15	-0.08	0.25	0.09	-0.23	-0.47	-0.19	0.95	-0.02	0.15
BY	-0.01	-0.07	0.14	1.71	-0.56	-0.26	-0.09	0.09	-0.28	0.67

Residual effect=0.46

DF=Days to 50% flowering; DM=Days to maturity; PH=Plant height at maturity (cm); NPB=Number of primary branch plant⁻¹; NSB=Number of secondary branch plant⁻¹; NPP=Number of pod plant⁻¹; TSW=Thousand seed weight (g); BY=Biological yield plot⁻¹ (g).

keeping other characters constant, increasing one of these characters will increase seed yield, which implied that these characters are the major contributors for improvement of seed yield at the genotypic level.

Negative direct effect was exerted on seed yield by days to flowering, plant height and biological yield. These results are in agreements with that of Mustefa (2006) and Fikreselassie *et al.* (2012). Earlier studies have also indicated positive direct effect of number of pods (Sade *et al.* 1996), plant height (Singh *et al.* 1993) day to maturity (Raghuvanshi & Singh 1984) seeds pod⁻¹ and

branch numbers (Pant *et al.* 1983), on seed yield. However, 1000- seed weight (Singh *et al.* 1993), pod number (Singh *et al.* 1993; Raghuvanshi & Singh 1984) and plant height (Raghuvanshi & Singh 1984) had direct negative effects on seed yield.

The phenotypic direct and indirect effect of different characters on seed yield is presented in Table 6. Number of seed pod⁻¹, number of secondary branch, plant height at maturity 1000-seed weight, and number of pods plant⁻¹ had exerted positive direct effect on seed yield at phenotypic level. However, day of flowering,

Table 6. Estimates of direct (bold-and under line diagonal) and indirect effects (off-diagonal) at phenotypic levels of 11 traits on seed yield plot⁻¹ in fenugreek landraces

	DF	DM	PH	NPB	NSB	NPP	NSP	TSW	BY	Rp
DF	-0.18	0.26	-0.96	0.23	-0.34	0.81	0.18	-0.06	-0.03	-0.09
DM	0.16	-0.38	0.21	0.11	0.02	0.31	-0.39	0.07	0.04	0.15
PH	0.09	0.12	0.18	-0.39	0.09	0.27	0.31	0.17	0.29	1.13
NP	0.07	0.05	-0.23	-0.32	0.09	0.12	0.11	-0.17	0.54	0.26
NS	0.06	0.14	0.32	-0.57	0.42	0.2	-0.64	-0.48	0.5	-0.05
NPP	0.02	0.02	0.01	0.01	0.02	0.05	-0.07	0.04	-0.04	0.06
NSP	0.07	0.09	-0.69	0.04	0.07	0.14	0.46	0.12	-0.47	-0.17
TSW	0.2	0.13	0.04	0.05	0.03	0.02	-0.19	0.15	-0.34	0.09
BY	0.12	-0.05	0.12	-0.16	-0.07	0.04	-0.09	0.12	-0.19	-0.16

Residual effect=0.38

DF=Days to 50% flowering; DM=Days to maturity; PH=Plant height at maturity (cm); NPB=Number of primary branch plant⁻¹; NSB=Number of secondary branch plant⁻¹; NPP=Number of pod plant⁻¹; TSW=Thousand seed weight (g); BY=Biological yield plot⁻¹ (g).

days to maturity, number of primary branches plant⁻¹ and biological yield had negative direct effect on seed yield.

The trend with respect to phenotypic path coefficient of seed yield with other traits was more or less the same. The residual effect was somehow low for both phenotypic and genotypic level indicating that the traits for genotypic and phenotypic level included in this study accounted for almost the whole variation in seed yield plant⁻¹. An overall analysis of path coefficient suggested that selection should be appropriate to provide for plants with high number of primary branches, followed by number of seed pod⁻¹ to increase seed yield plant⁻¹ on fenugreek. Phenotypic coefficients of variation values were low for days to flowering and days to maturity; medium for plant height at maturity; and it was high for the rest of the characters. Genotypic coefficients of variation (GCV) values were low for days to flowering, day to maturity and plant height at maturity; medium for number of primary branches plant⁻¹ and a thousand seeds weight; and high for the rest of the characters. Correlation analysis showed that seeds yield plant⁻¹ had positive and highly significant genotypic correlations with day to maturity, number of primary and secondary branches plant⁻¹, number of pods plant⁻¹, number of seeds pod⁻¹, biomass yield, thousand seeds weight and harvest index. Number of primary branches plant⁻¹ and number of seeds pod⁻¹ were the important contributors to seed yield and the two traits could be used as an indirect selection criterion.

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