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Studies on the genetic variability of Ethiopian fenugreek genotypes (*Trigonella foenum-graecum* L.)

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Abstract

Fenugreek is multipurpose plant originated in the Mediterranean region. Lack of information on phenotypic characteristics is main problems in fenugreek production. Field experiment was conducted at Jamma district of South Wollo, Amhara National Regional State in 2018-19 main rainy seasons to estimate genetic variability, heritability in broad sense, genetic advance, among Ethiopian fenugreek genotypes. Sixty two nationally collected fenugreek genotypes along with standard and local checks were evaluated in simple lattice design. Analysis of variance showed the presence of significant ($p<0.05$) difference among genotypes for most of the traits examined, indicating the presence of genetic variability. Seed yield ranged from 651 kg ha^{-1} to 2148 kg ha^{-1}.A total of 30 and 35 genotypes had yield advantage up to 85 % and 98% than local and standard checks respectively. Seed yield ha^{-1} and biomass yield ha^{-1} were characterized with high GCV (29.3, 23.5), PCV (30.7, 27.5), h^2 (90.7, 72.3) and GAM (57.6, 41.2). Days to maturity showed the lowest GCV (0.8), h^2 (2.3) and GAM (0.3); while the lowest PCV was recorded for days to flowering (4.7).

Key words: Fenugreek, simple lattice and variability

Introduction

Fenugreek (*Trigonella foenum-graecum*) is an annual, self-pollinating legume grown mainly as a spice. It is also recognized for its medicinal and nutraceutical properties having 16 chromosome numbers (Sauvaire *et. al*., 1996). Fenugreek is believed to be originated from the Mediterranean region (Petropoulos, 2002). The genus *Trigonella* is one of the largest genera of the tribe *Trifoliate* in the family of *Fabaceae* and sub-family *Papilionaceae* (Balodi and Rao, 1991).

In Ethiopia, fenugreek ranked first out of spice crops in terms of area coverage and production (CSA, 2016). Fenugreek-growing regions of Ethiopia are the high characterized by subtropical climate of wet and dry seasons (Beteleihm Belete, 2018). In Ethiopia fenugreek occupies 32,507 ha with 87,041 ton productions in 2015 cropping season (CSA, 2016). South Wollo has the highest share in both in acreage and production in fenugreek production.

The amount of variability and extent of desirable traits heritability that exists in the population or germplasm collection of any crop is of the utmost important towards development of better varieties (Azeb Hailu *et. al*., 2016 and Yadav *et. al*., 2017). Genetic variability for the character of interest is a basic prerequisite for its improvement through selection or other breeding methods (Engida Tsegaye *et. al*., 2007). The presence of wide variations among fenugreek genotypes in phenotypic expression and heritability of yield and other quantitative traits allow the crop cultivation throughout the world under various environment conditions from the sea level to 4000 meter above sea level (Alberino *et. al*., 2004). It is also a well established fact that the yield potential of crop genotypes varies due to genotypic differences (G), environmental influences (E) and genotype by environment interactions (Becker and Leon, 1988). Therefore, examining the presence of genetic variability among fenugreek genotype and estimating heritability of traits are critical initial steps to develop fenugreek varieties adaptable to semi-arid areas. Proper understanding of the magnitude of correlations among various yield related traits is very important in developing high yielding genotypes (Tadele Tadesse *et. al*., 2009). For example it has been suggested that desirable drought phenotypic traits must be genetically associated with yield under stress, highly heritable, genetically variable, easy to measure, stable within the measurement period, and must not be associated with a yield penalty under unstressed conditions (Okogbenin *et. al*., 2013).

Despite its extraordinary importance Ethiopia is one of the highest producers in the world. The yield of fenugreek under farmers' conditions is very low due to many problems (1.1 t ha^{-1}) (CSA, 2016) compared to attainable (1.7 t ha^{-1}) and genetic potential yield of the crop. The wide gap in yield is attributed to: lack improved variety, lack of information variability, heritability, association of characters and genetic distance among fenugreek genotypes in Ethiopia (Mihretu Fufa, 2017). Poor agronomic practices, poor soil fertility, shortage of rain at flowering and podding stage, diseases (powdery mildew and wilt) and insect pests (borer) had also their own contribution to reduce fenugreek yield (Girma *et. al*., 2015). Therefore, in order to best exploit the available genetic wealth, assessing out the information on the extent and nature of genetic diversity of the population and the interrelationships among characters that would help in formulating efficient scheme of selection based on multiple trait of important. Therefore, this research was conducted to assess genetic variability of traits among fenugreek genotypes for yield and yield related traits.

Materials and methods

Description of the experimental site

The experiment was conducted at Jamma research site of Sirinka Agricultural Research Center (SARC) at Jamma District during the main growing season of 2018. Jamma is located at 10°27'N and 39°16'E on an altitude of 2622 meters above sea level, South Wollo, Amhara National Regional State, Ethiopia. Based on the last ten years (2008-2017) meteorological data obtained from Ethiopian Meteorological Agency, Kombolcha station, Jamma receives an average annual rainfall of 1047 mm and minimum and maximum temperature of 9.2 °C and 26.2 °C, respectively. Jamma is 120 km and 320 km away from Dessie and Addis Ababa, respectively. The dominant soil type in the District is Vertisol.

Experimental materials, design and procedure

Sixty two fenugreek accessions collected from Debre-Zeit Agricultural Research Center (DZARC) along with local and standard checks were evaluated at Jamma testing site of SARC. The experiment was laid out using simple lattice design (8x8) on plot size of 1.6 m^2, with an inter-row of 20 cm and intra-row spacing of 5 cm. The accessions were collected from different parts of the country. Clean fenugreek seeds were sowed of 20 and 5 cm between rows and plants, respectively, as per the national recommendation. Each genotype was planted on a gross plot size of 1.6 m^2 (0.8 m width x 2 m length). The distance between plots and blocks were maintained at 0.5 m and 1 m, respectively. Being fenugreek is leguminous crop, fertilizer were not applied at all. Weeding and thinning were practiced at the appropriate time. Data were recorded from the central two rows with net plot size of 0.8 m^2 (0.4 m x 2 m).

Table 1: Passport data of accessions

S.No.	Accession Number	Region	Zone	S.No.	Accession Number	Region	Zone
1	53003	Oromiya	N/Shewa	33	201627	NA	
2	53008	Amhara	S/ Gondar	34	201632	NA	
3	53009	Amhara	S/Gondar	35	202121	NA	
4	53014	Amhara	S/ Wollo	36	202122	NA	
5	53016	Oromiya	W/ Harerge	37	202124	NA	
6	53021	Amhara	E/Gojam	38	202125	NA	
7	53023	Oromiya	N/ Shewa	39	202126	NA	
8	53026	Amhara	E/Gojam	40	202127	NA	
9	53027	Amhara	E/Gojam	41	202129	NA	
10	53028	Amhara	E/Gojam	42	202132	NA	
11	53035	Amhara	E/Gojam	43	202133	NA	
12	53037	Amhara	E/Gojam	44	207361	Amhara	S/ Gondar
13	53039	Amhara	E/Gojam	45	207362	Amhara	N/ Gondar
14	53040	Amhara	E/Gojam	46	207363	Amhara	N/Gondar
15	53041	Amhara	E/Gojam	47	207364	Amhara	N/ Gondar
16	53042	Amhara	E/Gojam	48	207365	Amhara	N/ Gondar
17	53045	Amhara	E/Gojam	49	207390	Amhara	N/Gondar
18	53055	Amhara	E/Gojam	50	207391	Amhara	S/ Gondar
19	53056	Amhara	E/Gojam	51	207394	Amhara	S/ Gondar
20	53057	Amhara	E/Gojam	52	208680	Oromiya	E/ Harerge
21	53058	Amhara	E/Gojam	53	210864	NA	
22	53059	Amhara	E/ Gojam	54	212549	Amhara	N/ Shewa
23	53080	Amhara	E/ Gojam	55	212552	Amhara	N/ Shewa
24	53085	Oromiya	Bale	56	212777	Amhara	E/ Gojam
25	53086	Oromiya	N/Shewa	57	213115	Amhara	S/ Wollo
26	53094	SNNP	S/Omo	58	213116	Amhara	S/ Wollo
27	53097	Amhara	E/ Gojam	59	214942	Amhara	N/ Shewa
28	53098	Amhara	E/ Gojam	60	215056	Oromiya	Borena
29	53099	Amhara	E/ Gojam	61	216898	Oromiya	Arssi
30	53106	Amhara	N/ Shewa	62	216899	Oromiya	Arssi
31	53108	Amhara	N/Gondar	63	Jamma		
32	201577	NA		64	Local		

NA = not identified

Data collection

Data from plot basis or plant basis were recorded from the central two rows, leaving a guard row from either sides of the plot. The following data were recorded from plot basis.

Days to 50 % flowering: Days to 50% flowering was recorded as the number of days from planting to the time when 50 % of the plants in the plots produced flower.

Days to 90 % maturity: was recorded as number of days from planting to the time when 90 % of the plants in the plot reach physiological maturity.

Pod filling period: Number of days from flowering or exertion of pods to the time when 50% of the pod forms seeds.

Biomass yield (Above ground): Was taken as the total above-ground biomass weight of the plants from the central two rows. Total above-ground biomass was harvested and sun-dried and weighed using spring balance

Seed yield: was taken from the central two rows. Entire plants were harvested, threshed and winnowed. Clean seed were measured using electronic sensitive balance.

Thousand seeds weight: Thousand seeds were counted and weighed using electronic sensitive balance for each replication.

Harvesting index: It was calculated as the ratio of seed yield to biomass yield in percent

Plant height: plant height was measured from the main stem, measured from the ground level to the tip of the plant using measurement tape at 90% physiological maturity.

Pod length: pod length was measured from the tip to petiole of the pod at 90% physiological maturity.

Number of branches plant^{-1}: The total number of branches arising from the main stem was counted at 90% physiological maturity.

Number of pods plant^{-1}: The total number of pods per plant was counted at physiological maturity.

Number of seeds pod^{-1}: The total number of seeds per pod was counted at physiological maturity.

Data analyses

Analysis of variance (ANOVA) for each trait was analyzed using SAS statistical software package, version 9.0 as per Gomez and Gomez (1984). Means of traits for each treatment were separated by Duncan Multiple Range Test (DMRT) based on significant level. Variance components, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and heritability (h^2) were carried-out using output generated by SAS software.

The ANOVA was computed using the following model for simple lattice design:

$Yijk = \mu + Rj + Tk + Bi(j) + eijk$

Where; μ= overall mean, Rj = replication effect of the jth genotype, Bi(j) = random effect of block j within replication i, Tk = effect of treatment k, and eijk = the environmental effect of the ijkth observation.

Phenotypic and genotypic coefficients of variation

Phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were estimated according to Burton (1951) as:

$$PCV= \frac{\sqrt{\sigma^2 p}}{\overline{X}} *100$$

$$GCV= \frac{\sqrt{\sigma^2 g}}{\overline{X}} *100$$

Where $\overline{X}$ = mean value of the trait; $\sigma^2 p$ = Phenotypic variance of the character; $\sigma^2 g$ = genotypic variance of the character; PCV=Phenotypic coefficient of variation; GCV= Genotypic coefficient of variation.

Genotypic variance ($\sigma^2 g$) = (MSg – Mse)/r; Error variance (MSe) = $\sigma^2 e$

Where r = number of replications; MSg = mean square of genotype; MSe =mean square of error; $\sigma^2 g$ = genotypic variance; $\sigma^2 e$ = error variance

$\sigma^2 p$= phenotypic variance= $\sigma^2 g + \sigma^2 e$

Heritability (h^2)

Broad sense heritability values were estimated based on the formula of Falconer and Mackay (1996) as follows:

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Genetic advances

Genetic Advance (GA): Using the methods described by Johnson *et al.* (1955). Genetic advance and GA as percentage of the mean expected from selection of the best 5% of the genotypes were estimated as:

$GA = h^2 .k. \sigma_p$

Genetic advance as percentage of mean = $\frac{\text{GA}}{\bar{x}} x100$

Where, k is a constant, which at a selection intensity of 5% is about 2.06; σp is the phenotypic standard deviation; h^2 is broad sense heritability ratio; and x is the grand mean of the trait under considerations.

Results and discussion

Variability of traits

The mean squares from analysis of variance (ANOVA) showed significant variation (P<0.05) among the sixty four fenugreek genotypes for the traits considered except for days to flowering and maturity, seed filling period, number of branch plant^{-1} and pod length (Table 2). These indicated that the presence of adequate genetic variability among fenugreek genotypes and the possibility of improving yield and yield related traits through selection.

In harmony with the present results, Anubha *et. al*., (2013*)* reported significant amount of variability in fenugreek germplasm for almost all morphological traits studied, except for pod length. Million Fikrselassie *et. al*., (2012) also reported significant variations among 144 fenugreek genotypes for most of the traits considered. Similarly, Aman *et al*. (2018) reported significant variation among 124 fenugreek genotypes for all the traits considered, except for days to maturity. In addition to these authors, Wojo *et. al*., (2015), Mamatha *et. al*., (2017) and Pushpa *et. al*., (2010) reported the presence of significant differences among fenugreek genotypes for most traits studied. However, in contrast to the present findings, Betelhiem Belete (2018) reported that there was significant differences among 49 fenugreek genotypes in days to maturity and number of branch plant^{-1}, while no significant difference in number of seed plant^{-1}.

Mean performance of genotypes

A wide range of variation was observed in traits like plant height, number of branch plant^{-1}, biomass yield, number of pod plant^{-1}, number of seed plant^{-1}, seed yield, harvesting index and thousand seed weight. This indicated the presence of diverse genotypes for these traits. This variation can provide sufficient scope for further selection and improvement on these fenugreek traits (Table 2). Plant height and biomass ranged from 20 to 36.4 cm and 2.5 to 101.5 ton ha^{-1}, respectively. The mean height and biomass were 27.8 cm and 5.9 ton, respectively. Local check was the shortest in plant height and lowest in biomass yield, while the standard check was highest for plant height and intermediate for biomass yield, respectively. Totally, 45% of genotypes for the two traits had above the grand mean of plant height and biomass yield.

Genotypes also varied in number of branch plant^{-1}, number of seed plant^{-1} and seed yield with mean values of 3.1, 7.6 and 1224 kg, respectively. Some of the genotypes were better than the local and standard checks for these traits. In addition, 57%, 71% and 42% of the genotypes had mean values greater than the grand mean for branch plant^{-1}, number of seed plant^{-1} and seed yield, respectively. These results indicated the possibility of finding fenugreek genotypes that can perform better than the existing varieties for the study area and similar agro-ecologies to increase productivity; and to use as parents for hybridization program. Similarly, the highest variability for number of pods per plant and plant height for fenugreek accessions was reported by Mihretu Fufa (2017). Preeti (2017) also reported considerable variation among genotypes for number of seed per plant.

Table 2: Mean squares for different sources of variation, range and the corresponding coefficient of variation (CV) for the 12 characters studied

	Rep(df=1)	TRT(df=63)	MSB(df=14)	MSE(df=49)	Range	CV
DF	0.28	11.303	22.4*	9.571	59-72	4.79
DM	3.445	18.701	18.3	16.731	144-167	2.65
PP	60.5*	11.889	18.9	10.119	3-25	23.13
PH(cm)	3.96	16.582***	9.5	6.058	20-36.4	8.83
NB	0.04	0.253	0.22	0.193	2-4.6	14.03
BM(ton)	2094.8	4.53***	1444.2	0.71	2.5-11.25	14.35
NP	10.24	7.957**	4.1	3.283	3-14.2	23.90
NS	0.08	2.358**	8.5***	2.104	4.8-13	16.87
PL(cm)	0.00008	1.136	0.4	0.778	2.6-8.8	13.32
SY(ton)	148.9*	0.271***	14.5	0.013	5.5-22.65	9.39
HI	0.014*	0.007***	0.002	0.001	0.1-0.45	17.50
TSW(gm)	1.2	3.416***	0.9	1.194	14.6-23	17.50

Where, DF= days to flowering, DM= days to maturity, PP=seed filling period, PH=plant height, NB= number of branch per plant, BM=biomass, NP=number of pod/plant, PL=pod length, SY=seed yield, HI=harvesting index, TSW=thousand seed weight, Rep=replication, TRT=treatment, MSB= mean square of block and MSE= mean square of error and CV=coefficient of variation.

Estimation of variances

Estimates of phenotypic (σ^2p), genotypic (σ^2g) and environmental (σ^2_e) variances; phenotypic coefficient of variation (PCV) and genotypic coefficients of variations (GCV); heritability in broad sense, genetic advance and genetic advance as percent of means were score low to high for traits measured in fenugreek genotypes (Table 3).

Higher magnitude of differences of phenotypic and genotypic variances was observed among phenological traits (Table 3). These higher differences between phenotypic and genotypic variances indicated the existence of greater environmental influences for the expression of these traits and suggested the practical difficulty of improving these traits through selection.

The highest value of phenotypic variance was computed for days to maturity (17.7) while the lowest was for harvesting index (0.001). Genotypic variances were highest for plant height (5.26) and lowest for harvesting index (0.003). The high genotypic variance indicated that selection can be successfully applied in the population. These results were in agreement with the findings of Betelhiem Belete (2018) who reported relatively high environmental and phenotypic variance for phenological traits (days to flowering, maturity and pod filling period). According to Sivasubramanian and Madhavamenon (1973), genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) can be categorized as high (>20%), moderate (10-20%) and low (<10%). Depending on this classification, high value of genotypic coefficient of variation was recorded for biomass, number of pod plant^{-1}, seed yield ha^{-1} and harvesting index. These suggested that the influence of environmental factors for the expression of these traits is low; and traits are amenable to selection.

Table 3: Estimates of variance components, heritability and genetic advance of the 12 traits

Trait	σ^2g	σ^2_e	σ^2 p	GCV (%)	PCV (%)	h^2 (%)	GA	GAM(%)
DF	0.866	9.571	10.437	1.452	5.042	8.297	0.55	0.86
DM	0.985	16.731	17.716	0.643	2.725	5.560	0.48	0.31
PP	0.885	10.119	11.004	6.842	24.125	8.043	0.55	4.00
PH	5.262	6.058	11.320	8.229	12.069	46.484	3.21	11.51
NB	0.030	0.193	0.223	5.530	15.077	13.453	0.13	4.15
BM	1.91	0.71	2.62	23.442	27.456	72.901	2.43	41.22
NP	2.337	3.283	5.620	20.169	31.276	41.584	2.03	26.78
NS	0.127	2.104	2.231	4.146	17.376	5.693	0.17	1.98
PL	0.179	0.778	0.958	6.387	14.776	18.685	0.37	5.59
SY	0.129	0.013	0.142	29.343	30.568	92.143	0.71	58.01
HI	0.003	0.001	0.004	25.317	32.684	60.002	0.08	36.98
TSW	1.111	1.194	2.305	5.247	7.557	48.200	1.50	7.47

Where, DF=days to flowering, DM= days to maturity, PP=pod filling period, PH=plant height, NB= number of branch plant^{-1}, BM=biomass, NP=number of pod plant^{-1}, NS= number of seed pod^{-1}, PL=pod length, SY=seed yield, HI=harvesting index, TSW=thousand seed weight, σ^2g=genotypic coefficient of variance, σ^2e=environmental coefficient of variance, σ^2p=phenotypic coefficient of variance, GCV=genotypic coefficient of variation, PCV=phenotypic coefficient of variation, h^2 =heritability, GA= genetic advance and GAM =genetic advance as percent of means.

Estimation of genotypic coefficient of variation provides measure for comparing variability in the various metrical traits and better improvement through selection (Kumar *et. al.*, 2013). However, the rest traits had low genotypic coefficient of variation suggesting marked influence of environmental factors for their expression.

In harmony to the present results, Millon Fikreselassie *et. al.*, (2012) reported low genotypic coefficient of variation for days to flowering, plant height, number of seed plant^{-1} and thousand seed weight, however, these authors oppositely reported low genotypic coefficient of variation for number of pod plant^{-1}, seed yield ha^{-1} and harvesting index. Un like to the present findings, Sarada *et. al.*, (2008) reported high genotypic coefficient of variation for number of pod plant^{-1}and number of seed pod^{-1}; medium GCV for plant height, number of branch plant^{-1}and seed yield ha^{-1}; and low GCV for pod length.

The calculated value for phenotypic coefficient of variation was high for pod filling period, biomass, number of pod plant^{-1}, seed yield ha^{-1} and harvesting index (Table 3). Plant height, number of branch plant^{-1} and number of seed pod^{-1} had medium phenotypic coefficient of variation, while days to flowering, days to maturity and thousand seed weight had low phenotypic coefficient of variation. For most traits, phenotypic and genotypic coefficient of variation showed small differences indicated that environmental factors have little influence on their expression; and the possibility of fenugreek improvement through selection for these traits. In agreement with the present results, Aman *et. al.*, (2018), Preeti *et. al.*, (2017) and Sarada *et al.* (2008) reported nearly equal phenotypic and genotypic coefficient of variance for all traits studied. Preeti *et. al.*, (2017) also reported high GCV and PCV for seed yield, medium PCV for plant height, number of branch plant^{-1}, pod length and number of seed pod^{-1} and low GCV and PCV for days to flowering.

The low values for genotypic coefficient of variations (GCV) and higher differences in magnitude with the corresponding phenotypic coefficient of variations (PCV) was observed in pod filling period, number of branch plant^{-1}, number of seed plant^{-1} and number of pod plant^{-1}. This indicated the existence of higher influence of environmental factors in masking the expression of these traits of fenugreek genotypes; and suggested practical difficulty of fenugreek genotypes improvement of these traits through selection. Similarly, Million Fikreselassie *et. al.*, (2012) reported GCV and PCV values exhibiting greater differences almost for all the traits studied. Low values for both genotypic coefficient of variations (GCV) and phenotypic coefficient of variation (PCV) were observed for traits such as days to flowering, days to maturity and harvesting index. These results indicated the presence of large influence of environment on the expression of these traits and the practical difficulty of their improvement via selection. Similar findings were reported by Millon Fikreselassie *et. al.*, (2012) on days to flowering and Betelheim Belete (2018) on days to flowering and maturity.

Heritability and genetic advance

The values of heritability and genetic advance varied from low to high magnitudes for the studied traits (Table 4). As suggested by Robinson *et al.* (1955), heritability in broad sense can be categorized as high (>60), moderate (30-60%) and low (<30%). The computed values for heritability in broad sense ranged from 5.56% (days to maturity) to 92.1% (seed yield). Highest heritability values were recorded for traits such as biomass yield plot^{-1}, seed yield plot^{-1} and harvesting index. Medium heritability values were obtained for plant height, number of pod plant^{-1}and thousand seed weight and low heritability values were recorded for days to flowering, days to maturity, seed filling period, number of branch plant^{-1}, number of seed plant^{-1}and pod length (Table 3). These results suggested that these traits are amenable for selection in the late generations. Environment had higher effect for lower heritable traits and vice versa. In agreement with Million Fikreselassie *et. al.*, (2012) reported high heritability for biomass yield and seed yield; and low heritability for days to flowering. Opposite to the present findings, Aman *et. al.*, (2018) and Mamatha *et. al.*, (2017) reported high heritability for days to flowering, pod length, number of pod plant^{-1} and number of branch plant^{-1}. Plant height scored low to high by Aman *et al.* (2018) and Mamatha *et. al.*, (2017), respectively but our results showed medium in heritability for the same trait.

The genetic advance as percent of means ranged from 0.31% (days to maturity) and 58.35% (seed yield) (Table 3). Therefore, the expected genetic gains from selecting the top 5% of the genotypes; as a percent of the mean, varied from 0.31% to 58.35%, indicating that selecting the top 5% of the genotypes can increase the yield of fenugreek up to 58.35% in the studied area. Therefore, fenugreek improvement can be made by selection for these traits under similar conditions. The next better genetic advance as the percent of means were recorded for biomass yield ha^{-1} and harvesting index. While low estimates of genetic gain were obtained for days to maturity and number of seed per plant. The low values of expected genetic advance of mean for the days to flowering, pod filling period, number of branch plant^{-1}, number of seed pod^{-1}, pod length and thousand seed weight were due to low variability for the traits indicated by the low GCV and PCV values.

In agreement with the present results, Nobret and Habtamu Matthew (2017) reported similar results except for plant height, number of seed plant^{-1} and harvesting index. Aman *et. al.*, (2018) reported similar result for most of the traits, low genetic advance in days to flowering, day to maturity and high genetic advance in number of pod plant^{-1} and seed yield, But opposite result for plant height, pod length, number of seed pod^{-1} and thousand seed weight. This shows as the importance of genetic variability in improvement of fenugreek genotypes through selection. Majumder *et. al.*, (2008) also reported high heritability estimates along with low genetic advance indicating that non additive type of gene action and high genotype environment interaction plays a significant role in the expression of the traits as observed in the present study. In this study, both heritability and genetic advance as percent of mean values were high for biomass yield, seed yield and harvesting index. So high heritability is due to additive gene effects and selection may be effective in early generations for these traits. These traits can be used as good chances of improvement of fenugreek through direct selection. Similar result was reported by Preeti *et. al*., (2017), Verma *et. al*., (2016), Mahendra *et. al*., (2015), and Saha and Kole (2001), Heritability estimates would be reliable if accompanied by a high estimate of genetic advance as percent of mean (Singh and Choudhry, 1985). Different studies suggested that, it is important to consider both genetic parameters (heritability and genetic advance) to suggest that whether the trait is amenable for selection or not for its improvement than depending on heritability of the trait alone (Ali *et. al*., 2008).

Conclusion

The current study results showed that the presence of exploitable variations among the locally collected fenugreek genotypes in which either selection breeding or crossing of distant genotypes with desirable traits to develop varieties for the study area and similar areas with similar fenugreek production constraints. However, this result is from single location, for high degree of certainty to make recommendation about the importance of evaluation of these genotypes, evaluation of genotypes will be conducted under location and year replicated trial at least for one more season to further promote the high yielding genotypes and evaluation at different locations that leads to variety development.

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