

## Research Article

# Diversity of Ethiopian Fenugreek (*Trigonella foenum-graecum* L.) Accessions Based on Agromorphological Traits

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Information on the diversity of landraces is necessary to improve crops through selection or hybridization. This study was conducted to show the diversity of fenugreek landraces and associated traits. A total of 160 accessions including one local and four improved standard checks were evaluated in an augmented block design at the Haramaya University research site in 2016. Data collected include days to flowering, days to maturity, seed yield (kg/ha), thousand seed weight (g), the number of primary branches, plant height at flowering (cm), the number of pods per plant, the number of secondary branches, average pod length (cm), the number of seeds per pod, and seed yield per plant (g/plant) of quantitative traits. The analysis of variance revealed the existence of significant differences between accessions of all parameters. Genotypic and phenotypic coefficients of variation departed from 5.95–56.91% and 6.47–58.88%. Heritability in the broad sense and expected genetic gain as percent mean varied from 60.9 to 96.1% and from 2.5 to 70.3%. The seed yield per plant, the number of secondary branches, and the number of pod per plant had positive direct effects on the yield at both genotypic and phenotypic levels and the number of primary branches, and the average pod length via seed yield per plant, while the number of seeds per plant through the number of primary branches and the number of pods per plant had a positive indirect effect on the yield at the genotypic level, suggesting that these traits could be considered for indirect selection of genotypes for yield. The genetic distances of genotypes measured by Euclidean distance ranged from 0.07 to 10.6, and the dendrogram was constructed by using the unweighted pair group method using arithmetic mean. The presence of variability among fenugreek accessions suggested possibilities to improve the crop through the crossing of distant genotypes. This was an excellent opportunity to contribute to farmers' food security and livelihoods by bringing about the improvement of fenugreek.

## 1. Introduction

Fenugreek (*Trigonella foenum-graecum* L.) is an annual self-pollinating diploid ( $2n = 16$ ) legume species [1]. It originated in countries bordering the eastern shores of the Mediterranean Sea and is now widely cultivated in China, Egypt, Ethiopia, Morocco, Ukraine, Greece, and Turkey [2]. Ethiopia is one of the countries where fenugreek is most widely cultivated [3], and an original homeland of a subspecies known as the Mediterranean ecotype, which is also found in Eritrea and Somalia [4]. In Ethiopia, fenugreek

growing regions are located at 1800–2300 meters above the sea level and are characterized by a subtropical climate. The distribution of fenugreek is similar to other cool-season food legumes such as faba bean, field pea, lentil, chickpea, and grass pea. During the 2014 cropping season, fenugreek was planted on 20,524 hectares with an estimated average yield of  $1.224 \text{ t ha}^{-1}$ . Fenugreek ranks 9<sup>th</sup> among highland pulses in Ethiopia in terms of total production.

Fenugreek is primarily grown by Ethiopian farmers using landrace seed stocks that have been adapted to certain agroecological conditions. The agricultural research facilities

at Sinana, Sirinka, and Debreziet have made six improved cultivars accessible for planting. Fenugreek has received less attention from the national agricultural research system than other highland pulse crops as a result of the lack of evaluated genotypes of fenugreek that were discovered in the hands of farmers and the Ethiopian Biodiversity Institute. As a result, in order to develop new varieties, it is essential to evaluate the genetic diversity of the crop by systematic analysis across various agroecological conditions [5].

Yield per unit area is the result of many characteristics, each of which is polygenic, and the inheritance of yield-related traits is known to be highly influenced by the environment [6]. Therefore, the selection of genotypes for high yield alone is difficult because of its complex nature. It is important to study agronomic characters along with genetic diversity to understand their combined effects on the yield. To this end, some previous research activities generated valuable information on the genetic diversity of Ethiopian fenugreek accessions and their association with agronomic characters. 36 fenugreek accessions were studied at the Sinana Agricultural Research Center; 144 accessions were evaluated at Ambo and Adadi; 36 accessions were tested in Gesah district [7].

The present study builds on these previous efforts by analyzing 160 accessions gathered from everyone throughout Ethiopia at the research site Raare in the East Hararge Zone of Haramaya University, and the current study makes improvements on these earlier initiatives. The objectives of the study are to estimate genetic diversity for yield and yield-related traits.

## 2. Material and Methods

A field experiment was conducted at Raare Haramaya University's experimental site during the 2016 cropping season in Ethiopia at a latitude of 9° 26' N, a longitude of 42° 3' E, and an altitude of 1980 meters above the sea level. Haramaya University is situated 520 kilometers east of Addis Abeba. The location represents a subhumid midaltitude agroclimatic zone and has a bimodal rainfall pattern. The long rainy season lasts from July to September, whereas the short rainy season lasts from October to December. The year 2016 saw a total of 377.7 mm of precipitation with a temperature range of 11.3 to 23.7°C. The soil at the test site is categorized as fluvisols and has the texture of sandy clay loam.

Four standard checks, one local check, and 155 collections from Ethiopian Biodiversity Institute's national gene bank were used in the field experiment (EBI). The summary of the accessions is presented in Table 1.

Due to the 160 accessions used, the experiment used an augmented block design. Replications were not possible due to the small amount of seed, but checks were replicated in each block. The experiment has five blocks which contain 36 entries, including four standard checks (the "Chala," "Hunda'ol," "Eibbsa," "FGP #1," and local checks). While each accession was assigned only once during the experiment, the checks were distributed randomly within each block and replicated once in each block. A plot was divided into two rows, each measuring 2 m in length, with each row

0.25 m, making each plot 2 × 2 × 0.25 m, or 1 m<sup>2</sup>. There were 40 plants total in each plot (2 m × 2 rows × 10 cm) due to the 10 cm space between plants. Data collection was conducted using plants that were cultivated in both rows. All other agronomic procedures were followed as per the recommendation for fenugreek.

Five plants were chosen at random from each plot, and data collected include their days to flowering, days to maturity, seed yield (kg/ha), thousand seed weight (g), the number of primary branches, plant height at flowering (cm), the number of pods per plant, the number of secondary branches, average pod length (cm), the number of seeds per pod, and seed yield per plant (g/plant).

All datasets were subjected to analysis of variance (ANOVA) using the Statistical Package for Augmented Design (SPAD) software [8]. For significantly affected parameters, means were separated using critical differences in each category. Correlation and genetic distance were computed as per the method of Sharma [9] using SAS computer software version 9.1 (2000) and Statistica basic-7. Further genetic analyses were conducted for the traits for which genotypes exhibited significant mean squares. The phenotypic and genotypic variances were estimated according to the method suggested by Burton and De Vane [10]. The coefficients of variation at phenotypic and genotypic levels were estimated using the formula adopted by Johnson et al. [11].

Heritability (H<sup>2</sup>) in a broad sense was computed using the formula adopted by Allard [12]. Genetic advance as part of the mean (GA) for each character was computed using the formula adopted by Fehr [13]. Phenotypic and genotypic correlations between the yield and yield-related traits were estimated using the method described by Miller et al. [14]. The coefficients of correlation at a phenotypic level were tested for their significance by comparing the value of the correlation coefficient with the tabulated t-value at a g-2 degree of freedom. However, the coefficients of correlation at a genotypic level were tested for their significance using the formula described by Robertson [15].

The direct and indirect effects of yield-related traits on the yield were estimated through path coefficient analysis, and residual effects were estimated. The analysis was conducted following the method suggested by Dewey and Lu [16]. At 1% and 5% level of significance, the calculated t-value was compared to the tabulated "t" value at g-2 degree of freedom, where g = number of genotypes:

$$SE_{gxy} = \sqrt{\frac{(1 - r^2)gxy}{2hx \cdot hy}} \quad (1)$$

The Euclidean distance (ED) calculated from the yield and yield-related traits for all pair-wise combinations of fenugreek landraces was used to estimate the genetic distance of 160 fenugreek accession and checks. As described by Sneath and Sokal [17], Euclidean distance (ED) was computed from phenotype data collected for landraces after standardization (subtracting the mean value and dividing it by the standard deviation) as described by Sneath and Sokal

TABLE 1: Summary of fenugreek accessions collected from different geographic regions of Ethiopia.

No	Geographic region	Administrative zones of collection	No. of accessions	Altitudinal range (m.a.s.l.)
1	Northern Ethiopia	Tigray	8	2410
2	Northeastern Ethiopia	North and South Wollo	16	1910–2880
3	Northwestern Ethiopia	North and South Gonder, East and West Gojjam, Metekel	96	2330–2700
4	Central Ethiopia	Arsi and North Shewa	22	2000–2700
5	Western Ethiopia	East and West Wellega	2	1950
6	Southeastern Ethiopia	Bale and Borena	4	1730–2560
7	Southwestern Ethiopia	Gamo Gofa	2	Not known
8	Eastern Ethiopia	East and West Hararghe	5	1700
9	Released varieties		4	
10	Local check		1	

Source: Ethiopian Biodiversity Institute (EBI).

[17]. The distance matrices from phenotypic traits were used to construct a dendrogram based on the unweighted pair group method with arithmetic means (UPGMA) by Sneath and Sokal [17]. K-means clustering was used to specify the number of clusters to be generated. The results of the cluster analysis were presented in the form of the dendrogram. In addition, the mean average distance (ED) was calculated for each accession by averaging particular accession's distance to others. The calculated average distance (ED) was used to determine which fenugreek accession (s) is the closest to or farthest away from others [18].

### 3. Results

The ANOVA (Table 2) results reveal the presence of highly significant ( $p < 0.01$ ) differences among entries of days to 50% flowering, days to 90% maturity, the number of pods per plant, the number of seeds per pod, the number of primary branches, the number of secondary branches, thousand seed weight, plant height at flowering, and seed yield in kg per hectare. In addition, the entries showed a significant ( $p < 0.05$ ) difference in average pod length and seed yield per plant.

The four released and one local variety were used as a reference point against which other accessions to be evaluated or standard checks showed highly significant differences ( $p < 0.01$ ) for the number of primary branches, days to 50% flowering, days to 90% maturity, seed yield per hectare, and plant height at flowering while the standard checks showed nonsignificant differences for other traits.

The ANOVA also revealed highly significant ( $p < 0.01$ ) differences between check varieties vs. entries/tests for days to 50% flowering, days to 90% maturity, plant height at flowering, the number of pods per plant, the number of seeds per pod, the number of primary branches, and the number of secondary branches, while a significant ( $p < 0.05$ ) difference was seen in thousand seed weight and seed yield kg per hectare. However, the mean squares for seed yield per plant and average pod length for check varieties versus test entries were nonsignificant.

**3.1. Phenotypic and Genotypic Coefficient of Variations.** The genotypic (GCV) and phenotypic (PCV) coefficient of variations ranged from 5.95 to 56.91% and 6.47 to 58.88%,

respectively, where the lowest and highest values were calculated for the days of flowering (DF) and the number of pods per plant (NPPP), respectively (Table 3). Estimates of PCV and GCV were moderate for average pod length (APL) and the number of seeds per pod (NSPP). The PCV was estimated at 13.33 and 18.57% for APL and NSPP, respectively, whereas GCV was estimated at 10.41% and 16.27% for APL and NSPP, respectively. The high estimates of PCV ranged from 27.10% to 58.88% and GCV ranged from 24.47 to 56.91% when calculated for plant height at flowering, the number of pods per plant, the number of primary branches, the number of secondary branches, seed yield per plant, thousand seed weight, and grain yield per hectare.

#### 3.2. Heritability in a Broad Sense and Genetic Advance.

The proportion of phenotypic variance is attributable to an overall genetic variance for the genotype [19]. Estimates of heritability in a broad sense for 11 traits of 160 fenugreek accessions ranged from 60.98 to 96.05%, while estimates of expected genetic gain as percent mean ranged from 2.53 to 70.33% (Table 3).

#### 3.3. Correlation Coefficient of Grain Yield with Other Characters.

Grain yield per hectare had a positive and highly significant ( $p \leq 0.01$ ) correlation coefficient with the number of pods per plant at both genotypic and phenotypic levels (Table 4). In addition, grain yield per hectare was positively and significantly ( $p \leq 0.05$ ) correlated both at the genotypic and phenotypic levels—with the number of secondary branches, number of primary branches, and seed yield per plant. Average pod length showed a negative and significant ( $p \leq 0.01$ ) correlation with grain yield per hectare both at genotypic and phenotypic levels (Table 4).

Path analysis was conducted to partition the genotypic and phenotypic correlation coefficients of traits into direct and indirect effects on the grain yield. The results of genotypic path analysis are presented in Table 5, and the results of phenotypic path analysis are presented in Table 6. Seed yield per plant, the number of secondary branches, and the number of pods per plant exerted a positive direct effect on the grain yield both at genotypic and phenotypic levels and had positive and significant genotypic and phenotypic

TABLE 2: Mean squares from analysis of variance for 11 traits of 160 fenugreek accessions.

Trait	Mean squares						
	Block (4)	Treatment (159)	Among checks (4)	Among tests (154)	Tests vs. checks (1)	Error (16)	CV (%)
DF	2.74 <sup>ns</sup>	9.59**	9.38**	17.14**	11.1**	1.39	2.3
DM	48.90 <sup>ns</sup>	78.17**	102.08**	68.38**	1489.92**	25.48	4.19
PHF	73.97**	58.46**	56.66**	47.44**	1763.13**	10.63	10.63
NPPP	282.34**	62.86**	7.41 <sup>ns</sup>	60.57**	637.20**	3.65	13.80
NSPP	1.45 <sup>ns</sup>	4.75**	2.93 <sup>ns</sup>	4.76**	10.06**	1.14	8.17
NPB	0.04 <sup>ns</sup>	1.47**	0.27**	1.05**	71.17**	0.05	9.56
NSB	0.78**	0.61**	0.10 <sup>ns</sup>	0.62**	1.41**	0.11	19.67
APL	0.37 <sup>ns</sup>	1.10*	1.50 <sup>ns</sup>	1.08*	1.99 <sup>ns</sup>	0.53	7.61
SYPP	0.57 <sup>ns</sup>	0.99*	0.77 <sup>ns</sup>	1.00*	0.42 <sup>ns</sup>	0.45	17.75
Yhkg	21746.3 <sup>ns</sup>	130778.6**	130256**	131178**	71357.6*	15973	12.46
TSW	11.21 <sup>ns</sup>	24.09**	16.68 <sup>ns</sup>	24.20**	37.45*	6.56	13.65

Ns = nonsignificant, \* and \*\* = significant and highly significant at  $p < 0.05$  and  $p < 0.01$ , respectively. Numbers in parenthesis represented degree of freedom. DF = Days to 50% flowering, DM = Days to 90% maturity, PHF = Plant height at flowering, NPPP = Number of pods per plant, NSPP = Number of seeds per pod, NPB = Number of primary branches, NSB = Number of secondary branches, APL = Average pod length, SYPP = Seed yield per plant in gram, Yhkg = Yield in kg per hectare, TSW (g) = Thousand seed weight in gram and CV (%) = Coefficient of variation in percentage.

TABLE 3: Estimates of range, mean, genetic components of variance, heritability, and genetic advance of fenugreek accessions at Haramaya 2016.

Traits	Range	Mean	$\sigma_p^2$	$\sigma_g^2$	PCV (%)	GCV (%)	H <sup>2</sup>	GA	GAM (5%)
DF	41.14–57.04	51.25	10.98	9.31	6.47	5.95	84.81	5.80	4.70
DM	97.67–138.21	120.21	103.65	73.07	8.47	7.11	70.50	14.81	3.20
PHF	10.86–52.14	30.67	69.09	56.33	27.10	24.47	81.54	13.98	12.19
NPPP	0.19–39.23	13.85	66.51	62.13	58.88	56.91	93.41	15.72	28.62
NSPP	4.20–19.10	13.07	5.89	4.52	18.57	16.27	76.77	3.84	15.00
NPB	0.85–4.49	2.37	1.52	1.46	52.02	50.98	96.05	2.44	65.95
NSB	0.30–3.88	1.70	0.72	0.59	49.91	45.11	81.67	1.43	70.33
APL	4.32–12.30	9.58	1.63	0.99	13.33	10.41	60.98	1.61	13.23
SYPP	0.72–5.91	3.80	1.44	0.90	31.58	24.97	62.50	1.55	32.73
Yhkg	250.09–2275.00	1035.50	146751.60	127584	36.99	34.49	86.94	687.10	2.53
TSW	10.05–36.97	18.75	30.65	22.78	29.53	25.45	74.32	8.49	15.54

$\sigma_p^2$  = Phenotypic variance,  $\sigma_g^2$  = Genotypic variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic Coefficient of Variation, H<sup>2</sup> = Broad sense heritability, GA = Expected Genetic advance and GAM (5%) = Genetic Advance as percent of the Mean, DF = Days to 50% flowering, DM = Days to 90% maturity, PHF = Plant height at flowering, NPPP = Number of pods per plant, NSPP = Number of seeds per pod, NPB = Number of primary branches, NSB = Number of secondary branches, APL = Average pod length, SYPP = Seed yield per plant, TSW = Thousand seed weight, and Yhkg = yield per hectare in kg.

TABLE 4: Estimates of genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients among 11 traits studied in 160 fenugreek accessions.

Variable	DF	DM	SYPP	PHF	NPB	NSB	APL	NPPP	NSPP	TSW	Ykgha <sup>1</sup>
DF		0.31**	-0.03 <sup>ns</sup>	-0.13 <sup>ns</sup>	-0.02 <sup>ns</sup>	0.05 <sup>ns</sup>	0.02 <sup>ns</sup>	-0.08 <sup>ns</sup>	-0.15 <sup>ns</sup>	-0.01 <sup>ns</sup>	-0.13 <sup>ns</sup>
DM	0.31**		0.11 <sup>ns</sup>	0.074 <sup>ns</sup>	0.22**	0.11 <sup>ns</sup>	-0.05 <sup>ns</sup>	0.17*	-0.07 <sup>ns</sup>	-0.11 <sup>ns</sup>	0.12 <sup>ns</sup>
SYPP	-0.04 <sup>ns</sup>	0.09 <sup>ns</sup>		0.061 <sup>ns</sup>	0.05 <sup>ns</sup>	0.04 <sup>ns</sup>	0.01 <sup>ns</sup>	0.23**	-0.01 <sup>ns</sup>	-0.05 <sup>ns</sup>	0.18*
PHF	-0.12 <sup>ns</sup>	0.07 <sup>ns</sup>	0.05 <sup>ns</sup>		0.21**	0.07 <sup>ns</sup>	0.02 <sup>ns</sup>	0.24**	0.12 <sup>ns</sup>	-0.02 <sup>ns</sup>	0.06 <sup>ns</sup>
NPB	-0.02 <sup>ns</sup>	0.22**	0.04 <sup>ns</sup>	0.20**		0.85**	-0.15*	0.21**	0.00 <sup>ns</sup>	-0.09 <sup>ns</sup>	0.15*
NSB	0.06 <sup>ns</sup>	0.11 <sup>ns</sup>	0.04 <sup>ns</sup>	0.05 <sup>ns</sup>	0.83**		-0.16*	0.13 <sup>ns</sup>	-0.09 <sup>ns</sup>	-0.06 <sup>ns</sup>	0.16*
APL	0.03 <sup>ns</sup>	-0.02 <sup>ns</sup>	0.00 <sup>ns</sup>	0.02 <sup>ns</sup>	-0.15*	-0.15*		-0.10 <sup>ns</sup>	0.20**	-0.11 <sup>ns</sup>	-0.16*
NPPP	-0.09 <sup>ns</sup>	0.14*	0.21**	0.23**	0.20**	0.07 <sup>ns</sup>	-0.10 <sup>ns</sup>		0.13 <sup>ns</sup>	0.05 <sup>ns</sup>	0.43**
NSPP	-0.15*	-0.06 <sup>ns</sup>	-0.01 <sup>ns</sup>	0.10 <sup>ns</sup>	0.00 <sup>ns</sup>	-0.09 <sup>ns</sup>	0.21**	0.12 <sup>ns</sup>		-0.03 <sup>ns</sup>	-0.04 <sup>ns</sup>
TSW	-0.01 <sup>ns</sup>	-0.10 <sup>ns</sup>	-0.04 <sup>ns</sup>	-0.02 <sup>ns</sup>	-0.09 <sup>ns</sup>	-0.06 <sup>ns</sup>	-0.10 <sup>ns</sup>	0.05 <sup>ns</sup>	-0.02 <sup>ns</sup>		-0.02 <sup>ns</sup>
Ykgha <sup>1</sup>	-0.13 <sup>ns</sup>	0.13 <sup>ns</sup>	0.17*	0.07 <sup>ns</sup>	0.15*	0.15*	-0.15*	0.41**	-0.04 <sup>ns</sup>	-0.02 <sup>ns</sup>	

\* = significance at probability level of 0.05, \*\* = significant at probability level of 0.01 and ns = Nonsignificant, DF = Days to 50% flowering, DM = Days to 90% maturity, PHF = Plant height at flowering, NPPP = Number of pods per plant, NSPP = Number of seeds per pod, NPB = Number of primary branches, NSB = Number of secondary branches, APL = Average pod length, SYPP = Seed yield per plant, TSW = Thousand seed weight, and Ykgha<sup>1</sup> = yield in kg per hectare.

TABLE 5: Estimates of direct (bold-diagonal) and indirect effects (off-diagonal) of path at genotypic levels of the 10 traits on seed yield per plant in 160 fenugreek accessions.

Variable	SYPP	NPB	NSB	APL	NPPP	rg
SYPP	<b>0.07</b>	-0.01	0.01	0.00	0.09	0.18*
NPB	0.00	<b>-0.13</b>	0.17	0.01	0.08	0.15*
NSB	0.00	-0.11	<b>0.20</b>	0.01	0.05	0.16*
APL	0.00	0.02	-0.03	<b>-0.09</b>	-0.04	-0.16*
NPPP	0.02	-0.03	0.03	0.01	<b>0.40</b>	0.43**

Residual = 0.13, SYPP = Seed yield per plant, NPB = Number of primary branches, NSB = Number of secondary branches, APL = Average pod length, and NPPP = Number of pods per plant.

TABLE 6: Estimates of direct (bold-diagonal) and indirect effects (off-diagonal) path at phenotypic levels of the 10 traits on seed yield per plant in 160 fenugreek accessions.

Variable	SYPP	NPB	NSB	APL	NPPP	rp
SYPP	<b>0.07</b>	-0.01	0.01	0.00	0.08	0.17*
NPB	0.00	<b>-0.18</b>	0.20	0.01	0.08	0.15*
NSB	0.00	-0.14	<b>0.24</b>	0.01	0.03	0.15*
APL	0.00	0.03	-0.04	<b>-0.09</b>	-0.04	-0.15*
NPPP	0.01	-0.04	0.02	0.01	<b>0.38</b>	0.41**

Residual 0.13, SYPP Seed yield per plant, NPB Number of primary branches, NSB Number of secondary branches, APL Average pod length, and NPPP Number of pods per plant. The bold values shows direct effects on yield, so we can choose those parameters to improve the crop.

correlations with yield. Although the number of primary branches exhibited positive and significant genotypic and phenotypic correlations with the yield, this trait exerted a high and negative direct effect on the grain yield both at genotypic and phenotypic levels. Several primary branches had a positive indirect effect on the yield via average pod length, the number of secondary branches, and several pods per plant both at genotypic and phenotypic levels. Average pod length had negative and significant genotypic and phenotypic correlations with the yield.

**3.4. Distance Analyses Based on the Geographic Origin.** The accessions were grouped into eight geographic regions. Together with the five checks and the mean of released varieties, a total of 14 groups were analyzed to assess the relationships among accessions based on their geographic origins. For 11 agromorphological traits, the mean values of each group and variety were used to estimate genetic distances in terms of Euclidean distances, as shown in Table 7 and Figure 1.

## 4. Discussion

The ANOVA (Table 2) results reveal the presence of highly significant ( $p < 0.01$ ) differences among entries such as days to 50% flowering, days to 90% maturity, the number of pods per plant, the number of seeds per pod, the number of primary branches, the number of secondary branches, thousand seed weight, plant height at flowering, and seed yield kg per hectare. In addition, the entries showed significant ( $p < 0.05$ ) differences in average pod length and seed yield per plant. The four released and one local variety used as standard checks showed highly significant differences ( $p < 0.01$ ) for the number of primary branches, days to 50% flowering, days to 90% maturity, seed yield per hectare, and

plant height at flowering while the standard checks showed nonsignificant differences for other traits. The ANOVA also revealed highly significant ( $p < 0.01$ ) differences between check varieties vs. entries/tests for variables such as days to 50% flowering, days to 90% maturity, plant height at flowering, the number of pods per plant, the number of seeds per pod, the number of primary branches, and the number of secondary branches, while a significant ( $p < 0.05$ ) difference was seen in thousand seed weight, and seed yield kg per hectare. However, the mean squares for seed yield per plant and average pod length for check varieties versus test entries were found to be nonsignificant.

The significant differences among test accessions for all traits showed the presence of variation. The results suggest an opportunity for crop improvement based on the traits of interest in the selected accessions. Other workers in Ethiopia also reported the presence of significant differences among fenugreek accessions for variables such as days to flowering, days to maturity, plant height at 90% maturity, the number of primary branches, the number of secondary branches, the number of pods per plant, the number of seeds per plant, thousand seed weight, and seed yield. Studies conducted in other countries [20] reported the presence of significant differences among fenugreek germplasm for variables such as the number of primary branches, the number of secondary branches, plant height, and the number of seeds per pod. Sharma et al. [21] also reported significant variation among 50 fenugreek genotypes for grain yield, the number of pods per plant, seed yield per plant, and eight other traits.

**4.1. Phenotypic and Genotypic Coefficient of Variations.** The genotypic (GCV) and phenotypic (PCV) coefficient of variations ranged from 5.95 to 56.91% and 6.47 to 58.88%, respectively, where the lowest and highest values were calculated for days of flowering (DF) and the number of

TABLE 7: Dendrogram generated based on the UPGMA clustering method depicting relationships among accessions of eight geographic regions and five checks based on groups mean values for 11 agromorphological traits.

Group	CE	SEE	WE	EE	NWE	NEE	NE	SWE	MRV	Chala	Ebbisa	Hunda'ola	FGP #1	Local	Overall
CE		1.77	1.50	1.66	0.98	1.19	1.23	3.10	2.44	2.52	2.96	3.28	2.00	2.16	
SEE			1.47	2.28	1.96	2.02	2.06	3.66	2.94	3.07	3.53	3.53	2.51	2.61	
WE				1.96	1.49	1.78	1.47	3.66	2.86	3.27	3.12	3.40	2.60	2.43	
EE					2.28	2.49	2.45	3.39	2.97	3.25	3.17	3.45	2.96	2.85	
NEW						1.09	0.70	3.01	2.56	2.67	3.12	3.31	2.12	2.27	
NEE							1.42	3.36	2.98	2.82	3.67	3.92	2.19	2.58	
NE								3.06	2.75	2.95	3.20	3.40	2.38	2.46	
SWE									3.38	3.26	3.88	3.71	3.49	3.72	
MRV										1.13	1.36	1.19	1.24	1.11	
Chala											2.41	2.11	0.98	1.50	
Ebbisa												1.37	2.41	1.90	
Hunda'ola													2.33	1.98	
FGP #1														1.10	
Local															
Min	0.98	1.47	1.47	1.66	0.70	1.09	0.70	3.01	1.11	0.98	1.36	1.19	0.98	1.10	0.70
Max	3.28	3.66	3.66	3.45	3.31	3.92	3.40	3.88	3.38	3.27	3.88	3.92	3.49	3.72	3.92
Mean	2.06	2.57	2.39	2.70	2.12	2.42	2.27	3.44	2.22	2.46	2.78	2.84	2.18	2.21	2.48
SD	0.76	0.72	0.82	0.56	0.84	0.92	0.84	0.28	0.87	0.80	0.83	0.92	0.72	0.72	0.76
CV (%)	36.75	28.18	34.29	20.79	39.84	37.85	37.01	8.13	39.02	32.62	29.80	32.50	33.17	32.58	31.61

Min = Minimum, Max = Maximum, SD = Standard deviation, CV (%) = Coefficient of Variation in percent, SWE = Southwestern, NE = Northern, CE = Central Ethiopia, SEE = Southeastern, WE = Western, EE = Eastern, NEW = Northwestern, Chala, Ebbisa, Hunda'ola, FGP #1, LC = Local check, and MRV = Mean of Released varieties.

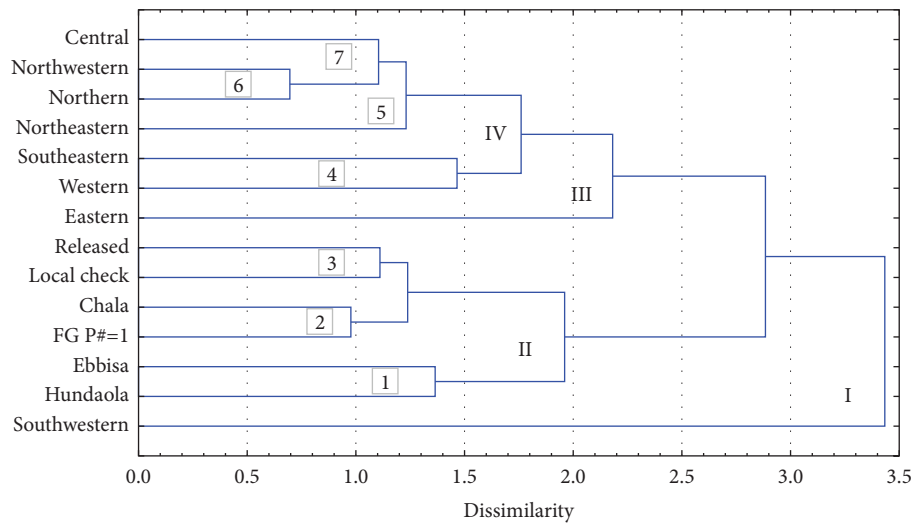


FIGURE 1: Dendrogram generated based on the UPGMA clustering method depicting relationships among accessions of eight geographic regions and five checks based on groups mean values for 11 agromorphological traits.

Pods per plant (NPPP), respectively (Table 3). GCV and PCV are categorized as low (<10%), moderate (10–20%), and high (>20%) [22]. Accordingly, both PCV and GCV estimates were low (6.47 to 5.95%) for days to 50% flowering (DF) and days to 90% maturity (DM). The PCV was greater than the GCV for both traits; however, the magnitude of the difference was low, suggesting the influence of environmental factors on the phenotype expression of traits. However, the low GCV estimates for DF and DM indicate the limited scope of improvement of these traits through selection depending on phenotype expression. It also reported a low genotypic coefficient of variation for days to flowering.

Estimates of PCV and GCV were moderate for average pod length (APL) and the number of seeds per pod (NSPP). The PCV was estimated to be 13.33% and 18.57% for APL and NSPP, respectively, whereas GCV was estimated to be 10.41% and 16.27% for APL and NSPP, respectively. High estimates of PCV ranged from 27.10% to 58.88% and GCV ranged from 24.47% to 56.91%, calculated for variables such as plant height at flowering, the number of pods per plant, the number of primary branches, the number of secondary branches, seed yield per plant, thousand seed weight, and grain yield per hectare. The magnitude of the differences between PCV and GCV was low for all traits, suggesting a high chance of success in identifying genotypes to be

developed as new varieties through selection based on phenotypic expression. In agreement with these study results, Yadav et al. [23] reported a high estimate of PCV along with GCV in fenugreek genotypes for most traits. Panwar et al. [24] reported high estimates of PCV and GCV for the number of pods per plant. Dashora et al. [25] also reported high GCV for the number of pods per plant. Pathak et al. [26] and Singh et al. [27] reported high PCV for seed yield per plant and the number of pods per plant. In addition, Singh et al. [27] reported high PCV for the number of secondary branches, number of primary branches, and number of seeds per pod.

**4.2. Heritability in a Broad Sense and Genetic Advance.** The estimates of heritability in a broad sense for 11 traits of 160 fenugreek accessions ranged from 60.98 to 96.05%, while estimates of expected genetic gain as percent mean ranged from 2.53 to 70.33% (Table 3). According to Johnson et al. [11] and Robinson et al. [28], heritability values < 30, 30 to 60, and >60% are categorized as low, moderate, and high, respectively, while according to Pramoda and Gangaprasad [29], heritability estimates should be classified as low (<40%), medium (40–50%), moderately high (60–79%), and very high ( $\geq 80\%$ ). Accordingly, the estimates of heritability in a broad sense for 11 traits of the 160 fenugreek accessions in the present study could be categorized as high according to Pramoda and Gangaprasad, which suggests that selection could be fairly easy and improvement is possible using selective breeding for these traits.

Falconer and Mackay [30], Deshmukh et al. [22], and Johnson et al. [11] classified genetic advance having the percent of mean as low (<10%), moderate (10–20%), and high (>20%). Accordingly, the estimates of genetic advance as percent of the mean for 11 traits of 160 fenugreek accessions could be categorized as moderate to high. It was suggested that the importance of considering both the genetic advance and heritability of traits is indicative of the progress that could be made through selection [31]. In this study, high heritability accompanied by high genetic advance was observed for the number of pods per plant, the number of seeds per pod, the number of primary branches, the number of secondary branches, and seed yield per plant. For other traits, including average pod length, plant height at flowering, the number of seeds per pod, and thousand seed weight, high heritability was coupled with moderate genetic advance. This indicates that the traits considered in this study were highly heritable and the selection of high-performing genotypes is possible to improve the traits. The high heritability of these traits is due to the relatively small contribution of the environment to the phenotype and most likely due to additive gene effects [32, 33].

The present study results agree with the results reported by Jain et al. [34] that high heritability was coupled with high genetic advance for the number of pods per plant and seed yield per plant in 50 diverse genotypes from different geographic and genetic origins. While Mishra [35] reported that high heritability was coupled with high genetic advance for the number of primary branches and the number of pods

per plant in 16 fenugreek accessions collected from diverse geographic regions. They also reported that high heritability was coupled with moderate genetic advance for average pod length, plant height at flowering, and the number of seeds per pod. Kumar et al. [31] and Prajapati et al. [36] also reported low genetic advance as the mean for days to flowering. Pathak et al. [26] and Singh [20] reported that high percent of heritability for the variables the number of pods per plant and the number of primary branches.

**4.3. Correlation Coefficient of Grain Yield with Other Characters.** Grain yield per hectare had a positive and highly significant ( $p \leq 0.01$ ) correlation coefficient with the number of pods per plant at both genotypic and phenotypic levels (Table 4). This indicates that plants bearing many pods per plant will give higher seed yield per plant, leading to high seed yield per hectare. Thus, selection for the number of pods per plant alone leads to improvement in grain yield per hectare. In addition, grain yield per hectare was positively and significantly ( $p \leq 0.05$ ) correlated—both at the genotypic and phenotypic levels—with the number of secondary branches, the number of primary branches, and seed yield per plant. This indicates that more branching can hold many pods per plant that lead to high seed yield per plant.

In Ethiopia, Wojo et al. [7] and Maurya et al. [37] conducted studies of the associations between traits in fenugreek. These authors reported similar results to the current study that seed yield had a positive and significant association with the number of branches and the number of pods per plant. In addition, many authors [26, 34, 36–39] reported a positive and significant association between seed yield with the number of pods per plant, the number of secondary branches, the number of primary branches, and seed yield per plant. At genotypic and phenotypic levels, others have reported positive and significant correlations with seed yield in fenugreek, such as Maurya et al. [37] for several branches per plant and pods per plant and Kole and Saha [39] for several pods per plant. These authors suggested that the selection of accessions based on high mean values for numbers of primary branches, secondary branches, seed yield per plant, and the number of seeds per pod is akin to the selection of genotypes for high seed yield. Average pod length showed a negative and significant ( $p \leq 0.01$ ) correlation with grain yield per hectare both at genotypic and phenotypic levels (Table 4). This suggests that the selection of fenugreek accessions with high mean values of pod length should not be used for yield improvement. Based on the present study, the selection of fenugreek accessions for high mean values of average pod length should not be used as a criterion to improve seed yield. Contradicting the current study, Singh and Pramilla [40] and Sharma and Sastry [41] reported a positive and significant association of average pod length with seed yield among fenugreek accessions.

**4.4. Phenotypic and Genotypic Path Analysis.** Path analysis was conducted to partition the genotypic and phenotypic correlation coefficients of traits into direct and indirect effects on the grain yield. The results of genotypic path

analysis are presented in Table 5, and the results of phenotypic path analysis are presented in Table 6. Seed yield per plant, the number of secondary branches, and the number of pods per plant exerted a positive direct effect on the grain yield both at genotypic and phenotypic levels and had a positive and significant genotypic and phenotypic correlation with the yield. This indicates that the correlation of these traits with the grain yield was largely due to the direct effect and that selection based on these traits is predicted to improve grain yield. This result is supported by several previous studies in which the same traits had positive direct effects on the grain yield of fenugreek, such as Singh and Kakani [42] for the number of pods per plant and number of secondary branches and Yadav et al. [23] for number of pods per plant and number of branches.

Although the number of primary branches exhibited a positive and significant genotypic and phenotypic correlation with the yield, this trait exerted a high and negative direct effect on the grain yield both at genotypic and phenotypic levels. The number of primary branches had a positive indirect effect on the yield via average pod length, the number of secondary branches, and the number of pods per plant both at genotypic and phenotypic levels. This indicates that selection based on the number of primary branches would lead to a selection of accessions with low grain yield; therefore, the selection of genotypes for high grain yield should be through the selection of traits in which this trait exerted a high indirect effect on the yield. Wojo et al. [7] also reported that the number of primary branches had a negative direct effect on the grain yield phenotypically but a positive direct effect on the grain yield genotypically. The results partially agree with Singh and Kakani's study [42], which reported a high and negative direct effect of the number of primary branches on the grain yield both at genotypic and phenotypic levels.

Average pod length had negative and significant genotypic and phenotypic correlations with the yield. In addition, average pod length exerted a negative direct effect on the grain yield at both genotypic and phenotypic levels, indicating that it is difficult to enhance grain yield through selection based on average pod length. Similarly, Yadav et al. [23] reported that average pod length had a negative direct effect on the grain yield at the phenotypic level.

The residual effect was low for both genotypic and phenotypic levels (0.13 and 0.12 s, respectively) indicating that the 11 traits included in this study account for almost all variation in seed yield per hectare. In other words, the total genotypic and phenotypic variation explained 87% and 88% of the variation in the grain yield.

*4.5. Distance Analyses Based on the Geographic Origin.* Eight geographical regions were used to classify the accessions. A total of 14 groups were analyzed, together with the five checks and the mean of the released varieties, to determine the correlation between accessions based on their geographic origins for 11 agromorphological traits. To calculate genetic distance in terms of Euclidean distances, the mean values of each group and variety were utilized

(Table 7 and Figure 1). The genetic distance between accessions from southwestern Ethiopia and all other groups was the greatest, ranging from 3.01 to 3.88. The central Ethiopian accessions, however, had the closest genetic kinship to the majority of other groupings, with a mean ED of 2.06. The mean ED of the newly released accessions Hundao'la (2.84) and Ebbisa (2.78) from eastern (2.7) and southeastern Ethiopia (2.57) was higher than the mean ED of all clusters combined. These groups of accessions and newly released varieties could be thought of as being further away from other groups of accessions. Typically, the geographic regions where the accessions were collected were used to classify them.

Genetic distance analyses revealed that geographic location was one of the factors that affected the diversity of accessions either by facilitating free exchange of accessions between close geographic regions (for example, western, southwestern, northwestern, northern, and northeastern Ethiopia are all relatively close) or by impeding exchange between distant geographic regions (as between southwestern and eastern Ethiopia). The findings of the present study are consistent with those of Refs. [43, 44] who found that fenugreek genotypes from various geographic origins are quite diverse and suggested that crop improvement might be achieved by hybridization and accessions chosen from various clusters. Meena et al. [45] and Sefidan et al. [46], in contrast, showed that fenugreek genotypes from various geographic regions lacked genetic difference.

## 5. Conclusions

Accordingly, the highest values of genotypic and phenotypic coefficients of variations were estimated for the number of pods per plant. Moreover, high values of broad sense heritability were accompanied by high values of genetic advance for multiple traits, including the number of pods per plant, the number of seeds per pod, the number of primary branches, the number of secondary branches, and seed yield per plant. This indicates that these traits are highly heritable and the selection of high-performing genotypes is possible for the improvement of these traits. However, both the same values were low for other characters, indicating the higher influence of environmental factors on the expression of those traits, suggesting it would be difficult to improve based on the selection of genotypes for high mean values.

Grain yield per hectare had a significant positive association with the number of pods per plant, the number of secondary branches, the number of primary branches, and seed yield per plant at both genotypic and phenotypic levels. Thus, the selection of these traits can lead to improvement in grain yield per hectare. Moreover, seed yield per plant, the number of secondary branches, and the number of pods per plant exerted a positive direct effect on the grain yield both at genotypic and phenotypic levels, indicating that direct selection for these traits will improve the grain yield. Other traits, such as average pod length, had a negative and significant association with the grain yield, suggesting that selection based on this trait would not result in the improvement of yields.



Genetic distances among accessions were calculated as estimated interims of Euclidean distances. A total of 160 accessions of fenugreek were grouped into clusters based on the Euclidean distance matrix, and a dendrogram was constructed using the unweighted pair group method with arithmetic means (UPGMA). The clustering of accessions based on geographic origins revealed that much of the diversity was based on the origin. Accessions from south-western Ethiopia showed the maximum genetic distance from all other groups, ranging from 3.01 to 3.88. In contrast, accessions from central Ethiopia had lower genetic distances than most of the other groups, with a low mean ED of 2.06. This showed that geographical location has been an important factor that contributes to diversity by enhancing the possibility of the free exchange of proximate breeding materials or hindering movement due to distance.

Generally, the results of this analysis indicate that the accessions of fenugreek were diverse and suggested possibilities to improve the crop through the crossing of distant genotypes or direct selection of accessions for the high mean performance of traits of interest. However, as the evaluation of accessions was conducted in one location and one year, it is recommended that the experiment should be repeated at more locations over years to confirm the results reported here. Nevertheless, there is an excellent opportunity to contribute to farmers' food security and livelihoods by bringing about the improvement of fenugreek through selection and hybridization and by crossing distant accessions from different clusters with different combinations of advantageous traits.

## Data Availability

The data are not included due to third party right.

## Conflicts of Interest

The authors declare that they have no conflicts of interest.

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