Journal of Plant Breeding and Crop Science Vol. 4(3), pp. 39-48, 23 February, 2012
Available online at http://www.academicjournals.org/JPBCS
DOI: 10.5897/JPBCS11.078
ISSN 2006-9758 © 2012 Academic Journals

*Full Length Research Paper*

# Genetic variability of Ethiopian fenugreek (*Trigonella foenum-graecum* L.) landraces

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Accepted 20 February, 2012

**Keeping in view the lack of information on genetic diversity in Ethiopian, 144 random samples of fenugreek accessions with standard check were used to determine the extent and pattern of genetic diversity and associations with their geographic origins. The field experiment was conducted at Adadi and Ambo during 2006 and 2007 cropping seasons. Treatments were arranged in a 12 ×12 simple lattice design and data were subjected to the ANOVA performed by the SAS software. The mean squares of the accessions were highly significant for most of the characters, implying that a wide range of variability has been obtained for the traits studied. The GCV ranged from 1.65 to 68.95%, while the PCV from 3.30 to 158.06%. The estimated broad sense heritability ranged from 2.92 to 82.02%. The first four PC accounted for more than 88% of the total variation. The 144 germplasm materials were grouped into six clusters based on Mahalanobis' $D^2$ statistic. It was asserted that geographic diversity should not necessarily be used as an index of genetic diversity and parental selection but should be based on systematic study of genetic diversity in a specific population.**

**Key words:** Genetic variability, *Fenugreek, Trigonella foenum-graecum L., Landraces.*

## INTRODUCTION

The genus *Trigonella* is one of the largest genera of the tribe *Trifoliate* in the family Fabaceae and sub-family Papilionaceae (Balodi and Rao, 1991). Among *Trigonella* species, *Trigonella foenum-graecum* (commonly known as fenugreek) is an annual species, with autogamous flowers occasionally visited by insects. It is indigenous to countries on the Eastern shores of the Mediterranean, but widely cultivated in India, Egypt, Ethiopia, Morocco and occasionally in England (Polhil and Raven, 1981; Davoud et al., 2010). The principal use of fenugreek in Ethiopia includes: 1) as a rotation crop, it improves both the soil structure and fertility; 2) it also fetches high revenue for farmers and producers; 3) its flour is used as a flavoring of the traditional bread (loaf) and maintains soft texture of "*tef-injera*" in relatively cooler zones of the country where the latter is a staple food (Jemal, 1998). The flour of fenugreek is used in various spice makings. In a typical case of such a use, the powder is soaked over-night and the water poured off the next morning while the remnant is mixed with honey which becomes a delicious beverage. In the absence of milk, fenugreek is a substitute of infant feed.

The production distribution of fenugreek in Ethiopia is nearly similar to those of other cool season food legumes such as fababean, field pea, lentils, chickpea, and grass pea, etc. Its cultivation and economic importance in the Ethiopian agriculture date back to a long period of history. Although, the present production scale makes it rank 6$^{th}$ among the highland pulses. Fenugreek stands as number one in generating cash. Thus, improving this crop means opening a new vista of market opportunity in the face of the ever expanding world trade for the country in general and for the resource-poor farmer in particular. One additional advantage of fenugreek is the wide variety of its uses at different crop stages such as green manuring, leaf vegetable and seed production for the international market of condiments or feed (Beyene, 1965).

Knowledge of the extent and pattern of variability particularly of genetic variability present in a population of

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a given crop is indisputably essential for further improvement. As is true for a long list of plant species, Ethiopia is endowed with a bounty of genetic resources also for fenugreek which, nevertheless, is still being cultivated using age-old methods of farming without any significant coverage of better cultivars developed through intentional and systematic selection other than the one made by nature.

Further neglect and under-use of this locally important crop will inadvertently entail the risk of loosing some important germplasm material that has been developed over thousands of years of cultivation. One important factor, however, restricting its large-scale production and development of better varieties is that very little information is available about its genetic diversity. Therefore, in order to best exploit the available genetic wealth, unraveling the information on the extent and nature of genetic diversity of the population and the inter-relationships among characters that would help in formulating efficient scheme of selection based on multiples of traits is of utmost importance. However, only little of such vital information on fenugreek landraces is present under Ethiopian conditions. In view of filling up such a technical gap, this piece of research work was conceived to address the major objectives subsequently given. To determine the extent and pattern of genetic diversity for morpho-physiological traits and associations between the geographic origins of the germplasm and genetic diversity and to establish such fundamental genetic facts as heritabilities and covariances of traits is of interest for further improvement of the crop.

## MATERIALS AND METHODS

The field experiment was conducted at two locations in Ambo and Adadi during 2006 and 2007 main cropping seasons. Ambo has an altitude of 2300 m.a.s.l. and average annual rainfall of 1000 mm, while Adadi has an altitude of 2050 m.a.s.l. and average annual rainfall of 900 mm. The soil at Ambo is characterized as a vertisol with a pH of 6.1 while that of Adadi is light vertisol with a pH of 7.5.

One hundred and forty-three random samples of fenugreek accessions along with one commercial variety (*Challa*) were considered in this study. The accessions were collected by the Institute of Biodiversity Conservation (IBC) from the most important production complexes of Ethiopia representing different agro-ecologies of varying altitude, rainfall, temperature and soil type.

Treatments were arranged in a 12 × 12 simple lattice design. Seeding was done in a plot of four rows with 2 m length and regular spacing of 10 cm between plants and 25 cm between rows. The layout and randomization were as per the standard procedure set by Cochran and Cox (1957). Two seeds per hole were placed carefully to ensure the first germination. Thinning was made at the true leaf stage. Weeding and other cultural practices were done as per the recommendations adopted for the respective sites.

The following data were collected in both 2006 and 2007 either from the whole plot or from ten plants sampled randomly from each plot with respect to days prior to flowering, plot uniformity, thousand seed weight, number of pods per plant, plant height, number of seeds per plant, number of seeds per pod, seed colour, seed shape, seed yield/plant, biomass yield per plot and per plant, harvest index. Before proceeding with the analysis of variance for each variable, tests were made for homogeneity of variances using the $F_{max}$ test. The data were subjected to the analyses of variance (ANOVA) and combined analysis of variance over environment for simple lattice design was performed using the SAS program software (SAS, 1996). The total variability for the traits was quantified using pooled analyses of variance over two years and locations using the following model:

$$P_{ijmkt} = \mu + y_m + l_t + r_{i(m)(t)} + b_{j(i)(t)(m)} + g_k + (gy)_{km} + (yl)_{mt} + (gl)_{kt} + (ylg)_{mtk} + e_{ijmkt}$$

where $P_{ijmkt}$ = phenotypic value of $k^{th}$ genotype under $i^{th}$ replication during $m^{th}$ year at $t^{th}$ location and $j^{th}$ incomplete block with replication i, location t and year m; $y_m$= $m^{th}$ year; $l_t$= $t^{th}$ location; $r_{i(m)(t)}$ = the effect of replication i with in year m and location t; $b_{j(i)(t)(m)}$ = the effect of incomplete block j with in replication i, location t and year m; $g_k$ = the effect of $k^{th}$ accession; $\mu$= grand mean and $(gy)_{km}$, $(yl)_{mt}$, $(gl)_{kt}$ and $(ylg)_{kmt}$ = the interaction effects and $e_{ijmkt}$ = random error.

Partitioning of the total variation into components due to genotype ($\sigma_g^2$), environment ($\sigma_e^2$) and genotype by environment interaction ($\sigma_{ge}^2$) deviations was performed from the analyses of variance by calculating the expected mean squares and similarly, the components from pooled analysis of variance over years and locations were calculated. The coefficients of variations at phenotypic and genotypic levels were estimated using the formula adopted by Johnson et al. (1955) as:

$$PCV = [\sigma p / \bar{X}] \times 100$$

$$GCV = [\sigma g / \bar{X}] \times 100$$

Where σp = phenotypic standard deviation (σg + σe), σg= genotypic standard deviation, σe= environmental standard deviation and $\bar{X}$ = grand mean for the character x; PCV and GCV = phenotypic and genotypic coefficients of variation, respectively.

### Estimate of heritability

Broad-sense heritability ($h^2$) for traits was estimated for pooled analyses over two years and locations using the formula adopted by Allard (1960) as:

$$h^2 = \left[ \frac{\left(\sigma^2 g\right)}{\sigma^2 g + \sigma^2 gl/l + \sigma^2 gy/y + \sigma^2 gyl/yl + \sigma^2 r/lyr} \right] \times 100$$

Where $\sigma^2 g$ = genotypic variance, $\sigma^2 gl$= genotype by location variance, $\sigma^2 gy$ = genotypic by year variance, $\sigma^2 gyl$ = genotypic by year and location variance, $\sigma^2 r$ = replication variance, y= number of year, l= number of locations and r= number of replications.

Genetic advance in absolute unit (GA) and percent of the mean (GAM), assuming selection of the superior 5% of the genotypes, was estimated in accordance with the methods illustrated by Johnson et al. (1955) as:

$$GA = k\sigma p h^2$$

$$GAM = (GA / \bar{X}) \times 100$$

Where k = the standardized selection differential at 5% selection intensity (k = 2.063), σp = phenotypic standard deviation, $h^2$ = heritability and $\bar{X}$= Grand mean.

Genetic diversity between clusters based on correlation matrix was calculated using the SAS software package (SAS Institute, 1996).

**Table 1.** Analysis of variance for 9 traits of *T. foenum-graecum* landraces tested over two cropping seasons (2006 to 2007) and two locations (Adadi and Ambo).

| Traits | MSY (1)[β] | MSL (1) | MSR (1) | MSB (22) | MSG (143) | MSYL (1) | MSYG (143) | MSLG (143) | MSYLG (142) | MSE | CV (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| DF | 11413.472** | 597.879** | 0.116 $^{ns}$ | 16.585** | 12.746** | 1.104 $^{ns}$ | 13.854** | 9.5211** | 6.782 $^{ns}$ | 5.905 | 4.78 |
| PH | 35259.984** | 4.029 $^{ns}$ | 576.410** | 41.555* | 51.070** | 29608.629** | 17.646 $^{ns}$ | 17.704 $^{ns}$ | 28.754 $^{ns}$ | 24.404 | 14.67 |
| BMY | 7.573** | 20400.140** | 2.836* | 0.191* | 0.168** | 16908.312** | 0.066 $^{ns}$ | 0.070 $^{ns}$ | 0.152** | 0.274 | 18.85 |
| PPP | 56.723** | 2296.275** | 2205.85** | 1.039** | 0.667** | 12190.713** | 0.085 $^{ns}$ | 0.557** | 0.129$^{ns}$ | 0.397 | 15.73 |
| SPPL | 2292.350** | 1786759.95** | 6823.351* | 49.094 $^{ns}$ | 48.288* | 4168012.78** | 26.156 $^{ns}$ | 23.615$^{ns}$ | 5104.086** | 5.464 | 17.74 |
| SPP | 0.208 $^{ns}$ | 168.150** | 35.843** | 0.304** | 0.193** | 178.549** | 0.059 $^{ns}$ | 0.098$^{ns}$ | 0.087 $^{ns}$ | 0.291 | 16.32 |
| TSW | 1542.03** | 1216.57** | 68.84** | 6.30$^{ns}$ | 14.41** | 231.90** | 3.90$^{ns}$ | 4.81$^{ns}$ | 5.61$^{ns}$ | 4.281 | 11.90 |
| SY | 0.681** | 1698.739** | 0.384$^{*}$ | 0.013 $^{ns}$ | 0.017* | 1915.712** | 0.011$^{ns}$ | 0.009 $^{ns}$ | 0.024** | 0.103 | 18.51 |
| HI | 9312.604 ** | 665.136 ** | 499.636 ** | 30.774 $^{ns}$ | 43.251$^{ns}$ | 65.111 $^{ns}$ | 34.268 $^{ns}$ | 37.068 $^{ns}$ | 36.415 $^{ns}$ | 35.165 | 14.98 |

*, ** Significant at 0.05 and 0.01 probability level respectively and $^{ns}$ non -significant. MSY=Mean Square due to year, MSL=Mean Square due to location, MSR=Mean Square due to replication, MSB=Mean Square due to block, MSG=Mean Square due to genotypes, MSYL=Mean Square due to the interaction between year and location, MSYG=Mean Square due to the interaction between year and genotypes, MSLG=Mean Square due to the interaction between location and genotypes, MSYLG = Mean Square due to the interaction between year and location and genotypes, MSE=Mean Square due to error, CV%=Coefficient of variation in percentage. [β] Figures in parenthesis indicate degrees of freedom. DF=days to 50% flowering, PH=Plant height in cm, BMY=Biomass yield in g per plant, PPP=number of pods per plant, SPPL=Number of seeds per plant, SPP=Number of seeds per pod, TSW= thousand seeds weight in gram, SY=Seed yield in g per plant, HI=Harvest index in percentage.

Thus the analysis was computed based on multivariate analysis using Mahalanobis $D^2$ statistic (Mahalanobis, 1936). The important traits in each principal component that significantly contributed to the variation observed were identified as suggested by Johonson and Wichern (1988). Squared distance ($D^2$) for each pair of genotype combinations was computed using the following formula:

$$D^2_{ij} = (X_i - Xj)\, S^{-1}\, (X_i - X_j)$$

Where $D^2_{ij}$ = the square distance between any two genotypes i and j, $X_i$ and $X_j$ = the vectors of values for the $i^{th}$ and $j^{th}$ genotypes, and $S^{-1}$ = the inverse of pooled variance covariance matrix (Singh and Chaudhary, 1999). Based on the squared distances ($D^2$), clustering of genotypes was done using Tocher's method as described by Singh and Chaudhary (1999).

## RESULTS AND DISCUSSION

Results from the analysis of variance, using simple lattice design, are given in Table 1. In order to assess the extent to which the observed variation is due to genetic effect, parameters like estimates of minimum, mean and maximum values, variances and coefficients of variation at phenotypic ($\sigma^2 p$) and genotypic ($\sigma^2 g$) levels, heritability in broad sense ($h^2$), expected genetic advance in absolute (GA) and as percent of mean (GAM) for the nine traits of the accessions of *T. foenum-graecum* tested are presented in Table 2. The detail accounts of each of these are discussed.

Before proceeding with the analysis of variance, test was made to confirm the homogeneity of variances which all turned out to be so. It can be seen from Table 1 that the mean squares due to year were significant (P≤0.05) for all traits except number of seeds per pod. Similarly, with the exception for plant height, the mean squares due to location were highly significant for all traits indicating that there are differences between the four environments, which are significant enough to see the genetic performance of fenugreek germplasm. It is evident from the results that mean squares due to genotypes were significant for all traits except for harvest index, indicating the existence of sufficient genetic variability which is in consistent with the reports of Davoud et al. (2010).

Mean squares due to the interaction between year and location were highly significant for all the traits studied, except for days to flowering and harvest index. Mean squares due to the interaction between location and genotype were non-significant for all traits, except for days to flowering and number of pods per plant. Mean squares due to the interaction between year, location and genotype were highly significant for biomass yield, number of seeds and seed yield per plant, whereas for the rest of the traits studied, it was non-significant difference.

The Ethiopian fenugreek landraces evaluated in this study showed significant phenotypic variability in terms of plant morphology, phenology and yield attributes. These results are similar with the findings of other scholars like Banyai (1973),

**Table 2.** Estimates of minimum, mean and maximum value, variance and coefficient of variation at phenotypic ($\sigma^2p$), genotypic ($\sigma^2g$) level, heritability in broad sense ($h^2$%), genetic advance in absolute (GA) and percent of mean (GAM) for nine traits of *T. foenum-graecum.*

| Trait | Minimum | Mean | Maximum | $\sigma^2p$ | $\sigma^2g$ | GCV (%) | PCV (%) | $h^2$ (%) | GA | GAM |
|---|---|---|---|---|---|---|---|---|---|---|
| DF | 47.68 | 50.87 | 54.36 | 7.952 | 1.996 | 2.78 | 5.54 | 14.77 | 0.86 | 1.69 |
| PH | 25.33 | 33.59 | 41.95 | 35.284 | 8.857 | 8.86 | 17.68 | 67.15 | 8.23 | 24.50 |
| BMY | 4.14 | 7.789 | 14.38 | 9.000 | 2.250 | 19.26 | 38.52 | 60.85 | 3.77 | 48.35 |
| PPP | 8.46 | 16.170 | 26.67 | 38.938 | 9.723 | 19.28 | 38.59 | 37.35 | 4.81 | 29.73 |
| SPPL | 89.25 | 174.677 | 268.14 | 3398.89 | 849.468 | 16.69 | 33.38 | 82.02 | 98.64 | 56.47 |
| SPP | 7.16 | 10.988 | 16.27 | 13.250 | 3.299 | 16.53 | 33.13 | 49.40 | 3.71 | 33.76 |
| TSW | 13.75 | 17.39 | 20.99 | 8.880 | 2.226 | 8.58 | 17.14 | 81.97 | 5.04 | 28.98 |
| SY | 1.47 | 3.03 | 4.36 | 1.082 | 0.271 | 17.19 | 34.32 | 74.06 | 1.59 | 52.44 |
| HI | 33.92 | 39.55 | 45.68 | 25.806 | 6.458 | 6.43 | 12.84 | 37.12 | 3.89 | 9.84 |

DF= days to 50% flowering, PH= Plant height in cm, BMY= Biomass yield in g per plant, PPP= number of pods per plant, SPPL= Number of seeds per plant, SPP= Number of seeds per pod, TSW= thousand seeds weight in gram, SY= Seed yield in g per plant, HI= Harvest index in percentage.

Provorov et al. (1996) and Feysal (2006). In this study, the general efficiency of simple lattice design was generally trait specific.

The maximum seed yield per plant (4.36 g) was recorded for the germplasm FgColl53078 and the minimum (1.47 g) for the germplasm FgColl234027 with the over-all mean seed yield per plant of 3.03 g (Data not present). The result from this investigation is in agreement with the previous reports of Cornish et al. (1983), Pant et al. (1983), Schneiter et al. (1994) and Feysal (2006). In general, the accessions showed shorter days to flowering which may be suitable to lower rainfall regions whereas, the late types can be adapted to the highland areas with dependable rainfall. 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. Seed size is associated with seedling vigor, emergence of seed and stress tolerance (McCormick, 2004). Larger seeds have greater cotyledon reserves and therefore, can provide energy to young seedlings at a faster rate. All except FgColl215406, FgColl53078 and FgColl213114 exhibited smooth seed shape/surface, while the rest of the tested material showed wrinkled seed surface. In a similar manner, FgColl215406, FgColl207356, FgColl207376 and FgColl239064 exhibited mixed populations while the rest of the tested material tends to be uniform. From the results, the broad spectrum of variability observed among these collections of fenugreek for different characters generally indicated possibilities for genetic improvement of the crop through selection and cross breeding.

Genotypic coefficient of variation (19.28%) was observed to be high for number of pods per plant followed by biomass yield per plant (19.26%), seed yield per plant (17.19%), and number of seeds per plant (16.69%) and per pod (16.53%), but low for the temporal data such as number of days to flower (2.78%). The estimated values of phenotypic variances were in the range of 1.082 for seed yield per plant to 3398.89 for number of seeds per plant (Table 2). The lowest and highest genotypic variances were found for seed yield per plant (0.271) and number of seeds per plant (849.468), respectively.

The results depicted in Table 2 showed that estimates of heritability in broad sense were high for number of seeds per plant, thousand seed weight, seed yield per plant, plant height and biomass yield per plant. These characters, therefore, may respond effectively to phenotypic selection. Moreover, moderate heritability was observed for number of seeds per pod, number of pods per plant and harvest index. However, low values of heritability were estimated for number of days to flowering, indicating limited possibility of improvement for this character through selection. In earlier studies, high heritability estimates for seed weight (Shukla and Sharma, 1978), seeds per pod, plant height, harvest index and seed yield (Feysal, 2006) were reported. These findings, thus, only partially agree with the results obtained in the present investigation. The probable cause of the disparity could be due to the fact that the heritability of a given trait refers to a particular population under a particular condition or environment. Generally, heritability determines the effectiveness of selection. The effectiveness of selection for a trait depends on the relative importance of the genetic and environmental factors in the expression of phenotypic differences among genotypes in a population. The components of yield that were most heritable in this fenugreek population were plant height, biomass yield and thousand seed weight. Therefore, the simultaneous selection for these traits could lead to an increase in harvest index and seed yield.

Genetic gains expected from selecting the top 5% of the genotypes, as a percent of the mean, varied from 1.69% for days to flower to 56.47% for number of seeds per plant, indicating an increase of 1.69 to 56.47%. The same magnitude can be made by selection based on

**Table 3.** The eigen values and vectors of the correlation matrix for 9 traits of 144 *T. foenum-greacum* landraces.

| Parameter | PRIN1 | PRIN2 | PRIN3 | PRIN4 |
|---|---|---|---|---|
| Eigen value | 3.842 | 2.175 | 1.067 | 0.896 |
| Variance (%) | 42.69 | 24.17 | 11.86 | 9.96 |
| Cumulative | 43.69 | 66.87 | 78.72 | 88.69 |
| **Character** | | | | |
| DF | -0.109 | -0.314 | -0.356 | 0.731 |
| PH | 0.435 | -0.146 | 0.166 | -0.161 |
| BMY | 0.474 | -0.014 | 0.111 | 0.024 |
| PPP | 0.381 | -0.189 | -0.501 | 0.004 |
| SPPL | 0.398 | 0.355 | -0.295 | 0.126 |
| SPP | -0.038 | 0.602 | 0.180 | 0.067 |
| TSW | 0.185 | -0.348 | 0.672 | 0.327 |
| SY | 0.483 | 0.140 | 0.063 | 0.189 |
| HI | -0.031 | 0.464 | 0.086 | 0.539 |

PRIN1, PRIN2, PRIN3, PRIN4 =Principal component 1, 2, 3 and 4 respectively, DF=days to 50% flowering, PH=Plant height in cm, BMY=Biomass yield in g per plant, PPP=number of pods per plant, SPPL=Number of seeds per plant, SPP=Number of seeds per pod, TSW=thousand seeds weight in gram, SY=Seed yield in g per plant, HI=Harvest index in percentage.

these traits under similar conditions in this study. The next better gains were recorded for seed and biomass yield per plant and number of seeds per pod. In contrast, low estimates were obtained for harvest index and days to flowering. The low values of expected genetic advance for the traits like harvest index and days to flowering are due to low variability for the traits indicated by the low GCV and PCV values. This indicates the importance of genetic variability in improvement through selection. This result is also in conformation with that of Feysal (2006). Raghuvanshi and Singh (1984) as well as, Feysal (2006) reported high estimates of genetic advance for plant height and seed weight which were in general in agreement with the results of the present study. Plant height, number of seeds per plant and thousand seed weight had higher estimates of heritability and genetic advance as compared to other yield contributing traits. This suggests that they may serve as important traits in indirect selection for higher seed yield. As observed in the present investigation, the low expected genetic advance for days to flowering and harvest index were due to low variability for the traits. Therefore, if heritability estimates provide basis for selection on phenotypic performance, the estimates of heritability and genetic advance should always be considered simultaneously, as high heritability is not always associated with high genetic advance (Johnson et al., 1955).

In order to assess the pattern of variations, principal component analysis was done by considering all the nine variables simultaneously. Four of the nine principal components accounted for more than 88% of the total variation in the Ethiopian fenugreek landraces (Table 3). The first principal component accounted for 44% of the total variation, while six of the nine traits considered exerted positive effects on this component, the rest three traits exerted negative effects of different magnitudes. Among those traits having positive and greater influence include: seed and biomass yield, plant height, number of seeds and pods per plant in same order. Conversely, days to flowering, number of seeds per pod and harvest index had all negative weights on this component. The second component accounting for an additional 24% of the total variation primarily illustrates the patterns of variations in number of seeds per pod, harvest index, number of seeds per plant and seed yield which were found to have positive impacts on the second component while thousand seed weight, days to flower, number of pods per plant, plant height and biomass yield had negative coefficients. The third principal component accounted for 12% of the total variation and was alluded with the variations in thousand seed weight, number of seeds per pod, plant height and biomass yield exhibiting positive effects on one hand; and number of pods per plant, days to flowering and number of seeds per plant with negative impacts on the other**.** The traits that contributed most for the first principal component (biomass yield per plant and number of pods per plant) were phenotypically negatively associated with the major traits of the second principal component (number of seed per pod and harvest index) (Table 4). This indicates that there is variability among the traits of the fenugreek accessions considered in this investigation.

Genetic diversity plays an important role in plant breeding because hybrids between lines of diverse origin generally display a greater heterosis than those between closely related strains. The average linkage technique of

**Table 4.** Estimates of correlation coefficients at phenotypic (above diagonal) and genotypic (below diagonal) levels of 9 traits in *T. foenum-graecum* landraces.

| Traits | DF | PH | BMY | PPP | SPPL | SPP | TSW | SY | HI |
|---|---|---|---|---|---|---|---|---|---|
| DF | | -0.12* | -0.34** | -0.15* | -0.40** | -0.33** | -0.14* | -0.39** | -0.06 |
| PH | -0.21* | | 0.50** | 0.54** | 0.41** | -0.17** | 0.33** | 0.48** | -0.19** |
| BMY | -0.17* | 0.82** | | 0.60** | 0.86** | 0.32** | 0.60** | 0.93** | -0.25** |
| PPP | 0.05 | 0.62** | 0.61** | | 0.59** | -0.37** | 0.25** | 0.59** | -0.22** |
| SPPL | -0.26** | 0.55** | 0.74** | 0.53** | | 0.45** | 0.26** | 0.90** | 0.03 |
| SPP | -0.31** | -0.15 | 0.07 | -0.54** | 0.36** | | 0.04 | 0.38** | 0.24** |
| TSW | 0.09 | 0.45** | 0.43** | 0.13 | -0.14 | -0.31** | | 0.60** | -0.08 |
| SY | -0.22** | 0.75** | 0.91** | 0.57** | 0.82** | 0.17* | 0.38** | | -0.02 |
| HI | -0.15 | -0.23** | -0.16 | -0.18* | 0.23** | 0.42** | -0.16 | 0.12 | |

*, **Significant at 0.05 and 0.01 probability level respectively. DF=days to 50% flowering, PH=Plant height in cm, BMY= Biomass yield in g per plant, PPP=number of pods per plant, SPPL=Number of seeds per plant, SPP=Number of seeds per pod, TSW=thousand seeds weight in gram, SY=Seed yield in g per plant, HI=Harvest index in percentage.

clustering produced a more understandable portrayal of the 144 fenugreek accessions by grouping them into six clusters, whereby different members within a cluster is being assumed to be more closely related in terms of the trait under consideration with each other than those members in different clusters. Similarly, members in clusters with non-significant distance were assumed to have more close relationship with each other than they are with those in significantly distant clusters. Table 5 indicates the range (minimum and maximum), mean, standard deviation and CV% of genetic divergence in morphological and seed traits of the six clusters and Table 6 showed grouping of the accessions into different diversity classes. The detail account of the characteristics of each cluster is presented:

**Cluster I:** It consisted of 52 landraces which were collected from the entire regions of collection. Members in this cluster laid on intermediate value in all the traits under consideration.

**Cluster II:** It consisted of 58 landraces, which were early in days to flowering, tall in height, intermediate in biomass yield, number of pods and seeds per plant and number of seeds per pod. Accessions in this cluster also exhibited high, with thousand seed weight, seed yield per plant and harvest index.

**Cluster III:** It consisted of 12 landraces characterized by intermediate in days to flowering; low in seed and biomass yield and number of seeds and pods per plant. Accessions in this cluster also exhibited intermediate, in plant height, number of seeds per pod and harvest index; high in thousand seed weight.

**Cluster IV:** It had 17 landraces which exhibited early growth periods of days to flowering; low in thousand seed weight and intermediate in both biomass yield and number of pods per plant. These accessions also exhibited higher values of seed bearing traits such as seed yield per plant, number of seeds per pods and per plant, harvest index and exhibited taller in plant height.

**Cluster V:** It consisted of four landraces, two collected from Central Tigrai and each one from East Tigrai and West Hararghe. The accessions under this category were relatively inferior in most of the traits investigated. It was characterized by intermediate days to flowering; exhibited lowest in all traits under studied except thousand seed weight and harvest index which exhibited higher value

**Cluster VI:** It consisted of one landrace from South Wello. It was found to be the most superior accession regarding the traits studied. This accession was characterized by low in thousand seed weight and harvest index. However, this particular accession also required longer period to flower and gave higher in plant height, seed and biomass yield per plant, number of seeds and pods per plant and seeds per pod.

In general, the differences between the clusters were mainly attributed to the variation in thousand seed weight. Other traits such as days to flowering, biomass yield and number of seeds per plant have contributed equally well for cluster constellations. In addition, these traits were also the major contributors to the principal one and two. From the estimated distance analysis, under this investigation, out of fifteen possible pairs of clusters, differences between thirteen pairs were highly significant ($P \leq 0.01$) and one pairs were significant ($P \leq 0.05$) while between the rest (one pair) of cluster was non-significant (Table 7). The details of each pair of cluster distances are discussed.

The maximum distance was found between cluster five and six ($D^2$=497.26). Cluster five constitutes accessions from West Hararghe, Central and East Tigrai

**Table 5.** Mean and range of genetic divergence in morphological and seed traits of the nine clusters of *T. foenum-graecum*.

| Character | Cluster | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | I | | | | | II | | | | | III | | | | |
| | Min. | Mean | Max. | SD | CV (%) | Min. | Mean | Max. | SD | CV (%) | Min. | Mean | Max. | SD | CV (%) |
| DF | 47.68 | 51.17 | 54.36 | 1.41 | 2.76 | 48.15 | 50.73 | 53.67 | 1.38 | 2.72 | 50.27 | 51.13 | 52.44 | 0.74 | 1.45 |
| PH | 28.64 | 33.21 | 38.98 | 2.96 | 8.91 | 29.80 | 34.88 | 41.95 | 2.61 | 7.48 | 26.69 | 30.02 | 33.93 | 2.38 | 7.93 |
| BMY | 4.97 | 7.23 | 9.39 | 1.50 | 20.75 | 6.30 | 8.57 | 14.38 | 1.29 | 15.05 | 4.34 | 5.81 | 7.34 | 0.84 | 14.46 |
| PPP | 11.37 | 15.76 | 21.61 | 3.12 | 19.80 | 12.33 | 17.48 | 22.09 | 2.18 | 12.47 | 9.00 | 11.32 | 14.97 | 1.57 | 13.87 |
| SPPL | 142.72 | 159.57 | 172.53 | 29.15 | 18.27 | 174.92 | 188.27 | 209.80 | 8.08 | 4.29 | 116.58 | 126.82 | 139.10 | 7.80 | 6.15 |
| SPP | 7.16 | 10.28 | 13.99 | 1.82 | 17.70 | 7.87 | 10.98 | 15.18 | 1.51 | 13.75 | 8.79 | 11.34 | 14.14 | 1.57 | 13.84 |
| TSW | 13.75 | 17.54 | 20.42 | 1.49 | 8.49 | 14.47 | 17.51 | 20.99 | 1.46 | 8.34 | 16.20 | 17.56 | 19.24 | 1.05 | 5.98 |
| SY | 2.13 | 2.81 | 3.51 | 0.52 | 18.51 | 2.71 | 3.31 | 4.04 | 0.32 | 9.67 | 1.85 | 2.24 | 2.46 | 0.19 | 8.48 |
| HI | 33.92 | 38.97 | 44.21 | 2.54 | 6.52 | 35.12 | 39.71 | 45.04 | 2.39 | 6.02 | 35.46 | 39.61 | 42.53 | 2.19 | 5.53 |
| | IV | | | | | V | | | | | VI | | | | |
| DF | 47.89 | 49.97 | 51.84 | 1.14 | 2.28 | 50.12 | 51.67 | 53.55 | 1.51 | 2.92 | - | 52.27 | - | - | - |
| PH | 31.08 | 34.02 | 39.50 | 2.22 | 6.53 | 25.33 | 27.84 | 31.20 | 2.86 | 10.27 | - | 36.51 | - | - | - |
| BMY | 7.39 | 8.67 | 11.46 | 1.17 | 13.49 | 4.14 | 5.11 | 6.26 | 0.92 | 18.00 | - | 11.18 | - | - | - |
| PPP | 13.75 | 17.28 | 26.67 | 3.10 | 17.94 | 8.46 | 10.48 | 12.71 | 1.75 | 16.70 | - | 23.61 | - | - | - |
| SPPL | 209.89 | 219.51 | 235.72 | 7.28 | 3.32 | 89.25 | 103.66 | 110.27 | 9.72 | 9.38 | - | 268.14 | - | - | - |
| SPP | 9.17 | 13.25 | 16.27 | 1.85 | 13.96 | 8.17 | 9.54 | 10.58 | 1.02 | 10.69 | - | 11.28 | - | - | - |
| TSW | 14.70 | 16.35 | 18.92 | 1.25 | 7.65 | 16.11 | 17.94 | 19.78 | 1.81 | 10.09 | - | 16.32 | - | - | - |
| SY | 3.08 | 3.56 | 4.36 | 0.36 | 10.11 | 1.47 | 1.88 | 2.17 | 0.31 | 16.49 | - | 4.31 | - | - | - |
| HI | 37.43 | 41.05 | 45.68 | 2.67 | 6.50 | 35.42 | 38.00 | 41.23 | 2.86 | 7.53 | - | 40.42 | - | - | - |

Min, Mn and Max stands for minimum, mean and maximum value, SD= standard deviation, DF= Days to 50% flowering, PH=Plant height in cm, BMY=Biomass yield in g per plant, PPP=number of pods per plant, SPPL=Number of seeds per plant, SPP=Number of seeds per pod, TSW=thousand seeds weight in gram, SY=Seed yield in g per plant, HI=Harvest index in percentage.

respectively, while cluster six constitutes a single accession from South Wello (Table 6). The second most divergent clusters were cluster three and six ($D^2$= 380.79). Cluster three constitutes 12 accessions collected from Arssi (2 accessions), South Tigrai (1 accession), South Wello (1 accession), East Gojam (3 accessions), North Gondar (3 accessions), North shoa (1accession) and the commercial variety, *Challa*.

The third most divergent clusters were cluster four and five ($D^2$=243.32). Cluster four constitutes 17 accessions from North Shoa (four accessions), Bale (six accessions), South Wello (two accessions), North Gondar (two accessions), East Hararghe (one accession), East Gojam (one accession) and Arssi (one accession). The forth most divergent clusters were between cluster one and six ($D^2$=229.52), cluster one was constituted from 52 accessions from all region under consideration for the study followed by cluster four and three ($D^2$=153.75), cluster two and five ($D^2$=138.66), cluster two and six ($D^2$=135.98), cluster two and three ($D^2$=73.86).

Genotypes grouped into the same cluster presumably diverge little from one another as the aggregate characters are measured. Generally, maximum genetic segregation and genetic recombination is expected from crosses that involve parents from the clusters characterized by significant distances. In the present investigation,

**Table 6.** Grouping of 144 Ethiopian *T. foenum-graecum* landraces into different clusters and collection regions.

| Cluster | Number of accessions | Accessions included | Origin |
|---|---|---|---|
| $C_1$ | 52 (36.11%) | FgColl53072, FgColl53075, FgColl216897, FgColl53006 | Arssi |
| | | FgColl53064, FgColl230072, FgColl230073 | Bale |
| | | FgColl234028, FgColl234033, FgColl237511, FgColl207599, FgColl234024, FgColl234025, FgColl234026 | Central Tigrai |
| | | FgColl212775, FgColl212776, FgColl236622, FgColl53050, FgColl239062 | East Gojam |
| | | FgColl53017, FgColl230880 | East Hararghe |
| | | FgColl234030, FgColl234031, FgColl234034 | East Tigrai |
| | | FgColl241140 | Jijiga |
| | | FgColl53005, FgColl207376, FgColl207370 | North Gondar |
| | | aFgColl53086, FgColl53087, FgColl53088, FgColl53106, FgColl212550 | North Shoa |
| | | FgColl53007, FgColl215261 | North Wello |
| | | FgColl53009 | South Gonder |
| | | FgColl207360 | South Tigrai |
| | | FgColl53014, FgColl53102, FgColl215729, FgColl215731, FgColl226090, FgColl53019, FgColl213110, FgColl213115 | South Wello |
| | | FgColl53096 | West Gojam |
| | | FgColl53016, FgColl219250, FgColl223350, FgColl223351, FgColl223352, FgColl223353 | West Hararghe |
| C2 | 58 (40.28%) | FgColl216898, FgColl232194, FgColl236992 | Arssi |
| | | FgColl53063 | Awi |
| | | FgColl53091, FgColl212876, FgColl212878, FgColl237984, FgColl239727 | Bale |
| | | FgColl234032, FgColl235133, FgColl234023 | Central Tigrai |
| | | FgColl53071, FgColl53080, FgColl53097, FgColl53107, FgColl53079, FgColl53098, FgColl53099, FgColl212777, FgColl215334, FgColl215335 | East Gojam |
| | | FgColl239061, FgColl239063, FgColl239064 | East Hararghe |
| | | FgColl53018, FgColl208680, FgColl230536, FgColl230540 | North Gonder |
| | | FgColl53062, FgColl53108, FgColl53109, FgColl207356, FgColl207367 | North Shoa |
| | | FgColl53003, FgColl212552, FgColl214942, FgColl229245, FgColl229246, FgColl239073 | North Wello |
| | | FgColl53010 | South Gonder |
| | | FgColl53008, FgColl207391 | South Tigrai |
| | | FgColl215585 | South Wello |
| | | FgColl53104, FgColl53105, FgColl212658, FgColl53012, FgColl53013, FgColl213111, FgColl213112, FgColl213114, FgColl213117 | West Gojam |
| | | FgColl239068, FgColl239065, FgColl239066 | |
| | | FgColl208679 | West Hararghe |
| | | FgColl237982 | West Shoa |
| $C_3$ | 12 (8.33%) | FgColl53103 | S. Wello |

**Table 6.** Cont.

| | | | |
|---|---|---|---|
| | | FgColl235134 | S. Tigrai |
| | | FgColl226091, FgColl212779, FgColl53061 | N. Gondar |
| | | FgColl 53021, FgColl53026, FgColl236621 | E. Gojam |
| | | FgColl212549 | N. Shoa |
| | | FgColl53074, FgColl216899 | Arssi |
| | | *Challa* | Commercial |
| | | FgColl212657, FgColl213109 | S. Wello |
| | | FgColl205176, FgColl207365 | N. Gondar |
| | | FgColl53078 | E. Gojam |
| $C_4$ | 17 (11.81%) | FgColl215096,FgColl53023, FgColl229247, FgColl53002 | N. Shoa |
| | | FgColl232195 | Arssi |
| | | FgColl212877, FgColl53085, FgColl53100, FgColl215406 ,FgColl230070, FgColl215405 | Bale |
| | | FgColl230883 | E.Hararghe |
| | | FgColl234029, FgColl234027 | C. Tigrai |
| $C_5$ | 4(2.78%) | FgColl207359 | E.Tigrai |
| | | FgColl223349 | W. Hararghe |
| $C_6$ | 1(0.69%) | FgColl212656 | S.Wello |

**Table 7.** Pair wise generalized squared distance ($D^2$) among 6 clusters constructed from 144 *T. foenum-graecum* landraces.

| Cluster | $C_1$ | $C_2$ | $C_3$ | $C_4$ | $C_5$ | $C_6$ |
|---|---|---|---|---|---|---|
| $C_1$ | 2.04 | 16.19 | 26.23** | 66.23** | 67.76** | 229.52** |
| $C_2$ | | 1.82 | 73.86** | 22.47** | 138.66** | 135.98** |
| $C_3$ | | | 4.97 | 153.75** | 21.18* | 380.79** |
| $C_4$ | | | | 4.27 | 243.32** | 67.30** |
| $C_5$ | | | | | 7.17 | 497.26** |
| $C_6$ | | | | | | 0 |

*, **, significant at 5 and 1%, respectively.

therefore, crossing of accessions from cluster five and six will give rise to maximum genetic segregation. Among the six clusters formed, cluster five showed the maximum intra-cluster $D^2$ value of 7.17 followed by cluster three with 4.97. Since cluster six contains a single accession, the intra-cluster $D^2$ value is zero (Table 6). The result revealed that even though cluster two contains the largest number of accessions (40.28% of the total accessions), it had the shortest intra-cluster distance. This indicates that the accessions grouped in this cluster are more similar as compared

with the rest of the accessions in the rest of the clusters. In a similar fashion, there were only four accessions for cluster five, but it was more divergent as compared with the accessions present in the rest of the clusters (Table 6).

## Conclusion

A collection of 144 fenugreek accessions representing about 38% of the country's fenugreek germplasm collection was evaluated. From this investigation, the fenugreek accessions were highly variable for several traits, including phenology and yield components indicating the possibilities for genetic improvement of the crop through selection and cross breeding. The varying characters of the superior accessions have implications for further work. Thus, the variation for the different characters found in fenugreek accessions included in this study could be exploited and used in fenugreek breeding programs. The results obtained in this study indicated that single plant or pure line selection for the number of seeds per plant and thousand seed weight may be effective for improvement of seed yield in fenugreek. As a breeding strategy, recurrent or family selection will be employed for the improvement of the traits that had low heritability and genetic advance.

There are implications from the variations among high performing accessions in this study that will provide a basis for a genetically diverse breeding program and provide diversity. Crossing these accessions in a breeding program should result in segregating populations. Therefore, there is a high chance of genetic improvement and of increasing the level of desirable traits in new accessions. Although, such strong relationship of diversity and geographical origin may be possible and was observed in the present investigation, more emphasis has to be put at population level than at geographical level as a source of diversity.

## ACKNOWLEDEGMENTS

This report is part of M.Sc. research thesis work of the first author. The financial assistance from Canadian Education and Training Awards for Africa (CETAA), International Center for Agricultural Research in the Dry Areas (ICARDA) and Holetta Agricultural Research Center (HARC) for the research work is highly acknowledged. The authors also wish to thank all the staff of the Highland Pulse Research Program at Holetta Research Center who managed the trial.

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