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RESEARCH PAPER

Genetic divergence among Ethiopian linseed (*Linumusitatissimum* L) genotypes

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Abstract

Knowledge of genetic divergence of traits in any crop population is important for the continued improvement of the crop as well as for its development in the agricultural system. The study was designed to assess genetic diversity of traits in linseed (Linumusitatissimum L) genotypes evaluated at Ambo University Gudar campus during 2019 cropping season. The experiment was conducted using simple lattice design with two replications consisted fifty six genotypes. Using Euclidean distance value (D2) the studied genotypes were grouped into seven different clusters. Among the clusters cluster III and IV consisted largest number of genotypes while cluster VI and VII consisted small number of genotypes. Maximum inter cluster genetic divergence (D=71.64) was revealed between cluster II and VI, while minimum genetic divergence (D=19.74) was manifested between cluster V and VI. Whereas maximum (11.85) intra clusters distance was manifested for cluster V, while minimum (7.14) intra cluster was revealed for cluster VII. Genotypes in cluster II revealed highest mean value for seed yield per hectare. Principal component analysis (PCA) showed that the first four principal components accounted for 75.96 of the total variation, of which nearly 53.08 % was contributed by the first two principal components (PCA1 and PCA2). Therefore the result of this study suggests existence of genetic divergence for seed yield and other agronomic traits in the studied linseed genotype, which should be exploited in linseed breeding program.

Keywords: cluster, Genetic divergence, Genotypes, principal component

Introduction

Linseed (Linumusitatissimum L., 2n=30) belongs to family linaceae and the genus Linum is one of the earliest crop cultivated for its seeds and fibre. Almost every part of the linseed plant is utilized commercially either directly or after processing (Paul et al., 2017).Among the oilseed crops, linseed contributes an important share to Ethiopian economy. Linseed covered 0.64% (about 80,353.74 hectares) of the grain crop area and 0.30% (about 879,116.55 quintals) of the grain production (CSA, 2017).

Ethiopia is the fifth world producer in linseed and considered as a centre of diversity (Vavilov, 1926). It is known for its high quality oil, and its use as a raw material for agro-industries. Linseed is grown for oil production and shows high variability in flower color, plant height, flowering and maturity periods, and capsule size and wilt resistance (Biru and Dareje, 2014)

Despite of its contribution to local oil industry and hard currency earning, average productivity of linseed in Ethiopia during 2016/17 cropping season was 10.94 quintals per hectare (CSA, 2017), but in developed country greater than 15 q/ha (FAO, 2018).

Among various production constraints limiting productivity of linseed, was limited access to improved varieties is the major that is the reason why Less than 10 percent of Ethiopian farmers only utilize improved seeds (FAO/WFP, 2010).

Genetic diversity is crucial to success in any crop breeding and it provides information about the quantum of genetic divergence and serves a platform for specific breeding objectives (Bindroo and ManthiraMouthy, 2014). Therefore understanding the genetic diversity of linseed (Linumusitatissimum L.) is important for the continued improvement of this crop as well as for its development in the agricultural system. Germplasm characterization is an important link between the conservation and utilization of plant genetic resources. The diversity among genotypes can be assessed based on morphological characterization thus; the genetic diversity is referred to the diversity present within different genotypes of same species. This is due to contrasting alleles of a gene in different individuals producing contrasting phenotypes (Mulusew et al., 2014; Nag et al., 2015; Bhandari et al., 2017). Diversity in plant genetic resources provides opportunity for plant breeders to develop new and improved cultivars with desirable characteristics, which include both farmer-preferred traits (high yield potential, large seed, etc.) and breeder-preferred traits (pest and disease resistance and photosensitivity, etc.) (Rahman et al.,2016; Bhandari et al.,2017).

On other hand genetic variability is a measure of the tendency of individual genotypes in a population to vary from one another. Genetic variability in a population is important for biodiversity because without variability, it becomes difficult for a population to adapt to environmental changes and therefore makes it more prone to extinction and genetic variation and mode of inheritance of quantitative and qualitative traits are of prime importance in planning the breeding programme (Shah et al., 2015; Kumar et al., 2016).

Analysis based on multivariate methods using D2 statistic is useful in providing information for more efficient variety development programmes (Leul,M.2014).Assessment of variability for yield and other characters becomes absolutely essential before planning for an appropriate breeding strategy for genetic improvement (Kumar et al., 2019).Understanding the genetic diversity of linseed is important for the continued improvement of this crop as well as for its development in the agricultural system. Germplasm characterization is an important link between the conservation and utilization of plant genetic resources. Therefore present study was carried out with the objective to identify genetic divergence among Ethiopian linseed genotypes.

Materials and methods

Experimental materials and management

Genetic variability and characterization of 56 linseed genotypes for yield and other Agronomic traits were studied at Ambo University, Gudar Campus. Among the studied materials 48 genotypes were taken from Ethiopian Institute of Biodiversity (EIB), which was collected from different agro-ecology region of Ethiopia (Table 1), while one local variety and 7 released varieties were collected from Sinan and Kulumsa Agricultural research center.

The experiment was conducted in simple lattice design with two replications. Each replication consisted of two rows of each genotype. Row to row distance was 20 cm with row length of 2 meter and plant to plant distance was 10 cm was maintained by thinning. Appropriately cultural practices were carried out as recommended for linseed. Data was recorded on five randomly selected plants for plant height, number of primary branch, number of secondary branch, number of capsule per branch, number of seed capsule, characters while days to 50 per cent flowering, lodging percentage, days to maturity, harvest index and seed yield data was recorded on plot basis. Harvest index calculated as Harvest index (%) = Seed yield per plot/ Aerial biomass per plot x 100

Table 1. Description of the test genotypes collected from different Ethiopia region

Geographical origin	No of Geno types	Name of genotypes (serial numbers in bracket are codes used in this study)
Oromia	24	13628(2),15475(7),17417(8),17597(9),17598(10),17603(11),17607(12),17608(13),17610(14),17615(15),18792(16),19008(17),19009(18),19010(19),19013(20),13755(3),208360(25),208801(27),212512(28),212854(29),219333(32),219334(34), 216892 (31)
Amhara	6	13522(1),237491(47),235784(46),229802(36), 226032(37), 202501(22),
SNNP	4	13758(4),208358(24),211478(30),2406439(33)
Tigray	10	235170(43),238471(44),235177(45),235158(41),235277(42) 219966(35),19079(21),15248(6), 235784(46), 233996(48)
Benishangul Gumuz	4	23544(39),23545(40),207970(23),
National releases	7	Jitu(49),Belay-96(50), Bekelcha(51), Yadeno(52), Kuma(53), Berene(54), Jeldu(55)
Local variety	1	Local

Statistical analysis

Analysis of variances

All collected data were subjected to analysis of variance using appropriate computer software (SAS, version 9.3,2011) and Tukey's range Test (critical difference) at probability of 0.05 was used to separate the means and ranges for significant parameters with the corresponding statistical model;-

$Yij = \mu + Gi + Rj + \varepsilon ij$,

Where Yij is the plot value of each trait of the i^{th} genotype and the j^{th} replication, μ is the trial mean of the a given trait, Gi, is the effect of genotypes, Rj is the effect of replications, and εij is the plot error

Genetic divergence and Cluster Analysis

Genetic divergence and Cluster analysis was carried out through R software 3.4.4 version using Euclidean distance with average method. The means of traits for clusters were obtained from cluster analysis. Distance between intra and inter clusters was calculated by Minitab software using Euclidean formal as indicated in (Anderberg, 1973)

$$D = \sqrt{\varepsilon(xi - xj) + (yi - yj)}$$

The principal component analysis (PCA) was done using the same software employed in estimating the genetic distance (cluster analysis).

Result and discussion

The analysis of variance for Days to flowering, plant height, primary branch per plant, secondary branch per plant, number of capsule per branch, lodging percent, number of seed per capsule, days to maturate, harvest index and yield per hectare revealed that statistically significant differences among the studied genotypes. The genetic divergence and cluster analysis was carried out only for characters which revealed significant difference among the studied genotypes. The result of cluster analysis made on 56 linseed genotypes is presented in Table 2 and Fig 1. The 56 genotypes of linseed from six sources (Table 1) were clustered into seven diversity classes based on D value computed for ten characters

Cluster and Genetic divergence analysis

The cluster analysis revealed that the genotypes were placed into seven clusters (Table 2 and Fig.1) of which the third and fifth cluster

encompasses the largest number of genotypes each contain fifteen (15)genotypes , while the first , fourth , second, sixth and seventh cluster each contains twelve (12),six (6), four (4), two (2) and two (2) genotype respectively. Similarly different clustering patterns were also reported by different researchers in linseed genotypes (Paul et al., 2017; Patial et al., 2019).

Genetic improvement through selection and hybridization depends upon the extent of genetic diversity between parents. Genetically divergent parents could lead to the development of desirable recombinants and transgressive segregants, that in turn, may lead to the development of better performing varieties than the released varieties (Legesse, B.2010). In present study linseed genotypes originated from five different regions (Table 1) were randomly distributed to the different clusters with no definite pattern showing their distinct diversity. There was no observed clear cut relationship between the original sources of the tested genotypes and their genetic diversity since genotypes from the different sources fell into the same cluster and genotypes of the same source were distributed into different clusters, indicating that genotypes from the same origin may have different genetic background and genotypes from different origins might have the same clusters.

Table 2. Clustering of fifty six linseed genotypes using mean of ten characters

S.No.	Cluster	Number of genotypes	Genotypes codes
1	I	12	Acc. Nos. 13522, 13628, 13758, 19013, 15248, 17608, 19079, 212512, 212854, 211478, 238471, 235177
2	II	4	13755, 13756, 17598, 17610
3	III	15	17597, 17603, 17607, 15475, 19008, 202501, 208358, 208360, 229802, 226032, 23534, 23544, 235784, Yadeno, Jitu
4	IV	6	Belay- 96, Bale Local, Bekelcha, Berene, 17417,208801
5	V	15	19009, 19010, 17615, 211892, 240643, 219334, 219966, 235158, 235170, 23396, Kuma, Jeldu, 208749, 18792, 207970,
6	VI	2	219333, 23545
7	VII	2	235277, 237491

Table 3. Estimates of average intra and inter- cluster distances for the 7 clusters in 56 Linseed genotypes

	I	**II**	**III**	**IV**	**V**	**VI**	**VII**
I	**11.00**	38.87	24.79	22.34	20.97	39.12	40.0
II		**8.69**	23.21	28.64	37.44	71.64	64.47
III			**9.36**	22.75	28.48	58.89	54.17
IV				**9.32**	19.74	53.19	47.40
V					**11.85**	38.16	28.84
VI						**7.25**	19.84
VII							**7.14**

NB. Bold figure represent intra-cluster distance

Genetic distances (D2) of fifty six genotypes are presented in (Table 3). The estimates of within and between cluster diversity presented by intra and inter cluster (D2) values revealed that the genotypes of same cluster had little divergence from each other with respect to the aggregate effect of 10 characters under study (Table 3). Inter-cluster Euclidean distances (D2) values ranged from 19.74 (between clusters C IV and C V) to 71.64 (between clusters C II and C VI). The largest genetic divergence are revealed between cluster II and VI (D2=71.64), followed by cluster II and VII(D2=58.89), indicating that superior hybrids or recombinants can be realized by mating between the lines of these clusters, while the lowest genetic divergence is revealed between cluster IV and V(19.74), followed by cluster VI and VII(19.84). Intra cluster distance range from 11.85 for cluster V to 7.14 for cluster VII.

The largest intra cluster distance were revealed for cluster V followed by cluster I and cluster III, while smallest intra cluster distance were manifested for cluster VII, followed by cluster VI and cluster II. The clusters characterized by maximum distances reveal superior heterosis effect and variation from their crosses (Gemechu et al., 2018). Similarly (Chaudhary et al., 2016) reported different genetic distances among linseed genotypes in his studies. Similarly (Mulusew et al, 2013) reported as genetic diversity plays an important role in plant breeding since hybrids between lines of diverse origin generally display a greater heterosis than those between closely related strains

Table 4. Mean differences among the seven clusters of 56 linseed genotypes for mean performance for Yield and other Agronomic traits.

Cluster	FD	PH	Pbr	Sbr	Cbr	LG	SC	MD	HI	Yield/ha
I	60.42	69.58	2.55	4.99	3.81	8.54	7.34	114.87	0.10	9.67
II	84.12	87.37	2.37	5.55	3.02	2.87	8.55	137.62	1.17	17.34
III	64.43	75.53	2.60	4.9	3.17	4.47	8.69	137.50	0.21	14.69
IV	62.67	90.08	2.35	5.35	4.31	10.08	7.13	121.50	0.13	11.32
V	63.83	78.8	2.55	5.10	3.52	25.90	6.94	120.23	0.09	8.41
VI	52.5	54.25	2.87	5.75	7.70	38.75	8.40	97.00	0.16	8.64
VII	58.25	65.25	2.5	4.82	3.86	47.50	7.42	108.50	0.05	4.88
Grand mean	63.7	74.4	2.54	5.2	4.2	19.7	7.9	119.6	0.27	10.7

Where;-Cbr= number of capsule per branch, FD=days to flower, MD= days to maturity, HI=harvest index, LG=lodging percent, Pbr=number of primary branch per plant, PH= plant height, Sbr=number of secondary branch per plant Sc=number of seed per capsule, Yldha= Seed yield per hectare

Mean value for each cluster (Table 4) revealed that genotypes in cluster II had highest values for yield per hectare followed by harvest index, days to flowering and days to maturate, cluster III had highest values for number of seed per capsule, cluster IV had highest values for plant height, cluster VI showed highest value for primary branch per plant followed by secondary branch per plant and number of capsule per branch, VII had highest values for lodging percent, while cluster V had lowest value for days to flowering and days to maturate. Cluster analysis revealed wide range of genetic divergence, which is useful for future hybridization breeding programme to getting desirable transgressive segregantes. In present study a cluster II which showed highest days to mature revealed highest yield performance, this mean that it is important for an area which has long rain season, while a cluster VI which manifested short days to maturate are important for an area with short rain season.

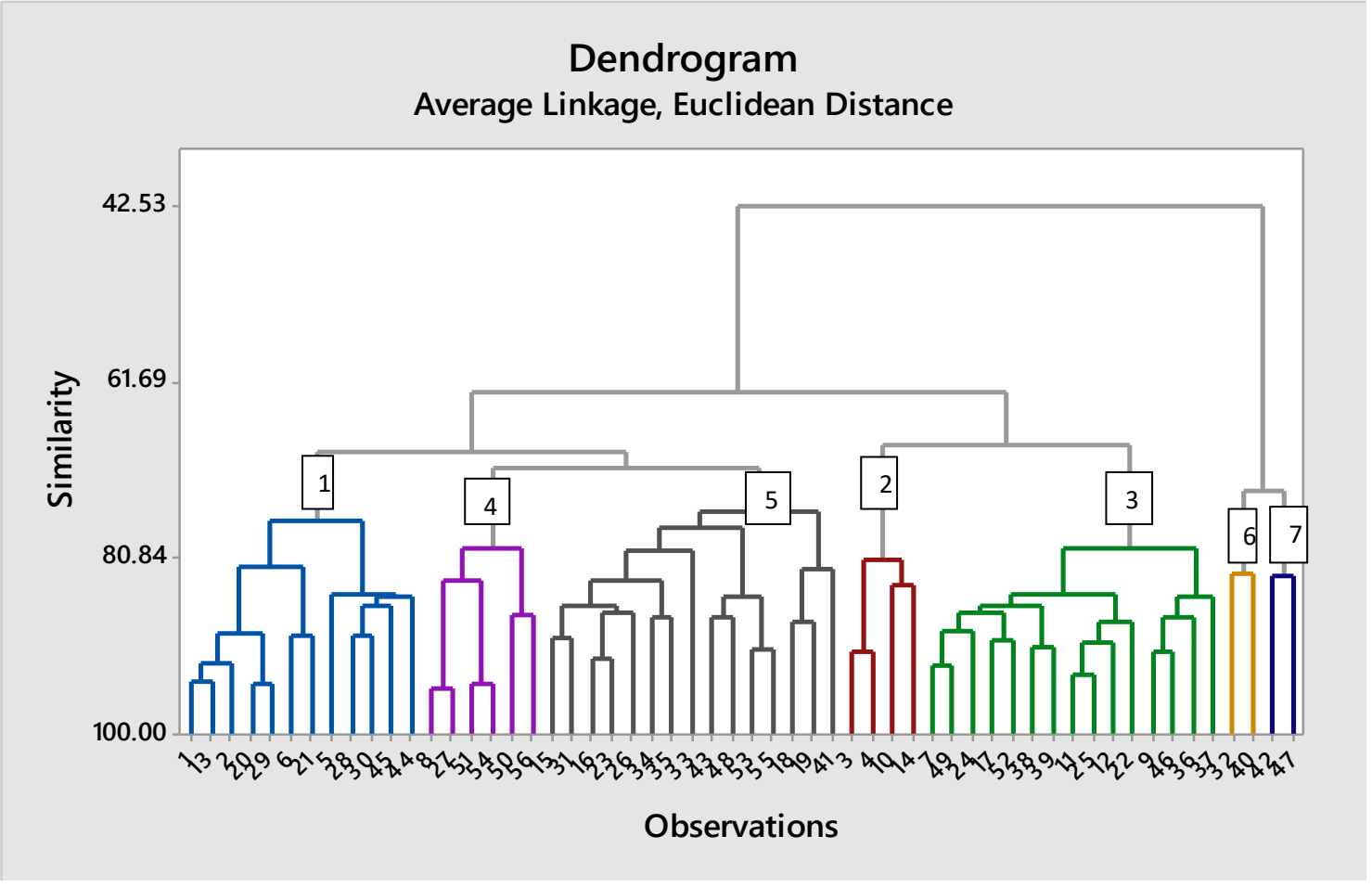

Fig.1 Relationship among 56 linseed genotypes revealed by cluster analysis based on ten traits

Principal Component Analysis

Principal component analysis is a method that reduces data dimensionality without much loss of information. Principal component analysis shows the importance of the largest contributor to the total variation at each axis for differentiation (Sharma, 1998).Four principal components (PCs) extracted about 75.96 % (Table 5) of the entire variation of the genotypesconsidering only PCA Eigen values in PC score greater than 1.In present study about 37.57 % of the total variance explained by the first PCA was due chiefly to variation in harvest index, seed yield per hectare,anddays to maturity. About 15.51% of the whole variance explained by the second PC originated mainly from variation in the primary branch per plant, number capsule per plant, number of seeds per capsule. The third PC accounting for about 12.45% of the entire variance resulted largely from variation in secondary branch per plant, plant height, number of capsules per branch. The fourth PC constituted 10.44% of the variation and demonstrated mainly by primary branch per plant, secondary branch per plant and days to flowering. Characters with relatively larger absolute values of eigenvector weights in PC1 had the largest contribution to the differentiation of the genotypes into clusters as it is normally assumed that characters with larger absolute values closer to unity within the first principal component influence the clustering more than those with lower absolute values closer to zero (Chahal and Gosal, 2002; Legesse 20210).

Table 5. Percent and cumulative variances and Eigenvectors on the first four principal components in 56 genotypes of linseed.

Parameters	PCA1	PCA2	PCA3	PCA4
Variance (%)	37.57	15.51	12.45	10.44
Cumulative (%)	37.57	53.07	65.52	75.96
Characters		**Eigenvectors**		
FD	0.31	-0.29	0.22	0.45
PH	0.25	-0.33	0.43	-0.078
Pbr	0.02	0.45	-0.31	0.57
Sbr	0.013	0.31	0.60	0.46
Cbr	-0.22	0.44	0.41	-0.32
LG	-0.38	0.04	0.05	0.15
SC	0.34	0.44	0.04	-0.17
MD	0.45	-0.09	-0.11	0.14
HI	0.39	0.29	-0.28	-0.12
Yieldha	0.41	0.14	0.19	-0.25

Conclusion

The present study manifested good existence of genetic divergence and variability potential among the Ethiopia linseed genotypes. Based on principal component analysis value (PCA1) days to maturity and seed yield characters has played great role for diversity of studied genotypes. Therefore, the breeder should adopt suitable breeding methodology such as hybridization and selection to utilize in future breeding program for the studied genotypes, since varietal and hybrid development will go a long way in the breeding programmers especially in case of linseed. In future to strengthen the obtained result, repeating the study using molecular markers can make more credible since this study was carried out only based on morphological characterization.

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