

## GENETIC DIVERGENCE IN LINSEED GERmplasm

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### ABSTRACT

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Genetic diversity study on 81 linseed genotypes were conducted at two locations, Sinana and Robe in the highlands of Bale, in order to assess the nature and magnitude of genetic diversity for yield, yield related traits and oil content. The D<sup>2</sup> analysis allowed the 81 genotypes of linseed to be identified into ten distinctive clusters. The analysis indicated that genetic diversity was not necessarily related with geographic diversity. The observation suggested that accessions from different agro ecological zones fall in the same cluster and, thus, indicated their closeness. On the other hand, accessions from the same agro ecology were distributed to different clusters. Therefore, accessions from different regions might have the same genetic background and those from the same origin might have different genetic background. Maximum distance was observed between cluster I and IV (D<sup>2</sup>=762.3) at Sinana and between cluster I and III (880.65) at Robe whereas the minimum distance was between cluster VIII and IX (D<sup>2</sup> = 17.4) at Sinana and between cluster IX and X (D<sup>2</sup> = 20.837) at Robe. However, the analysis suggested that there is considerable diversity among the germplasm accessions included in the present study. There is good scope to bring about improvement through hybridization and selection by crossing accessions from different clusters.

**Keywords:** Genetic divergence, Linseed, Variability, Clusters

### INTRODUCTION

*Linum usitatissimum* L. (n=15), also called flax, is an important oilseed crop which belongs to the family linaceae having 14 genera and over 200 species. Linseed is the only widely grown and economically important species. The genus *Linum* has both cultivated and wild species. The wild species have little economic value. Almost all the species are annual herbs and some are shrubs. *Linum usitatissimum* L. is the only species with non-dehiscent or semi-dehiscent capsules suitable for modern cultivation of the family linaceae (Getinet and Nigussie, 1997). *Linum usitatissimum* L. is one of the oldest plant species cultivated for oil and fiber (Lay and Dybing, 1989). The crop is predominantly self pollinated, but out crossing (less than 2%) occasionally results from insect activity (Dilman, 1928).

Ethiopia is considered to be the center of diversity for linseed (Vavilov, 1926). The principal linseed growing regions in Ethiopia are located at altitudes between 1800 and 2800m, although it occasionally grows at altitudes as low as 1680m or as high as 3430m (CSO, 1984).

Knowledge of the extent and pattern of variability, particularly of genetic variability present in a population of a given crop is essential for further improvement of the crop. Similarly, information on the extent and nature of interrelationship among characters help in formulating efficient scheme of multiple trait selection. Besides this, knowledge of the naturally occurring diversity in a population helps to identify diverse groups of genotypes that can be used for hybridization program. This naturally occurring diversity in traits of agronomic importance is studied through D<sup>2</sup> analysis (Mahalanobis, 1936). The D<sup>2</sup> statistics measures the degree of diversification and determines the relative proportion of each component character to the total divergence. In Ethiopia, the information on these aspects in linseed is very scarce. Therefore, there is a need to generate information on interrelationships of yield and yield related traits and the genetic divergence among linseed genotypes.

Keeping this in view, the present study was conducted with the following objective; Assessment of nature and magnitude of genetic diversity for yield, yield related traits and oil content in some Ethiopian linseed genotypes.

**MATERIALS AND METHODS****Testing location and season**

Table 1. The List of linseed accessions and their origin

No.	Accession No.	Collection place/area	No.	Accession No.	Collection place/area
1.	PGRC/E 10002	Shewa/J.meacha	42.	PGRC/E 13736	Wello/Ambasel
2.	PGRC/E 10005	Sidamo	43.	PGRC/E 10155	Gonder
3.	PGRC/E 10007	Kefa/Jima	44.	PGRC/E 10013	Harerge
4.	PGRC/E 10008	Gonder/D.tabor	45.	PGRC/E 10015	Illubabor
5.	PGRC/E 10010	Kefa	46.	PGRC/E 10012	Gojjam
6.	PGRC/E 10022	Wollo	47.	PGRC/E 13673	Gojjam/Mota
7.	PGRC/E 10026	Gojjam/ Koladamot	48.	PGRC/E 13658	Bako
8.	PGRC/E 10037	Sidamo/Jemjem	49.	PGRC/E 10014	Shewa
9.	PGRC/E 10039	Eritria/Seraye	50.	PGRC/E 10082	Harerge/Alemaya
10.	PGRC/E 10041	Bale/Ginner	51.	PGRC/E 10173	Gojjam/Bichena
11.	PGRC/E 10046	Wellega/Nekamt	52.	PGRC/E 10122	Sidamo/Arero
12.	PGRC/E 10061	Gamogofa	53.	PGRC/E 10092	Shewa/Yefitana timug
13.	PGRC/E 10068	Gojjam/ Bahrdar	54.	PGRC/E 10044	Tigray/Shire
14.	PGRC/E 10080	Harar	55.	PGRC/E 10158	Sidamo/awassa
15.	PGRC/E 10085	Harar	56.	PGRC/E 10047	Illubabor/Bunobedelle
16.	PGRC/E 10104	Shewa/J.M	57.	PGRC/E 10133	Tigray/Agame
17.	PGRC/E 10109	Shewa/J.Meacha	58.	PGRC/E 10048	Tigray/Shire
18.	PGRC/E 10111	Shewa/ Merabete	59.	PGRC/E 10081	Harerge/Habro
19.	PGRC/E 10118	Shewa/J.Mmeacha	60.	PGRC/E 10172	Gamugofa/Garadula
20.	PGRC/E 10120	Sidamo	61.	PGRC/E 10139	Welega/Horegudru
21.	PGRC/E 10125	Tigray/Inderta	62.	PGRC/E 10132	Tigray/Agame
22.	PGRC/E 10138	Wellega/Horogudru	63.	PGRC/E 13673	Gojjam/Mota
23.	PGRC/E 10144	Wellega	64.	PGRC/E 10073	Gojjam/Debremarkos
24.	PGRC/E 10159	Gonder/Wegera	65.	PGRC/E 10161	Gonder/Denbi
25.	PGRC/E 10162	Gonder	66.	PGRC/E 10180	Shewa/Menagesha
26.	PGRC/E 10169	Gonder	67.	PGRC/E 10182	Shewa
27.	PGRC/E 10176	Gojjam/Metekel	68.	PGRC/E 10178	Shewa/K.Hadiya
28.	PGRC/E 10179	Shewa	69.	PGRC/E 10043	Gojjam/Koladdamot
29.	PGRC/E 10204	Wollo/Awsa	70.	PGRC/E 10191	Shewa/Jibatenameach
30.	PGRC/E 10006	Illubabor	71.	PGRC/E 10171	Gamugofa/Gamu
31.	PGRC/E 10042	Tigray/Axum	72.	PGRC/E 10088	Shewa/Teguletbulga
32.	PGRC/E 10047	Illubabor/Buno	73.	PGRC/E 10051	Bale/Genale
33.	PGRC/E 10062	Bale/Meliyu	74.	PGRC/E 10177	Gojam/Debremarkos
34.	PGRC/E 10235	Gonder	75.	PGRC/E 10071	Gojam/Dejen
35.	PGRC/E 10064	Gamogofa/Hambako	76.	PGRC/E 10174	Gojam/Koladegadamo
36.	PGRC/E 10072	Gojam/Debremarkos	77.	PGRC/E 10164	Gonder/Wegera
37.	PGRC/E 10073	Gojam/Debremarkos	78.	PGRC/E 10121	Sidamo/Jemjem
38.	PGRC/E 10060	Gonder	79.	PGRC/E 10147	Wello/Yeju
39.	PGRC/E 13737	Wello/Ambasel	80.	PGRC/E 10207	Wello/Kallu
40.	PGRC/E 13731	Wello/Ambasel	81.	PGRC/E 10200	Wello/Kalu
41.	PGRC/E 13738	Wello/Ambasel			

The experiment was carried out at two locations, at the experiment field of Sinana Agricultural Research Center's on-station, and the other at a site in the farmer's field near

Robe town in the highlands of Bale. The experiment was conducted at each location on vertisol clay loam soil under rain fed conditions during the meher season (August-January) of 2001/2002 cropping season.

Eighty-one genotypes (Table 1) collected from fourteen districts of the country was laid out in, 9 x 9 simple lattice design with two replications. Each experimental plot has plot size of 1.6m<sup>2</sup> i.e. two rows at 4m long with inter-row spacing of 20-cm. Seeding rate was 25 kg/ha. Fertilizer was applied at the rate of 23/23 kg/ha N/P<sub>2</sub>O<sub>5</sub>. Data were recorded on both plant and plot basis. The following data was taken on plant basis, i.e. data was collected from five plants which were tagged just before heading and all data to be collected on plant basis were recorded on these five plants. The data on plant basis was expressed as average of five plants in each experimental plot. The parameters taken at plant basis are plant height (cm), number of primary branches, number of secondary branches, number of capsules per plant, number of seeds per capsule, seed yield (g/plant), and number of tillers. Where as days to flower, days to maturity, biological yield (g/plot), harvest index (%), thousand seed weight (g), seed yield (g/plot), and percent oil content (%) was taken on plot basis. Genetic diversity was studied following Mahalanobis's (1936) generalized distance ( $D^2$ ) extended by Rao (1952) using MSTATC and Minitab computer software. Tocher's method (Rao 1952) was followed for grouping the 81 genotypes into different clusters.

## RESULTS AND DISCUSSION

### Cluster analysis (Clustering groups based on quantitative traits at sinana)

Clustering was done based on quantitative traits both at Sinana and Robe independently by Minitab computer software. The data was standardized to a mean of zero and a variance of unity to avoid differences in scales used for recording data on the different characters before under taking a series of multivariate analysis. The result of clustering gave ten groups at each location. A summary of cluster group with the number of genotypes in which each cluster had in it and the place of collection are given in Table 1 for Sinana and Robe. Table 3 and Table 4 indicate summary of means of the cluster at Sinana and Robe respectively. Figure 1 and Figure 2 represents the cluster dendrogram at the respective site. The components of cluster means and Figure 1 at Sinana for different characters indicated considerable differences between clusters for all the characters considered.

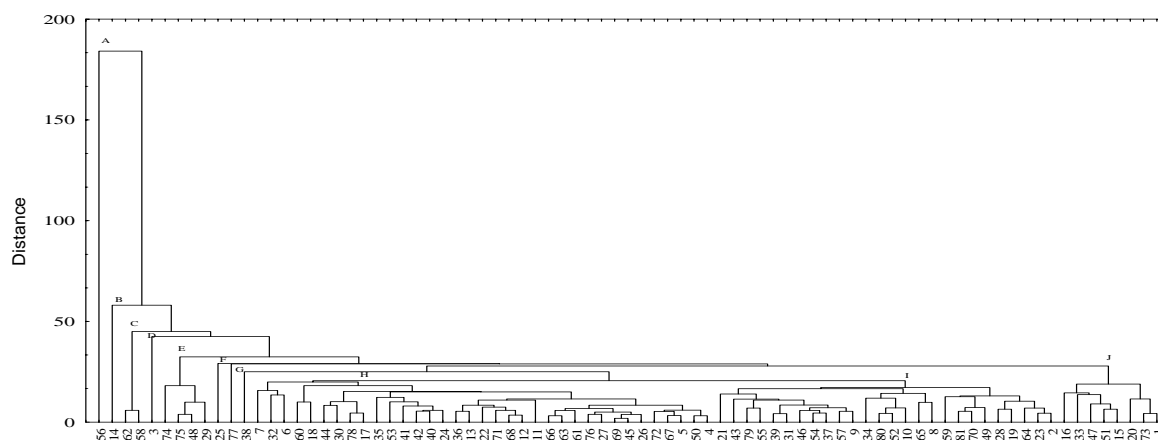


Figure 1. Cluster groups of 81 linseed entries based on 14 different related traits at Sinana

The  $D^2$  analysis allowed the 81 genotypes of linseed to be identified into ten distinct clusters for both sites with the assumption that those within the same cluster having smaller  $D^2$  values among themselves than those belonging to other clusters (Table 3).

At Sinana cluster A consists of only one genotype which was collected from Illubabor and had the characteristics of late maturing with more number of primary branches and more number of capsules per plant. Cluster B had only one genotypes collected from Harar. This cluster was characterized by early flowering, early maturity with low number of seeds per capsules, low biomass, low seed yield per plant, low seed yield per plot, and with low percent oil content. Cluster C contains two genotypes both collected from Tigray. This cluster was characterized by tall genotypes with the largest seed weight, the highest harvest index, highest seed yield and with high percent oil content but with low number of primary and secondary branches.

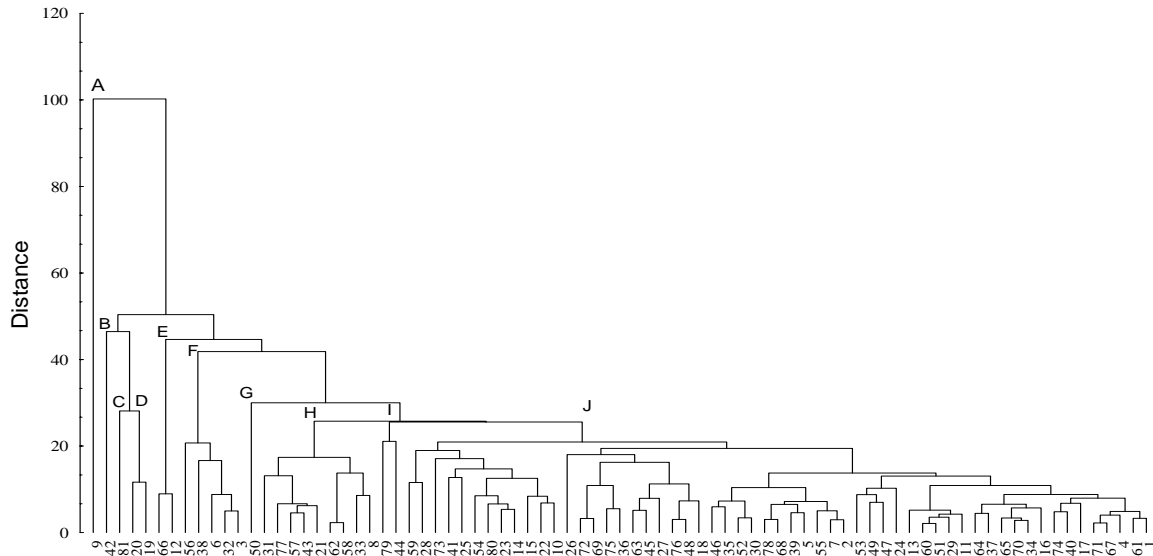


Figure 2. Cluster groups of 81 linseed entries based on 14 different related traits at Robe

Cluster D also had only one genotype. It was late flowering and late maturity types with low harvest index and low seed yield per plant and relatively with medium to high percent oil content. It was a collection from Kefa. Cluster E had 4 genotypes, which was different in their origin (Wello, Wellega, Gojam and Gondar). They were characterized by high numbers of seeds per capsules and tillers per plant with low number of secondary branches. Cluster F consisted of two genotypes originated from Gondar. They possessed high number of secondary branches, more biomass and relatively high percent oil content.

Cluster G also had only one genotype of Gondar origin. Its performance was average with respect to all traits. Cluster H was the largest group and it had 35 genotypes. This was collected from different localities. This group was characterized by medium to high percent oil content, medium in their height with medium to late flowering and maturing types.

Cluster I was the second largest group with 26 genotypes. They were relatively early flowering and maturing types with high harvest index and medium to high percent oil content. Cluster J consisted of 8 genotypes. This group was characterized by high seed yield per plant, high percent oil content and medium to high biomass. They were also the second in their seed yield per plot.

#### Cluster Analysis (Clustering groups based on quantitative traits at Robe)

Based on quantitative traits at Robe, 81 entries were clustered into ten groups as it is summarized in Figure 2 and Table 2.

Cluster A had one entry which was obtained from Eritria and it was characterized by early flowering, medium maturity and height, low number of primary branches, high seeds weight, high harvest index and seed yield per plot (Table 2). Cluster B also had one entry collected from Wello. It was characterized by relatively early in flowering and maturity and it had high number of capsules per plant and high percent of oil content. Cluster C also had one entry with high biomass and average performance in other traits. It was collected from Wello.

Table 2. Summary of 81 linseed genotypes in ten clusters along with the number of genotypes with in each cluster for Sinana and Robe

Cluster group	Sinana			Robe		
	Entries by Identification No.	Total No.	Place of Collections/origin	Entries by Identification No.	Total No.	Place of Collections/origin
A	56	1	Ilubabor	9	1	Eritria
B	14	1	Harar	42	1	Wello
C	58,62	2	Tigray	81	1	Wello
D	3	1	Kefa	19,20	2	Shewa and Sidamo
E	29,48,74,75	4	Wello, Wellega, Gojam and Gondar	12,66	2	Gamogofa and Shewa
F	25,77	2	Gondar	3,6,32,38,56	5	Kefa, Wello, Illubabor (2) and goder
G	38	1	Gondar	50	1	Harar
H	4,5,6,7,11,12,13,17,18,22,24,26,27,30,32,35,36,40,41,42,44,45,50,53,60,61,63,66,67,68,69,71,72,76,78	35	Gondar (3), Kefa, Wello (4), Gojjam(7), Welega (3), Gamogofa (4), Shewa (7), Ilubabor (3), Harar (2), Sidamo (1)	8,21,31,33,43,57,58,62,77	9	Sidamo, Tigray (5), Bale, Gondar (2)
I	2,8,9,10,19,21,23,28,31,34,37,39,43,46,49,52,54,55,57,59,64,65,70,79,80,81	26	Sidamo (4), Eritira, Bale, Shewa (4), Tigray (4), Welega, Gondar (3), Gojam (3), Wello (4), Harar,	44,79	2	Harar and Wello
J	1,15,16,20,33,47,51,73	8	Shewa (2), Harar, Sidamo, Bale (2), Gojam (2)	1,2,4,5,7,10,11,13,14,15,16,17,18,22,23,24,25,26,27,28,29,30,34,35,36,37,39,40,41,45,46,47,48,49,51,52,53,54,55,59,60,61,63,64,65,67,68,69,70,71,72,73,74,75,76,78,80	57	Shewa (11) Sidamo (4), Gondar (6), Kefa, Gojam (14), Bale (2), Welega (5), Harar (3), Wello (5), Illubabor (2), Gamogofa (3), Tigray
Total		81			81	

Number in parenthesis indicated that the number of entries obtained from that region

Cluster D had two entries, one from Shewa and the other from Sidamo. They were tall types and gave high mean values for seed yield per plot and tillers per plant. Cluster E had two entries (from Gamo Gofa and Shewa). This group was characterized by late flowering and late maturity with high number of primary and secondary branches, high tillers per plant, and low numbers of seeds per capsules and seeds weight. Cluster F this cluster had five entries collected from Kefa, Wello, Illubabor (2 entries) and Gondar. The group included entries with very late in maturity, very tall types with low numbers of capsules per plant, seed yield per plot, harvest index and seed yield per plot. Cluster G contained only one entry collected from Harar. It had high mean value for seeds per capsules with low biomass and low percent oil content. Cluster H was the second largest group next to cluster J. It contained nine entries. They included entries with early in flowering and maturity with high seed weight and relatively high percent oil content.

Table 3. Clusters Means for 14 characters in 81 linseed genotypes grown at Sinana

Variables	Clusters									
	A	B	C	D	E	F	G	H	I	J
DF	90	52	75	103	85	72	87	81	76	82
DM	166	128	139	165	145	143	162	141.6	138.7	143.6
PH	80	63	90.5	76	70	72.5	79	71.5	73.6	79.4
TPP	5	3	3	3	6	3	4	4	4	4
NPB	66	27	13	13	25	20	21	18.6	21	28
NSB	2	2	1	2	1	3	1	1	2	2
NCPP	133	52	38	37	66.8	49.5	70	42.7	53	63.4
NSPC	7	3	7	4	8	4	6	5	6	5.3
TSW	3.0	4.6	5.6	2.7	3.5	4.1	4.4	3.6	4.4	4.2
SY/pl	1.0	0.6	1.15	0.6	1.75	0.90	1.0	0.91	1.22	1.96
HI	15.0	19.0	25.0	14.0	20.5	20.0	18.0	19.2	21.7	20.1
SY/plot	127.0	116.0	361.0	203.0	231.5	220.5	209	212.9	257	302.9
BM	975.0	725.0	1337.5	1275	1193	1513	1150	1162	1257	1443
POC	31.0	29.5	34.6	30.6	32.2	33.0	30.5	31.4	32.9	32.5

DF= Days to flowering; DM= Days to maturity; PH= Plant height (cm); TPP= Tillers per plant; NPB= No. of primary branches; NSB= No. of secondary branches; NCPP= No. of capsules per plant; NSPC= No. of seeds per capsule; TSW= Thousand seed weight (gm); SY/pl= Seeds yield per plant; HI = Harvest index per plot (%); BM = Biomass per plot; SY/plot= Seed yield per plot (g/plot); POC= Percent of Oil

Table 4. Clusters Means for 14 characters in 81 linseed genotypes grown at Robe

Variables	Clusters									
	A	B	C	D	E	F	G	H	I	J
DF	69	70	82	74	86	83	81	67	66	77
DM	140	131	139	141	142	158	140	129	129	137
PH	63	61	69	71	60	71	63	65	57	63
TPP	3	5	4	5	6	4	3	3	3	4
NPB	9	18	22	23	32	15	28	12	10	14
NSB	3	3	2	2	3	2	3	2	2	1
NCPP	37	85	50	78	67	32	37	37	32	42
NSPC	6	8	7	7	5	6	10	7	9	7
TSW	5.4	4.8	4.6	4.5	3.1	3.9	4.0	5.4	3.4	3.9
SY/pl	1.0	2.0	2.0	3.5	1.0	0.8	1.0	1.0	1.0	1.2
HI	48	25	19	20	21	11	28	23	22	23
SY/plot	593.0	211.0	250.0	242.0	223.0	109.0	228.0	231.3	199.5	217.3
BM	1217	846	1652	1202	1095	970	834	1015	913	958
POC	34.6	40.0	35.0	35.7	34.2	33.2	31.7	35.0	32.6	33.7

DF= Days to flowering; DM= Days to maturity; PH= Plant height (cm); TPP= Tillers per plant; NPB= No. of primary branches; NSB= No. of secondary branches; NCPP= No. of capsules per plant; NSPC= No. of seeds per capsule; TSW= Thousand seed weight (g); SY/pl= Seeds yield per plant; HI = Harvest index (%); SY/plot= Seed yield per plot (g/plot); BM = Biomass ; POC= Percent oil content

Cluster I had two entries obtained from Hara and Wello and characterized with very early flowering and maturity. They were short types with relatively high numbers of capsules per plant. Cluster J was the largest group with fifty-seven entries. These entries were medium in flowering and had low number of secondary branches.

Cluster A of Sinana had five entries in common with cluster H of Robe. Clusters J of Sinana and Robe had six entries in common. However, cluster A, B, and G of both Sinana and Robe had only one entry even though the entries were not the same.

Table 5. Squared distance between cluster groups based on 14 different related traits for 81 linseed entries grown at Sinana (above diagonal) and Robe (below diagonal).

Cluster	A	B	C	D	E	F	G	H	I	J
A		743.6**	756.8**	762.3**	747.8**	744.5**	748.5**	750.5**	748.8**	752.6**
B	632.1**		176.4**	164.8**	143.4**	81.4**	106.0**	64.5**	83.7**	148.1**
C	880.6**	236.1**		189.1**	115.4**	101.9**	108.3**	87.1**	54.3**	77.5**
D	626.2**	115.9**	115.9**		120.4**	95.6**	77.6**	54.7**	104.7**	116.6**
E	530.3**	111.3**	161.2**	90.79**		69.6**	60.8**	41.6**	37.5*	62.9**
F	677.0**	190.9**	178.6**	100.9**	89.2**		84.2**	32.0**	20.7*	47.2**
G	513.2**	220.7**	194.2**	145.3**	58.7**	128.2**		46.0**	64.5**	90.7**
H	505.7**	114.2**	148.4**	92.6**	67.9**	89.9**	88.3**		17.2	47.8**
I	573.5**	153.9**	143.3**	105.5**	95.9**	97.4**	104.4**	43.7**		20.4
J	475.5**	116.5**	126.9**	64.7**	49.35**	64.0**	73.9**	21.5	20.8	

\*, \*\* indicates significant at 5 % and 1 % probability levels, respectively

The observation suggested that accessions from different agro ecological zones fall in the same cluster and, thus, indicated their closeness. On the other hand, accessions from the same agro ecology were distributed to different clusters. Therefore, accessions from different regions might have the same genetic background and those from the same origin might have different genetic background. Furthermore, the geographic and genetic diversity are not necessarily related. i.e. germplasm accessions collected from the same geographic collection region fall in different cluster groups whereas those collected from different geographic region tended to be clustered in the same cluster. However, the analysis suggested that there is considerable diversity among the germplasm accessions included in the present study. There is good scope to bring about improvement through hybridization and selection by crossing accessions from different clusters. For example, an accession from cluster C of sinana that had the highest yield per plot, the highest oil content, high biomass and the largest seed could be crossed with an accession from another cluster having low/medium height as well as more branches and tillers to combine these traits.

#### Distance analysis

Summary of pair wise squared distance ( $D^2$ ) among the ten clusters for Sinana and Robe are given in Table 5. Maximum distance was observed between cluster A and D ( $D^2 = 762.3$ ) at Sinana and between cluster A and C (880.65) at Robe. The minimum distance was between cluster H and I ( $D^2 = 17.4$ ) at Sinana and between cluster I and J ( $D^2 = 20.837$ ) at Robe. The information presented here suggested that the linseed germplasm under study is a good source of parents for improvement through hybridization and selection.

#### SUMMARY AND CONCLUSION

The 81 linseed accessions were clustered into ten groups at both locations based on Mahalanobis's  $D^2$  values. This cluster classification showed that geographic and genetic diversity were not necessarily related, i.e., germplasm accessions collected from the same geographic region fall into different cluster groups whereas those collected from different geographic regions tended to be clustered in the same cluster. Maximum distance was observed between cluster I and IV ( $D^2=762.3$ ) at Sinana and between cluster I and III (880.65) at Robe whereas the minimum distance was between cluster VIII and IX ( $D^2 = 17.4$ ) at Sinana and between cluster IX and X ( $D^2 = 20.837$ ) at Robe.

In conclusion, the present investigation indicated that there is wide range of genetic variability and diversity in Ethiopian linseed germplasm though the present investigation was conducted on only a part of it. There is large scope of simultaneous improvement in seed yield as well as oil content through selection. Hybridization among accessions from different clusters identified in this study could lead to considerable genetic improvement by following appropriate selection strategies in the segregating generations. However, it would be worthwhile to study more available germplasm over years and locations to identify more diverse accessions as well as to confirm the importance of the traits identified as predictors of yield and/or oil content.

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