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Genetic Variation of Different Crosses of Linseed (*Linum usitatissimum* L.) Genotypes for Some Agro-morphological Traits

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ABSTRACT

Linseed is among the most important oilseeds in the highlands of Ethiopia, for which yield enhancement is among the breeding objectives. Variability of the genotypes is paramount importance for selection in any breeding programs. This study was carried out in 2012/13 cropping season to determine the genetic variability of 25 linseed genotypes derived from various crosses including checks. The experiment was laid out using a 5×5 simple lattice design with two replications. The analysis of variance revealed that the genotypes showed significant differences for most of the traits measured. High phenotypic and genotypic coefficients of variation were recorded for number of seeds/plant and number of capsules/plant. High heritability along with high genetic advance was observed for number of seeds/plant which indicates selection of this trait at early generation would be effective. Number of primary branches, number of secondary branches, number of capsules and number of seeds/plant showed highly significant positive correlation with seed yield/plant. But, 1000 seed weight had highly significant negative correlation. In cluster analysis it has been shown that the genotypes were placed into six groups, for which further effective selection/hybridization could be done.

Key words: Correlation, cluster, genetic advance, heritability, selection

INTRODUCTION

In Ethiopia, Linseed (*Linum usitatissimum* L.) has been cultivated since ancient time (Wakjira *et al*., 2004). It is the second most important oilcrops in the highland areas of the country. According to the Central Statistical Authority (CSA, 2012) it covered an area of 116, 541.4 ha of land with production of 112, 760.7 tones and productivity of 0.97 t ha^{-1}. Ehiopia is the fifth world producer of linseed after Canada, China, USA and India (Wakjira, 2007). It is traditionally grown on marginal and sub-marginal lands with minimum frequency of plowing and no weeding (Teklewolde *et al*., 1992).

Linseed oil has drying and hardening properties which is emanated from its high linolenic acid content, due to this property, it had been used mostly for industrial purposes such as manufacture of paints, varnishes, soaps, printing inks and linoleum (Wakjira *et al*., 2004). Linseed oil is extracted locally for edible purpose which is often blended with other vegetable oil such as noug (*Guizotia abyssinica* Cass) in order to minimize the oxidation effect of the linolenic acid such as rancidity and bad taste (Teklewolde *et al*., 1992). Hence, this linolenic acid which is oxidatively

unstable fatty acid content of the extracted oil has to be reduced to ensure the keeping qualities of linseed oil for cooking purpose. The residue after the extraction of oil from linseed is a good source of protein which can be used as animal feed. The seeds are usually roasted, ground, mixed with spices and water and served with various local breads. It is also consumed in soups, with porridges and cooked potatoes, etc. (Burako, 2010). There are also interests for whole seed linseed in the backing and confectionery industries where its health benefits are recognized, for which the traditional varieties are suitable. In this regard, therefore, developing high yielding varieties and application of improved agronomic practices are paramount importance in increasing the yield of linseed.

Genetic variability is crucial in breeding/selection program of any crops. In line with this, various researches have been done by different investigators on various crops like linseed itself (Kandil *et al*., 2012; Ottai *et al*., 2012; Wakjira, 2011; Tadesse *et al*., 2011; Choferie, 2008), Brassica (Abideen *et al*., 2 013; Fahmi *et al*., 2012; Belete, 2011; Khan *et al*., 2008a), Wheat (Mohammed *et al*., 2012; Mohibullah *et al*., 2011; Khan *et al*., 2010; Kotal *et al*., 2010; Khan *et al*., 2008b, 2002), Teff (Ayalneh *et al*., 2012; Chanyalew *et al*., 2009) and Barely (Jalata *et al*., 2011; Zakova and Benkova, 2004; Kebebew *et al*., 2001). Wakjira (2011) studied genetic variability of 60 accessions of linseed and found that these accessions showed wide diversity for the traits measured. In this study the lowest phenotypic and genotypic coefficients of variation was recorded by days to maturity (6.26 and 5.46%, respectively), while the highest was recorded by seed yield/plant (54.97 and 50.18, respectively). In similar study, seeds/capsule and days to 50% flowering showed the lowest (67.38 %) and the highest (91.38%) predicted broad sense heritability values, respectively. High heritability along with high genetic advance was shown by seed yield per plant. High heritability along with high genetic advance was also reported for traits such as plant height, number of capsules/plant and seed yield/plant (Ottai *et al*., 2012; Kandil *et al*., 2012). High genetic and phenotypic coefficients of variation as well as high heritability were recorded for traits such as secondary branches/plant and seed yield/plant in 81 linseed germplasms evaluated at Sinana (Tadesse *et al*., 2011). In this study, seed yield per plant showed positive and significant association with plant height, number of capsules/plant, thousand seed weight and seed yield/plot at phenotypic level.

The objective of this study was to determine the genetic variability of different crosses of linseed genotypes based on their agro-morphological traits.

MATERIALS AND METHODS

Plant material: The genotypes were segregants from crosses such as CI-1652 (standard) X R12N27G (regenerant from tissue culture), R12D33 (regenerant from tissue culture) X Chilalo (standarad), CDC1747 (Canadian variety) × CI 1652 (standard variety) and CDC 1747 (Canadian variety) X Chilalo (standard) (Table 1).

Field experiments: Twenty two genotypes along with three checks were evaluated in two replications using a simple lattice design (5×5) at Holetta Agricultural Research Center during 2012/13 cropping season. These genotypes were grown on plots consisted of 6 rows of 3 m length with between rows distance of 20 cm. All agronomic practices were followed as recommended for growing linseed in the areas. The studied traits were 50% days to flowering, days to maturity, plant height (cm), number of secondary branches/plant, number of capsules/plant, number of seeds/capsule, seed yield/plant (g) and thousand seed weight (g).

Table 1: Different crosses of linseed genotypes and their pedigree

Genotypes	Pedigree
9-21-1	CI-1652 (standard)×R12N27G (regenerant from tissue culture)
15-27-2	CI-1652 (standard)×R12N27G (regenerant from tissue culture)
6-36-2	R12D33 (regenerant from tissue culture) X Chilalo (standarad)
3-39-1	CDC1747 (Canadian variety)×CI 1652 (standard variety)
10-46-1	CI1652 (standard)×R12N27G (regenerant from tissue culture)
1-68-2	CDC 1747 (Canadian variety)×Chilalo (standard)
1-68-3	CDC 1747 (Canadian variety)×Chilalo (standard)
2-69-1	CDC 1747 (Canadian variety)×Chilalo (standard)
2-69-3	CDC 1747 (Canadian variety)×Chilalo (standard)
3-70-1	CDC 1747 (Canadian variety)×Chilalo (standard)
4-71-2	CDC 1747 (Canadian variety)×Chilalo (standard)
5-72-1	CDC 1747 (Canadian variety)×Chilalo (standard)
7-74-1	CDC 1747 (Canadian variety)×Chilalo (standard)
7-74-2	CDC 1747 (Canadian variety)×Chilalo (standard)
12-80-1	CDC 1747 (Canadian variety)×Chilalo (standard)
16-83-2	CDC 1747 (Canadian variety)×Chilalo (standard)
22-89-1	CDC 1747 (Canadian variety)×Chilalo (standard)
24-91-1	CDC 1747 (Canadian variety)×Chilalo (standard)
Berene-SPS-1	Berene
4-95-2	CDC1747 (Canadian variety)×Chilalo (standard)
5-96-2	CDC1747 (Canadian variety)×Chilalo (standard)
6-97-3	CDC1747 (Canadian variety)×Chilalo (standard)
Checks	
Kasa-2 (currently released variety)	
Jeldu-1 (currently released variety)	
Local	

Statistical analysis: Data were subject to analysis of variance using AGROBASE™ software (Agronomix Software Inc., Canada). The genotypic and phenotypic variances were computed following Omidi *et al.* (2009). Phenotypic and genotypic coefficients of variation were calculated according to Burton (1952). Heritability (h^2), Genetic Advance (GA) and genetic advance as percent of mean (GAM) were computed as described by Allard (1960). Pearson correlation and cluster analysis were done using SAS statistical software version 9.00 (SAS, 2002).

RESULTS AND DISCUSSION

The result of analysis of variance showed a significant genetic difference among the genotypes for the traits measured except days to maturity and number of seeds/capsule (Table 2). The mean and range value of the traits are presented in Table 3. Plant height ranged from 66 cm in the genotype local check to 100 cm in the genotype 2-69-1. Number of primary branches/plant ranged from 3 (6-36-2, 1-68-2 and 5-96-2)-6 (local check). Number of secondary branches/plant ranged between 5 (6-36-2, 1-68-2, 2-69-1, 3-70-1, 3-70-2 and 4-95-2) and 8 (3-39-1, 10-46-1, 4-95-2 and local check). The highest number of capsules/plant was recorded by the genotype local check, while the lowest was recorded by the genotype 9-21-1. Similarly these genotypes showed the highest and the lowest number of seeds/plant, respectively but the reverse for 1000 seed weight. See yield/plant ranged from 5.65 g in genotype 1-68-3-11.7 g in genotype 4-95-2.

Table 2: Mean squares from analysis of variance for 10 traits in 25 genotypes

Traits	EMS	GMS	BMS	CV
DF	2.052	12.528**	0.180	1.74
DM	4.540	3.622^{ns}	5.780	1.33
PH (cm)	4.225	96.703***	54.080	2.61
NPB	0.028	0.507***	0.336	4.45
NSBP	0.088	2.049***	0.106	4.65
NCPP	8.748	35.448***	0.320	14.59
NSPC	4.693	7.655^{ns}	1.280	28.16
NSPP	467.937	6234.816***	3306.471	13.82
SYPP (g)	1.282	6.8***	9.159	14.21
TSW (g)	0.022	0.413***	0.003	2.89

**, ***significant at p≤0.01 and p≤0.001 level, respectively. DF: 50% days to flowering, DM: Days to maturity, PH: Plant height, NPBP: Number of primary branches/plant, NSBP: Number of secondary branches/plant, NCPP: Number of capsules/plant, NSPC: Number of seeds/capsule, NSPP: Number of seeds/plant, SYPP: Seed yield/plant, TSW: Thousand seed weight, EMS: Error mean squares, GMS: Genotypes mean squares, BMS: Block mean squares, CV: Coefficients of variation, us: Non-significant

Table 3: Range, mean, standard error and least significance differences for 10 traits of the 25 genotypes

	Agronomic traits									
Genotypes	DF	DM	PH	NPB	NSBP	NCPP	NSPC	NSPP	SYPP	TSW
9-21-1	85	161	83	4	6	13	5	63	6.40	5.95
15-27-2	84	161	78	4	7	16	7	108	5.70	5.30
6-36-2	81	161	74	3	5	15	12	180	5.95	5.35
3-39-1	81	161	76	4	8	26	4	102	5.80	5.70
10-46-1	81	160	81	4	8	26	7	195	10.40	5.35
1-68-2	80	161	76	3	5	19	6	124	6.25	4.85
1-68-3	83	161	78	4	6	17	6	108	5.65	5.20
2-69-1	83	161	100	4	5	19	8	129	9.40	5.80
2-69-3	79	160	73	4	6	26	6	146	7.00	4.80
3-70-1	82	160	77	4	5	15	9	133	6.05	5.05
4-71-2	80	160	75	4	5	20	8	156	7.75	5.05
5-72-1	87	160	85	4	6	18	5	81	6.80	4.95
7-74-1	83	160	83	4	6	20	9	170	8.15	4.75
7-74-2	84	160	78	4	7	23	9	203	7.95	4.95
12-80-1	84	159	78	4	7	20	8	152	7.90	5.20
16-83-2	85	159	71	4	7	19	8	152	7.40	5.25
22-89-1	83	160	82	4	6	16	8	132	6.75	5.15
24-91-1	83	165	85	4	7	20	10	199	10.00	5.05
Berene-SPS-1	87	162	89	4	7	26	6	166	9.80	4.80
4-95-2	76	159	73	4	8	26	9	222	11.70	5.25
5-96-2	81	160	73	3	5	16	9	140	7.65	5.55
6-97-3	86	162	72	4	6	20	7	143	7.60	5.30
Kasa-2	85	164	83	4	6	23	7	167	9.30	5.60
Jeldu-1	84	162	86	4	7	22	9	197	11.20	5.65
Local	82	160	66	6	8	27	12	347	10.65	3.65
Range	76-87	159-165	66-100	3-6	5-8	13-27	4-12	63-347	5.65-11.7	3.65-5.95
Mean	82.42	160.46	78.76	3.76	6.37	20.27	7.69	156.47	7.97	5.18
SE	1.4	2.13	2.06	0.17	0.30	2.96	2.17	21.63	1.13	0.15
LSD (0.05)	2.47	ns	3.54	0.29	0.51	5.10	ns	37.31	1.95	0.26

SE: Standard error, LSD: Least significance difference. DF: 50% days to flowering, DM: Days to maturity, PH: Plant height, NPBP: Number of primary branches/plant, NSBP: Number of secondary branches/plant, NCPP: Number of capsules/plant, NSPC: Number of seeds/capsule, NSPP: Number of seeds/plant, SYPP: Seed yield/plant, TSW: Thousand seed weight

Table 4: Phenotypic variance, genetic variance, phenotypic coefficient variation, genotypic coefficient of variation, heritability, genetic advance and genetic advance as percent of mean for 8 traits in 25 genotypes

Traits	PV	GV	PCV	GCV	h^2	GA	GAM
DF	6.58	5.55	0.03	0.03	0.84	4.45	5.39
PH	40.04	37.93	0.08	0.08	0.95	12.40	15.75
NPB	0.20	0.19	0.12	0.12	0.93	0.86	22.82
NSBP	1.02	0.98	0.16	0.16	0.96	2.00	31.40
NCPP	19.13	14.75	0.22	0.19	0.77	6.95	34.28
NSPP	2644.32	2410.35	0.33	0.31	0.91	96.54	61.7
SYPP	2.09	1.45	0.18	0.15	0.69	2.06	25.82
TSW	0.21	0.2	0.09	0.09	0.95	0.90	17.34

PV: Phenotypic variance, GV: Genotypic variance, GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, h^2: Broad sense heritability, GA: Genetic advance, GAM: Genetic advance as percent of mean. DF: 50% days to flowering, DM: Days to maturity, PH: Plant height, NPBP: Number of primary branches/plant, NSBP: Number of secondary branches/plant, NCPP: Number of capsules/plant, NSPC: Number of seeds/capsule, NSPP: Number of seeds/plant, SYPP: Seed yield/plant, TSW: Thousand seed weight

Table 5: Pearson correlation coefficients between 8 traits

Traits	DF	PH	NPB	NSBP	NCPP	NSPP	SYPP
DF							
PH	0.416**						
NPB	0.221	-0.001					
NSBP	-0.023	-0.122	0.661**				
NCPP	-0.122	-0.039	0.597**	0.719**			
NSPP	-0.188	0.291*	0.566**	0.511**	0.677**		
SYPP	0.018	-0.173	0.613**	0.512**	0.662**	0.767**	
SW	0.079	0.356*	-0.378**	-0.157	-0.339*	-0.125	-0.553***

*, **, ***significant at p≤0.05, p≤0.01 and p≤0.001 level, respectively. DF: 50% days to flowering, DM: Days to maturity, PH: Plant height, NPBP: Number of primary branches/plant, NSBP: Number of secondary branches/plant, NCPP: Number of capsules/plant, NSPC: Number of seeds/capsule, NSPP: Number of seeds/plant, SYPP: Seed yield/plant, TSW: Thousand seed weight

The phenotypic and genotypic coefficients of variation (PCV and GCV, respectively), heritability and genetic advance of the traits are shown in Table 4. The highest PCV and GCV were shown for number of capsules/plant (0.19 and 0.22, respectively) and number of seeds/plant (0.33 and 0.31, respectively) which indicates environmental influence on the performance of these traits was less. Similarly, Kandil *et al.* (2012) reported high PCV and GCV values for number of capsules/plant. The broad sense heritability value ranged from 0.69 for seed yield/plant-0.96 for number of secondary branches/plant. Wakjira (2011) reported high heritability (0.91) for days to flowering. The highest genetic advance as percent of mean (61.70) was recorded for number of seeds/plant, while the lowest value for this parameter (5.39) was recorded for days to flowering. High heritability value along with high genetic advance was shown by number of secondary branches plant, number of capsules/plant and number of seeds/plant. Ottai *et al.* (2012) and Kandil *et al.* (2012) reported similar result for capsules/plant. The highest genetic advance as percent of mean coupled with the high heritability value implies selection for the trait considered would be effective in early generation due to the likely additive gene action.

Pearson correlation coefficients between traits are presented in Table 5. Plant height showed positive significant correlation with days to flowering (0.416), number of seeds/plant (0.291) and 1000 seed weight (0.356). Number of primary branches/plant showed positive and significant correlation with number of secondary branches/plant (0.661), number of capsules/plant (0.597),

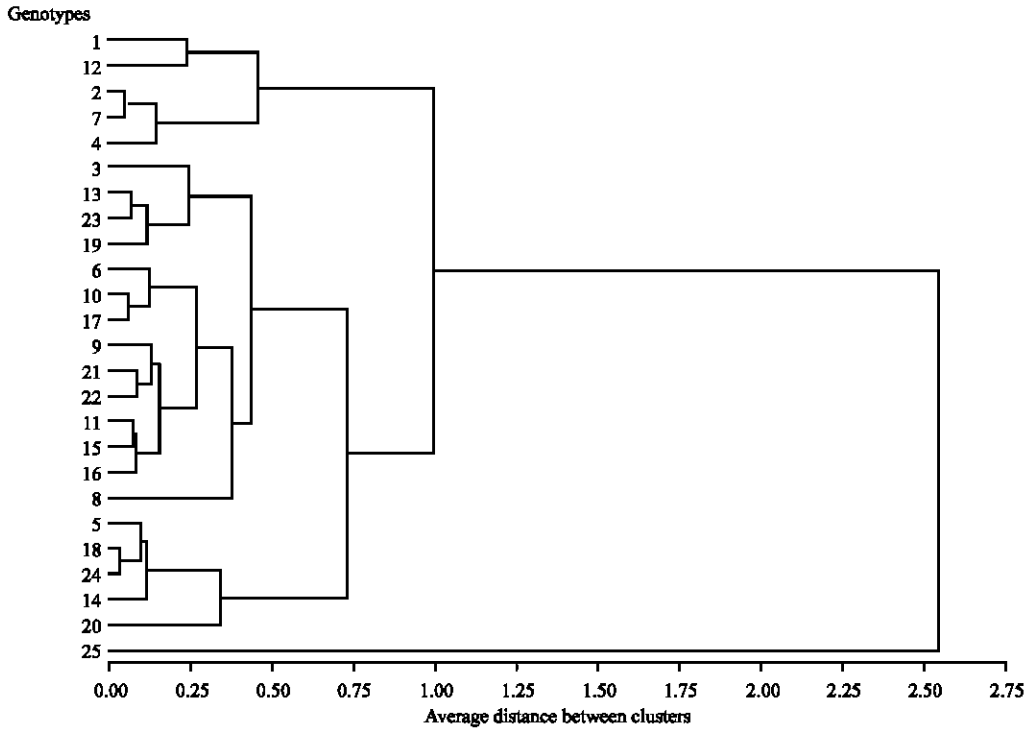

Fig. 1: Relationship among 25 linseed genotypes revealed by cluster analysis based on 8 traits

number of seeds/plant (0.566) and seed yield/plant (0.613), except 1000 seed weight (-0.378) which was negative and significant. Number of secondary branches/plant also showed positive and significant correlation with number of capsules/plant (0.719), number of seeds/plant (0.511), seed yield/plant (0.512), except 1000 seed weight (-0.157) which was negative though insignificant. Positive and significant correlation was also observed for number of capsules/plant with number of seeds/plant (0.677) and seed yield/plant (0.662). Number of seeds/plant showed positive and significant association with seed yield/plant (0.767), while 1000 seed weight showed negative and significant association with number of capsules/plant (-0.339) and seed yield/plant (-0.553). Hence, as an oilseed, in improving the seed yield of the genotypes in terms of number of branches/plant, number of capsules/plant and number of seeds/plant, we need to balance for 1000 seed weight. In agreement with the present investigation Pal *et al.* (2000) and Adugna and Labuschagne (2003) reported significant positive correlation of number of primary branches/plant and number of capsules/plant with seed yield, respectively. Contrarily, 1000 seed weight had positive significant correlation with seed yield (Akbar *et al.*, 2003; Adugna and Labuschagne, 2003).

The cluster analysis showed that the genotypes were placed into six groups, of which the fourth encompasses the largest number of genotypes (14), while the sixth contains only single genotype which is the local landrace (check) (Fig. 1).

CONCLUSION

This study indicates the presence of substantial genetic difference among the genotypes considered. Number of branches, number of capsule and number of seed are important traits for the improvement of seed yield of linseed. The genotypes can also be used for further crossing/hybridization program according to their classifications.

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