

GENETIC DIVERGENCE AND HETEROSIS IN LINSEED (*Linum ussitatissimum* L.)

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ABSTRACT

Cluster analysis can be used to identify cultivars with similar adaptation, which can be useful for sampling in subsequent studies and parental selection in hybridization breeding programs. Twenty-one flax genotypes differed in their origin and purpose were used in this study. Sixteen agronomic and yield characters were evaluated. Analysis of variance revealed significant differences for all studied characters indicating the presence of considerable amount of genetic variability. The variation due to parents, crosses were also significant for presence of most characters. Parents vs crosses were significant for most characters, indicating the heterotic effects. Significant positive heterosis over mid-Parents, better parent and commercial cultivars were observed for seed yield/fed, number of apical branches/plant and number of capsules/plant. The crosses exhibited heterosis for seed yield also showed significant heterosis for most yield components characters. The cross combination Sakha 3 x Gowhar surpassed all genotypes for oil content. The 85% of dissimilarity coefficients were significant.

The Twenty-one parents were grouped into seven major groups based on relative dissimilarity among them with significant differences between groups for most characters. The maximum distance observed between cluster V and VII, whereas the minimum distance between cluster III and VI. The forty one genotypes were grouped into ten clusters, while most F₁ combinations were distributed on seven differed clusters indicating that the progeny produced from crossing between two distantly related parents showed divergent distance and gave values surpassed their parents in most characters.

Keywords: Genetic divergence – heterosis – linseed

INTRODUCTION

Heterosis is a complex genetical phenomenon, which depends on the balanced of different combinations of gene effects as well on distribution of plus and minus alleles in the parents. Exploiting heterosis is one of the methods used to increasing yield, fiber and seeds that have stagnated in recent years. The knowledge of the nature and extent of genetic variability plays an important role in designing a successful breeding program.

It is an established fact that in any plant population greater the genetic variability greater the chance of obtaining the desirable gene recombinants with increase heterotic effects (Kumari and Rao, 2008). Few researches were made on the heterotic effect in linseed, for this regard Mahto *et al.* (2001), Rao *et al.* (2001), Kusalkar *et al.* (2002), Bhatia and Pathania (2003), Ewes (2006) and Mohammadi *et al.* (2010) studied heterosis in seed yield and its components characters and found that heterosis was observed in most yield characters .

Genetic divergence among parents is considered an important factor for obtaining heterotic effects. This diversity is one of the restraining tools for breeding programs based on hybridization, because it generate parameters

for identifying superior parents. This distance is essential to increase the chance of recovering superior genotypes. Cox *et al.* (1985), suggested crossing distantly related lines in an inbred improvement programmed to maximize the number of segregating loci in the F₂ and subsequent inbred generations.

Estimation of genetic diversity is an important step for a breeding program, but not the last one. Another helpful issue to be evaluated is the relative importance of the characters. The efficacy of the genetic divergence as a criterion for choosing parents for crossing programs has been reported by many workers (Verma, 1996; Mahto and Verma, 1998; Mansby *et al.* 2000; Adugna *et al.* 2005 Moreover, Chandra 1977, Kumari and Rao 2008 and Tadesse *et al.* 2009), Selected some genotypes from distinct cluster for hybridization program to obtain high heterotic expression and also to recover desirable transgressive segregates.

Hence, The objectives of this research was to determine the variability and heterotic effects among flax combinations and assess genetic diversity among 21 parents of flax as well as among parents and F₁ hybrids.

MATERIALS AND METHODS

The experiment was conducted at Gemmeiza Agric. Res. Station during the two growing seasons of 2007/08 and 2008/09. Twenty one parental genotypes belonging to (*Linum usitatissimum* L.) were used. These genotypes were differed in these origin and purpose. Origin and purpose of these genotypes are shown in Table 1.

Selfed seeds of 20 parents were sown and crossed as male with the local cultivars Sakha 3 as female parent to produce 20 F₁ hybrids in 2007/2008 growing season. The twenty one genotypes with twenty F₁ hybrids were growing and evaluated in a randomized complete blocks design with three replicates. Each entry was planted in a single row. The row to row distance was 20 cm and five cm within row with three meters row long for each studied genotype.

Data were recorded on ten individual guarded plants from each genotype on days to first flower, days to 50% flowering, days to maturity, plant high, technological stem length, fruiting zone length, main stem diameter, number of apical branches / plant, number of capsules / plant, number of seeds / capsule, seed index, seed yield / fed, fiber yield / plant, fiber length, fiber fineness and oil content %.

The data were subjected to two methods of statistical analysis. Initially, the analysis of variance (F test) for all sixteen characters was done to detect the significance of the observed differences as described by Sokal and Rohlf (1995). The amount of heterosis was calculated as follows.

$$\text{Mid parent heterosis} = \frac{F_1 - \overline{MP}}{\overline{MP}} \times 100$$

$$\text{Better parent heterosis (heterobeltiosis)} = \frac{F_1 - \overline{BP}}{\overline{BP}} \times 100$$

Superiority of F_1 hybrids over the standard commercial check variety:

$$\text{Superiority} = \frac{F_1 - \overline{CC}}{\overline{CC}} \times 100$$

L.S.D for mid parent, better parent heterosis and commercial cultivar were estimated.

Where, F_1 , \overline{MP} , \overline{BP} and \overline{CC} refer to means of F_1 generation, mid parent, better parent and commercial cultivar, respectively.

After this step, multivariate technique was used to assess the dissimilarities among flax genotypes. This technique was found to resolve several phenotypic measurements into fewer more interpretable and more easily visualized dimensions (Johnson and Wichern, 1988). Therefore, Hierarchical clustering procedure using ward's minimum variance method, which minimize within group sum of squares across all partitions, was applied to determine the genetic diversity and distance as outlined by Anderberg (1973) and developed by Johnson and Wichern (1988). The Euclidean distance was computed and the results from clustering analysis are presented as dendrograms, the dendrogram is constructed on Euclidean distance base. All computations were performed using Minitab (1998) and SPSS (1995) computer procedures.

Table 1. Genotypes and pedigree of parents.

No.	Genotypes	Performance	Pedigree or origin	Purpose
1-	Giza 4	Local cultivar	Pink Giza x Oil Giza	Dual purpose cultivar
2-	Giza 6	Local cultivar	Hindi x Giza 4	Dual purpose cultivar
3-	Giza 8	Local cultivar	Giza 6 x Senta catalina	Dual purpose cultivar
4-	Sakha 2	Local cultivar	L.2348 x Hera	Dual purpose cultivar
5-	Romania 20	Introduced variety	Romania	Fiber production
6-	Gowhar	Introduced cultivar	India	Oil production
7-	Bombay	Introduced cultivar	India	Oil production
8-	Hermes	Introduced cultivar	Netherlands	Fiber production
9-	L1	Local elite line	Fiber crops Res. Sec.	Oil production
10-	L3	Local elite line	Fiber crops Res. Sec.	Oil production
11-	L4	Local elite line	Fiber crops Res. Sec.	Oil production
12-	L5	Local elite line	Fiber crops Res. Sec.	Oil production
13-	L6	Local elite line	Fiber crops Res. Sec.	Oil production
14-	L15	Local elite line	Fiber crops Res. Sec.	Oil production
15-	L16	Local elite line	Fiber crops Res. Sec.	Oil production
16-	402	Local elite line	Fiber crops Res. Sec.	Oil production
17-	435	Local elite line	Fiber crops Res. Sec.	Oil production
18-	533	Local elite line	Fiber crops Res. Sec.	Oil production
19-	2419	Local elite line	Fiber crops Res. Sec.	Oil production
20-	2467	Local elite line	Fiber crops Res. Sec.	Oil production
21-	Sakha 3	Local cultivar	L.2096x telinka2E	Elite fiber flax line

RESULTS AND DISCUSSION

Results of the analysis of variance (Table 2) revealed that the differences between the genotypes were significant for all studied characters, indicating the presence of considerable amount of genetic variability. The variation due to parents was also significant. Such variations could be attributed to the varied in genetic background of parents. Chandra (1977), working on the diversity of flax, reached similar conclusion with regard to the varied back ground of flax landraces. The crosses showed significant differences in most characters, revealed that this variability could be transmitted to the progeny. Also, the variation due to parents vs crosses was also significant for most characters, indicating the heterotic response for these characters.

The obtained results of heterosis for yield and yield components characters are presented in (Table 3). The data revealed significant heterosis over mid-parents levels and better parent for seed yield / fed. Sixteen F₁ combinations showed significant positive heterosis over better parent for seed yield, while seven combinations gave Superiority over commercial parent. The combinations Sakha 3 x Romania 20, Sakha 3 x Giza 8, Sakha 3 x L 5 and Sakha 3 x Gowhar gave the best values. Regarding to yield components character number of apical branches / plant , five cross combinations exhibited desirable heterosis over better parent, positive values, and two combinations showed the same trend over commercial parent. The cross combinations Sakha 3 x Giza 6 and Sakha 3 x L 5 gave best values over better and commercial parents. On the other side, two combinations showed significant negative values for such characters. Thus it was desirable for fiber propose.

For number of capsules / plant (Table 3) fourteen and eight crosses exposed significant useful heterosis over better parent and also found Superiority over to commercial parents respectively. No crosses exceeded better parent for number of seeds / capsule, but thirteen combinations surpassed commercial parent for this character.

Concerning to oil content, no any combination crosses exhibited significant useful heterosis over better parent, also, four combinations showed Superiority over commercial parent. The combinations Sakha 3 x Gowhar surpassed all genotypes, parents and crosses, for oil content , this might due to the Indian genotype Gowhar might possess most dominant genes which control in oil content and this characters could transmitted to the progeny. In the same trend Sakha 3 x Sakha 2, Sakha 3 x 2467 and Sakha 3 x 2419.

It is interesting to note that , the higher yield / fed dose not necessarily depend on the high heterotic behavior of the combination of all yield components which are ultimately associated with yield be sufficient to enhance the yield. Roa *et al.* (2001), Kumar *et al.* (2002) Singh *et al* (2009) and Mohammadi (2010) also reported almost identical .

Table 2. Analysis of variance for the studied characters of flax genotypes.

S.O.V	Df	M.S.															
		First flowering	50% flowering	Days at Maturity	Plant height	Stem length	Main stem diameter	Fruiting zone length	N. of apical branches	N. of Capsules / plant	N. of Seeds/ Capsule	Seed index	Seed yield / fed.	Fiber Yield/ plant	Fiber length	Fiber Fine-ness	Oil content %
Reps	2	7.54	12.54	2.74	0.25	7.83	0.0249	8.61	1.309	10.49	0.285	0.024	333.00	0.0036	1.24	216.00	1.489
Genotypes	40	43.08	19.42	15.03	58.57	53.53	0.2384	40.20	0.331	40.82	0.476	1.269	23241.00	0.058	49.19	470.7	4.85
Parents	20	59.56	34.26	28.12	68.32	67.45	0.3517	56.15	0.333	33.31	0.354	1.72	13852.00	0.087	62.57	352.00	2.434
Crosses	19	27.82	4.85	1.99	13.79	19.1	0.0695	23.63	0.312	24.27	0.146	0.776	21743	0.026	18.51	617.45	7.581
P.VSC	1	3.45	3.11	1.15	714.40	429.26	1.185	36.11	0.869	505.5	9.206	1.585	239481	0.073	364.52	56.04	1.281
Error	80	5.36	4.06	0.915	5.71	4.05	0.0281	7.52	0.159	3.79	0.134	0.254	387	0.002	2.58	36.5	0.454

*, ** Significant and Highly Significant At 0.05 and 0.01 Level of Probability Respectively.

Table 3. Heterosis over mid-parents, MP, better parent, BP and commercial cultivar, CC, for yield and yield components characters

No.	Genotypes	Seed Yield / fed (kg)			No. of apical branches			No. of capsules / plant			No. of seeds / capsules			Seed index "gm"			Oil Content "%"		
		MP	BP	CC	MP	BP	CC	MP	BP	CC	MP	BP	CC	MP	BP	CC	MP	BP	CC
1	Sakha3*Giza6	51.485**	21.886**	5.776	5.963	-0.391	6.250	12.062*	-8.403	-13.834**	-3.493	-5.007	-2.708	20.623**	12.319*	13.139*	42.495*	16.568*	34.47**
2	Sakha3*L16	52.736**	26.846**	1.462	6.318	0.898	7.625*	16.427**	3.061	-20.158**	-1.641	-3.022	-1.012	16.535*	9.630	8.029	42.982**	35.270**	11.26-3
3	Sakha3*L5	59.907**	17.065**	33.340**	5.929	4.688	11.667**	22.946**	7.428	-14.229**	-6.022*	-7.194*	-5.574	24.409**	13.333**	15.326**	56.826**	48.954**	21.502**
4	Sakha3*L3	40.237**	25.089**	-15.642**	-1.976	-3.12	3.333	15.014*	0.495	-19.763**	3.131	2.919	2.103	-2.527*	-14.557**	-1.46	30.451**	9.464	18.43C*
5	Sakha3*L1	17.911**	5.036	-28.952**	4.703	0	6.667*	8.598	-12.245*	-15.020**	-1.569	-2.854	-1.061	-3.150	-8.869	-10.219	36.219**	33.482**	2.046B
6	Sakha3*402	65.566**	55.365**	-6.312	5.027	0.781	7.500*	5.600	-11.607*	-21.739**	3.142	2.969	2.083	8.502	4.688	-2.19	52.926**	45.684**	18.066*
7	Sakha3*2467	73.631**	71.409**	-6.997	2.058	-3.125	3.333	8.635	-6.250	-22.925**	5.760*	5.649	4.811*	19.679**	14.615**	8.759	54.177**	41.628**	3.925*
8	Sakha3*2419	60.396**	52.363**	-10.478*	7.171*	5.078	12.083**	4.278	-12.556*	-22.925**	4.194	2.989	4.592*	11.197	2.857	5.109	51.440**	45.116**	25.597**
9	Sakha3*4termes	74.282**	38.922**	23.621**	8.730**	3.633	10.542**	12.113*	-2.451	-21.344**	-6.668*	-6.143*	-6.348*	24.696**	24.167**	8.759	36.384**	34.234*	1.706-
10	Sakha3*Giza6	104.204**	56.602**	55.109**	1.21	-1.963	4.583	41.311**	24.000**	-1.976	2.172	0.907	2.648	11.969	3.571	5.638	33.676**	5.834	33.106**
11	Sakha3*Bombay	77.022**	44.689**	20.511**	1.02	1.417	7.333*	21.246**	5.941	-15.415**	2.094	0.898	2.500	6.967	4.4	-4.745	33.638**	31.532**	-0.34F
12	Sakha3*533	53.819**	31.857**	-2.425	1.181	0.391	7.083*	7.050	-11.838*	-18.972**	-0.818	-2.169	-0.228	21.962**	20.492**	7.299	26.807**	25.455*	-5.802*
13	Sakha3*L6	27.701**	24.214**	-30.535**	4.593	0.808	7.208*	15.341*	0.986	-18.763**	-5.465*	-5.611	-6.070*	1.527	-6.963	-2.92	35.242**	28.452**	4.778
14	Sakha3* Sakha2	53.524**	17.345**	17.345**	3.750	0.808	7.208*	-4.950	-24.111**	-24.111**	4.780	4.364	4.364*	0	-6.569	-6.569	33.485**	15.700	15.700D
16	Sakha3*435	23.625**	-2.335	-10.977*	8.687**	5.078	12.083**	-2.747	-16.901**	-30.040**	0.671	-0.863	1.26	7.087	0.741	-0.73	27.684**	24.176*	-3.584
16	Sakha3*Giza4	38.005**	8.936	-0.481	3.393	1.172	7.917*	11.717*	-5.093	-18.972**	1.035	0.52	-0.278	8.745	-0.694	4.38	42.007**	18.266*	30.375**
17	Sakha3*Gohar	102.949**	75.312**	27.379**	-0.398	-2.344	4.167	34.513**	21.277**	-9.881*	8.891**	3.119	14.432**	6.299	0	-1.46	27.083**	15.094	4.086
18	Sakha3*L4	0.938	-23.630**	-21.325**	0.398	-1.562	5.000	15.183**	-4.762	-13.043**	1.109	-0.33	1.775	-3.273	-14.744**	-2.92	-10.747	-26.647**	-16.362**
19	Sakha3*L15	49.253**	46.413**	-19.530**	6.250	-0.38	6.250	8.527	-11.017*	-16.996**	0.607	0.25	-0.546	1.186	-4.478	-6.569	13.669	3.226	-7.167
20	Sakha3*Romania20	79.096**	36.156**	38.301**	3.026	2.311	10.667**	3.743	-13.004	-23.320**	-4.635	-6.924**	-4.077**	12.941	5.862	5.109	41.131**	21.477**	23.549**
	LSD 5%	27.821	32.125	32.125	0.517687	0.597774	0.597774	0.712741	0.823003	0.823003	0.953	1.100	1.100	0.564	0.651	0.651	2.753	3.179098	3.179098
	LSD 1%	37.00174	42.72593	42.72593	0.686524	0.795039	0.795039	0.947946	1.094594	1.094594	1.267	1.46	1.46	0.750007	0.866033	0.866033	3.661729	4.228201	4.228201

*, ** Significant and highly significant at 0.05 and 0.01 level respectively

Hierarchical clustering analysis:

This procedure, using disjoint cluster analysis on the basis of Euclidean distance, was applied to illustrate relative genetic distance and genetic divergence within a given germplasm base.

a- Among parental genotypes:

The actual values of Euclidean distance corresponding to the 210 possible comparisons, taking two genotypes at time are given in Table 4. These estimates that treated as Chi-square values showed that about 85% of the values were significant. Euclidean distance was ranged from 8.029 between Romania 20 and Sakha 2 to 221.4 between Gowhar and L 5.

The genetic divergence based on Euclidean distances between the twenty one parental genotypes is graphically illustrated as dendrogram, tree diagram, in Figure 1.

The 21 parents were grouped into seven major clusters according to hierarchical clustering analysis based on the relative dissimilarity among 21 parents and 16 agronomic characters. It is clear that, the parent Gowhar, L 5 and Herms formed a wide three groups having divergent distance from the other genotypes and from each other. The dendrogram showed that the divergence between Romania 20, Sakha 2, Giza 8 and L 4 was not clearly pronounced, since these parental genotypes appeared to be closely related with average coefficient 10.8 inter cluster.

Distribution of flax parental genotypes in clusters is given in Table 5. The twenty one flax genotypes were grouped into seven major clusters revealed a large amount of genetic variability. Cluster I represented 19% of total material consisted of four genotypes, Romania 20, L 4, Giza 8 and Sakha 2 with the lowest average dissimilarity coefficient 10.838. These genotypes were varied in purpose, but agreement in large seed yield with it's attribute (number of seeds/capsules and number of capsules/plant. Cluster II contained four genotypes which accounted 19% of total material also. Most of these genotypes were local elite line and tester (Sakha 3) with average coefficient 28.066. This cluster was large divergent distance with the other clusters. The genotypes of this cluster characterized by decrease in seed yield with its attributes. Cluster III consists of five genotypes (23.8%) such as Bombay (Indian genotype), two local cultivars (Giza 4 and Giza 6) and two local elite line, with average coefficient 25.496. Cluster IV contained five local elite line (23.8%) and characterized by high straw yield with very late in maturity and decrease in seed yield with the second small average coefficient within cluster 14.248. Contrarily, clusters V, VI and VII consisted of one genotype (4.8% of total material) for each. L 5, Herms and Gowhar, respectively. These genotypes were highly significant distance with the other genotypes. The divergent distance was obtained among cluster V and VII. El-Mansy *et al.* (2010) reported that chose parents which have greatest genetic divergence in order to obtain the best combination. However, not only genetic divergence might be used to choose parents for crossing, but also their performance.

Table 4. Squared Euclidean dissimilarity coefficients among the flax genotypes.

Case	Euclidean Distance																			
	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
1	177.4	99.8	67.0	170.8	39.3	123.3	9.7	38.4	45.6	13.3	149.1	123.8	168.7	59.1	8.0	59.1	154.4	164.7	78.0	107.8
2		81.8	45.9	72.0	72.0	36.2	113.5	71.8	221.4	99.0	51.1	34.2	69.5	74.9	101.5	57.8	56.4	68.2	38.6	81.7
3			34.1	71.6	63.0	60.7	105.7	64.7	144.6	91.4	51.2	27.8	69.6	65.9	94.0	52.8	56.4	66.8	24.4	24.1
4				104.7	29.8	60.0	73.2	34.1	111.8	59.4	83.8	58.3	102.5	48.6	61.1	32.0	89.7	99.8	17.3	114.8
5					133.1	50.9	176.3	134.9	215.4	162.2	24.4	50.2	11.2	132.3	165.1	121.6	21.5	13.8	93.4	34.1
6						87.2	44.6	16.0	83.0	32.2	111.3	86.0	130.9	46.4	33.5	37.4	117.3	127.3	41.7	142.8
7							128.6	86.6	167.8	114.9	31.8	27.7	51.1	86.9	118.1	73.5	34.5	44.0	45.9	36.9
8								43.6	39.9	16.3	154.3	129.1	174.1	63.9	14.5	66.2	159.6	169.8	83.6	183.4
9									82.2	31.7	113.0	89.4	133.2	42.8	33.9	28.2	118.2	128.6	42.2	142.9
10										54.8	193.3	167.9	213.3	97.2	51.4	102.7	198.7	208.9	122.6	151.0
11											140.1	114.4	159.5	50.8	8.6	53.8	145.3	155.7	70.3	168.8
12												29.6	23.2	111.7	143.3	101.4	10.1	18.4	72.2	44.4
13													46.1	87.6	117.5	79.6	35.9	45.6	49.9	23.5
14														129.8	162.6	120.1	20.9	17.1	92.2	35.1
15															54.6	40.9	114.4	125.2	52.2	130.7
16																55.1	148.7	159.1	72.8	172.2
17																	105.4	116.5	35.7	126.3
18																		12.7	77.4	35.5
19																			87.4	33.4
20																				102.8
21																				

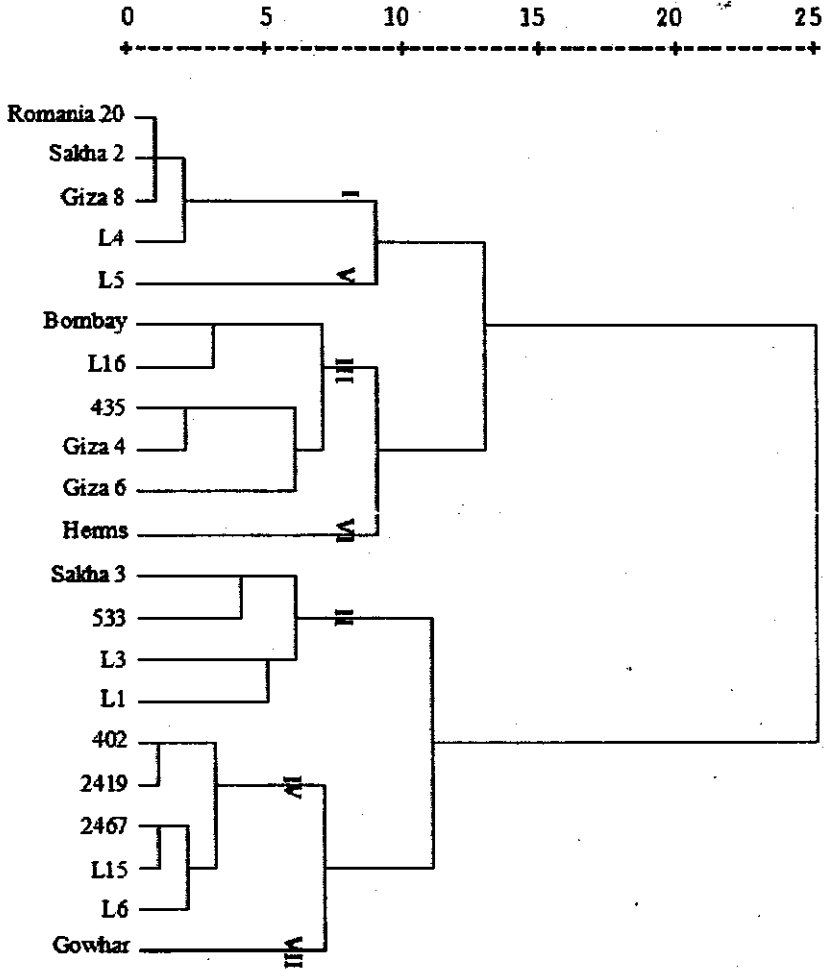


Figure 1. dendrogram presentation of the studied parental flax genotypes .

Table 5: Distribution of 21 parental genotypes in different clusters.

Clusters No.	N. of genotypes	genotypes
I	4	Romania20, L4, Giza8 and Sakha2
II	4	533, L3, Sakha3 and L1
III	5	Bombay, 435, Giza4, Giza6 and L16
IV	5	2467, 402, L15, 2419 and L6
V	1	L5
VI	1	Herms
VII	1	Gohar

Therefore, these clusters might be consisted of diverse genotypes on the basis of quantitative characters. The selected genotypes from various clusters are suggested to be used in crop improvement in future, (Singh *et al.* 1997). Inter-cluster distance is a good indication to select diverse parental lines. It is suggested that superior pure line from diverse cluster may be chosen for hybridization due to better performance of hybrids (Ghafoor *et al.* 2001).

b- Among parents and F₁ hybrids:

The studied flax genotypes, parents and F₁'s were subjected into clustering analysis based on Euclidean distance between them. The clustering pattern of these genotypes are graphically illustrated as diagram in Figure 2 .The distribution pattern of F₁ heterozygous was more or less influenced by their parents as expected on the basis of close affinity between the parents and their F₁ hybrids. The 41 flax genotypes, 20 F₁ hybrids and 21 parents, were grouped at ten major clusters (Figure 2) while the F₁'s were grouped at seven cluster (Table 6). Cluster I was the largest one and included 13 genotypes, seven of them were F₁ and six were parental genotypes with the smallest coefficients 5.346, most of F₁ hybrid's in this cluster between the two distinct parents. Cluster II contained three F₁ genotypes. All these genotypes were among diverse parents with average coefficient 27.7. This cluster was widely divergent from the other clusters specially cluster I and closely related with cluster V and VII with coefficient 58.28. In the same trend, cluster VIII contained one F₁ genotype Sakha 3 x Giza 4. Such conclusion might indicate that considerable divergence could be created by hybridization, since F₁'s were widely dispersed from their parents. Cluster IV aggregate six genotypes two of them were F₁ and the other were parents. The mean dissimilarity coefficient among the six genotypes was 17.92.

It is worth to note that, the Indian variety Gowhar was grouped in wide cluster and wide divergence from the other clusters, this variety was the earliness genotypes with largest oil content. Cluster VII consisted of three genotypes, two F₁ with one inbred line (L 5) with average dissimilarity coefficient 21.25. In contrary, cluster IX consisted of six genotypes one of them F₁ heterozygous resulting of crossing between two distinctly parents Sakha 3 and Giza 8 with average coefficient 18.69 and this cluster was closely related with clusters III and IV. The Netherland cultivar formed unique group and closely related with cluster VIII.

Most F₁ combinations were distributed in a different cluster and no fall around the parents in the same cluster. The observation suggested that, the genotypes from different origin and different parents fall in the same cluster and, thus indicated their closeness. On the other hand, the genotypes from the same origin " Parents " were distributed to different clusters. (Tadess *et al.* 2009).

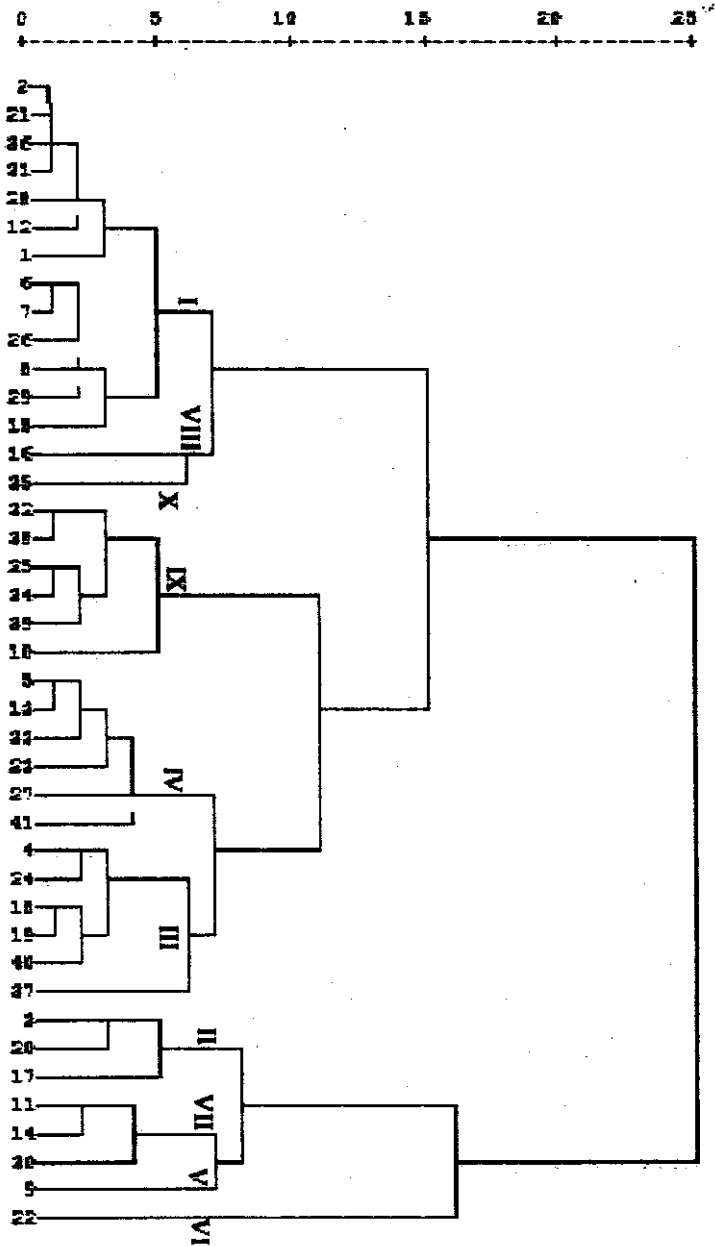


Figure 2. dendrogram presentation of the studied flax genotypes (parents and F₁).

Table 6. Distribution of 41 parental and F₁'s genotypes in different clusters.

Clusters No.	N. of genotypes	Genotypes
I	13	Sakha3 X L16, Romania20, Sakha2, Giza8, L4, Sakha3 X 533, Sakha3 X Giza6, Sakha3 X 402, Sakha3 X 2467, 435, Sakha3 X 2419, Giza4, Sakha3 X 435
II	3	Sakha3 X L5, Sakha3 X Romania20, Sakha3 X Gohar
III	6	Sakha3 X L3, Sakha3 X L4, Sakha3 X L15, Bombay, L16, Giza6
IV	6	Sakha3 X L1, Sakha3 X L6, Sakha3, L1, L3, 533
V	1	Sakha3 X Herms
VI	1	Gohar
VII	3	Sakha3 X Bombay, Sakha3 X Sakha2, L5
VIII	1	Sakha3 X Giza4
IX	6	Sakha3 X Giza8, L6, L15, 2467, 2419, 402
X	1	Herms

Results in Table 7 illustrated cluster means of 16 studied characters, involved in Euclidean clustering analysis, for each cluster. Cluster II characterized by high seed yield with significance with the other clusters, with superiority in other yield attributes. While, it was approximately early. Whereas, cluster VI was superior in all earliness characters with oil content ratio and fiber yield " straw yield " on the other hand, cluster VII gave the best value for fiber length.

Based on genetic divergence between genotypes and cluster means, it can be concluded that genotypes of the selected clusters II, VI, VII and the cultivated variety Sakha 3 could be selected for a breeding programs aimed to improvement yield and quality in flax. Our results were agreement with Kumari and Roa (2008).

It is evident to note that crossing of distantly related parents may give best hybrids which surpassed their parents in most characters and should higher variance in most characters in segregating generation rather than crossing between closed related parents, which agree with Ali *et al.* (1995). While, Sandhu and Boparai (1997) reported that genetically diverse genotypes when used as parents in hybrid breeding program generate a wide range of variability and provide transgressive segregants in a hybridization program, thereby enhancing the probability of new genotypic expression due to accumulation of maximum desirable genes.

Flax breeders desire to increase genetic diversity among new cultivars, while at the same time maintaining the complex of desired agronomic and quality traits present in existing popular cultivars. Developing such a combination can be difficult, as the introgression of new genetic material is expected to disturb genetic complex responsible for desirable traits. The use of cross among divergent cultivars could be a means to achieve both ends.

Table 7: Cluster Means of the Contributed Clusters in Each Cluster.

No. Cluster	No. Of Genotypes	Contributed Characters															
		Plant height	Stem length	Main stem diameter	Fruiting zone length	N. of apical branches	N. of Capsules / plan	N. of Seeds/ Capsule	Seed index	Seed yield / fed.	Fiber Yield/ plant	Fiber length	Fiber Fineness	Oil content%	First flower	50% flowering	Days at Maturity
I	13	93.24	66.81	2.43	26.43	4.77	21.24	8.42	6.99	347.99	1.76	57.98	225.84	33.99	109.62	49.56	134.33
II	3	97.21	67.38	2.52	29.84	4.86	22.74	8.72	7.10	279.00	1.79	59.59	223.78	35.66	104.78	118.22	133.67
III	6	91.08	67.4	2.17	23.68	4.41	18.00	8.22	7.13	304.17	1.78	58.27	224.20	33.25	109.93	119.98	134.23
IV	6	91.53	68.26	2.16	23.26	4.39	17.58	8.36	6.93	341.57	1.91	59.117	231.52	33.31	109.78	120.11	134.44
V	1	97.27	67.23	2.40	30.03	4.97	19.87	8.84	6.63	445.20	1.64	58.43	268.47	31.47	105.67	118.67	134.33
VI	1	86.53	64.27	2.54	22.27	4.50	17.67	8.20	6.27	261.67	1.94	55.77	228.21	37.29	94.33	106.00	121.33
VII	3	95.87	69.39	2.50	26.48	4.37	19.33	8.50	6.76	422.27	1.67	60.77	225.81	34.57	108.67	119.33	134.78
VIII	1	95.33	67.7	2.52	27.63	4.77	25.47	8.63	6.83	358.40	1.88	59.07	269.78	33.51	40.67	118.00	133.00
IX	6	93.27	68.03	2.07	24.556	4.00	17.567	7.902	7.44	263.68	1.94	60.122	228.31	33.61	110.83	118.94	134.22
X	1	96.27	66.03	1.88	30.23	4.00	14.8	7.73	6.80	320.47	1.88	57.67	265.14	34.26	108.00	119.67	136.33
L.S.D		3.90	3.29	0.27	4.47	0.65	3.17	0.59	0.82	32.15	0.07	2.62	9.86	1.10	3.78	3.29	1.65

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التباعد الوراثي وقوة الهجين في الكتان

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** قسم بحوث الألياف - الجميزة - مركز البحوث الزراعية .

أجرى هذا البحث بمحطة البحوث الزراعية بالجميزة خلال موسمي الزراعة ٢٠٠٧/٢٠٠٨ و ٢٠٠٨/٢٠٠٩م. تم استخدام واحد وعشرون تركيب وراثي من الكتان تابعه للنوع (*Linum usitatissimum* L.) في صفاتها وهي : جيزة ٤ ، جيزة ٦ ، جيزة ٨ ، سخا ٢ ، رومانيا ٢٠٠٧ ، جوهر ، بومبي وهيرمس ، السلالات ١ ، ٢ ، ٣ ، ٤ ، ٥ ، ٦ ، ١٥ ، ١٦ ، ٤٠٢ ، ٤٣٥ ، ٥٣٣ ، ٢٤١٩ ، ٢٤٦٧ ، وسخا ٣.

يهدف هذا البحث لدراسة الاختلافات الوراثية للأبء والجيل الأول وكذلك دراسة قوة الهجين لصفات محصول البنور ومكوناته أيضا دراسة التباعد الوراثي بين الأبء وكذلك بين الأبناء والجيل الأول باستخدام التحليل المتمد اعتمادا على عدم التشابه النسبي .

تم دراسة صفات ارتفاع النبات والطول الفعال للساق وحجم المنطقة الثمرية ، عدد الأفرع القمية ، قطر الساق الرئيسي ، محصول البنور / ف ، عدد الكبسولات / نبات ، عدد البذور / كبسولة ، وزن ١٠٠٠ بذرة ، محصول القش ، طول الليفة ، النعومة ، محتوى الزيت % .
وكانت أهم النتائج المتحصل عليها كالآتي :

- أظهر تحليل التباين اختلافات معنوية بين التركيب الوراثية لجميع الصفات مما يدل على وجود كمية كبيرة من الاختلافات الوراثية ، كما كانت الاختلافات بين الأبء وكذلك الهجن معنوية لمعظم الصفات .
- أظهر تفاعل الأبء مع الهجن معنوية لمعظم الصفات مما يدل على وجود التأثير الهجينى .
- أظهرت النتائج أن هناك معنوية لقيم قوة الهجين على أساس متوسط الأبوين وكذلك هناك تفوق بين الهجن والصف التجاري لصفة محصول الحبوب / فدان ، عدد الأفرع القمية / نبات ، عدد الكبسولات / نبات ، كما وأن الهجن التي أظهرت قوة هجين لصفة المحصول، وقد أظهرت قوة هجين أيضا لمعظم صفات مكونات المحصول .
- أظهرت النتائج أن التركيب الهجين سخا ٣ × جوهر قد تفوق على كل التركيب الوراثية بالنسبة للمحتوى الزيتي .
- كانت ٨٥% من القيمة معنوية لمعامل عدم التشابه النسبي .
- تم توزيع التركيب الأبوية " ٢١ " الى سبع مجاميع رئيسية ، وذلك على أساس عدم التشابه النسبي بينهما مع وجود اختلافات معنوية بين المجاميع لمعظم الصفات .
- كان التجمع رقم (٥) أكثر تباعدا عن التجمع رقم (٧)، بينما أظهر التجمع رقم (٣) والتجمع رقم (٦) قرابة نسبية .
- توزعت للتركيب الوراثية " الأبوية والهجينية " على عشر مجاميع رئيسية مع توزيع التركيب الخليطية على سبع مجاميع ، كما أظهر للنتائج من التهجين بين أباء متباعدة درجة كبيرة من عدم التشابه النسبي والتباعد الوراثي ، كما أعطى فيما تفوق قيم آباتها لمعظم الصفات .
- وعلى ذلك فإن المربي يمكنه استخدام هذه التركيب الوراثية في برامج التربية المختلفة التي تهدف لتحسين صفات محصول البذرة أو الألياف في الكتان .

قام بتحكيم البحث

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