Efficiency of Two Breeding Methods on Flax Population

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Abstract

The experiment was carried out at the Etay El-Baroud Experiment Station, El-Beheira Governorate, Egypt during the three successive seasons of 2014-2015, 2015-2016 and 2016-2017. The present study aimed at measuring the efficiency of two methods of selection used in the flax breeding program namely; pedigree method (PM) and bulk method (BM) on one flax population droved from previous work by the other (self) in 2014. F_2 seed from the previous work furnished the source material for subsequent generations of flax populations (S2465/1 × Giza 8). In 2017 season, the high yielding selected lines (20) from each methods of breeding (two methods *i.e.* pedigree and bulk). Comparison between two breeding methods, mean square due to breeding methods were significant for days to flowering , No. of capsules / plant , length of fruiting zone , No. of seeds / capsule , seed index , seed yield /plant , technical stem length , and oil percentage. This result indicated the difference between breading methods. The pedigree methods gave the highest value for all traits**.** The pedigree method proved to be more efficient than bulk method for selection based on these traits may be due to the two parent good combiner for most traits. Also, gave the earliness of days to flowering. These result in this cross where a two parent were good combiner for most trait. For days to flowering, the result indicated that the pedigree method produced more superior lines than bulk method compared the best parent with fifteen and sixteen lines respectably. The best line was No. 7 of pedigree method. As for No. of capsule/ plant , 20 and 9 lines showed significant higher than best parent for pedigree and bulk method gave the highest number of capsules/ plant . Regarding to No. of basal branches/plant, the pedigree method produced consistently none superior parent compared the best parent, with three and four lines for pedigree and bulk, respectively. For No. of seeds / capsules, only the line No. 14 of pedigree method of breeding gave the highest no. of seeds / capsule. Concerning seed index, all lines of pedigree and bulk methods surpassed the best parent. Also, the line No. 9 of pedigree method gave the behavior seed index. With regard to seed yield/plant, four and six lines surpassed significant seed. Yield compare the best parent. The best line was No. 19 of pedigree followed by No. 2 of bulk method of breeding. For total length, sixteen lines of both breeding methods surpassed significant compare the best parent. The best line was No. 1 of pedigree method (123, 67). Regarding technical stem length, fourteen and nine lines showed significant higher than the best parent for pedigree and bulk methods, respectively the best line was No. 6 (112. 67) followed by No. 5 (111 . 33) of pedigree method . For fiber percentage, none of lines showed significant compare the best parent or over mean.

Keywords: Breeding methods, Pedigree, modified bulk and flax.

Introduction

Flax (*Linum usitatissimum L.*) also known as flax is cultivated for seeds and fibers. Its oil is largely of drying type and non-edible because of high amount of saturated fatty acids namely; palmitic acid and stearic acid along with unsaturated fatty acids viz., oleic, linoleic and linoleinic acids. Its oil content ranges from 33-45% with protein content of 24% (Gill, 1987). Singh and Marker (2006) reported that its oil is high in omega-3 fatty acid which is believed to be helpful in lowering cholesterol level when included in the diet chain. Linseed cake is a superior supplement for the dairy cattle due to its excellent palatability. Its meal contains 3% oil and 36% protein and serves as nutritious feed for cattle. It is a good source of calcium (170 mg100g-1), phosphorus (370 mg100g-1), potassium, manganese, waxes (0.012-0.450 %), sterols and phospholipids (0.11-0.21 %).

In self-pollinating crops, such as flax (*Linum usitatissimum L.*), breeding programs must include a three step process for developing germplasm: (1) recombination of genes for enlarging variation, (2) identification and selection of recombinant genotypes according to their agronomic types and (3) Fixation of genes in homozygous genotypes. Pedigree selection (PS) is the conventional method of accumulating genetic recombination in each generation. The heterozygosity in early generations makes the efficient identification and selection of recombinant genotypes more difficult. Repeated pedigree selection can increase homozygosity, but many generation cycles are required to reach homozygosity in loci associated with agronomic traits. The single-seed descent (SSD) method can be used to obtain homozygous inbreds by accelerating generation cycles, but its application is dependent on growth habit of the plant materials used **(Inagaki, *et al*., 1998)**.

Several methods of selection can be used in segregating generations after crossing in self-pollinated crops. The information for each method of selection as well as the relationship between these methods of selection and yield would help in determining the best method of selection for breeding program to obtain high yielding cultivars of wheat and to apply this method in the following breeding program.

Selection for seed yield and production of the cultivars with high yield potential is the main objective of breeding programs. Many researchers **(Quarrie et al., 1999; Richards, 1996)** believed that genetic improvement of yield must be done via genetic improvement of physiological traits. In determining the potential of genetically different lines and cultivars, breeders have to observe many different characters that influence yield. Accurate evaluation of these characters is made more difficult by the genotype by environment interaction **(Tadesse and Bekele, 2001).**

The main objectives of the present investigation were to evaluate the efficiency of two breeding methods, i. e., pedigree and modified bulk method on one flax population by using the lines produced from F_5.

Materials and Methods

The experiment was carried out at the Etay El-Baroud Experiment Station, El-Beheira Governorate, Egypt during the three successive seasons of 2014-2015, 2015-2016 and 2016-2017. The present study aimed at measuring the efficiency of two methods of selection used in the flax breeding program namely; pedigree method (PM) and bulk method (BM) on one flax populations droved from previous work by the other (self) in 2014. F_2 seed from the previous work furnished the source material for subsequent generations. Used in this study one flax (***Linum usitatissimum, L.***) populations (2n = 30 chromosomes) **(Table 1)**.

Table 1. The pedigree of the parents of flax population

Parental name	Pedigree	Origin
Population1 (S2465/1 × Giza 8)		
(P_1) S2465/1	Selection from indian	Indian
(P_2) Giza 8	Giza6 × Santa catalina	Egyptian

In 2013/2014 season, one groups of random plants were taken from each F_2 population, each group consisted of 400 plants. The group of random plants was handled by taken single seed from each plant to produce (SSD), and then plants were harvested in mass to produce bulk population. The group of random plants was threshed each plant separately and recorded the following characters, high 5% approximately of plants for yield were used as pedigree method. Selection was practiced twice in the season, at heading and maturity stages, on the basis of yield and yield components.

Pedigree method (PM): Each selected F_2 plant was taken and sown in a separate row represented F_3 families on the basis 30 seeds per row during 2014/2015 season. Seeds were spaced at 10 cm, while row spacing was 30 cm. Selection between and within families was practiced as described earlier, primary selection was practiced at heading stage, and final selection at maturity stage. Forty families were selected from 90 F_3 families from three population under study were grown in three replications in a randomized complete block design (RCBD). Also, high selected plants for pedigree methods, for the studied traits to raise F_4 families in 2016/2017 season for each population. The same method was practiced on F_4 generation during 2015/2016 season and selection was done between and within growing families. Twenty families were selected from F_4 generation for each population and retained to be

raised as F_5 generation in the final evaluation trial during 2016/2017 season.

Modified bulk method (MB): Few Seeds from each selected plant from each F_2 generation were mixed to form the population seed bulk. The mixed seeds were planted in a 20 rows per plot; a row was three meters in length, 30 cm. between rows and 10 cm. between grains, during 2014/2015 growing season as F_3 generation. Selection was practiced on the basis of best plants per each population. Seeds of the selected plants were mixed to form grains bulk and grains sample were taken to be raised as F_4 generation during the growing season of 2015/2016. Seeds of the F_4 generation were sown in a 20 rows /plot; a row was three meters in length, 30 cm between rows and 10 cm between grains. Similarly, twenty plants per population were selected. Seeds from each plant were kept and planted separately as F_5 generation during 2016/2017 growing season.

In2016/2017 season, the high yielding selected lines (20) from each methods of breeding (two methods *i.e.* pedigree and bulk). Also, the parents. were represented by one row per plot, a row was three meters in length, 20 cm between rows and 10 cm between seeds were evaluated in nested design with three replications in each cross

Characters studied; the following characteristics were measured on random sample of 10 guarded plants in each plot for each in F_3 and F_4 in pedigree method and each line in F_5 generation of all studied

methods. The mean of the 10 plants were subjected to the statistical and genetic analysis for: Days to flowering: number of days from sowing date up to the initiation of the first flower, Plant height (cm), measured as the distance from the cotyledonary nodes up to the uppermost capsule branch, Technical stem length (cm), from the cotyledonary nodes to the first apical branch of the main stem and Stem diameter (mm), at the middle region of stem to the nearest 0.1 mm. Number of basal branches/plant, Number of fruiting branches /plant, Length of fruiting zone (cm), Number of capsules/plant, counted at full maturity in the field, Number of seeds/capsule, average number of seeds per capsule determined from 5 capsules selected at random for each individual plant, Seed index (g): expressed as the average of 1000 seeds weight and Oil yield/fed (Kg), by multiplying the seed yield/fed and oil percentage. Total fiber percentage (%) and oil percentage, as given by the A.O.A.C. (2000) using a Soxhlet apparatus and petroleum ether with a bailing range of 60-80°C as solvent for six hours.

Results and Discussion

Comparison between two breeding methods, mean square due to breeding methods were significant for days to flowering , No. of capsule / plant , length of fruiting zone , No. of seeds / capsule , seed index , seed yield /plant , technical stem length , and oil percentage . The other trait showed insignificant **(Table 2)** this result indicated the difference between breading methods. The pedigree methods gave the highest value for all traits **(Table 3)**. The pedigree method proved to be more efficient than bulk method for selection based on these trait may be due to the two parent good combiner for most traits. Also, gave the earliness of days to flowering . these result in this cross where an the two parent were good combiner for most trait .

Deghais and Aurian (1993) applied three breeding methods (pedigree , modified bulk and single seed descent)in six crosser and 20 familiar per cross (F6 or F7) , selected by each methods were yield tested . The pedigree and sing seed descent method proved to be more efficient than the modified bulk method for selection based on grain yield . Mobark (2007) estimated the efficiency of three breeding methods i.e., pedignee , modified bulk and sign seed descent methods in two bread wheat populations , each on 30 familiar . They found that significant difference among the F_3 and F_4 familiar in both populations for all stuched trait. Pedigree method possessed higher value of phenotypic and genotypic coefficients of variability and broad sense heritability for No. of spike/plant, No. of kernels, 1000 kernel weight and grain yield/plant.

Whan et al (1982) found the effect of selection using the means of lines from the F_3 and F_4 rather than the individual F_2 or F_3 derived lines can be assessed by the yields obtained in the following generation. The improvement obtained in the F_5 by selecting F_2 derived lines was much greater in the first cross, when selection is carried out in an early generation is the response to selection in a late generation e. g. the F_5 when lines are approaching homogy gosity, In the simulated schemer considered here, the selected lines could not be re selected, and the available date enabled each selected line to be continued with one random line only. This caused a loss of variation for yield and the gain from selection an often reduced in the generations following selection.

Table 2. Mean squares of the breeding methods of the F_5 lines for the studied traits in the (S2465/1 × Giza 8).

S.O.V	d.f	Days to flowering	Stem diameter	Number of fruiting branches /plant	Number of capsules /plant	Number of basal branches /plant	length of fruiting zone	Number of seeds /capsule.
Rep	2	0.058	0.000	0.233	0.025	0.625	4.275	2.925
Lines	39	0.914**	0.000	0.641	6.391**	0.810**	4.632	1.674*
Methods	1	3.008*	0.001*	0.208	200.208**	0.208	32.033**	5.633*
L/M	38	0.859*	0.000	0.652	1.291	0.826**	3.911	1.570*
Error	78	0.477	0.000	0.943	1.957	0.360	3.625	0.976

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

Table (2): Cont.

S.O.V	d.f	Seed index	Seed yield/plant	Total Length	Technical stem length	Total fiber percentage (%).	Oil percentage
Rep	2	0.026	0.220	1.433	11.433	0.055	0.026
Lines	39	0.029**	2.684**	10.201**	18.256**	0.067**	0.027
Methods	1	0.217**	4.819**	0.133	88.408**	0.030	0.261**
L/M	38	0.024**	2.628**	10.466**	16.410**	0.068**	0.021
Error	78	0.011	0.670	2.083	7.681	0.036	0.028

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

Table 3. Mean performance of the breeding methods of the F5 lines for the studied traits in the (S2465/1 × Giza 8).

Breeding methodology	Days to flowering	Stem diameter	Number of fruiting branches /plant	Number of capsules/plant	Number of basal branches/plant	length of fruiting zone	Number of seeds /capsule
Pedigree	95.850	0.324	7.383	22.017	2.183	32.517	8.067
Bulk	96.167	0.317	7.300	19.433	2.267	31.483	7.633
LSD 5%	0.251	0.006	0.353	0.508	0.218	0.691	0.359
LSD 1%	0.333	0.008	0.468	0.674	0.289	0.917	0.476

Table (3): Cont.

Breeding methodology	Seed index	Seed yield/plant	Total Length	Technical stem length	Total fiber percentage (%).	Oil percentage
Pedigree	9.332	3.863	120.050	107.767	13.620	42.467
Bulk	9.247	3.462	120.117	106.050	13.588	42.373
LSD 5%	0.038	0.297	0.524	1.006	0.069	0.061
LSD 1%	0.050	0.394	0.695	1.335	0.092	0.081

Also, the efficiency of the breeding methods in the present study was evaluated based on the numbers of superior lines having higher of traits than the best parent. Date presented in (**Table 4).**

For days to flowering, the result indicated that the pedigree method produced more superior lines than bulk method compared the best parent with fifteen and sixteen lines respectably. The best line was No. 7 of pedigree method. As for No. of capsule/plant , 20 and 9 lines showed signification higher than best parent for pedigree and bulk method gane the highest number of capsule/plant .

Regarding to No. of basal branches/plant, the pedigree method produced consistently none superior parent compared the best parent, with three and four lines for pedigree and bulk, respectively.

For No. of seeds/capsules, only the line No. 14 of pedigree method of breeding gave the highest no. of seeds/capsule.

Concerning seed index, all lines of pedigree and bulk methods surpassed the best parent.

Also, the line No. 9 of pedigree method gave the behavior seed index.

With regard to seed yield/plant, four and six lines surpassed significant seed. Yield compare the best parent. The best line was No. 19 of pedigree followed by No. 2 of bulk method of breeding.

For total length, sixteen lines of both breeding methods surpassed significant compare the best parent. The best line was No. 1 of pedigree method (123, 67).

Regarding technical stem length, fourteen and nine lines showed significant higher than the best parent for pedigree and bulk methods, respectively the best line was No. 6 (112. 67) followed by No. 5 (111. 33) of pedigree method .

For fiber percentage, none of lines showed significant compare the best parent or over mean.

Table 4. Mean performance of the selected F_5 lines of breeding methods and two parents in the (S2465/1 × Giza 8).

Breeding methods	No. of line	Days to flowering	Stem diameter	Number of fruiting branches /plant	Number of capsules/plant	Number of basal branches/plant	length of fruiting zone
pedigree	1	95.67	0.33	7.33	22.67	1.67	33.33
	2	96.67	0.31	8.33	22.33	2.67	34.33
	3	96.00	0.34	7.00	22.33	1.67	33.33
	4	96.33	0.32	8.33	21.67	2.00	31.00
	5	95.33	0.33	7.00	22.00	2.00	33.67
	6	96.67	0.34	6.67	21.33	2.67	33.33
	7	95.00	0.32	7.67	22.00	2.00	32.33
	8	95.67	0.33	7.33	21.00	1.67	32.67
	9	95.67	0.32	7.33	22.67	2.67	31.33
	10	95.67	0.33	7.67	21.33	1.67	32.33
	11	96.00	0.32	7.33	23.33	2.00	30.00
	12	95.33	0.33	6.67	22.33	1.33	32.67
	13	96.67	0.32	7.67	21.00	2.00	34.33
	14	95.67	0.32	8.00	21.33	3.00	32.00
	15	96.00	0.32	7.33	22.00	2.67	32.67
	16	95.33	0.31	7.00	23.00	2.00	31.00
	17	95.67	0.33	7.00	21.67	2.00	31.67
	18	97.00	0.32	7.67	22.67	2.00	32.33
	19	95.33	0.33	6.67	22.33	3.00	32.67
	20	95.33	0.30	7.67	21.33	3.00	33.33
Bulk	1	96.33	0.32	7.67	18.33	2.00	34.33
	2	97.00	0.32	7.00	21.00	3.00	33.33
	3	96.00	0.30	7.67	19.67	1.67	31.67
	4	95.33	0.32	7.33	19.67	1.67	31.33
	5	96.33	0.32	7.33	19.00	2.33	31.67
	6	96.00	0.30	7.33	18.67	2.67	33.00
	7	95.33	0.31	6.33	19.33	2.67	31.33
	8	96.33	0.31	7.00	20.00	2.67	29.67
	9	97.00	0.32	7.67	19.67	3.00	31.67
	10	96.33	0.33	7.67	18.33	2.00	31.33
	11	96.00	0.32	7.67	19.00	2.33	30.33
	12	96.00	0.31	7.00	19.33	2.00	30.33
	13	96.00	0.33	6.67	20.00	2.67	31.33
	14	96.33	0.32	7.33	19.67	1.67	30.33
	15	96.00	0.31	6.67	19.67	1.67	32.33
	16	95.67	0.32	8.00	19.33	1.67	30.33
	17	96.33	0.31	7.00	20.33	1.67	32.33
	18	97.00	0.32	7.33	19.00	2.67	30.33
	19	95.33	0.32	7.67	19.33	3.33	31.33
	20	96.67	0.32	7.67	19.33	2.00	31.33
P1		98.00	0.31	7.33	17.33	2.00	35.33
P2		97.67	0.32	8.67	17.33	2.00	33.33
Over mean		96.10	0.32	7.37	20.56	2.21	32.11
LSD 5%		1.09	0.03	1.53	2.29	0.97	3.03
LSD 1%		1.43	0.04	2.01	3.01	1.27	3.99

Table (4): Cont.

Breeding methods	No. of line	Number of seeds/capsule.	Seed index	Seed yield/plant	Total Length	Technical stem length	Total fiber percentage (%).	Oil percentage
	1	9.00	9.40	2.28	123.67	109.00	13.60	42.47
	2	7.67	9.30	3.95	120.67	108.67	13.47	42.50
	3	7.00	9.40	2.38	121.00	107.00	13.50	42.50
	4	8.33	9.27	3.09	121.00	110.00	13.60	42.53
	5	8.00	9.30	3.13	120.67	111.33	13.67	42.40
	6	6.67	9.37	3.44	122.00	112.67	13.70	42.47
	7	7.00	9.23	2.44	116.00	107.33	13.50	42.43
	8	9.00	9.40	2.49	121.67	107.33	13.43	42.50
	9	8.00	9.60	4.40	119.00	109.00	13.80	42.47
Pedigree	10	7.67	9.23	2.41	117.00	104.67	13.50	42.43
	11	9.00	9.40	3.72	122.33	109.67	13.73	42.40
	12	7.67	9.30	2.05	119.33	104.33	13.60	42.50
	13	7.67	9.20	2.70	119.67	106.67	13.53	42.40
	14	7.67	9.30	4.22	119.67	107.33	13.77	42.47
	15	9.67	9.23	4.44	119.67	108.33	13.53	42.40
	16	8.33	9.30	2.93	119.00	108.67	13.70	42.50
	17	7.67	9.40	3.08	117.67	105.00	13.50	42.57
	18	8.67	9.30	3.61	122.00	107.33	13.83	42.40
	19	8.33	9.13	5.10	118.33	103.00	13.67	42.53
	20	8.33	9.57	4.00	120.67	108.00	13.77	42.47
	1	8.00	9.23	2.72	121.00	107.67	13.60	42.47
	2	8.67	9.27	5.04	120.67	109.00	13.37	42.40
	3	7.67	9.23	2.40	118.67	104.67	13.70	42.27
	4	7.67	9.30	2.29	120.00	105.00	13.73	42.43
	5	6.67	9.37	2.74	121.00	108.33	13.60	42.27
	6	8.33	9.23	3.86	119.33	106.00	13.77	42.37
	7	7.33	9.27	3.78	121.00	103.00	13.43	42.53
	8	7.33	9.10	3.68	115.00	109.33	13.70	42.37
	9	7.00	9.30	3.85	121.00	107.33	13.30	42.43
Bulk	10	7.00	9.23	2.37	118.33	104.00	13.37	42.40
	11	7.00	9.23	2.84	122.33	110.00	13.90	42.37
	12	9.00	9.30	3.25	120.00	107.33	13.57	42.47
	13	6.67	9.23	3.29	119.00	104.00	13.63	42.47
	14	7.67	9.20	2.37	119.33	104.67	13.73	42.30
	15	8.33	9.27	2.58	118.67	103.00	13.33	42.37
	16	7.67	9.27	2.33	123.67	108.00	13.70	42.07
	17	7.00	9.30	2.13	119.33	102.00	13.40	42.47
	18	7.67	9.20	3.53	121.00	105.00	13.83	42.30
	19	8.67	9.20	5.25	122.33	105.00	13.57	42.47
	20	7.33	9.20	2.61	120.67	107.67	13.53	42.27
	P1	8.00	8.63	2.38	116.33	102.00	14.00	42.37
	P2	8.00	8.87	2.50	115.33	102.67	13.37	41.60
Over mean		7.86	9.26	3.18	119.88	106.69	13.61	42.40
LSD 5%		1.59	0.17	1.81	2.51	4.47	0.33	0.29
LSD 1%		2.10	0.22	2.38	3.30	5.87	0.43	0.38

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