



# Analysis of Heritability, Genetic and Principal Components of Seed Yield and its Traits in Flax Genotypes (*Linum Usitatissimum L.*)

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## Abstract

The field experiment was conducted in a lattice design to analyze heritability, genetic advance and Principal components of seed yield and its agronomic traits in flax genotypes at Holetta and Kulumsa research locations, Ethiopia. 36 genotypes of flax were analyzed for heritability, genetic advance and principal component characters that presented in the tested flax resources. The analysis of variance showed that there were significant differences between genotypes of flax for each and every one characters analyzed except plant height. These point out towards the presence of genetic variability between the genotypes of flax that is important for improvement program. The highest heritability was recorded for the weight of thousand seed (50%), flowering date (43.264%), oil yield (41.723%), seed yield (40.699%), maturity date (32.961%) and plant height (32.2936%). This implies that greater quantity of the entire variance was due to high genotypic and less environmental variance. Hence, a better improvement can be made if some of these characters are well thought-out as selection criteria for the improvement of seed yield and its agronomic characters of flax types. Principal component analysis showed that 99.99% of the difference was contributed by the first seven principal components for seed yield and its agronomic characters. Oil yield, thousand seed weight, maturity date and stand percent were the most important seed yield positive contributors of the difference in the first principal component in which 48.60% of the variation revealed. The current study concealed the existence of substantial high principal component contributor characters between genotypes for oil yield, thousand seed weight, plant height and stand percent characters analyzed. Therefore, these characters can serve as choice indices in genetic enhancement of flax seed yield and its agronomic characters.

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## Introduction

Flax (*Linum usitatissimum* L.) (fiber type) is one of the earliest cultivated plant species and a versatile crop grown up for production of strong stem fiber and seed oil used for the paints, varnishes, inks, putty, linoleum and other industrial applications [1]. Cultivated flax can be classified into two main types, namely fiber and oil or linseed types [2]. In Ethiopia, oil-bearing type Linseed (*Linum usitatissimum* L.) is the second most important next to noug in the high land parts of the country cultivated for seed yield and oil traits. It is often grown on well-drained and organic matter rich soils. Linseed crop is adapted to cool, elongated growing season and high rainfall areas at elevation between 1600 and 2800 meters and best performed at elevation between 2200 to 2800 meters above sea level. The national average productivity and oil content is low as compared to some

**Table 1:** List of thirty-six flax seeds genotypes with few features used in the study.

No	Flax seed genotypes	Technical stem length in cm	Plant height in cm
1	Falx-34663	71	107
2	Flax-89577	81	100
3	Falx-34514	86	106
4	Flax-35151	76	96
5	Flax -35282	81	98
6	Falx-35121	77	102
7	Flax- 35312	85	98
8	Flax- 83030	81	98
9	Flax- 35245	82	100
10	Flax-35153	80	83
11	Flax- 35326	83	110
12	Falx-34454	83	98
13	Flax -35287	83	89
14	Flax -35293	84	99
15	Flax -35307	77	91
16	Flax- 35288	72	86
17	Flax- 35889	71	78
18	Flax-92373	70	80
19	Falx-34586	80	100
20	Flax-35146	76	105
21	Flax-35137	74	105
22	Flax-35150	73	91
23	Flax-35149	82	94
24	Flax-35140	77	97
25	Flax-35139	78	112
26	Flax-35148	74	101
27	Flax- 35328	74	89
28	Flax- 35277	87	90
29	Flax-35141	79	93
30	Flax- 88722	80	90
31	Flax- 35279	78	87
32	Belay-96	74	85
33	Bekoji	75	88
34	Jeldu	73	81
35	Berene	74	82
36	Kasa-2	73	81

of potentially high yielding varieties developed in research center. In addition high oil-bearing linseed genotypes understanding performance of genetic potential of flax type genotype in seed yield and oil behavior is important for alternative use. Under such a situation, it becomes very important to identify flax type genotypes, which can show best performance in seed yield and oil content over different environments or locations. Only best performing genotypes can guarantee a good yield and oil content with decreased risk of losing production and allow the plant breeders to make general recommendations. Keeping these facts in to consideration, therefore the present experiment was executed to analyze broad sense heritability, genetic advance and principal component analysis for yield and its agronomic characters by considering 36 flax type genotypes comprising five standard checks at Holetta and Kulumsa agricultural research locations.

## Material and methods

The field experiment was conducted at Holetta & Kulumsa Research locations in 2019/2020 main cropping season. Holetta (West Shewa Zone) and Kulumsa (West Arsi Zones of Oromia Region) are located at latitude 9° N and longitude 38° E, altitude of 2400 m a. s. l., (8° 01' N latitude and 39° 09' E longitude, latitude of 2200 m. a. s. l), respectively. These locations are the representatives of linseed growing areas in the central highlands of Ethiopia.

Thirty-six flax type genotypes of breeding materials lines were used in this study. The majority of the materials were selected lines from flax type genotypes and that are maintained at Holetta agricultural research center of High and mid land oil crop improvement program.

### Experimental design and season

The experiment was conducted in 2019/2020 by using simple lattice Design with two replications. A plot of four central rows each 3-meter long and 20 cm spacing between rows were used for data collection. Each replication was represented by 36 plots. The path between replication was 1.5 m and the spacing between plots within was also 0.4 m. A rate of 25 kg/ha and urea, phosphorous and Sulphur fertilizers were applied at the rates of 23/23 kg/ha N/P<sub>2</sub>O<sub>5</sub>.

### Data collected on plot and plant basis

1. Flowering date: The numbers of days from sowing date to a stage at which 50% of the plants in a plot open flowers.
2. Maturity date: The number of days from date of sowing to a stage at which 50% of the plants have reached physiological maturity. It is the time when 50% of the capsules change their color into brown.
3. Seed yield: Seed yield per plot measured in grams after moisture of the seed was adjusted to 7%.
4. Oil yield: The amount of oil in grams obtained by multiplying seed yield per plot by corresponding oil percent.
5. Stand percent: The proportion of plants at harvesting stage in percentage.
6. Thousand Seed weight: The weight (g) of thousand seeds.
7. Plant height: The average height of five randomly selected plants was measured in centimeters from the ground surface to the top of the main stem at maturity.

**Table 2:** The mean squares for different sources of variation for seven characters studied.

Characters	Genotype (35)	Loc(1)	Rep/Loc(2)	Bloc/Rep(10)	Loc*Trt(35)
Flowering Date	68.19**	6574.5	3.67	69.04	26.1
Maturity Date	18.98**	45120.8	2.5	12.1	10.08
Yield kg/ha	181722.23**	381409.174	4958.75	185205.70	44328.988
Oil yield kg/ha	34.0880**	51.361	0.625	38.83	8.161
Plant height	279.33**	5605.01	45.33	146.25	161.58
Stand percent	84.24ns	258.67	62.67	131.92	77.816
Thousand seed weight	1.175**	3.702	0.018	1.914	0.129

\*\*significant at  $p = 0.01, 0.05$  significance level, respectively; ns: Non-Significant.

## Results and discussions

The analysis of mean squares of variances are shown in **Table 2**. The analysis of variance revealed that the mean square due to genotypes for seed yield and its related agronomic characters traits were highly and significantly different for all traits studied except stand percent. This revealed that there was a considerable magnitude of variability among the different genotypes for all the traits compared. Similar findings were reported by Akbar [3]. The high quantity of genetic variability in the studied genotypes for the most important yield contributing characters indicated that the possibility of further improvement of these traits [4]. Sonal Upadhyay reported similar findings pertaining to the presence of high genetic variability for different agronomic traits including seed yield.

### Heritability in the broad sense

Breeders can create speedy advancement where heritability is high by using selection methods that are dependent only on phenotypic distinctiveness. However, where heritability is low methods of selection based on families and offspring testing are more effectual and efficient. Heritability in the broad sense of the characters is presented in **Table 3**. In this study, heritability values were found to be sufficiently high for most important yield component characters. Dabholkar generally classified heritability estimates as low (5-10%), medium (10-30%) and high (30-60%) [5]. Based on this classification, thousand seed weight (50.00%), flowering date (43.26404%), oil yield (41.72287%), seed yield kg/ha (40.69694%), maturity date (32.96125%) and plant height (32.29355%) exhibited high heritability estimates. Thousand seed weight was found to be the most heritable character in the genotype, with heritability of 50.00%, followed by flowering date (43.26404%), oil yield (41.72287%) and seed yield (40.69694%). This indicates that selection for this character in the genotype would be most effective for the expression of this character in the succeeding generations. Therefore, better improvement can be made if some of these characters are considered as selection parameter in future improvement program. Similar findings had been reported by Adugna [6]. For thousand weight, flowering date, oil yield, seed yield and for maturity date. High heritability value for thousand weight, flowering, maturity, oil yield, seed yield, and plant height recorded in the current study was also recorded by Yared [7]. According to Singh, if the heritability of a character is high, selection for such character is fairly easy as selected character will be transmitted to its offspring [8]. This is because there would be a close correspondence between the genotype and phenotype due to a relatively similar contribution of the environment to the genotype. On the other hand only stand (6.578857%) exhibited low heritability estimates.

### Genetic advance

Relating to the genetic advance at 5% intensity the highest genetic gain was predicted for oil yield (119.14 kg/ha), seed yield (107.22kg/ha) followed by thousand weight (26.58gm) while the lowest genetic advance was predicted for plant stand percent (2.07). Genetic advance as a percent mean ranged from 1.021554% stand percent to 119.14% for oil yield (Table 3). Within this range, a relatively high genetic advance as a percent mean was observed for oil yield (119.14%) and seed yield (107.22%) and followed by thousand seed weight (26.58%). On the other side high genetic advance with high heritability was shown thousand seed weight and oil yield which may be because of the presence of both additive and non-additive gene action [9]. Those traits having medium heritability along with better genetic advance could be improved using breeding procedure such as pedigree method. On the other hand, the lowest genetic gain as percent of means was observed for date of 50% maturity 1.021554% followed by stand percent 1.797173%. Low genetic advance as percent means observations in this study indicates that characters probably were under environmental influence than the genotypic expression and that selection based on these traits would be ineffective.

**Table 3:** Broad sense heritability, genetic advance and Genetic advance as percent of mean of studied agronomic characters.

No	Traits	h <sup>2</sup> b	GA=K*PV*H <sup>2</sup>	GA as means%
1	Flowering Date	43.264	8.97	3.52266
2	Maturity Date	32.9613	2.22	1.02155
3	Seed yield kg/ha	40.6969	107.22	2.95846
4	Oil yield kg/ha	41.7229	119.14	9.83351
5	Plant height	32.2936	13.04	3.84138
6	Stand percent	6.57886	2.07	1.79717
7	Thousand seed weight	50.00	26.58	122.759

h<sup>2</sup>b: Broad Sense Heritability; GA: Genetic Advance; K: Selection Intensity; GA as means%: Genetic Advance as Percent of Mean.

### Principal component analyses

In order to evaluate the patterns of variations, Principal Component Analysis (PCA) was done by considering seven characters for seed yield and agronomic traits. As shown as in **Tables 4** principal component analysis showed that 99.99% of the variation was contributed by the first seven principal components for agronomic traits. Oil yield, thousand seed weight, maturity date and stand percent were the most important of seed yield positive contributors of the variation in the first principal component in which 48.60% of the variation revealed. Seed yield, oil yield, thousand seed weight and date of 50% maturity, stand

percent had relatively high positive weight. Date of 50% flowering and plant height had negative weight. Additional 20.61% variation in the second principal component was mainly observed through agronomic character such as plant height, date of 50% flowering, stand percent and date of maturity. The third principal component was accounted for another additional 13.86% of the variation in which date of flowering, maturity and thousand seed weight were the major contributor. Stand percent had the highest negative weight. Principal component 4 and 5 contributed 7.89% and 5.95% additional variations, respectively. Stand percent in principal component 4 and thousand seed weight in principal component 5 were among the major contributors. Plant height in principal component 4 and

date of maturity in principal component 5 had the most negative weight. Oil yield and plant height in principal component 6 contributed 2.76 % additional variations and seed yield per plot in principal component seven are major variation contributor. In general, it is assumed that traits with larger absolute values closer to unity within the first principal component influence the clustering more than those with lower absolute values closer to zero [10]. In this study, most of the traits individually contributed small effects ( $\pm 0.01222$ -  $-0.6973$ ) to the total variation and, therefore, differential grouping of genotypes was mainly attributed by the cumulative effect of the individual traits. However, traits which had relatively greater weight in the first principal component largely contributed to the total variation and they were accountable for differential grouping of genotypes.

**Table 4:** Component scores of the first seven principal components of thirty six flax type genotypes based on their agronomic traits.

No.	Traits	Scores of components						
		PCA1	PCA2	PCA3	PCA4	PCA5	PCA6	PCA7
1	Flowering	-0.1463	0.63503	0.49122	0.36068	0.01222	0.45132	-0.0106
2	Maturity	0.37769	0.26768	0.44857	-0.3572	-0.5077	-0.4442	-0.0421
3	Seed yield	0.52289	-0.0629	-0.0717	-0.1133	-0.0761	0.44522	0.70757
4	Oil yield	0.52055	-0.0684	-0.0635	-0.1657	0.07764	0.44796	-0.6973
5	Plant height	-0.0781	0.64507	-0.4261	-0.5372	0.32077	-0.0474	0.05012
6	Stand	0.30388	0.31493	-0.5536	0.59055	-0.3264	-0.2067	-0.0632
7	1000 seed	0.43946	0.03403	0.2455	0.25434	0.7217	-0.3938	0.06929
	Eigen value	3.4022	1.44263	0.97046	0.55228	0.41656	0.1933	0.02257
	Variance %	48.6	20.61	13.86	7.89	5.95	2.76	0.32
	Cumulative	48.6	69.21	83.07	90.97	96.91	99.67	99.99

## Conclusion

In this study, thirty-six flax genotypes were evaluated in simple lattice design with two replications at Holetta and Kulumsa locations, with the objectives of evaluating broad sense heritability, genetic advance and principal component analysis for yield and its traits in flax genotypes at Holetta and Kulumsa locations, Ethiopia. The analysis of variance showed the existence of highly significant differences between the tested genotypes for the all of characters studied except stand percent, showing the existence of genetic variability between the tested genotypes of flax type for these characters. In this study, heritability values were found to be sufficiently high for most important yield component characters. Based on the Dabholkar classification thousand seed weight (50.00%), flowering date (43.26404%), oil yield (41.72287%), seed yield (40.69694%), maturity date (32.96125%) and plant height (32.29355%) exhibited high heritability estimates. Thousand seed weight was found to be the most heritable trait in the genotype, with heritability of 50.00 %, followed by days to flowering (43.26404%), oil yield (41.72287%) and seed yield (40.69694%). This shows that selection for these traits in the genotype would be most effective for the expression of these traits in the succeeding generations. Therefore, better improvement can be made if some of these traits are considered as selection criteria in future improvement program. High heritability value for thousand seed weight, date to flowering, oil yield, seed yield, and days to maturity and plant height recorded in the current study was also recorded by Yared. According to Singh [10], if the heritability of a character is high, selection for such character is fairly easy as selected character will be transmitted to its progeny. This is be-

cause there would be a close correspondence between the genotype and phenotype due to a relatively similar contribution of the environment to the genotype. At the same time only stand percent (6.578857%) and exhibited low heritability estimates.

Principal component analysis showed that 99.99% of the variation was contributed by the first seven principal components for seed yield and agronomic traits. Oil yield, thousand seed weight, maturity date and stand percent were the major seed yield positive contributors of the variation in the first principal component in which 48.60% of the variation revealed.

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in genetic improvement of flax type linseed yield and its component traits.

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