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Variability, Genetic Advance and Trait Association of Advanced Ethiopian Noug Genotypes

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Abstract: **Noug (*Guizotia abyssinica* (L. F.) Cass.) is an important oilseed in Ethiopia. Genetic improvement of the crop is largely dependent on the scale of genetic variability. The research was conducted in the experimental field of Holetta agricultural research center main station and Ghinchi sub-center during 2016. The research trial was laid out in randomized complete block design and thirteen quantitative traits were recorded. Seventeen advanced lines of noug were studied for genetic variability and association of traits. The combined analyses of variance revealed highly significant ($p < 0.01$) differences among the genotypes for all the studied characters except for days to maturity and oil yield. The genotypic coefficient of variation ranged from 1.4 % for oil content to 23 % for oil yield while phenotypic coefficient of variation ranged 1.3 % for oil content and days to maturity to 17 % for shattering. The broad sense heritability varied from 16.5 % for oil yield to 91.7 % for oil content. The expected genetic advance as percentage of mean ranged from 1.5 % for days to maturity to 31 % for shattering. High heritability estimates along with high genetic advance was observed for seed filling period and shattering; Correlation studies revealed that seed yield was positively and significantly correlated with seed filling period and oil yield at genotypic and phenotypic level. The study indicates the presence of ample variability among the tested genotypes which implies the possibility of the crop for future improvement.**

Keywords: **Genetic advance, Genotypic Correlation, Heritability, Noug, Phenotypic Correlation, Variability.**

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1. INTRODUCTION

Oilseeds are important plants whose oil can be used for human consumption. Edible oil plays a very important role in human nutrition as a high-energy component of food and they are important for meeting the calorie requirements. Among the most important oilseeds grown in Ethiopia, noug is the second most widely-produced oilseed accounting about a quarter of total oilseed production and 33 percent of area planted to oilseeds. More than 95 percent of noug production in Ethiopia is concentrated in the highlands of Amhara and Oromiya regions of Gojjam, Gonder and Wellega (CSA, 2018).

In Ethiopia noug Seeds are mainly used for local oil extraction and export earnings. The oil from noug seeds makes up about 44 percent of total edible oil production in the country. The noug cake, which is the by-product from noug seed oil extraction process is used for livestock feed. The local production of edible oil has tremendous growth potential and is expected to rapidly expand in the coming years. Even though noug is a principal oilseed, which plays a significant role in the national economy of Ethiopia; over the last several years, production has shown steady growth. Besides its excellent oil quality and good agronomic performance under stress and low management; productivity is very low compared to other oilseeds. The low average yield of noug is due to cultivation of traditional landraces, low availability of high yielding varieties, limited Agricultural extension interventions, poor mangemental practice and mono cropping of cereal crops.

Therefore, it necessitates studying noug genotypes to identify elite varieties to boost the production. The principal aim of the genetics and breeding research of noug is to avail high yielding and better quality varieties which are adaptable to potential growing areas by increase seed yield and oil content, reduce shattering with uniform maturity, resistance to diseases, pests and lodging (EIAR, 2016). An increase in oil content and seed yield appears feasible because of existing genetic variability, which can be used in breeding research.

Noug is a self-incompatible and open pollinated species with great phenotypic and genotypic diversity (Adarsh *et al.*, 2014, Dempewolf et al. 2015). For that reason, mainly breeders have adopted population improvement programmes such as mass and recurrent selections. Understanding the variability, genetic advance, heritability and correlation among traits are valuable in any noug selection program. The present study was undertaken to investigation the variability and interrelation of traits among Ethiopian advanced noug genotypes developed by continuous cycle of mass and recurrent selections.

2. MATERIAL AND METHODS

The experiment consisted of 16 advanced noug genotypes derived from mass and recurrent selections and one standard check evaluated during 2016 main cropping season at Holetta Agricultural research center (2400 m altitude, 35 km west of Addis Ababa) and Ghinchi sub-center (2200 m altitude, 85 km west of Addis Ababa). Even though, the two sites are only 38 km apart, Ghinchi soil has higher clay content than Holetta. A field experiment was laid out in randomized complete block design with four replications. Each treatment was grown in six row of 5m length with a spacing of 0.30 m between rows, 2m and 0.6 m spacing between blocks and rows respectively. All recommended management practices were followed for good establishment of the crop during the growth period.

Description of Collected Data

Days to flowering (DF): Number of days from date of emergency to the date 50**%** of plants in a plot and their flower buds show blooming.

Days to maturity (DM): Number of days from date of emergency to the date at which 90% of all heads of entire population are matured**.**

Seed filling period (SFP): The period from 50**%** of plants in a plot flower (DF) to 90% plants mature (DM).

Plant height (PH): The average measurement of 10 sample plants in centimeter selected from the harvestable plots (central rows) from ground to tip of the head on the main stem during 90% of all heads of entire population is matured.

Seed yield: the amount of seed obtained from each plot in grams adjusted to 7% moisture content.

Thousands seed weight (TSW): Measuring the weight of 1000 seeds in gram taken from the harvestable plots (central rows).

Oil content (OC): The proportion of oil in the seed to the total oven dried seed weight as measured by nuclear magnetic resonance spectroscope (NMRS).

Oil yield /ha (OY): The amount of oil in kg obtained by multiplying seed yield per hectare by corresponding oil percentage.

Data analysis: Data were subjected to analysis of variance (ANOVA) using the SAS statistical package V 9.3 (SAS Institute, 2010). The genotypic and phenotypic variances were estimated as described by Allard (1960).

Genotypic variance ($\delta^2 g$) = (MSg-MSe)/r; Environmental variance ($\delta^2 g$) = MSe/r and Phenotypic variance ($\delta^2 p$) = $\delta^2 g + \delta^2 e$

Where: MSg- mean sum of square of genotype; MSe- mean sum of square of error.

Phenotypic and genotypic coefficients of variation were estimated as suggested by Johnson *et al.* (1955). Using SAS varcomp procedure;

Phenotypic coefficient of variation (PCV) = ($\sigma p / \boldsymbol{x}$) x 100

Genotypic coefficient of variation (GCV) = (σg /x) x100

Where: σp = phenotypic standard deviation, σg= genotypic standard deviation, and ***x*** = grand mean for the character x.

Heritability in broad sense was computed according to (Allard, 1960).

$h^2b = (\sigma^2 g / \sigma^2 p)$ x100

Where: $\sigma^2 g$=genotypic variance, and $\sigma^2 p$=Phenotypic variance

The heritability percentage categorized as low for less than 30%, 30-60% moderate and high if value is greater than or equal (≥) 60%, high as given by Robinson *et al.* (1949).

Genetic advance (GA) and Genetic advance as percent of the mean (GAM) estimated using;

GA = $k\sigma p h^2 b$

GAM = (GA/x) x 100

Where: GA = expected genetic advance from selection and K = the selection differential (K = 2.06 at 5% selection intensity), σp= phenotypic standard deviation and h^2b= broad sense heritability

Phenotypic and genotypic correlation coefficients were estimated using the standard procedure proposed by Singh and Chaudhary (1985).

Phenotypic correlation coefficient (rpxy) $= \frac{\sigma Pxy}{\sqrt{\delta 2px \, * \, \delta 2py}}$

Genotypic correlation coefficient (rgxy) $= \frac{\sigma gxy}{\sqrt{\delta 2gx \, * \, \delta 2gy}}$

Where: rpxy = phenotypic correlation coefficient between characters x and y;

rgxy= genotypic correlation coefficients between characters x and y;

σp and σg =phenotypic and genotypic standard deviation respectively,

$\delta^2 p$ and $\delta^2 g$ = phenotypic and genotypic variance respectively.

3. RESULT AND DISCUSSION

Analysis of variance (ANOVA)

The combined analysis of variance revealed highly significant differences among the 17 advanced noug genotypes for all the characters except Days to maturity and oil yield; indicating the existence of sufficient amount of variability among the genotypes for significant traits (Table 1). The mean performance of genotypes indicates the presence of variation among the treatments (Table 2). Similar results were reported for days to 50% flowering, plant height, 1000 seed weight, oil content (%) and seed yield by Kumar and Bisen (2016) and Suryanarayana *et al.* (2018) but both authors reported contradictory result for days to maturity. The result suggests the presence of tremendous variation among the studied genotypes. The presence of wide genetic variability provides an indication of a better scope for genetic improvement of noug.

Phenotypic and genotypic coefficient of variation:

The phenotypic coefficient of variation (GCV) ranged from 1.4 (oil content) to 23.0 (oil yield). Similarly, genotypic coefficient of variation (GCV) ranged from 1.3(oil content) to 17.0 (shattering) (Table 3). In this study the magnitude of GCV lower than the PCV value indicating that environment has important role in the expression of the traits. The variation of characters was not only due to genotypes but also due to the influence of environment. The result was in agreement with the findings of Ahirwar *et al.* (2017) for Days to 50% flowering, Days to maturity, Plant height, 1000 Seed weight and Seed yield. Tiwari and Ahirwar (2018) reported high PCV for Plant height, 1000 seed weight and seed yield.

Table 1 : Combined Analysis of variance for 10 traits of advanced noug genotypes tested at Holetta and Ghinchi in 2016

TRIATS	FD	MD	SFP	PH	YELDK	TSW	OC	OYK	SHA	ST
MSG	90.9***	46.6ns	122.6***	249.6***	75798.3**	0.3***	1.2***	119ns	3.6***	15.3***
MSR	92.6**	66.9ns	11.4ns	145.3ns	102746.8ns	0.07ns	0.01ns	16318.7ns	1.8*	6.6ns
MSE	14.7	32.4	15.4	94.0	57316.1	0.1	0.1	9953.1	0.72	6.8
CV%	3.9	3.9	7.9	5.9	20.7	7.2	4.8	18.5	17.15	2.9

*, ** and *** Significant at 0.05, 0.01 and 0.001 probability level respectively; ns non-significant MSG= Mean Square due to genotypes, MSE= Mean Square due to error, CV%= Coefficient of variation in percentage, DF=days to flowering, DM=days to maturity, SFP= Grain filling period, PH= plant height, YELDK=Seed yield per hectare (kg), TSW=Thousand seed weight and OC= oil content, OYK= Oil yield per hectare (kg), SHA = Shattering, ST = stand percentage.

Quantitative traits such as yield are controlled by many genes and highly influenced by environmental factors. Therefore, GCV and PCV values help to determine the influence of environment on trait expression and group variability into heritable and non-heritable components. The highest PCV and GCV value for oil yield, seed filling period and shattering showed selection of these traits based on phenotype may be useful for yield improvement. The high PCVs and GCVs indicate the presence of high genetic variations among the tested genotypes for the studied traits.

Broad sense heritability (H^2) and Genetic advance under selection (GA):

Heritability estimates were ranged from 16.5 (oil yield) to 91.7 (oil content). According to the heritability class given by Robinson *et al.* (1949) seed yield and oil yield grouped as low heritable traits (< 30%). Patil *et al.* (2013) obtained similar result for seed yield. Days to maturity and stand percent grouped as moderately heritable traits (30-60%) contradict with Patil *et al.* (2013) who reported low heritability score for yield per plot and days to maturity. The rest traits grouped as highly heritable traits (≥ 60 %). Low heritability result could be due to high environmental effect.

Heritability values are helpful in predicting the expected progress to be achieved through the process of selection. GCV along with heritability estimate provides a reliable estimate of the amount of genetic advance to be expected through phenotypic selection. Low heritability along with low phenotypic and genotypic coefficients of variations of these traits, indicating limited possibility of improvement for those characters through selection because of environmental effect. Even though heritability determines the effectiveness of selection; to increase selection efficiency estimating of heritability and genetic advance should always be considered simultaneously. Because heritability estimates alone are not satisfactory for selection criteria (Johnson *et al.*, 1955).

High estimates of genetic advance were reported for seed yield (60.1); genetic advance as percent of mean ranged from 1.5 (days to maturity) to 31.2 (shattering). Heritability estimates along with high genetic advance is usually more helpful in predicting gain under selection than heritability estimates alone. The range of GAM was classified as low less than 10 %, 10-20 % moderate and greater than 20 % high (Johnson *et al.*, 1955).

Therefore, based on this demarcation; days to flowering, days to maturity, plant height, oil content, oil yield and stand percentage classified as low GAM.

Table 2 : Mean comparison of advanced noug genotypes for various plant characters evaluated in 2016 at Holetta and Ghinchi

Genotypes	Traits									
	FD	MD	SFP	PH	YELDK	TSW	OC	OYK	SHA	ST
Collection/34/2	97.4	145.1	47.8	164.6	478.7	3.2	39.9	190.7	4.0	89.4
Collection/45/2	99.6	145.1	45.5	158.9	544.2	3.1	39.5	213.9	4.1	91.9
Collection/45/3	98.9	144.4	45.5	160.0	561.5	3.1	40.5	224.9	4.5	90.0
Collection/57/2	97.3	145.9	48.6	163.0	504.0	3.2	39.6	199.6	4.4	89.4
KLR-1(AW)2008	97.0	145.4	48.4	172.3	687.6	3.3	40.5	278.3	5.3	93.1

KLR-3(AW)2008	101.3	150.0	48.8	159.0	519.9	3.3	40.5	210.6	5.8	92.5
N07-001(1)(Weliso)	96.9	147.8	50.9	157.8	530.8	2.6	39.5	209.6	5.0	91.9
N07-045	98.0	141.3	43.3	177.0	452.8	3.1	39.7	179.6	5.8	90.6
N07-046	99.6	146.5	46.9	166.8	507.9	2.9	40.2	204.1	5.5	93.1
N08-54	94.8	150.4	55.6	162.3	469.6	3.2	39.8	186.9	5.5	91.9
NO8-028/1	97.9	146.4	48.5	165.0	443.0	3.1	39.8	175.7	4.0	90.6
NO8-029/1	96.9	144.6	47.8	157.0	532.5	3.2	39.3	208.1	4.5	89.4
NO8-032/1	98.8	145.3	46.5	162.4	505.8	3.1	39.9	200.2	4.1	89.4
PI508077	93.9	149.3	55.4	168.4	551.4	2.9	39.7	219.2	5.8	91.9
SPS- early	86.1	143.0	56.9	157.6	574.4	3.1	40.1	231.4	5.5	91.9
SPS-Very early	94.3	148.3	54.0	169.5	784.7	3.5	40.4	317.4	5.5	90.0
Ghinchi-1	98.1	147.0	49.0	162.6	579.3	3.2	39.7	229.9	5.0	89.4
Mean	96.9	146.2	49.4	163.8	542.8	3.1	39.9	216.5	4.9	90.9
CV%	3.9	3.9	7.9	5.9	20.7	7.2	4.8	18.5	17.15	2.9
LSD	3.80	5.64	3.9	9.6	272.8	0.2	0.3	108.1	0.8	2.6

*, ** and *** Significant at 0.05, 0.01 and 0.001 probability level respectively; ns non-significant MSG= Mean Square due to genotypes, MSE= Mean Square due to error, CV%= Coefficient of variation in percentage, DF=days to flowering, DM=days to maturity, SFP= Grain filling period, PH= plant height, YELDK= Seed yield per hectare (kg), TSW=Thousand seed weight and OC= oil content, OYK= Oil yield per hectare (kg), SHA = Shattering, ST = stand percentage.

High estimates of genetic advance were reported for seed yield and oil yield. High heritability coupled with high genetic advance was observed for seed filling period and shattering; suggesting that it can be improved through direct phenotypic selection due to predominant additive variation. High heritability coupled with low genetic advance observed for days to flowering, plant height, thousand seed weight and oil content revealed predominance of non-additive gene action.

This result was in agreement with Thakur and Reddy (2012) for thousand seed weight and Pulate *et al.* (2013) for oil content. However, the report conflict with Khuntey *et al*, (2015) who report high value for heritability coupled with high genetic advance for oil content. The variations may be because of the environmental influence on the expression of the traits and the genetic difference between the genotypes. Moderate heritability with low genetic advance was observed for days to maturity suggesting that environment played major role in character expression. Therefore, heterosis or recurrent breeding may be beneficial to improve the traits. Whereas, low heritability coupled high genetic advance was reported for seed yield indicates predominance of additive gene action.

Table 3 : Estimation of variance components for 13 traits of advanced noug genotypes tested at Holetta and Ghinchi in 2016

Traits	Minimum	Maximum	PCV	GCV	H^2	GA	GAM
DF	78	106	4.9	4.6	83.8	8.2	8.5
DM	124	158	2.3	1.3	30.4	2.1	1.5
SFP	29	67	11.2	10.5	87.5	10.0	20.2
PH	134	202	4.8	3.8	62.3	10.1	6.2
YELDK	79.2	1314.9	22.1	12.5	24.4	60.1	11.1
TSW	2.6	3.9	9.0	7.7	83.6	0.5	15.4
OC	38.8	41.4	1.4	1.3	91.7	1.1	2.7
OYK	31.5	523.3	23.0	10.3	16.5	17.0	7.9
SHA	3	7	19.0	17.0	79.8	1.5	31.2
ST	85	95	2.1	1.6	55.8	2.2	2.5

DF=days to flowering, DM=days to maturity, SFP= Grain filling period, PH= plant height, YELDK=Seed yield per hectare (kg), TSW=Thousand seed weight and OC= oil content, OYK= Oil yield per hectare (kg), SHA = Shattering, ST = stand percentage PCV=phenotypic coefficient of variation, GCV= genotypic coefficient of variation, H^2 = broad-sense heritability; GA = expected genetic gains and GAM= Genetic advance as percent of the mean.

Genotypic and phenotypic correlation of traits

Genotypic and phenotypic correlation coefficients among various traits are presented in Table 4. Seed yield showed positive significant genotypic and phenotypic correlation with seed filling period and oil yield. Were as; negative highly significant phenotypic correlation recorded for shattering and positive significant correlation for stand percentage. This indicates that genotypes with large number of seed filling period and high stand percentage with low shattering character had higher Seed yield. A selection for these characters would be helpful in improving the yield potential of noug.

Days to 50% flowering have non-significant negative correlation but days to maturity have non-significant positive correlation at phenotypic and genotypic level. Contrasting result was reported by Suryanarayana *et al.* (2018) for both characters which had significant negative correlation with seed yield at phenotypic and genotypic level.

Oil content exhibited highly significant and negative phenotypic correlation with days to 50% flowering, days to maturity and grain filling period; while it showed non-significant positive genotypic correlation with days to maturity and grain filling but negative with days to 50% flowering. Oil yield observed positive and highly significant genotypic and phenotypic correlation with grain filling period, oil content and Seed yield. But negative highly significant phenotypic correlation for shattering and stand. This indicates that genotypes with high grain filling period, oil content and high yielder genotypes had higher oil yield.

Genotypic correlation coefficient for most of the traits is non-significant with their respective character. The positive and significant association of pair of characters at phenotypic and genotypic level justifies the possibility of correlated response to selection. Most of the phenotypic correlation coefficients were lesser in magnitude than their respective genotypic correlation coefficients.

This showed that the expression of traits is mainly governed by the genetics of the genotypes and environment had little influence on them and selection for the correlated characters can be fruitful and give a better yield response for the improvement of noug. Similar results were reported by Ahirwar *et al.* (2017) and Suryanarayana *et al.* (2018).

Table 4 : Estimate of Genotypic (Below diagonal) and Phenotypic (above diagonal) for 10 characters in 17 advanced noug genotypes

Variable	FD	MD	SFP	PH	TSW	OYK	SHA	ST	OC	YELDK
FD	**1**	0.73***	0.20**	-0.32***	-0.03ns	-0.16ns	0.25***	0.20**	-0.30***	-0.15ns
MD	0.27ns	**1**	0.81***	0.49***	-0.03ns	0.05ns	0.33***	0.23***	-0.44***	0.07ns
SFP	-0.74***	0.44ns	**1**	-0.43***	-0.03ns	0.21**	0.26**	0.16ns	-0.37***	0.22***
PH	-0.01ns	-0.17ns	-0.11ns	**1**	-0.10ns	-0.06ns	0.29***	-0.08ns	0.33***	-0.07ns
TSW	0.01ns	-0.04ns	-0.03ns	0.26ns	**1**	-0.04ns	0.17ns	-0.02ns	0.27***	-0.05ns
OYK	-0.45ns	0.11ns	0.49*	0.13ns	0.43ns	**1**	-0.21**	-0.32***	-0.08ns	0.11*
SHA	-0.27ns	0.28ns	0.45ns	0.41ns	0.01ns	0.37ns	**1**	0.36***	0.44***	0.23**
ST	-0.05ns	0.24ns	0.21ns	0.09ns	-0.25ns	0.07ns	0.54	**1**	0.07ns	-0.32***
OC	-0.01ns	0.09ns	0.07ns	0.25ns	0.41ns	0.50*	0.36ns	0.31ns	**1**	0.07ns
YELDK	-0.45ns	0.10ns	0.50*	0.11ns	0.41ns	1.00***	0.35ns	0.04ns	0.46ns	**1**

DF=days to flowering, DM=days to maturity, SFP= Seed filling period, PH= plant height, YELDK=Seed yield per hectare (kg), TSW=Thousand seed weight and OC= oil content, OYK= Oil yield per hectare (kg), SHA = Shattering, ST = stand percentage.

4. CONCLUSION

Significant genetic variability were observed in the studied advanced noug materials which may be exploited in further breeding program to develop high seed yield and oil content. Among 17 tested genotypes two of them (SPS-very early and KLR-1(AW) 2008) and 12 genotypes had higher mean seed yield and oil content respectively than the standard checks (Ghinchi-1), this gives an opportunity for plant breeders for new variety release of the crop. The lower genotypic and phenotypic coefficient variability for days to 50 percent flowering days to maturity, plant height, 1000 seed weight, oil content and stand percentage indicated that there was less genetic variation for this trait in the material evaluated, which calls for search or development for variation in other material. Traits which have additive gene action (seed filling period and shattering) can be improved by simple selection methods, while days to flowering, plant height, 1000 seed weight and oil content can be improved through heterosis and recurrent selection. Traits which have significant and positive association given focus to improve seed and oil yield. Furthermore, genotypes possessing combination of associations are useful in future hybridization program to obtain desirable segregants.

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