Diversity Analysis in *Guizotia abyssinica* (L. f.) Cass. Germplasms Collected from Ethiopia

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Abstract: Noug Guizotia abyssinica (L. f.) Cass is an ancient and underutilized oilseed. In Ethiopia it is among the most important oilseed in terms of area coverage, volume of production and the main source of edible oil for local consumption. Determining the genetic diversity is fundamental in any noug improvement program. The objective of this study was to find out the extent and pattern of genetic diversity among noug genotypes. The experiment was carried out at Holetta, Ethiopia from June to December 2017 using 98 accessions and two improved varieties. The treatments were arranged in 10 x 10 simple lattice designs. Analysis of variance and variance components were estimated using SAS 9.3. The analysis of variance revealed significant difference ($p < 0.05$) among the genotypes for all the traits. The highest phenotypic coefficient of variation (78.8) was observed for number of heads per plant. Genotypic coefficient of variation ranged from 2.6 for yield per plot to 72.3 for number of heads per plant. The highest broad sense heritability (90.1) was observed for oil content and the lowest value (37.5%) noted for number of primary branch. The genetic gain ranged from 3.8 for yield per plot to 136.7 for number of head per plant. The study indicates the presence of genetic variability among the tested genotypes which implies the possibility for future improvement and the need for the initiation of a planned breeding and conservation programs by considering all growing areas as important source of desirable traits.

Keywords: Diversity, Ethiopia, Genotypes, Guizotia Abyssinica

1. Introduction

Noug (*Guizotia abyssinica* (L. f.) Cass.) is an indigenous and underutilized oil seed mainly cultivated in Ethiopia and India, which is grown for its edible oil and seed. In Ethiopia it is grown by over 0.77 million small holder farmers cultivated on 0.25 million hectare of land with production and productivity of 2.96 million tons and 1.1 tone ha⁻¹ respectively. It is the second widely grown oil seed next to sesame in the country [1].

Ethiopian farmers prefer to grow noug because of the capability of the crop to grow and giving a good seed yield under low soil fertility, moisture stress and poor management practices. In addition, noug tolerate crop pests and has fewer diseases and insect pests than other oilseeds. Furthermore, noug is suitable for soil conservation and rehabilitation. It is the main source of edible oil for local consumption in Ethiopia [2]. The pale yellow with nutty taste and pleasant odor noug oil is the primary choice for most Ethiopians.

Although Ethiopia is the center of origin and diversity for noug; it has remained among the poor yielder crop in the country. Its production and productivity is plagued by a number of critical drawbacks. The major factors are indeterminate growth habit leading to seed shattering, self-incompatibility, genetically low yielding characteristics, lodging, less or low response to management inputs, difficulty of pollination behavior, disease, insect and parasitic weeds. The availability of limited genetic information and semi domesticated nature of the crop has been an obstacle for further improvement programs [3].

Genetic diversity is the variation of heritable characteristics present in a population of the same species. It includes all the variability occurring among different genotypes which is the base for breeders to develop new and improved cultivars [4]. Assessment of genetic diversity provides critical information about substantial genetic divergence and serves as a platform for specific breeding objectives [5]. Even if there is no any accurate assessment regarding the level and patterns of diversity; it can be carried out using morphological, biochemical, molecular and cytological characterization [6]. But the first three markers are the most commonly used methods to evaluate genotypes, breeding lines and segregating populations. Morphological markers are the earliest and oldest markers based on phenotypic appearance considered as the first step in the genetic diversity assessment. They are inexpensive, simple to score and easy to apply for estimating genetic diversity [7, 8]. They play a major role in studying and characterizing germplasms since it requires no complicated laboratory facilities and procedures.

Diversity studies using morphological markers have been carried out for the assessment of noug genotypes [3, 9]. High variability was observed between noug genotypes and Ethiopia germplasms are considered as good source for high yield, late maturity, bold seed, resistance to water logging and drought [2]. Other authors also reported that Ethiopian noug genotypes have a high amount of variation for morphological traits and other breeding attributes [10]. Significant genetic variability for morphological traits was similarly reported [11]. Phenotypic and genotypic coefficients of variations; heritability and genetic advance are the commonly used genetic parameters.

Noug has received little attention by scientists and considered as underutilized or orphan crop; which is an obstacle for further improvement programs [3]. Hence, the success of crop improvement program depends upon the extent and magnitude of genetic variability available in the existing germplasms; exploration of genetic diversity in noug germplasms can open the door for crop improvement and provide relevant information for the scientific community. Germplasms collected from the diverse environment offers greater genetic diversity and may furnish useful traits to widen the genetic base of the crop. Local landraces are often heterogeneous and usually exhibit considerable genetic variation for desirable traits. Therefore, to exploit the genetic potential of the crop, understanding the morphological markers for better quality, high yielding and best agronomic traits is very essential. The present study was undertaken to assess the genetic diversity of Ethiopian noug genotypes in order to generate information on the status of genetic variation for further improvement and conservation program based on their morphological traits and oil content.

2. Material and Methods

2.1. Description of the Study Area

The experiment was carried out from June to December 2017 in the experimental field of Holetta Agricultural Research Center which is located 30 km west of Addis Abeba, 2400 m above sea level, $09^o 04^{'}$ N and $38^o 30^{'}$ E. Holetta received 1144 mm annual rainfall and 6^oC and 22^oC minimum and maximum temperature respectively.

2.2. Experimental Materials

Two improved varieties from Holetta Agricultural Research Center High and Midland Oil Crops Improvement Program and 98 collections obtained from the Ethiopian Biodiversity Institute were used in this experiment. The genotypes were collected from different agro-ecologies representing the major noug growing regions of Ethiopia (Table 1).

2.3. Experimental Design and Procedures

The experiment was arranged in a 10 x 10 simple lattice design. Planting was done in a plot of three rows with 2 m length and 0.3 m spacing between rows and 0.6 m distance between plots with 8 kg/ha of seed rate. The distance between the blocks was maintained to 3 m. Fertilizer were applied at the recommended rate of 50 kg/ha DAP and 30 kg/ha urea [11] and other agronomic practices were done as required.

2.4. Data Collection

Data were collected based on standard noug agro-morphological descriptors developed by Holetta Agricultural Research Center High and Midland Oil Crops Improvement Program of the Ethiopian Institute of Agricultural Research [12]. Days to 50% flowering (DF), days to 90% maturity (DM), grain filling period (GF), yield per plot (YPP), thousands seed weight (gm) and oil content were collected on plot basis. Whereas, number of primary branches (NPB), number of secondary branches (NSB), number of heads per plant (NH), number of seeds per head (NSH), number of seeds per plant (NSP) and plant height (PH) were collected from randomly selected ten plants from the central row of each plot. For phonological data the number of days was calculated taking date of emergency as a reference.

2.5. Statistical Analysis

After checking for outliers and normality of residuals data were subjected to analysis of variance (ANOVA) using the SAS statistical package [13]. The significant difference among the genotypes was tested at 1 and 5% level of probability.

2.6. Estimation of Variance Components

The genotypic and phenotypic variances were estimated as described by Allard [14]. Phenotypic and genotypic coefficients of variation (PCV and GCV) were expressed as percentage of the corresponding phenotypic and genotypic standard deviations estimated as suggested by Johnson [15]. The PCV and GCV values were ranked as low 0-10%,

medium 10-20% and > 20% high [16].

2.7. Broad Sense Heritability (H^2)

Heritability in broad sense was computed as the percentage of genotypic to phenotypic variance and the heritability percentage categorized as low for less than 30%, 30-60% moderate and high if value is greater than or equal ($\geq$) 60% [17].

2.8. Genetic Advance (GA) and Genetic Advance as Percent of the Mean (GAM)

Assuming selection of superior 5% of the genotypes was estimated in accordance with the method of Johnson and the GAM was categorized as 0-10% = low, 11-20 = moderate and > 20% high [18].

3. Results

3.1. Analysis of Variance (ANOVA) and Mean Performance of Genotypes

The analysis of variance revealed highly significant difference (P ≤ 0.01) among the genotypes for all the studied quantitative traits (Table 2). The studied genotypes showed wide range of variability for most of the traits evaluated in the study. A wide range of variability was observed for days to flowering ranged from 67 to 113 days with mean value 94.9 days. The number of primary branches per plant ranged from 4.2 to 25.5 with mean value of 11.9. Thousand seed weight ranged from 1.00 to 3.00 with a mean value of 1.8. The mean value of seed yield per plot recorded 102.8 gm ranging from 96.2 to 110.4 gm.

Table 1. *List of noug genotypes and their geographical origin tested at Holetta in 2017.*

Sr. No	Accession	Zone	Altitude	Sr. No	Accession	Zone	Altitude
1	15528	Agew awi	1650	51	15681	East Gojam	2420
2	208396	Agew awi	1710	52	15686	East Gojam	2490
3	15535	Arssi	2480	53	15692	East Gojam	2430
4	15587	Arssi	2470	54	15693	East Gojam	2360
5	216875	Arssi	2410	55	202242	East Gojam	1720
6	15520	Bahirdar special	1680	56	202245	East Gojam	1800
7	15746	Bahirdar special	1700	57	202254	East Gojam	1690
8	212731	Bahirdar special	1840	58	202255	East Gojam	1690
9	15079	Bale	2430	59	202264	East Gojam	1820
10	15560	Bale	2430	60	202266	East Gojam	1850
11	208830	Bale	2430	61	202269	East Gojam	1700
12	15092	South Gonder	1830	62	202270	East Gojam	1650
13	200428	South Gonder	1700	63	202271	East Gojam	1845
14	225962	South Gonder	2360	64	15683	East Gojam	2430
15	225964	South Gonder	2370	65	208400	East Gojam	2400
16	15779	South Wollo	2390	66	212721	East Gojam	2490
17	15780	South Wollo	2420	67	15121	East Shewa	1700
18	15781	South Wollo	2420	68	15056	East Wellega	1830
19	15787	South Wollo	1700	69	15080	East Wellega	1820
20	225954	South Wollo	2445	70	15574	East Wellega	2420
21	225955	South Wollo	2450	71	15659	East Wellega	2480
22	15008	Illubabor	1700	72	15617	East Wellega	1610
23	15012	Illubabor	1700	73	15622	East Wellega	1840
24	15115	Jimma	1740	74	15657	East Wellega	2410
25	9978	West Gojam	1828	75	15660	East Wellega	2420
26	15541	West Gojam	1800	76	15661	East Wellega	2430
27	15697	West Gojam	1810	77	15662	East Wellega	2490
28	15701	West Gojam	2440	78	15667	East Wellega	2480
29	15054	West Harerge	1820	79	15668	East Wellega	2480
30	208686	West Harerge	1770	80	15669	East Wellega	2460
31	15018	West Shewa	1700	81	15671	East Wellega	2360
32	15020	West Shewa	1800	82	208944	East Wellega	2460
33	15022	West Shewa	1660	83	208945	East Wellega	2480
34	15037	West Shewa	2400	84	15770	Oromia/kemise	1660
35	15066	West Shewa	1660	85	202454	Oromia/kemise	1730
36	15083	West Shewa	2390	86	15543	North Gondar	1760
37	15131	West Shewa	1800	87	15549	North Gondar	1770
38	15132	West Shewa	1630	88	15721	North Gondar	1760
39	15167	West Shewa	2390	89	15730	North Gondar	1800
40	15202	West Shewa	1700	90	15733	North Gondar	1850
41	15509	West Shewa	2390	91	214217	North Gondar	1620
42	203184	West Shewa	2400	92	225966	North Gondar	1830
43	203192	West Shewa	2470	93	15763	North Shewa	1850
44	203194	West Shewa	2450	94	15765	North Shewa	1820
45	203195	West Shewa	2430	95	202448	North Shewa	1620
46	15154	West Wellega	1650	96	202461	North Wollo	1640

Sr. No	Accession	Zone	Altitude	Sr. No	Accession	Zone	Altitude
47	202248	East Gojam	1700	97	202472	North Wollo	1735
48	202258	East Gojam	1760	98	202473	North Wollo	1690
49	15553	East Gojam	2450	99	Shambu	Improved variety	
50	15680	East Gojam	2430	100	Ginchi-1	Improved variety	

The oil content ranged from 26.5 to 43.0 with a mean value of 34.7%. The mean comparisons between the performances of the genotypes showed that there are some genotypes superior over the improved varieties (Table 3). For all the studied traits the top five best out smart genotypes for different trait were constituted from different geographic origin (Table 1).

Table 2. *Analysis of variance for 12 morphological traits of noug genotypes tested at Holetta in 2017.*

Traits	Source of variations				CV%	R-square
	MSR (1)[df]	MSB (18)	MSG (99)	MSE (81)		
DF	0.72ns	15.19ns	233.68***	44.65	5.23	0.88
DM	18.00ns	127.87***	66.07***	28.34	3.48	0.83
GFP	11.52ns	164.99**	164.72***	56.93	12.95	0.82
PH	561.13**	235.39***	206.14***	70.67	6.48	0.83
NH	372.65***	22.52*	69.93***	11.12	15.53	0.86
NPB	17.76***	5.01**	1.63**	0.96	12.99	0.79
NSB	57.89***	4.78*	24.48***	4.65	13.67	0.80
NSH	16.99ns	9.80ns	2147.91***	351.93	6.71	0.94
NSPP	282.74ns	208.10ns	9883.17***	1148.41	11.41	0.94
YPP	155.21***	72.75***	26.18***	12.46	3.43	0.77
TSW	4.59***	0.12***	0.15***	0.03	9.22	0.86
OC	3.20ns	0.50ns	18.15**	1.78	2.72	0.92

*, ** and *** Significant at 0.05, 0.01 and 0.001 probability level respectively and ns non-significant MSR= Mean Square due to replication, MSB= Mean Square due to block, MSG= Mean Square due to genotypes, MSE= Mean Square due to error, CV%= Coefficient of variation in percentage. ( )[df] figures in parenthesis indicate degrees of freedom, DF=days to flowering, DM=days to maturity, GFP= Grain filling period, PH= plant height, NH=number of heads, NPB=Number of primary branch, NSB=Number of secondary branch, NSPP= Number of seed per plant, YPP=yield per plot, TSW=Thousand seed weight and OC= oil content.

Table 3. *Elite genotypes identified on the basis of important morphological traits and oil content for future use.*

Trait of interest	Genotypes identified
Number of primary branch	15781, 225964, 15066, 15683 and 225966
Number of secondary branch	15781, 15787, 214217, 202245 and 202254
Number of head	214217, 202461, 15079, 202473 and 9978
Number of seed per head	15622, 15132, 15780, 15115 and 15131
Number of seed per plant	214217, 15115, 202245, 202264 and Ginchi-1
Thousand seed weight	15779, 15709, 214217, 9978 and 15012
Yield per plot	208945, 202473, 202264, 15779 and Ghinchi-1
Oil content	15779, 15709, 214217, 9978 and 15012

3.2. Phenotypic and Genotypic Coefficient of Variation

Genotypic coefficient of variation, phenotypic coefficient of variation, heritability, genetic advance and genetic advance as the percent of the mean were presented in table 4. The highest PCV and GCV value were observed for traits such as number of head (78.2 and 72.3), number of seed per plant (65.8 and 61.9) and number of seed per head (63.6 and 58.2) and the lowest PCV and GCV values were recorded for yield per plot (3.5 and 2.6), number of primary branch (7.5 and 4.6) and days to maturity (3.7 and 2.8). The PCV values were found superior to the GCV for all the characters and the PCV value for oil content slightly larger than the GCV value.

3.3. Broad Sense Heritability (H^2) and Genetic Advance under Selection (GA)

The highest broad sense heritability value was recorded for oil content (90.1) followed by number of seed per plant (88.4). Low heritability scores were revealed for number primary branch (37.5) and yield per plot (52.7). Highest magnitudes for genetic advance (GA) were recorded for number of seed per plant (128.0) and number of seed per head (56.4) whereas, the lowest value was observed for thousand seed weight (0.5), number of primary branch (0.7) and yield per plot (3.9). On the other hand, genetic advance as percent of mean (GAM) at 5% selection intensity was high for number of head (136.7) followed by number of seed per plant (119.8) but it was minimal for yield per plot (3.8) and days to maturity (4.4).

Table 4. *Estimation of variance components for 12 quantitative traits of noug genotypes.*

Traits	Mean ±SD	Range	PCV	GCV	H^2	GA	GAM
DF	94.9±12.8	67.0 - 113.0	11.4	10.2	80.9	18.0	19.0
DM	153.2±6.7	138.0 - 165.8	3.7	2.8	57.3	6.8	4.4
GFP	58.3±9.5	35.5 - 86.5	15.6	12.6	65.4	12.2	21.0
PH	129.7±10.6	102.5 - 151.1	7.8	6.3	65.7	13.7	10.6
NH	7.5±0.9	5.5 - 10.0	78.8	72.3	84.2	10.3	136.7
NPB	11.9±4.7	4.2 - 25.5	7.5	4.6	37.5	0.7	5.8

Traits	Mean ±SD	Range	PCV	GCV	H^2	GA	GAM
NSB	21.5±6.5	10.7 - 40.2	16.2	14.6	81.1	5.8	27.1
NSH	51.5±35.8	1.7 - 181.3	63.6	58.2	83.6	56.4	109.6
NSPP	106.8±78.1	3.5 - 399.8	65.8	61.9	88.4	128.0	119.8
YPP	102.8±3.1	96.2 - 110.4	3.5	2.6	52.7	3.9	3.8
TSW	1.8±0.3	1.0 - 3.0	14.4	13.3	85.7	0.5	25.5
OC	34.7±3.7	26.5 - 43.0	8.7	8.3	90.1	5.6	16.1

DF=days to flowering, DM=days to maturity, GFP= Grain filling period, PH= plant height, NH=number of heads, NPB=Number of primary branch, NSB=Number of secondary branch, NSPP= Number of seed per plant, YPP=yield per plot, TSW=Thousand seed weight and OC= oil content; SD = standard deviation; 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

4. Discussion

The observed significant phenotypic variability among the evaluated noug genotypes implied that the underutilized genetic variability of the crop should be future priority in noug improvement and genetic conservation programs. The present result was in harmony with the previous findings which reported significant variation for number of heads, plant height, number of primary branches and number of secondary branches [8, 10]. Likewise highly significant variability was reported for days to 50% flowering, days to maturity, 1000 seed weight, oil content (%) and seed yield per plant [19]. The wide range of variation observed among the genotypes for the studied traits revealed that there is an opportunities for genetic improvement through selection of superior genotypes or cross breeding.

Quantitative traits such as yield are controlled by many genes and highly influenced by environmental factors. Therefore, GCV, PCV, H, GA and GAM help to group variability into heritable and non-heritable components. The high PCVs and GCVs indicate the presence of high genetic variations among the tested genotypes for the studied traits. Based on the result the highest PCV and GCV value for number of head, number of seed per plant and number of seed per head showed that selection of these traits based on phenotype may be useful for yield improvement. High GCV and PCV for number of heads and number of seed per head and lowest GCV and PCV value for number of primary branch were reported [20, 21]. In addition high GCV for number of head were reported [10, 22, 23] which is in harmony with the present result and lowest GCV for number of primary branch was reported [24]. The superior PCV values over the GCV for all the traits indicate the influence of environment for traits expression. However the PCV value for oil content slightly larger than the GCV value; indicating very little influence of environment for their expression than the other traits and the trait is stable in its expression.

Heritable variation is useful for permanent genetic improvement. Highest heritability have been reported for number of heads, oil content and number of seed per plant [21, 24, 25]. Similarly low heritability score have been reported for number primary branch [22], yield per plot and days to maturity [10]. Low heritability result could be due to high environmental effect; along with low phenotypic and genotypic coefficients of variations of these traits, indicating limited possibility of improvement for those characters through selection because of high environmental effect. According to the heritability class number of primary branch, yield per plot and days to maturity grouped as moderately heritable (30-60%) traits but the rest were categorized as highly heritable traits (≥ 60%). Even though heritability determines the effectiveness of selection; estimating alone is not sufficient for selection criteria. Hence, to increase selection efficiency estimating of heritability and genetic advance should always be considered simultaneously [15].

High 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 [15]. Therefore, based on this demarcation; days to maturity, number of primary branch and yield per plot showed low GAM. While, days to flowering, plant height and oil content exhibited moderate value but other traits were grouped as high. In this study, high genetic advance along with high heritability was shown by number of seed per plant, number of seed per head and number of heads indicating the predominance of additive gene action for these characters. Hence, the improvement of these traits could be made through direct phenotypic selection. The result was in agreement with the previous reports [20, 24]. Similar finding for number of seed was reported [19, 21]. In other finding, similar result was reported [22] for number of heads. While in earlier report contradictory result high heritability coupled with high genetic advance for number of secondary branches per plant and plant height was reported [19].

On the other hand moderate heritability coupled with low genetic advance for number of primary branch, yield per plot and Days to maturity suggesting that environment had major role in their expression of these traits. Therefore, heterosis or recurrent breeding may be beneficial to improve these traits. High heritability coupled with low genetic advance was observed for oil content, thousand seed weight and days to flowering suggesting that predominance of non-additive gene action. Similar result was reported for thousand seed weight [22] and for oil content [20]. However, the report conflict with previous study who report high value for heritability coupled with high genetic advance for oil content [25]. The variations may be because of the environment influence on the expression of the traits and the genetic difference between the genotypes.

In order to achieving high expected genetic gain from selection of individuals; the present study clearly indicates

the significance of considering the interrelation of components than depending exclusively on one way. According to this result traits with high GCV and high H^2 resulted in high expected GA as compared to traits with low GCV and H^2.

5. Conclusion

Besides its importance noug improvement is lag behind and little were known about the diversity states of Ethiopian accessions. The study concludes the existence of genetic diversity among noug genotypes that can be beneficial for improvement. Number of head, number of seed per head and number of seed per plant exhibited high values of phenotypic and genotypic coefficient of variation, broad sense heritability and genetic advance. Thus, these traits can be considered as favorable attributes for noug improvement through effective phenotypic selection. On the other hand days to maturity, number of primary branch and yield per plot recorded lowest heritability and genetic advance; hence, improvement of these trait relay on either heterosis breeding or recurrent selection. Therefore, the information will be useful in future noug breeding and conservation programs.

Conflict of Interest

All the authors do not have any possible conflicts of interest.

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