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Genetic Variability of Ethiopian Mustard (*Brassica carinata* A. Brun) Accessions Based on Some Morphological Characters

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ABSTRACT

Ethiopian mustard is an important oil crop of Ethiopian origin and it has been grown in Ethiopia since antiquity both as an oilseed and vegetable crop. The study was conducted to assess the genetic variability of thirty six Ethiopian mustard accessions using ten morphological characters. The experiment was executed using 6×6 simple lattice design with two replications. Analysis of variance shows that the accessions were significantly ($p < 0.001$) different for most of the traits studied. High phenotypic and genotypic coefficients of variation were recorded for No. of seed pod⁻¹ (54 and 50, respectively), No. of seed plant⁻¹ (47 and 42, respectively) and seed yield plant⁻¹ (65 and 60, respectively). High heritability values (>70%) were recorded for all characters considered. Seed yield ha⁻¹ showed positive and significant correlation with No. of seed pod⁻¹ (0.488), No. of seed plant⁻¹ (0.565), seed yield plant⁻¹ (0.792) and 1000 seed weight (0.660), which indicates that indirect selection of these traits would improve seed yield ha⁻¹ of the population studied. Accessions were also clustered into seven distinct groups for which further crossing/breeding program could be employed.

Key words: Analysis of variance, cluster, coefficient of variation, correlation, heritability

INTRODUCTION

Ethiopian mustard (*Brassica carinata* A. Brun) is one of the major oil crops grown in the highlands of Ethiopia. It has been cultivated since ancient time. It is produced in an area of 45, 167.81 hectares with production and productivity of 74,666.6 tones and 1.7 ton ha⁻¹, respectively (CSA, 2012). About 80% of the edible oil in the country is imported, while only the rest 20% is produced locally for domestic consumption (Wijnands *et al.*, 2007). Therefore, to meet the increasing demand of vegetable oils as well as import substitution, enhancing the production and productivity of oil crops is paramount importance. In this regard, Ethiopian mustard is among the oil crops which could be a good potential source of edible vegetable oil. Breeding and genetics on this crop had been started four decades ago. So, in order to develop high yielding and stable varieties with high oil and meal quality and disease resistance, various breeding approaches and strategies have been employed. Since then, several improved varieties with high yield ranges from 2 to 3 tones ha⁻¹ and oil content ranges from 40 to 44% have been released for production.

Genetic variability is a prerequisite for any crop improvement programs. Several variability studies have been carried out for various oil crops such as *Brassica* species (Alemayehu and Becker, 2002; Aytac and Kinac, 2009; Belete, 2011; Belete *et al.*, 2012; Fahmi *et al.*, 2012;

Abideen *et al.*, 2013) Linseed (Fu *et al.*, 2002; Tadesse *et al.*, 2011; Wakjira, 2011; Kandil *et al.*, 2012; Ottai *et al.*, 2012; Ziarovska *et al.*, 2012; Belete and Yohannes, 2013), Safflower (Johnson *et al.*, 2007; Amini *et al.*, 2008; Chapman *et al.*, 2010; Safavi *et al.*, 2012) and Soybean (Gizlice *et al.*, 1993; Dong *et al.*, 2001; Li and Nelson, 2001; Ude *et al.*, 2003; Malik *et al.*, 2009). Phenotypic and genotypic coefficients of variation and heritability were commonly used genetic parameters. Information on correlation of characters was also used as crucial for indirect selection for improvement of complex character like seed yield.

This investigation was carried out to assess the genetic variability of 36 Ethiopian mustard accessions for ten morphological characters.

MATERIALS AND METHODS

Thirty six accessions (Table 1) including four checks were evaluated at Holetta Agricultural Research Center in 2012 cropping season (June to December). The accessions were laid out using 6×6 simple lattice design with two replications. Accessions were grown in six rows of length 3 m and between rows of 30 cm with all recommended agronomic practices. Data were recorded on days to flowering, plant height, No. of primary branch plant⁻¹, No. of secondary branch plant⁻¹, No. of pod plant⁻¹, No. of seed pod⁻¹, No. of seed plant⁻¹, seed yield plant⁻¹, seed yield ha⁻¹ and 1000 seed weight.

Data analysis: Data were subject to analysis of variance using AGROBASE™ software (Agronomix software Inc., Canada). Genotypic and phenotypic variances were calculated following Omidi *et al.* (2009) as follows:

$$\text{Genotypic variance (GV)} = \frac{(\text{MSt} - \text{MSe}) - \left[(\text{MSb} - \text{MSe}) \left(\frac{2}{k+1} \right) \right]}{2}$$

$$\text{Phenotypic variance (PV)} = \text{GV} + \text{MSe}/r$$

Phenotypic and genotypic coefficients of variation were estimated using the following equations:

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sqrt{\text{PV}}}{\bar{X}} \times 100$$

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sqrt{\text{GV}}}{\bar{X}} \times 100$$

Heritability values were calculated according to Allard (1960) as follows:

$$\text{Heritability (H)} = \frac{\text{GV}}{\text{PV}} \times 100$$

Correlation of characters was done using Pearson's correlation.

Table 1: Accessions used in this study

No.	Accession	Collection region/area	Altitude in m a.s.l
1	Acc. 21315	Oromia/T/Inchini	2410
2	Acc. 21336	Oromia/Dale Lalo	1480
3	Acc. 21338	Oromia/Dale Lalo	1680
4	Acc. 21349	Oromia/Darimu	1750
5	Acc. 21364	SNNP/Geshe	1780
6	Acc. 21371	Oromia/Sokoru	2030
7	Acc. 21374	Oromia/Amaya	1220
8	Acc. 21377	SNNP/Gumer	2840
9	Acc. 207915	Oromia/Horo	2400
10	Acc. 208355	SNNP/Selti	2000
11	Acc. 208404	Amara/Goncha siso enese	2650
12	Acc. 208406	Amara/Fogera	1850
13	Acc. 208407	Amara/Farta	2650
14	Acc. 208409	Amara/Farta	1850
15	Acc. 208412	Amara/Esete	2530
16	Acc. 208421	Amara/Dangela	1950
17	Acc. 208593	Oromia/Goro Gutu	2200
18	Acc. 208598	Harari/Harhar	1800
19	Acc. 208601	Oromia/Babile	1700
20	Acc. 208602	Provisiona/Gursum	1700
21	Acc. 208608	Oromia/Kurfa Chele	1840
22	Acc. 208807	Oromia/Dodotana Sire	1830
23	Acc. 208969	Oromia/Jima Horo	2350
24	Acc. 212665	Amara/Enemay	2540
25	Acc. 212666	Amara/Enarj Enawga	2600
26	Acc. 212668	Amara/Bahir Dar	2210
27	Acc. 212674	Amara/Farta	2650
28	Acc. 212901	SNNP/Sodo Zuria	1850
29	Acc. 216845	Oromia/Tiyo	2340
30	Acc. 219786	Tigray/Laeylay Maychew	2130
31	Acc. 237529	Tigray/Laeylay Maychew	2110
32	S-67 Brown seed	Check	
33	S-67 Yellow seed	Check	
34	Holetta-1 Brown seed	Check	
35	Holetta-1 Yellow seed	Check	
36	Yellow Dodolla	Check	

RESULTS AND DISCUSSION

Result of variance analysis shows that the accessions were significantly ($p < 0.001$) different for most of the characters studied. Non-significant differences were observed for No. of secondary branches plant⁻¹ and No. of pods plant⁻¹ (Table 2).

Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and heritability values of the characters are presented in Table 3. There were no or little differences between PCV and GCV for most of the characters measured. Aytac and Kinaci (2009) reported similar result in winter rapeseed. High PCV and GCV values were recorded for No. of seed pod⁻¹, No. of seed plant⁻¹ and seed yield plant⁻¹. High heritability values (>70%) were recorded for all

Table 2: Mean squares of the 10 morphological characters studied

Traits	EMS	GMS	BMS	CV
DF	6.90	301.94**	40.50	2.87
PH (cm)	273.36	1089.43**	590.91	9.73
NPB	0.63	1.77**	1.27	9.30
NSB	19.04	22.99NS	19.69	20.70
NP	5364.88	7615.23NS	7900.92	24.56
SP	6.02	23.52**	0.82	27.18
SEPP	657897.20	1514244.14**	2935787.58	31.30
SYP	9.04	29.67**	28.45	36.01
SY	14121.92	114063.44**	60106.21	2962.00
TSW	0.03	1.68**	0.07	5.44

**: Significant at $p < 0.001$, NS: Non significant, DF: Days to flowering, PH: Plant height, NPB: No. of primary branch, NSB: No. of secondary branch, NP: No. of pod, SP: Seed pod⁻¹, SEPP: No. of seed plant⁻¹, SYP: Seed yield plant⁻¹, SY: Seed yield ha⁻¹, TSW: 1000 seed weight, EMS: Error mean squares, GMS: Genotypic mean squares, BMS: Block mean squares, CV: Coefficient of variation

Table 3: Pearson's correlation coefficients of eight characters considered

Traits	DF	PH	NPB	SP	SEPP	SYP	SY
DF							
PH	0.273						
NPB	0.528**	0.217					
SP	-0.167	0.064	-0.142				
SEPP	-0.069	0.282	0.114	0.839**			
SYP	0.000	0.323	0.233	0.744**	0.811**		
SY	-0.146	0.361	0.278	0.488**	0.565**	0.792**	
TSW	0.236	0.283	0.326	0.367*	0.287	0.748**	0.66**

*, **: Significant at $p < 0.01$ and $p < 0.001$, respectively, DF: Days to flowering, PH: Plant height, NPB: No. of primary branch, SP: Seed pod⁻¹, SEPP: No. of seed plant⁻¹, SYP: Seed yield plant⁻¹, SY: Seed yield ha⁻¹, TSW: 1000 seed weight

characters considered, which indicates that these traits are more governed by genetic variance than environment. Khan *et al.* (2008) recorded high heritability for most of the characters they studied in brassica population. High heritability values along with high phenotypic and genotypic coefficient of variation were recorded for characters such as No. of seed pod⁻¹, seed yield plant⁻¹ and 1000 seed weight. This shows that selection at early generation would be effective as they are likely controlled by additive gene actions.

Correlation analysis (Table 4) reveals that seed yield ha⁻¹ positively and significantly correlated with No. of seed pod⁻¹ (0.488), No. of seed plant⁻¹ (0.565), seed yield plant⁻¹ (0.792) and 1000 seed weight (0.660). This implies that improving seed yield/hectare could be achieved through indirect selection of these characters. Thousand seed weight showed positive and significant correlation with seed yield plant⁻¹ (0.748). Similarly, Khan *et al.* (2005) reported that seed yield ha⁻¹ was positively and significantly correlated with seed yield plant⁻¹ and 1000 seed weight in *Brassica juncea*. No. of seed pod⁻¹ was positively and significantly correlated with seed yield ha⁻¹ in elite F₃: 4 *Brassica* populations (Khan *et al.*, 2008).

Accessions were also clustered into seven distinct groups regardless of their diverse geographic origin, which can be used for further breeding/crossing programs. The highest number of accessions (10) was grouped in third cluster. The solitary accession was identified in sixth cluster, while

Table 4: Mean, phenotypic and genotypic variance, phenotypic and genotypic coefficients of variation and heritability of the eight characters considered

Traits	Mean	PV	GV	PCV	GCV	H (%)
DF	91.44	301.94	298.49	19.00	19.00	98.86
PH	169.84	1089.43	952.75	19.00	18.00	87.45
NPB	8.56	1.77	1.46	16.00	14.00	82.20
SP	9.03	23.52	20.51	54.00	50.00	87.20
SEPP	2591.71	1514244.00	1185296.00	47.00	42.00	78.28
SYP	8.95	29.67	25.15	65.00	60.00	84.77
SY	1114.32	114063.40	107002.50	30.00	29.00	93.81
TSW	3.16	1.68	1.67	41.00	41.00	99.11

DF: Days to flowering, PH: Plant height, NPB: No. of primary branch, SP: Seed pod⁻¹, SEPP: No. of seed plant⁻¹, SYP: Seed yield plant⁻¹, SY: Seed yield ha⁻¹, TSW: 1000 seed weight, PV: Phenotypic variance, GV: Genotypic variance, PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation, H: Heritability

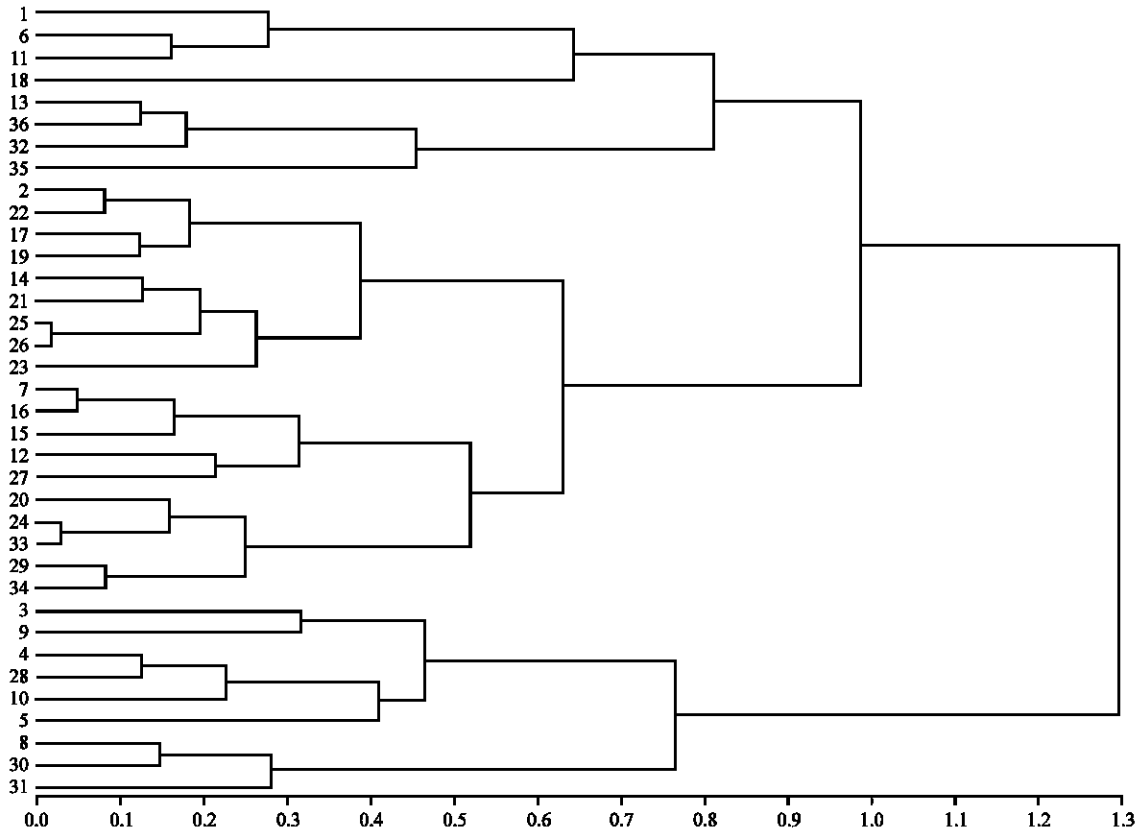


Fig. 1: Dendrogram of cluster analysis of 36 accessions of Ethiopian mustard based on morphological characters. Numbers indicates the accession studied (Table 1)

the remaining clusters such as the first, second, fourth, fifth and seventh comprised of 3, 6, 9, 4 and 3 entries, respectively (Fig. 1).

CONCLUSION

This study shows that early generation selection can be employed for No. of seed pod⁻¹, seed yield plant⁻¹ and 1000 seed weight in the improvement of the population considered.

It also indicates that indirect selection of traits such as No. of seed pod⁻¹, No. of seed plant⁻¹, seed yield plant⁻¹ and 1000 seed weight is helpful for enhancement of seed yield ha⁻¹.

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