Genetic Diversity in Ethiopian Mustard (*Brassica carinata* A. Braun)

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Abstract: A field experiment was conducted at Kulumsa Agricultural Research Center in order to estimate the extent of genetic variation in Ethiopian mustard (*Brassica carinata* A. Braun). In this study, genetic diversity in 60 Ethiopian mustard genotypes, collected from 16 regions of Ethiopia, were assessed using the techniques of cluster and principal component analyses based on 16 traits. All traits were significantly ($P < 0.01$) different and the genotypes were grouped into seven clusters. The largest and the smallest clusters comprised about 28.3 and 1.7%, respectively, of the studied genotypes. Genotypes in clusters II and VII showed better performance for the majority of traits of interest: seed yield/plot, seed yield/plant, biomass/plot, biomass/plant, plant height, number of pods/plant, 1000 seeds' weight and oil content. The clustering pattern of the tested genotypes indicated no relationships between genetic diversity and geographic origins since genotypes from the same origin were grouped into different clusters or vice versa. The average inter-cluster distances were significant for all clusters. The D^2 statistics analysis showed that the distance between clusters IV and V was minimum ($D^2 = 22.085$) while distance between clusters VI and VII was maximum ($D^2 = 1239.00$), suggesting the existence of diversity among the genotypes, and hence, parental materials can be selected and used for hybridization and subsequent improvement of Ethiopian mustard. Maximum variations in subsequent generations is expected if there is crossing of parents selected from clusters II and VII with those from clusters III, IV, and VI since the inter-cluster distances between these groups were large. On the other hand, crossing between clusters I, IV and V; I and II, and III and IV might not produce desirable recombinants since the inter-cluster distance between these groups was very small, indicating similarity of their genetic make-up. The first six principal components accounted for 92% of the total variations encountered. The first three principal components accounted for 36, 22 and 19% of the variations, respectively. Days to flowering, days to maturity, seed yield/plot, oil yield/plot and biomass/plot were the most important traits contributing to the total variation of the first principal component, implying the existence of great potential to improve these traits through selection.

Keywords: *Brassica carinata;* Cluster Analysis; Ethiopian Mustard; Genetic Diversity

1. Introduction

Brassica carinata is an amphidiploid species (BBCC, n = 17) containing the BB genome of *B. nigra* (n = 8) and CC genome of *B. oleracea* (n = 9) (Hemingway, 1995; Gomez-Campo and Prakash, 1999). It is believed to have originated in the plateaus of Ethiopia and has been cultivated there as an oilseed and vegetable crop since antiquity. In Ethiopia, the crop is traditionally used for many purposes, such as greasing traditional bread-baking clay pans, curing certain ailments and preparing beverages (Alemayehu, 2001). Furthermore, boiled and chopped leaves are mixed with butter, and served along with cheese and '*kitifo*' (slightly cooked, heavily chopped, and buttered beef). The bottom stalks remaining after harvest can be used for fences or as firewood. Similarly, the upper-branched parts are often used for making brooms for cleaning floors. Ethiopian mustard is also very beneficial in farming systems, as a potential rotational-crop for cereals and pulses. In its homeland, *B. carianata* is found to be better yielding, more tolerant to drought, more resistant to diseases and insect pests and seed shattering than *B. napus* (Tadesse and Bayeh, 1992; Alemayehu and Becker, 2002; Singh, 2003; Teklewold, 2005).

The industrial value of *Brassica carinata* oil is indeed immense in leather tanning, the manufacture of varnishes, paints, lubricants, soap and lamps (Doweny, 1971; Bhan, 1979). Recent investigations have witnessed that after transesterification, the oil exhibits physical and chemical properties suitable for bio-diesel (Cardone *et al*., 2003). The crop has the potential to be used as feedstock for oleochemicals (due to high erucic and linolenic acids) and bio-fumigant (due to its high glucosinolate) industries.

Genetic diversity measures individual variation and reflects the frequency of different types in a population (Frankel *et al*., 1995). Analysis of genetic relationships in crop species is an important component of crop improvement. It helps to analyze genetic variability of cultivars (Singh, 1983), select parental materials for hybridization for making new gene recombinations, select inbred parents or testers for maximizing heterotic response and identify materials that should be maintained to preserve maximum genetic diversity in germplasm sources (Thormann and Osborn, 1992).

Genetic diversity in crop plants arises as a consequence of inter-play of evolutionary forces (mutations, selections, migrations and random genetic drift) and the influence of man through selection and domestication (Allard, 1988). The genetic variation within a taxon is not uniformly distributed throughout the geographic area where it is growing (Frankel *et al*., 1995) and populations from areas very distant from each other are normally expected to accumulate higher genetic diversity than the population from the same vicinity (Chandel and Joshi, 1983). In diversity study, the inclusion of genotypes collected from different geographic areas has been adopted to capture maximum allelic diversity of a particular crop species.

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Detecting and quantifying the degree of dissimilarity among species, subspecies, populations and elite breeding materials is of primary concern in plant breeding and population genetics (Rief *et al.*, 2005).

Divergence analysis is usually performed by using D^2 techniques to classify genotypes for hybridization purposes. The genetic improvement through hybridization and selection depends upon the extent of genetic diversity between parents. The D^2 statistics is one of the important biometrical techniques used for assessing genetic divergence present in a population (Sharma, 1996). The D^2 values represent the index of genetic divergence among the genotypes both at intra-cluster and inter-cluster levels. It would, therefore, be logical to make crosses between genotypes belonging to the clusters which are separated by greatest generalized distance and show maximum divergence (Singh, 1983).

Information on genetic diversity is useful for making choices of parental materials of potential use in the breeding programs and it also enhances the efficienc of gene banks (Jain, 1977; Arunachalam, 1981). Although there are a large number of collections, thorough studies have not been carried out on genetic diversity in Ethiopian mustard genotypes. Therefore, an attempt is made in the present study to assess genetic divergence in Ethiopian mustard genotypes.

2. Materials and Methods

The field experiment was conducted at Kulumsa Agricultural Research Center (8° 01' N latitude and 39° 09' E longitude) in Arsi zone, southeastern Ethiopia, in the 2005/2006 cropping season using 60 Ethiopian mustard genotypes collected from 16 different parts of the country (Table 1). The genotypes were intentionally taken to represent different collections of the country (i.e., purposive sampling). Three released varieties (S-67, Yellow Dodolla and Holetta-1) were included for comparison and to see their position in the diversity pattern. Randomized complete block design with three replications was used in this study. Each genotype was planted in a plot consisting of two rows 5 m long with a spacing of 30 cm between rows. The recommended cultural practices were followed to raise the crop.

Data were recorded on 16 characters, including days to flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, biomass per plant, biomass per plot, seed yield per plant, seed yield per plot, harvest index per plant, harvest index per plot, thousand seeds weight, oil content and oil yield per plot. Fresh biomass weights were recorded and samples were also taken and dried to constant weight. Then total above ground dry matter and harvest index were calculated. Seed yield per plot was measured after the moisture of the seed was adjusted to 7%. Oil content (%) is the proportion of oil in the seed to the total oven dried seed weight as measured by Nuclear Magnetic Resonance Spectroscope. Oil yield per plot is the amount of oil obtained by multiplying seed yield per plot by corresponding oil percentage. The 16 characters were subjected to analysis of variance following the standard statistical analysis methods (Gomez and Gomez, 1984). Clustering of genotypes into different groups (i.e., based on 16 traits) was carried out using the average linkage method and the appropriate number of clusters were determined from the values of Pseudo F and Pseudo T statistics using the SAS computer software facilities (SAS, 2001). By employing the same software, F statistics and other test statistics were used to test the significances of the generalized squared distances between clusters and that of the clusters versus the traits, respectively.

The Mahalanobis generalized distances were utilized to estimate the distances between and within clusters using the SAS computer software package as per the following formula:

$$D^2ij = (Xi-Xj)' S^{-1}(Xi-Xj).$$

where, D^2ij = the distance between any two groups i and j; Xi and Xj are the vector mean of the traits for the i^{th} and j^{th} groups, respectively, and S^{-1} = the inverse of the pooled covariance matrix. In order to assess the total variations and supplement the cluster analysis, principal component analysis was also carried out using the SAS computer software facilities (SAS, 2001), involving all the 16 quantitative traits.

3. Results and Discussion

3.1. Analysis of Variance

Highly significant ($P < 0.01$) differences were noted for all traits measured (Table 2). The significance of genotype difference indicates the presence of variability for each of the characters among the tested genotypes. In characterizing genotypes of *B. carinata* collected from different parts of Ethiopia, Abebe *et al.* (1992) observed the presence of wide variation for morphological and agronomic traits. Alemayehu (2001) also evaluated 36 genotypes of Ethiopian mustard for agronomically important traits and reported the existence of an enormous amount of genetic variability. This wealth of diversity can be used for improving yield, quality and resistance to various biotic and abiotic stresses in future breeding programs. In this study, the total variations were assessed by carrying out principal component analysis by considering all 16 quantitative traits.

3.2. Cluster Analysis

Data on total variations which were assessed by carrying out principal component analysis by considering all the 16 quantitative traits are presented in Table 3. The 60 Ethiopian mustard genotypes were grouped into seven clusters (Table 4 and Figure 1) and the D^2 statistics were computed for all possible pairs of clusters as shown in Table 5. Cluster I, the largest of all seven, included 17 (28.3%) genotypes that comprised one released variety (Yellow Dodolla), one accession collected from the market, three accessions whose areas of collection were unknown and some accessions collected from seven different areas of Ethiopia. Similarly, the second cluster constituted 12 (20%) genotypes, one released variety (S-67), a selection from Kulumsa and some accessions collected from seven different regions. Cluster III was the

third smallest group and consisted of seven (11.7%) accessions from five zones. Cluster IV was the second largest group in the dendrogram, and contained 14 (23.3%) genotypes. Of these, four accessions were from Hararghe, three from Shewa, and the remaining accessions were from Illubabor, Sidamo, Welayita, Hediya, Wello and Arsi. Cluster V included eight (13.3%) accessions, two each from Shewa and Hararghe and the remaining four from Bale, Gojam, Gonder and Jimma each. Clusters VI and VII, the smallest clusters, constituted one (1.7%) genotype each. The genotype under cluster VI was collected from Gamo and that of Cluster VII was the recent variety (Holetta-1) that was released nationally in 2005. All the three released varieties were grouped under different categories, showing their distinct diversity. Generally speaking, this cluster analysis revealed that the Ethiopian mustard genotypes originating from different sources were randomly distributed into various subgroups with no definite pattern. Teklewold (2005) also reported similar results by grouping 43 accessions into four groups. This author reported that both dendrogram of cluster analysis and principal coordinate of analysis grouped the accessions in a very similar manner.

Table 1. List of the 60 Ethiopian mustard genotypes used in the diversity study of Ethiopian mustard.

Accession number	Area of collection[a]	Altitude
PGRC/E 211501	*	*
PGRC/E 208410	*	*
PGRC/E 21373	*	*
PGRC/E 20211	*	*
PGRC/E 21079	Arsi/Abomsa	2520
PGRC/E 21080	Arsi/Arba Gugu	3090
PGRC/E 21081	Arsi/Arba Gugu	2780
PGRC/E 21005	Arsi/Dodota	2450
PGRC/E 21002	Arsi/Shirka	1910
PGRC/E 21068	Bale/Adaba	2500
PGRC/E 215351	Bale/Ginir	*
PGRC/E 20109	Gamo	*
PGRC/E 20108	Gamo/Gardula	2100
PGRC/E 20162	Gojam/ Bahir Dar	1900
PGRC/E 208421	Gojam/Dangla	1950
PGRC/E 20110	Gojam/Inemay	2450
PGRC/E 208419	Gojam/Mecha	2050
PGRC/E 21257	Gojam/Shikudad	2090
PGRC/E 20112	Gojam/Tehnan	1980
PGRC/E 21033	Gonder	1930
PGRC/E 208004	Gonder/Dembiya	*
PGRC/E 21245	Gonder/Dembiya	1850
PGRC/E 208589	Hararghe/Chiro	2260
PGRC/E 208594	Hararghe/Goro gutu	1750
PGRC/E 20031	Hararghe/Habro	1750
PGRC/E 208596	Hararghe/Kersa	*
PGRC/E 208600	Hararghe/Kombolcha	2600
PGRC/E 208599	Hararghe/Kombolcha	2100
PGRC/E 212894	Hadiya/Angacha	2180
PGRC/E 20035	Illubabor/Chora	1800
PGRC/E 21358	Illubabor/Gumay	1820
PGRC/E 207928	Illubabor/Imboro Gechi	*
PGRC/E 21369	Jimma/Mana	1720
PGRC/E 213168	Kefa	*
PGRC/E 21058	Mentaweha market	*
Yellow Dodolla	Released in 1986	
S-67	Released in 1976	
Holetta-1	Released in 2005	
KARC-2000	Selection	
PGRC/E 20052	Shewa/Adis Alem	2540
PGRC/E 20068	Shewa/Ambo	2010
PGRC/E 20066	Shewa/Ambo	1950
PGRC/E 20125	Shewa/Ambo	1950
PGRC/E 208585	Shewa/Boset	1600
PGRC/E 20059	Shewa/Chaliya	1630
PGRC/E 20130	Shewa/Girar Jarso	2750
PGRC/E 20062	Shewa/Merhabete	1800
PGRC/E 21001	Shewa/Minjar	2755
PGRC/E 20159	Sidamo/Awasa	1750
PGRC/E 20076	Sidamo/Wenago	1853
PGRC/E 20168	Tigray	*
PGRC/E 20163	Tigray/Zal Anbesa	2300
PGRC/E 208860	Welayita/Sodozuriya	1820
PGRC/E 21328	Wellega/Arjo	2280
PGRC/E 21194	Wellega/Horo	1980
PGRC/E 21163	Wellega/Jima Arjo	2340
PGRC/E 208960	Wellega/Jima Genet	2280
PGRC/E 20090	Wellega/Naqamte	2140
PGRC/E 208717	Wellega/Seyo	1920
PGRC/E 21278	Welo/Desezuriya	*

[a]* = *Information not available*

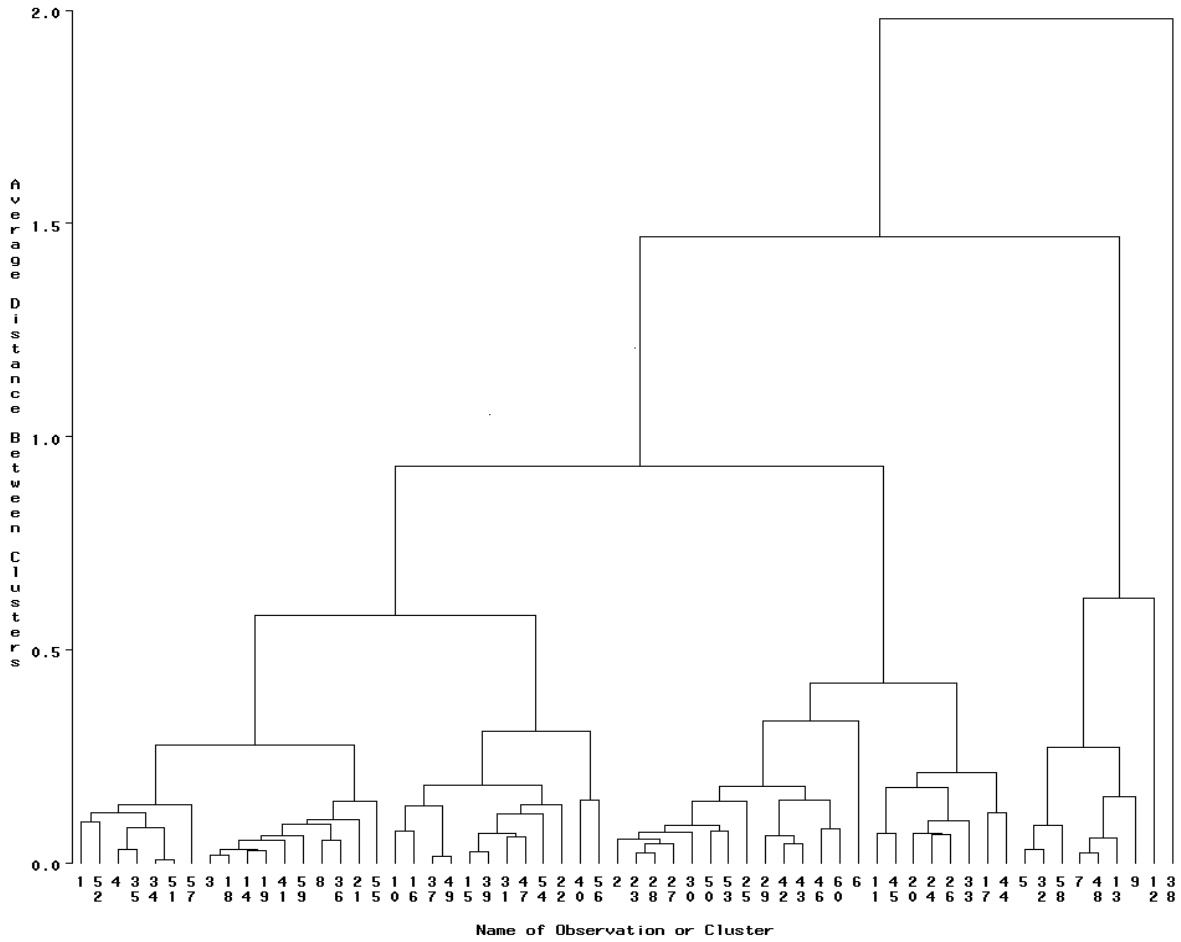

Figure 1. Dendrogram showing the clusters of 60 Ethiopian mustard genotypes.

Table 2. Mean squares of genotypes and error and the corresponding coefficient of variation for 16 characters studied.

Characters	Genotype (59)[b]	Error (118)	CV (%)
Days to flowering	125.258**	5.508	2.6
Days to maturity	324.254**	12.377	2.3
Plant height	529.660**	81.521	5.09
Primary branches per plant	4.892**	1.463	9.06
Secondary branches/plant	88.949**	52.727	23.80
Pods per plant	6547.463**	5963.013	24.42
Seeds per pod	1.238**	0.592	5.23
Biomass per plant	144.057**	106.723	21.66
Biomass per plot	3028892.429**	478780.452	20.69
Seed yield/plant	7.799**	6.147	25.26
Seed yield per plot	164861.548**	27782.425	24.20
Harvest index per plant	0.002**	0.001	13.26
Harvest index per plot	0.002**	0.001	11.78
1000 seeds weight	0.235**	0.035	6.06
Oil content	3.608**	1.174	3.13
Oil yield per plot	19312.379**	3278.271	24.04

[b]** = *Significance at P = 0.01; CV =* Coefficient of variation; *Figures in parenthesis are degrees of freedom*

3.3. Principal Component Analysis

In order to assess the total variations, principal component analysis was carried out by considering all 16 quantitative traits. The first six principal components accounted for 92% of the total variations encountered (Table 3). The first three principal components accounted for 36, 22 and 19% of variations, respectively. Among the traits considered in the study, days to flowering, days to

maturity, seed yield/plot, oil yield/plot and biomass/plot were the most important traits contributing to the total variation in the first principal component. Harvest index also had a relatively high positive weight on this component. Similarly, in the second principal component, seed yield/plant, number of pods/plant, number of secondary branches/plant and biomass/plant depicted a significant contribution. The third component emphasized plant height and 1000-seed weight, which increased but charged on harvest index/plant and plot.

The maximum variation (36%) depicted by the first principal component was based on quantitative traits such as days to flowering, days to maturity, seed yield/plot, oil yield/plot and biomass/plot. This emphasizes the importance of these traits for assessment of genetic diversity in Ethiopian mustard.

Table 3. Eigenvalues, total variance and cumulative variance for the 16 quantitative traits.

Character[a]	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6
Days to flowering	-0.38	0.10	0.15	0.05	0.13	-0.11
Days to maturity	-0.35	0.10	0.22	0.15	0.12	-0.16
Plant height	0.13	-0.06	0.48	-0.14	-0.08	-0.05
Primary branches per plant	-0.28	0.16	-0.02	-0.41	0.23	0.50
Secondary branches per plant	-0.16	0.42	-0.10	-0.19	0.10	0.26
Number of pods per plant	0.05	0.43	-0.18	-0.22	-0.40	-0.17
Number of seeds per pod	-0.29	0.08	-0.04	0.52	0.07	-0.31
Biomass per plant	-0.15	0.40	0.24	-0.07	-0.25	-0.21
Seed yield per plant	0.03	0.50	0.05	0.15	-0.12	-0.05
Harvest index per plant	0.22	0.23	-0.27	0.38	0.21	0.28
Biomass per plot	0.33	0.09	0.28	-0.12	0.14	-0.12
Seed yield per plot	0.37	0.14	0.18	-0.03	0.13	-0.09
Harvest index per plot	0.27	0.21	-0.23	0.29	0.03	0.13
Thousand seed weight	-0.03	0.14	0.44	0.19	0.45	0.21
Oil content	-0.06	-0.10	0.34	0.35	-0.61	0.56
Oil yield per plot	0.36	0.13	0.22	0.02	0.05	-0.03
Eigenvalues	5.75	3.56	3.11	1.06	0.66	0.64
%Total variance	36.0	22.0	19.0	7.0	4.0	4.0
%Cumulative variance	36.0	58.0	78.0	84.0	88.0	92.0

[a]*PC 1, PC 2, PC 3, PC 4, PC 5 and PC 6 are the first six principal components*

Table 4. Distribution of 60 Ethiopian mustard genotypes in different clusters.

Cluster I	PGRC/E 211501	PGRC/E 20162	PGRC/E 213168	PGRC/E 20168	PGRC/E 208717
	PGRC/E 21373	PGRC/E 21257	PGRC/E 21058	PGRC/E 20163	
	PGRC/E 20211	PGRC/E 20112	Yellow Dodolla	PGRC/E 21194	
	PGRC/E 21005	PGRC/E 208004	PGRC/E 20068	PGRC/E 208960	
Cluster II	PGRC/E 21068	PGRC/E 21245	KARC-2000	PGRC/E 20159	
	PGRC/E 208421	PGRC/E 21358	PGRC/E 20052	PGRC/E 21328	
	PGRC/E 20110	S-67	PGRC/E 20062	PGRC/E 21163	
Cluster III	PGRC/E 21079	PGRC/E 21002	PGRC/E 207928	PGRC/E 20090	
	PGRC/E 21081	PGRC/E 20108	PGRC/E 21001		
Cluster IV	PGRC/E 208410	PGRC/E 20031	PGRC/E 212894	PGRC/E 20125	PGRC/E 208860
	PGRC/E 21080	PGRC/E 208600	PGRC/E 20035	PGRC/E 20130	PGRC/E 21278
	PGRC/E 208589	PGRC/E 208599	PGRC/E 20066	PGRC/E 20076	
Cluster V	PGRC/E 215351	PGRC/E 21033	PGRC/E 208596	PGRC/E 208585	
	PGRC/E 208419	PGRC/E 208594	PGRC/E 21369	PGRC/E 20059	
Cluster VI	PGRC/E 20109				
Cluster VII	Holetta-1				

3.4. Distances among Different Clusters

Maximum generalized squared distance was observed between clusters VI and VII (D^2 = 1239), followed by that of clusters II and VI (D^2 = 757.217), and Clusters III and VII (D^2 = 734.628). In contrast, the smallest squared distance was obtained between clusters IV and V (D^2 = 22.085), indicating their close similarity. The average intra-cluster distance ranged from 2.522 (Cluster I) to 8.189 (Clusters VI and VII) as shown in Table 5. In fact, there was highly significant ($P < 0.01$) difference between the analyzed inter-cluster distances. This is additional proof of for the presence of wide diversity among the studied genotypes to be exploited in future variety improvement schemes.

3.5. Mean Values of Measured Characters for Different Clusters

The tallest genotypes were represented in cluster II, with recorded mean plant height of 187.94 cm, whereas the shortest with mean height of 159.05 cm was included in cluster III that had seven genotypes (Table 6). Others were grouped in cluster VII (181.00 cm) and cluster I (184.10 cm). Cluster VII exhibited the highest harvest index on a plant and plot basis (0.225 and 0.220, respectively) against the lowest of cluster VI, 0.184 and 0.164, respectively. The range of days to maturity was between 144 for cluster VII to 171 days for cluster VI. Genotypes grouped under cluster V and cluster II were relatively early maturing, with mean days to maturity of 146 and 148 days, respectively. However, genotypes classified under cluster III were relatively late maturing.

The highest biomass on plot basis was recorded for cluster VII (5950 g), while the lowest was for cluster VI (867 g). The second highest and lowest biomass per plot were recorded for cluster II and cluster III. On a plant basis, highest biomass was also recorded for cluster VII (58.17 g), whereas the lowest was registered for cluster V (42.48 g). The highest seed yields per plant (13.17 g) and per plot (1304.91 g) were recorded for cluster VII. The lowest seed yields per plant and plot were recorded for cluster VI (9.13 g and 151.38 g, respectively) compared to cluster II with high seed yield of 961.49 g/plot (Table 6). Genotypes in cluster III were low yielders, with mean seed yield per plot of 334.37 g.

Generally, clusters that contained early maturing genotypes such as clusters VII and II produced relatively high yield, more biomass and long stature but clusters with late maturing genotypes such as clusters VI and III were relatively shorter and produced low biomass. The general performance of genotypes was largely affected by the moisture stress occurring during the grain filling period and the effect was more pronounced on seed yield, 1000-seed weight and oil content. Early maturing genotypes in clusters II and VII relatively escaped moisture stress and produced better seed yield and yield components, suggesting that earlier reproductive development is obligatory for high yield and yield components in areas of terminal moisture stress. Among the genotypes, Holetta-1, PGRC/E 21068, 21163, 20052, 20110 and 21245 were the promising ones due to their better yielding ability and could be selected as parents to be crossed with genotypes in distant clusters, which were better in biomass, 1000-seed weight and oil content. The highest oil content (37.6%) was recorded from PGRC/E 21358 in cluster II and it could be a good candidate for crossing with distant genotypes for improving oil content. In short, cluster analysis showed the presence of high genetic divergence among the Ethiopian mustard genotypes collected from different agro-ecologies of Ethiopia. Hence, hybridization of these genetically divergent parents could lead to the development of desirable recombinants and transgresive segregants, that in turn, may lead to the development of better performing varieties than the released varieties. Crossing genotypes belonging to distant clusters for wide Mahalanobis distance (D^2) could maximize transgresive segregation (Amsalu and Endeshaw, 1999).

In conclusion, the current study has shown that there is sufficient evidence for the existence of ample diversity among the genotypes of Ethiopian mustard for optimizing the conservation and utilization of the mustard genetic resources which could have major impacts on the diverse needs of growers and consumers in view of future climatic, edaphic and biotic challenges.

4. Acknowledgment

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Table 5. Average intra- (bold face) and inter-cluster divergence D^2 value in 60 Ethiopian mustard genotypes.

Cluster	I	II	III	IV	V	VI	VII
I	**2.52226**	28.95500	200.47509	65.55999	24.05488	528.60367	188.37942
II		**3.21888**	360.03439	163.36467	86.17360	757.21718	85.12234
III			**4.29687**	46.54070	111.89223	118.44844	734.62849
IV				**2.91057**	22.08478	250.60659	439.52415
V					**4.02981**	376.12252	306.09072
VI						**8.18869**	1239.00
VII							**8.18869**

Table 6. Mean values of seven clusters for 13 characters of the 60 genotypes.

Cluster[b]	DF	DM	PH(cm)	PB/PL	SB/PL	PD/PL	SD/PD	BM/PL(g)	SY/PL(g)	HI/PL	BM/P(g)	SY/P(g)	HI/P
I	89.59	153.33	184.10	12.94	28.32	307.45	14.78	48.47	9.95	0.205	3765.88	780.68	0.207
II	87.17	148.19	187.94	12.71	29.13	314.76	14.22	47.43	10.14	0.213	4539.72	961.49	0.211
III	98.38	162.95	159.05	14.40	32.70	310.23	15.54	49.26	9.79	0.202	1730.00	334.37	0.194
IV	92.74	155.76	172.12	14.13	33.73	329.30	14.80	48.25	9.46	0.198	2675.24	528.33	0.197
V	85.17	145.67	173.46	12.75	28.53	314.05	14.36	42.48	9.36	0.220	3220.42	666.06	0.206
VI	100.33	171.00	162.00	14.00	31.93	265.60	15.80	49.67	9.13	0.184	866.67	151.38	0.164
VII	84.00	143.67	181.00	13.77	38.50	410.30	14.07	58.17	13.17	0.225	5950.00	1304.91	0.220

[b]*DF = Days to flowering; DM = Days to maturity; PH = Plant height; PB/PL = Number of primary branches per plant, SB/PL = Number of secondary branches per plant; PD/PL = Number of pods per plant; SD/PD = Number of seeds per pod; BM/PL = Biomass per plant; BM/P = Biomass per plot; SY/PL = Seed yield per plant; SY/P = Seed yield per plot; HI/PL = Harvest index per plant; HI/P = Harvest index per plot.*

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