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Studies on genetic divergence analysis of different Ethiopian mustard (*Brassica Carinata A.Braun*) genotypes growth in Debre Tabor, Ethiopia

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Research Paper

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The study was carried out with Ethiopian mustard genotypes to assess the genetic diversity for yield and yield related traits. The Euclidean genetic distances are the square roots of the sum of square of the distance between the multidimensional space values of the variables for any two genotypes. This had been used to classify pair of genotypes into different groups based on genotypes genetic distance. The genotypes were evaluate for 16 characters and showed wide variability for components studies. Cluster analysis had revealed that the 36 genotypes were grouped in 20 distinct clusters. The maximum average intra cluster D^2 was obtained in cluster XIII (D^2=715.4), at the same time as the lowest D^2 was recorded in cluster XIV (D^2=166.6), which shows the presence of less genetic variability or diversity within these clusters. Principal component analysis revealed that eleven PCs (PC1 – PC10), which are extracted from the original data and having latent roots greater than one, accounting just about 94.6% of the total variation. It was also renowned that differentiation of Ethiopian mustard genotypes into different clusters was because of the little contribution of few characters rather than the cumulative effect of a number of characters. The information obtained from this investigation can be used to diagram crosses and maximize the use of genetic diversity and expression of heterosis.

Key words: Cluster analysis, Ethiopian mustard, genetic divergence, principal component analysis

INTRODUCTION

Ethiopian mustard (BBCC n=2x=17) has evolved as a natural cross between *B. nigra* (BB n=8) and *B. oleracea* (CC n=9), followed by chromosome doubling, in the highlands of Ethiopia and the Mediterranean coast (Hemingway, 1995). It is self-pollinating amphidiploids species (Doweny and Röbbelen, 1989). Under open field conditions, an average of 30% out-crossing may result from pollination by wind and/or insects.

In Ethiopia, it is cultivated as an oilseed crop science ancient time and third in its production next to noug (*Guizotia abyssinca Casa*) and Linseed (*Linum ustatismum*). Ethiopian mustard oil, which is very often adulterated with oils from Niger seed (*Guizotia abyssinica*) or linseed (Linum ustatissimum), is the main commercial product (Nigussie and Becker 2002).For a successful plant breeding program, the presence of genetic diversity and variability play a fundamental role. Genetic diversity is essential to meet the diversified goals of plant breeding such as breeding for increasing yield, wider adaptation, desirable quality, pest and disease resistance. Genetic divergence analysis estimates the extent of diversity existed among selected genotype (Mondal, 2003). Precise information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization (Samsuddin,1985). Quantification and classification of genetic diversity among genotypes is essential for parental selection in breeding programs (Tsige *et al*., 2005). Knowledge of the naturally occurring diversity in a population helps to identify diverse groups of genotypes that can be used for hybridization program. In future studies, knowledge obtained from clustering of populations of *B. carinata* in the present study could be used as a benchmark for future collection and

characterization of landraces. Furthermore, molecular level characterizations need to be done in order to make comparison with present study and further determine the existing diversity at the gene level.

MATERIALS AND METHODS

Description of the experimental site

The field experiment was conducted at Debre Tabor testing of Adet Agricultural Research Center. The research station is located at 11º 89' N latitude and 39 º 09' E longitudes with an average elevation of about 2630 meter above sea level (m.a.s.l). The location is found in Amhara National Regional State, South Gondar Administrative Zone. The major portion of the total annual rainfall received between June and October with an average rainfall of 1235.63 mm per annum, and the average minimum and maximum temperature of the study area are 9.71^0c and 21.82^cc, respectively, with average temperature of 12.11^0c. The most dominant soil type of the area is well-drained red brown.

Experimental materials and procedures

A total of thirty six genotypes of Ethiopian mustard were used in the study. The genotypes were collected by Institute of Biodiversity and Conservation (IBC) from diverse agro-ecological areas of northern Ethiopia with an altitude range of 1600- 2700 meter above sea level, representing one of the major mustard production areas in the country. The genotypes and area of collection were described in (Table 1). The experiment was laid as 6 X 6 simple lattice designs using 5 m x 1.8 m plots with two replications. Single row plots, with each row 5m long and spacing between plots, rows and replications were 0.6 m, 0.3 m and 2 m, respectively. The rates of fertilizer application was 40.3 kg/ha and 150 kg/ha Urea and DAP respectively. Fertilizer were applied only at sowing and the seed rate was 10 kg/ha. Other cultural practices were followed as recommended for the area (Nigussie and Becker, 2002).

Data collection

The following data were collected from the experiment both per plot and per plant basis.
The following data was recorded from the central four rows.

1. Days to flowering (DF): It was recorded as number of days from planting to a stage when 50% of the plants in a plot produced flower.
2. Days to maturity (DM): The number of days from the date of sowing to a stage when 90% of plants have reached their physiological maturity.
3. Biomass (BM/P): The total above ground biological yield in grams obtained from each plot at harvest.
4. Harvest index (HI/P): The fraction of dry seed in the above ground biological yield on a plot basis.
5. Thousand Seed weight (TSW): The weight in grams of 500 seeds sampled from each plot and multiplied by two.
6. Seed yield (SY/P): Seed yield per plot was measured in grams after moisture of the seed is adjusted to 7%.
7. Oil content (OC): The proportion of oil in the seed to the total oven dried seed weight as measured by Nuclear Magnetic Resonance Spectrometer (NMRS).
8. Oil yield (OY/P): The amount of oil in grams obtained by multiplying seed yield per plot by corresponding oil percentage.

The data for the following characters were recorded from ten randomly taken plants each experimental plot and the average were considered per plant basis.

1. Primary branches per plant (PB/PL): The average number of primary branches per plant.
2. Secondary branches per plant (SB/PL): The average number of secondary branches formed on primary branches per plant.
3. Number of pods per plant (PD/PL): The average number of pods counted from the same sample plants.
4. Silique (Pod) Length (SL): The main Silique from the ten sampled plants were measured in cm and averaged to represent the pod length.
5. Number of seeds per pod (SD/PD): The average number of seeds per pod obtained from two randomly sampled pods of each of the 10 randomly taken plants.
6. Plant height (PH): The height of plants in each plot measured in centimeters from the ground surface to the top of the main stem at maturity.

Statistical Analysis

Multivariate analyses of cluster and principal component analyses of genotypic values were computed using the procedures CLUSTER (ward's minimum) and PRINCOMP, respectively using SAS software version 9.00 (SAS, 2001).The genotypic values were determined as the methods described by Zhu (1996) but considering the interaction component as nil (Falconer and Mackay,1996).Genetic distance between clusters was calculated using the generalized Mahalanbis D^2 statistics using the equation:

$$\mathbf{D^2_{ij} = (Xi- Xj)\, S^{-1}\, (Xi - Xj)}$$

Where, D^2_{ij} is the square distance between any two genotypes i and j, Xi and Xj are the vectors for the values for genotype i^{th} and j^{th} genotypes, and S^{-1} is the inverse of pooled variance covariance matrix.

Table 1. List of genotypes considered in the study and their origin.

Code	Acc.No.	Area of collection	Altitude (m)	Code	Acc.No.	Area of collection	Altitude (m)	Code	Acc.No.	Area of collection	Altitude (m)
1	PGRC/E 20052	Shewa/AdisAlem	2540	13	PGRC/E208558	*	*	25	PGRC/E 21001	Shewa/Jibat	2350
2	"20059	Shewa/Chaliya	1630	14	"208559	*	*	26	"21057	Gojjam	*
3	"20068	Shewa/Ambo	2010	15	"208560	*	*	27	"21069	Bale	2450
4	"20080	*	*	16	"208565	*		28	"21162	Bedele	1920
5	"20163	East Tigray	2300	17	"208570	*	*	29	"21163	Wellega/Jima Arjo	1820
6	"20168	Gondar	2400	18	"208571	*	*	30	"21266	Wollo/Borena	2570
7	"20169	*	*	19	"208572	*	*	31	"21278	Welo/Desezuriya	*
8	"208507	*	*	20	"208576	*	*	32	"21369	Jimma	1720
9	"208524	*	*	21	"208584	*	*	33	"213168	Kefa	*
10	"208528	*	*	22	"208585	Shewa/Boset	1600	34	YD	Released in 1986	
11	"208545	*	*	23	"208594	Hararghe	1750	35	Holetta-1	Released in 2005	
12	"208551	*	*	24	"208961	E. Wellega	2700	36	Local check	®	2240

*donated by foundation for agricultural plant breedingS.V.P.P.O.Box117 Wageningen, the Netherlands. - : Information not available. Code: Genotype by code. Acc. No: Genotype accession number.

RESULTS AND DISCUSSION

Genetic divergence

Information of the naturally occurring diversity in a population helps to identify diverse groups of genotypes that can be used for hybridization program. The interest of breeders in the use of measurements of genetic diversity dissimilarity as parameters of the indication of parental lines to be used in crosses is based on the biometric relationship between the heterosis manifested in hybrids and the divergence in the gene frequencies of parents (Falconer, 1981). More efforts have been devoted to the study of genetic divergence after proof was obtained for the existence of significant correlation between parental diversity and hybrid performance in different crops.

Cluster mean analysis

The genotypes in cluster I and XVIII may be used for improvement of oil content and seed yield per plot. From cluster mean values, genotypes in cluster I and XVIII deserve consideration for their direct use as parents in hybridization programs to develop high yielding Ethiopian mustard varieties. Cluster I contained two genotypes having the characteristic of relatively shorter duration of days to mature (145.5) next to cluster XI, very long plant height (217.5cm), lowest number of pod per plant (128) and high oil content (45%) .Cluster II contained two genotypes characterized for the most part all characters leveled in the middle value, as a result, this cluster had intermediate characters in other agronomic traits.

Cluster III had consisted of two genotypes characterized by the following features, the highest number of secondary per plant (39.0), the shortest pod length (3.5cm) except cluster XII, the lower number of primary branches per plant (11.5) except XIII, very light 1000-seed weight (2.3 gm) and least weight of biomass per plot (1300 gm). Cluster IV consisted of ten genotypes, that the first largest number of grouped including the standard check one released variety (Yellow Dodolla), which are characterized by the following features, herein cluster all characters leveled in the middle values ,for that reason, this cluster had intermediate characters in other agronomic traits. Cluster V had consisted of two genotypes. The cluster could be characterized by relatively early day to flowering (62), relatively heavy 1000-seed weight (4.6 gm) and lower number of secondary branches per plant (12.5).

Cluster VI had three genotypes with the second largest number of groups including the standard check one released variety (Holetta-1) that was released nationally in 2005. With a character feature, of the highest number of seed per pod (16.5), heavy seed yield per hectare (2366.9 gm) and relatively high oil yield per plot (103.6) except cluster VII.

Only two genotypes were grouped in Cluster VII. In this cluster had features of high number of primary branch per plant (24) and the highest number of pod per plant (307.5).From cluster VIII to XX one genotype (singleton) in each in Cluster. Among these clusters, VIII had the shortest plant height (126.5) and high oil yield per plot (117).

Table 2. Distributions of 36 Ethiopian mustard genotypes in different clusters.

Cluster	Total № of genotypes	Genotypes in each cluster[@]	% of clusters
I	2	12,32	5.56
II	2	7,9	5.56
III	2	27,31	5.56
IV	10	5,6,10,11,16,17,22,23,24,34	27.78
V	2	13,18	5.56
VI	3	1,3,35	8.3
VII	2	19,20	5.56
VIII	1	2	2.78
IX	1	4	2.78
X	1	8	2.78
XI	1	14	2.78
XII	1	15	2.78
XIII	1	21	2.78
XIV	1	25	2.78
XV	1	26	2.78
XVI	1	28	2.78
XVII	1	29	2.78
XVIII	1	30	2.78
XIX	1	33	2.78
XX	1	36	2.78
Total	36	36	100

Cluster IX, X, XVII, XVI and XX had the intermediate agronomic characters. Cluster XI were characterized by late flowering (105), early day to maturity (141) and early grain filling period (36). The lowest values of harvest index (139.3), seed yield per plot (696.3 gm), seed yield per hectare (1160.6 gm) and oil yield per plot (48.2) was described in cluster XII. Similarly, in cluster XIII was characterized for late grain filling period (95.5) and early day to flowering (57). Cluster XIV had one genotype characterized for very late day to maturing (170) and poor oil content (37.5%). However, the other characters almost were intermediate. The heavy weight biomass (6060 gm) and seed yield per plot (2182 gm) was described from cluster XV and XVIII respectively. Likewise, the lowest number of seed per pod (10) and least value of harvest index (623.6) it was found with in cluster XVII and XIX, respectively (Tables 2 and 3).

Estimation of intra and inter cluster square distances (D^2)

Average intra and inter cluster D^2 values were presented in (Table 4). Maximum average intra cluster D^2 was obtained in cluster XIII (D^2=715.4) followed by cluster XVI (D^2=478.9) and cluster XVIII (D^2=460.9) at the same time as the lowest D^2 was recorded in cluster XIV (D^2=166.6), which shows the presence of less genetic variability or diversity within these clusters.

The highest average inter cluster D^2 was recorded between cluster XV and cluster III (D^2=4933.6) followed by cluster XV and cluster XIII (D^2=4733.9) and cluster VIII and cluster III (D^2= 4247.2) which had shown these clusters were genetically more divergent from each other than any other clusters in this study. According to Ghaderi *et al.* (1984), increasing parental distance implies a great number of contrasting alleles at the desired loci, and then to the extent that these loci recombine in the F_2 and F_3 generation following a cross of distantly related parents, the greater will be the opportunities for the effective selection for yield factors.

Minimum inter cluster distance was observed between cluster XVII and cluster II (D^2=413.7) signifying that genotypes in these clusters were not genetically diverse or there were little genetic diversity with between these clusters. This signifies that, crossing of genotypes from these two clusters might not give higher hetrotic value in our breeding program in the succeeding generation in the F1 and not a wide range of variability observed in the segregating F2 population.

Maximum genetic recombination is expected from the hybridization of the parents selected from divergent cluster groups .In the present case, therefore, maximum recombination and segregation of the progenies is expected from crosses involving parents selected from cluster XV and cluster VIII and III, followed by cluster XVIII and XIII, however the breeder must specify his objectives in order to make best use of the characters where the characters are divergent.

Principal component analysis

Principal component analysis reflects the importance of the largest contributor to the total variation at each axis for differentiation (Sharma, 1998). The eigenvalues were

Table 3. Mean values of twenty clusters for 16 characters of the 36 genotypes.

	Clusters																			
Characters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	XIX	XX
DF	72.5	72.5	77.0	73.8	62.0	78.5	92.5	90.5	78.4	84.4	105.0	92.5	57.0	83.0	62.5	60.0	82.4	71.5	63.5	80.0
DM	145.5	152.3	169.0	159.8	151.0	158.0	166.0	174.0	156.2	159.9	141.0	156.5	152.5	170	151.5	163.5	161.1	154.0	153.8	147.0
GFP	73.0	79.8	92.0	85.9	89.0	79.5	73.5	83.5	77.9	75.0	36.0	64.0	95.5	86.8	89.0	103.5	78.9	82.5	92.5	67.0
PH	217.5	156.0	158.5	145.8	153.0	136.5	138.5	126.5	134.9	137.1	163.5	125.5	165.5	177.8	159.0	140.8	144.4	139.0	138.8	135.0
PBP	17.0	15.3	11.5	14.5	19.0	14.0	24.0	16.0	15.2	15.5	17.0	16.0	11.5	16.5	19.0	13.8	13.7	16.0	14.8	13.0
SBP	32.5	20.5	39.0	19.5	12.5	19.5	24.5	18.5	16.6	16.0	19.5	17.5	17.0	31.5	27.5	24.0	18.6	14.0	13.0	22.5
LP	5.0	5.3	3.5	4.2	4.0	4.5	4.5	4.5	4.2	4.1	5.0	5.0	3.5	4.0	4.5	4.5	4.4	4.5	5.5	4.5
NPP	128.0	199.8	268.5	162.3	184.5	184.0	307.5	139.0	163.5	133.2	116.5	100.0	61.5	124.3	113.0	149.0	179.1	146.0	246.5	195.5
NSP	15.0	12.0	14.5	13.8	11.0	16.5	11.0	15.5	12.5	13.9	14.0	11.5	13.0	13.0	11.0	10.5	11.1	12.5	10	12.0
BM	3800.0	2975.0	1300.0	4485.0	2465.0	4650.0	3450.0	5250.0	3562.1	4183.3	4350.0	5000.0	1470.0	4750.0	6060.0	902.5	3385.0	3600.0	2820.0	4300.0
HI	409.0	307.6	603.4	192.6	411.7	305.7	384.5	298.8	351.1	244.1	368.4	139.3	812.8	270.6	358.7	526.9	260.0	623.6	491.6	394.3
TSW	4.1	4.2	2.3	3.8	4.6	4.2	3.1	3.7	3.8	3.8	4.4	3.4	2.8	3.3	4.8	3.7	3.9	3.2	3.3	4.0
SY	1477.0	872.4	784.5	805.1	860.3	1420.2	1326.4	1568.3	1178.4	1006.3	1526.3	696.3	1194.8	1234.5	2047.7	953.3	871.9	2182.0	1274.0	1672.6
SYh	1412.8	1453.9	1307.4	1341.8	1433.8	2366.9	2210.7	2613.9	1584.2	1677.1	1482.6	1160.6	1991.4	1395.7	1355.8	1588.8	1453.1	1344.4	1905.2	2152.9
OC	45.0	44.6	41.5	42.7	42.1	40.8	40.6	44.8	40.0	43.3	39.0	41.7	42.8	37.5	42.2	42.1	41.7	36.4	41.6	39.0
OY	63.5	64.8	54.3	57.4	60.3	103.6	93.0	117.0	63.6	72.7	57.8	48.2	85.4	52.3	57.0	66.7	60.6	49.0	78.9	84.0

DF = Days to flowering, DM = Days to maturity, GFP =Grain filling period, PH = Plant height, PBP = Number of primary branches per plant, SBP = Number of secondary branches per plant, LP= Length of pod, NPP = Number of pods per plant, NSP =Number of seeds per pod, BM = Biomass per plot, SY(gm) = Seed yield per plot, SYh = Seed yield per hectare, HI = Harvest index per plot, TSW =Thousand seed weight, OC = Oil content and OY = Oil yield per plot

often used to determine how many factors to retain. When the principal component analysis was run on correlations, one rule of thumb is to retain those factors whose eigenvalues are greater than one. The sum of the eigenvalues is usually equal to the number of variables.

The coefficients defining the first ten principal components of these data were given in (Table 5). The coefficients were scaled to present correlations between observed variables and derived components. The principal component analysis were observed (Table 5) revealed that eleven principal components PC1, PC2 and PC3 with eigenvalues 3.1, 2.42 and 1.77 respectively, have accounted for 94.62% of the total variation. The first six principal components PC1, PC2, PC3, PC4, PC5, and PC6 with values of 19.04%, 15.13%, 11.04%, 9.99%, 7.37%, and 7.31%

Table 4. Average intra- (bold face) and inter-cluster divergence D2 value in 36 Ethiopian mustard genotypes.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	XIX	XX
I	296.3	1033.1	2608.2	989.7	1473.5	1287.8	907.0	1891.6	432.4	687.6	563.2	1481.9	2452.5	991.7	2333.1	1981.8	755.5	771.5	1127.9	921.0
II		407.0	1711.1	1520.5	521.6	1985.3	1011.8	2648.3	677.5	1239.7	1527.4	2063.5	1712.7	1814.8	3304.4	1107.6	413.7	1490.4	652.5	1701.0
III			246.2	3213.5	1193.4	3584.5	2405.1	4247.2	2329.2	2940.9	3157.1	3737.1	868.3	3499.3	4933.6	701.4	2122.0	2694.7	1709.5	3248.9
IV				231.3	2034.9	1213.2	1468.9	1674.0	1037.0	497.9	771.6	563.9	3171.8	516.2	2013.8	2620.1	1109.9	1692.8	1845.7	1219.8
V					263.9	2443.9	1345.3	3109.7	1154.3	1750.8	2002.7	2571.3	1260.9	2321.2	3787.9	603.6	933.1	1757.9	728.2	2132.3
VI						182.4	1222.8	667.6	1363.4	934.0	947.4	1462.9	3252.4	998.7	1848.1	2902.5	1655.3	1683.5	1903.4	490.6
VII							430.9	1870.3	670.9	987.8	1192.0	2002.0	2057.3	1553.3	2846.9	1723.0	904.4	1261.4	714.1	926.9
VIII								296.3	2017.0	1528.6	1451.0	1722.6	3884.6	1361.5	1574.5	3562.5	2306.0	2195.9	2558.4	1068.0
IX									349.0	660.9	870.8	1590.3	2183.7	1208.4	2655.4	1684.4	388.8	1068.2	830.8	1056.3
X										296.3	595.9	1021.2	2797.7	675.1	2173.7	2301.0	841.5	1406.6	1434.3	843.2
XI											357.0	1127.2	2978.3	516.4	1793.6	2522.7	1174.4	1040.1	1619.1	695.2
XII												300.0	3722.9	654.9	1743.3	3162.3	1657.2	2106.9	2406.0	1582.3
XIII													715.4	3378.7	4733.9	705.7	2093.5	2444.5	1405.2	2908.4
XIV														166.6	1545.3	2879.8	1415.1	1533.1	2013.2	996.0
XV															205.9	4309.0	2926.2	2478.3	3381.5	1970.8
XVI																478.9	1515.3	2112.2	1027.6	2570.2
XVII																	274.3	1381.4	862.8	1409.8
XVIII																		251.5	1332.7	1208.3
XIX																			460.9	1556.9
XX																				199.9

respectively contributed more to the total variation. Consistent with Chahal and Gosal (2002) characters with largest absolute values closer to unity with in the first principal component influence the clustering more than those with lower absolute values closer to zero. Therefore, in this study, differentiation of the genotypes into different cluster was because of a cumulative effect of a number of characters rather to the small contribution of each character (± 0.001-0.66). Accordingly, days to flowering, biomass per plot, number of seed per pod, length of pod, primary branch per plant, day to maturity, grain filling period ,number of pod plant and harvest index were the most important characters contributing to the first principal components (PC1).

The second component accounting for 15.13 % of the total variance had high loadings oil yield per plot seed yield per plot and hectare. The third component explaining 11 % of the total variance, had high loadings from length of pod, seed yield per plot, oil content and 1000 seed weight in (PC4); Days to flowering, plant height number of pod per plant, number of seed per pod, length of pod, biomass per plot and seed yield per plot in the (PC5); Days to flowering, length of pod, seed yield per plot, grain filling period, biomass per plot, 1000 seed weight, primary and secondary branches per plant in (PC6); plant height, seed yield per plot, number of primary and secondary branches per plant in (PC7); oil content, oil yield per plot, number of primary and secondary branches per plant in (PC8), 1000 seed weight, length of pod, number of pod plant, number of seed per pod, number of primary and secondary branches per plant in the (PC10) and secondary branches per plant, length of pod , plant height number of seed per pod biomass per plot (PC11) were the major contributors of each principal components. Therefore, the above-mentioned characters that load high positively or negatively contributed more to the diversity and they were the ones that mostly differentiated the clusters.

CONCLUSION

Genetic distance is very important for hybridization program to get better yield and best recombinant parents. Therefore, relative squared distance was estimated in this study. Thus based on these values (D^2) between any genotypes the 36 Ethiopian mustard genotypes were grouped by twenty (20) distinct clusters. The number of genotypes per cluster varied from one ten in cluster.

The maximum average intra cluster D^2 was obtained in cluster XIII (D^2=715.4) followed by cluster XVI (D^2= 478.9) and cluster XVIII

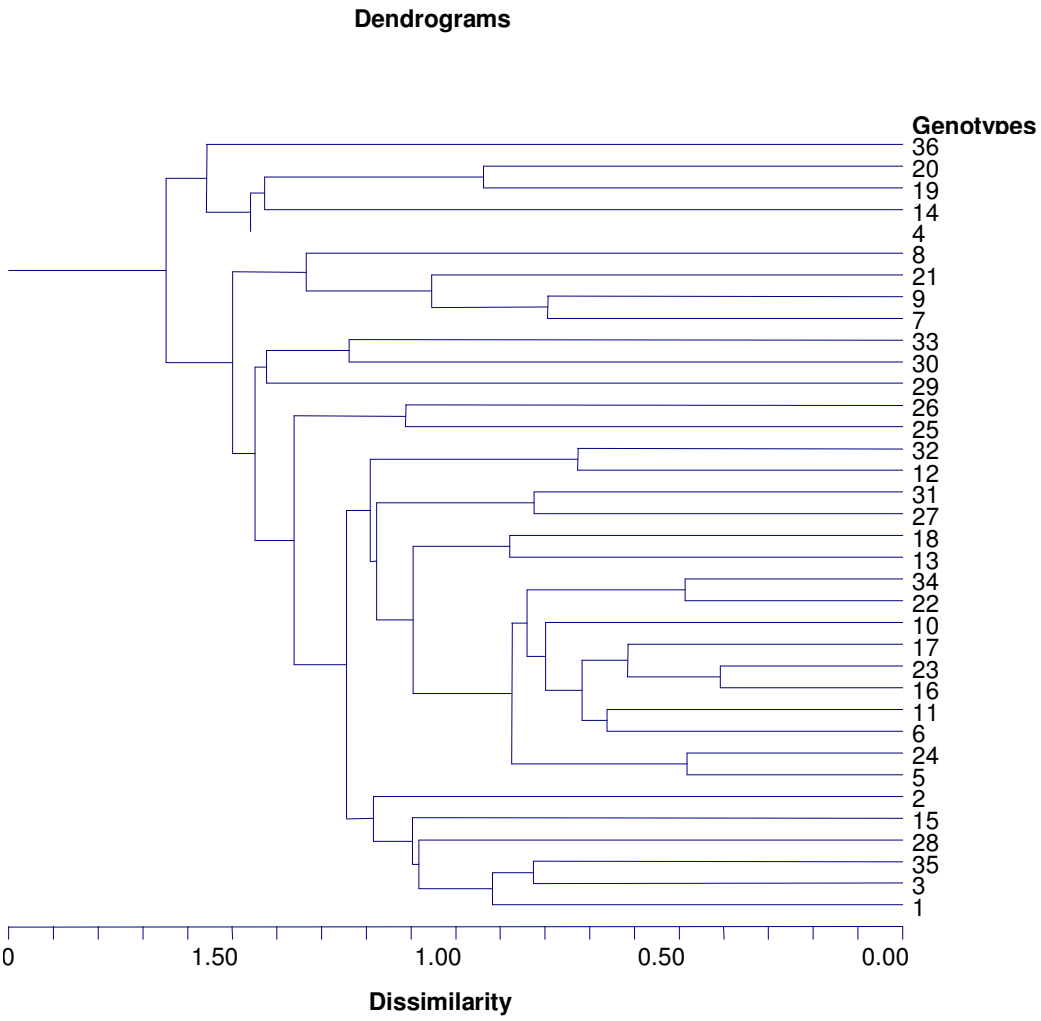

Figure 1. Dendrograms showing the clusters of 36 Ethiopian mustard genotypes.

(D^2=460.9) at the same time as the lowest D^2 was recorded in cluster XIV (D^2=166.6), which shows the presence of less genetic variability or diversity within these clusters (Figure 1).

The first six principal components PC1, PC2, PC3, PC4, PC5, and PC6 with values of 19.04%, 15.13%, 11.04%, 9.99%, 7.37%, and 7.31% respectively contributed more to the total variation. The first principal component influence the clustering more than those with lower absolute value closer to zero. Therefore, in the present study, differentiation of the genotypes into different clusters was because of relatively high contribution of few characters rather than small contribution from each character.

Therefore, the major contributing characters for the diversity in the third principal primary and secondary branches principal component seven (PC7),component two (PC2) were seed yield per plot, seed yield per hectare and oil yield per plot and days to maturity, harvest index and biomass principal component three (PC3); oil content principal component four (PC4); plant height, primary and secondary branches per plant principal component seven (PC7), similarly. primary and secondary per plant branches principal component eight (PC8). Usually it is customary to choose one variable from these identified groups.

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Table 5. Eigenvectors, total variance, cumulative variance and eigenvalues of the first eleven principal components (PCs) for 16 characters of 36 genotypes.

	Eigenvectors										
Characters	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**	**PC8**	**PC9**	**PC10**	**PC11**
Days to 50% flowering	0.36	-0.04	0.16	-0.29	0.28	-0.37	0.06	0.16	0.13	-0.04	0.12
Days to maturity	-0.31	-0.01	0.51	-0.04	0.15	0.04	-0.16	-0.01	-0.05	0.07	0.11
Grain filling period	-0.47	0.03	0.25	0.16	-0.08	0.28	-0.15	-0.11	-0.13	0.09	-0.01
Plant height (cm)	-0.04	-0.20	0.19	0.28	-0.27	0.04	0.48	0.07	0.57	0.01	-0.43
pods/plant	-0.29	0.06	0.18	-0.18	0.51	0.13	0.10	0.10	0.27	0.32	0.01
seed/pod	0.23	0.06	0.20	0.13	-0.43	-0.14	-0.33	-0.02	0.33	0.52	0.42
1^0 branches/plant	0.21	0.05	-0.02	-0.22	0.05	0.20	0.48	-0.65	-0.13	0.39	0.09
2^0 branches/plant	-0.19	-0.13	0.09	0.02	-0.17	-0.26	0.52	0.48	-0.45	0.26	0.23
Length of pod	0.21	0.07	-0.31	0.24	0.32	0.21	-0.16	0.35	-0.05	0.53	-0.30
1000 Seed weight (gm)	0.22	0.03	0.06	0.27	0.19	0.52	0.22	0.21	0.16	-0.31	0.57
Harvest index	-0.35	0.21	-0.45	0.001	-0.16	-0.08	0.08	-0.01	0.16	0.03	0.22
Biomass (kg/ha)	0.32	0.11	0.41	-0.18	-0.23	0.26	-0.05	0.16	-0.26	-0.03	-0.28
Seed yield(gm/plot)	-0.01	0.42	-0.14	-0.26	-0.33	0.38	0.05	0.21	-0.06	0.02	-0.03
Seed yield (Kg/ha)	-0.01	0.59	0.13	0.06	0.08	-0.22	0.11	0.02	0.09	-0.08	-0.07
Oil Content (%)	0.13	0.03	0.05	0.66	0.09	-0.09	0.02	-0.22	-0.33	0.01	0.001
Oil yield per plot (OY/P)	0.02	0.58	0.14	0.19	0.09	-0.09	0.02	-0.22	-0.33	0.01	0.001
Eigenvalue	3.10	2.42	1.77	1.60	1.18	1.17	1.12	0.81	0.76	0.65	0.56
Difference	0.68	0.65	0.17	0.42	0.01	0.05	0.31	0.06	0.11	0.09	0.02
% of total variance	19.40	15.13	11.04	9.99	7.37	7.31	7.00	5.08	4.72	4.06	3.50
% of cumulative variance	19.40	34.53	45.57	55.57	62.94	70.25	77.25	82.33	87.06	91.12	94.62

PC, Principal component

REFERENCES

Chahal GS, Gosal SS (2002). Principles and Procedures of Plant Breeding: Biotechnology and Conventional Approaches. Narosa Publishing House, New Delhi.

Doweny RK, RÖbbelen G (1989). Brassica Species. Oil crops of the world. McGraw-Hill New York: 339-359.

Falconer DS (1981). Introduction to quantitative genetics. 2nd ed. Longman, London.

Falconer DS, Mackay FC (1996). Introduction to Quantitative Genetics. Long man, New York.

Ghaderi A, Adamsand MW, Nassib AM (1984). Relationship between genetic distance and heterosis for yield and morphological traits in dry edible bean and faba bean. Crop science. 24:24–27.

Hemingway JS (1995). Mustards: Brassica spp. and Sinapis alba (Cruciferae). In Smartt J and Simmonds NW (eds) Evolution of crop plants, Longan Scientific and Technical, Singapore 2: 82-88.

Mondal MAA (2003). Improvement of potato (*Solanum tuberosum*) through hybridization and in vitro culture technique. PhD Thesis. Rajshahi University, Rajshahi, Bangladesh.

Nigussie A, Becker H (2002). Genotypic diversity and patterns of variation in a germplasm material of Ethiopian mustard (*Brassica carinata A. Braun*), Genetic Resources and Crop Evolution. 49: 573-582.

Samsuddin AKM (1985). Genetic diversity in relation to heterosis and combining analysis in spring wheat. Theor. Appl. Genet. 70: 306-308.

SAS Institute Inc (2001). Statistical Analysis System, Version 8.2. Cary, North Carolina, USA.

Sharma JR (1998). Statistical and Biometrical Techniques in Plant Breeding. New Age international publishers, New Delhi.

Tsige G, Labuschagne MT, Hugo A (2005). Genetic relationships among Ethiopian Mustard genotypes on oil content and Fatty acid composition. Afri. J. of Biotech. 4: 1256 - 1268.

Zhu J (1996). Analysis methods for seed models with genotypes x environment interactions. Yi Chuan Xue Bao. 21: 56-68.