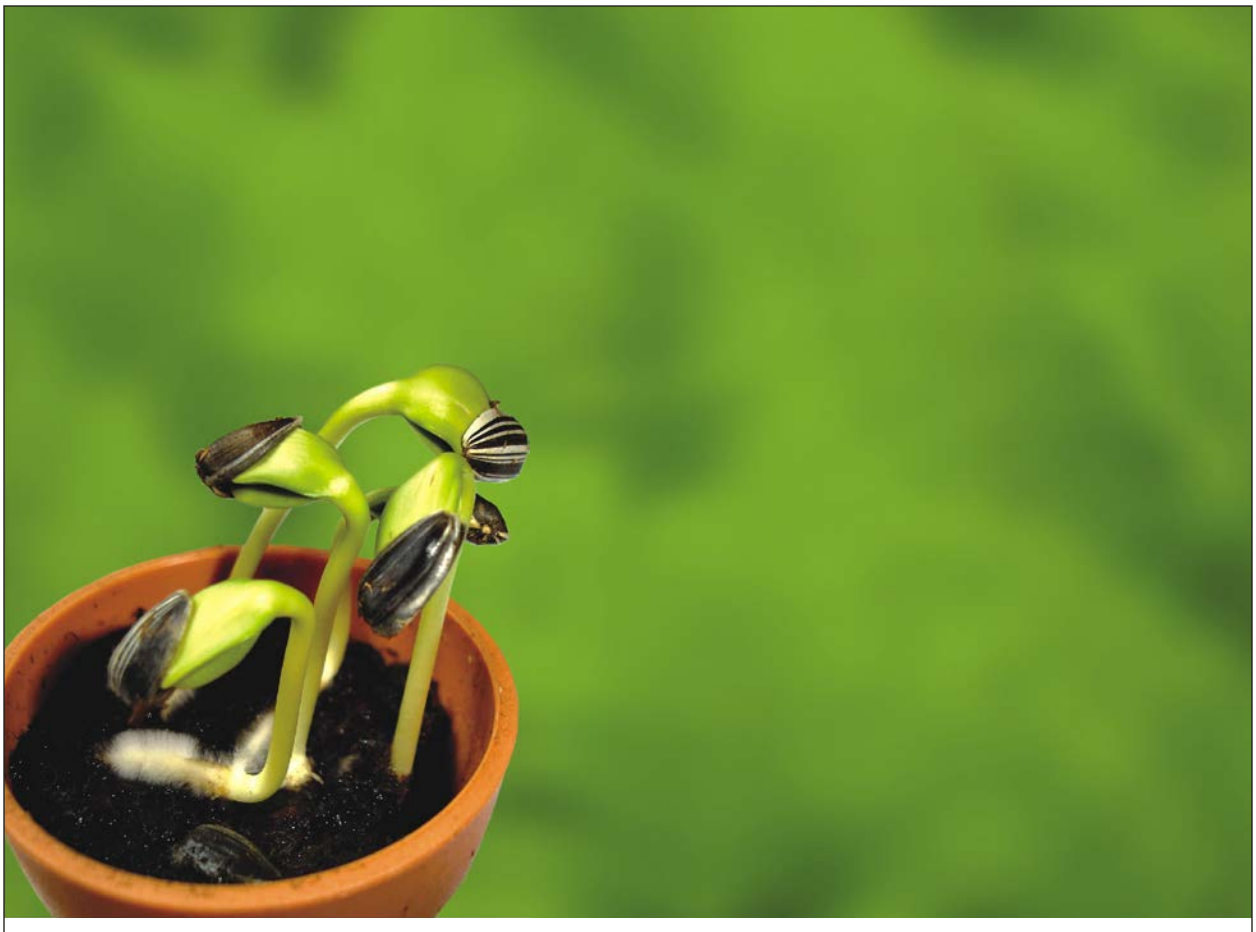

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Genetic Variability, Correlation and Path Analysis Studies in Ethiopian Mustard (*Brassica carinata* A. Brun) Genotypes

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ABSTRACT

Cultivation of Ethiopian mustard, as an oilseed, requires genetic improvement which relies on its genetic diversity and interrelationships among traits. A study was conducted to determine the extent and pattern of genetic divergence and the interrelationships among agronomic traits of Ethiopian mustard genotypes using simple lattice design at Holetta Research Center, Ethiopia. Univariate analysis has shown significant variation among genotypes in most traits. Cluster and principal component analysis resulted in the formation of seven clusters and has shown the presence of substantial genetic diversity among the genotypes. Genetic distances among clusters were significant from which selection of parents may be made for crossing in order to obtain genetic recombination and transgressive segregants. Apart from selecting genotypes from the clusters, which have higher inter-cluster distance, within a cluster performance of genotypes should also be considered for a particular trait of interest. The aggregate effect of individual traits contributed for the total variation and this was principally responsible for their respective cluster formation. Present investigation also showed that factors other than geographic diversity such as genetic drift, selection pressure, closeness in pedigree and environment may be responsible for differential grouping of genotypes. A correlation and path analysis study showed that seed yield per plot positively correlated with number of seeds per pod, number of seeds per plant and oil yield per plot. In this study, number of seeds per plant was found the most important component for improvement of the seed and oil yield of Ethiopian mustard genotypes.

Key words: Agronomic traits, cluster, Ethiopian mustard, genetic divergence, interrelationships, principal component, univariate analysis

INTRODUCTION

In Ethiopia, Ethiopian mustard (*B. carinata* A. Brun) is cultivated since ancient time and third in its production next to noug (*Guizotia abyssinica* Casa) and Linseed (*Linum ustatisumum* L.) in the highland areas of the country (Alemayehu and Becker, 2002). It is traditionally used for different purposes including: for greasing the traditional bread-baking clay pan (oven), the "Mitad", treating certain ailments and stomach upset and preparing beverages. Boiled leaves of young plants are consumed as vegetable relish. In the farming systems, it also serves as potential break-crops for cereals. This would increase crop diversity, reduce chemical use and thereby increase profits (Gan *et al*., 2007). The seed cake is used as high protein feed for animals, although the presence of glucosinolates is a limiting factor. In its native country, the oil, very often adulterated with premium oil from noug (Alemayehu, 1990, 2001), is the most important product. On the other hand, the oil shows physical and chemical properties suitable for bio-diesel

(Cardone *et al.*, 2003) which can also potentially contribute to the economic development of the country. There are opportunities which favor cultivation of oilseeds in general in the country which ranges from import substitution of edible oils to export of high value seed and oil. It is obvious that increasing the supply of oils and fats is imperative where its per capita availability is quite low. Despite the efforts made in the improvement of the Ethiopian Mustard, earliness and lack of high yielding varieties among the constraints for its production (EARO, 2000). Therefore, in order to enhance its cultivation, developing early and high yielding varieties remains the breeding policy to achieve agronomic objectives. Assessing the extent and pattern of genetic variability of Ethiopian mustard genotypes is thus a prerequisite which may help in identifying important genotypes for improvement of Ethiopian mustard. A number of methods have been used for analysis of genetic variability (Melchinger *et al.*, 1999; Rahman and Yutaka, 2004; Oboh, 2007; Raghu *et al.*, 2007).

Genetic diversity using SDS-PAGE analysis has been reported in cultivars of Bangladeshi Yellow Sarson and brown seeded *B. rapa* (Rahman and Yutaka, 2004). Further, Alsemaan *et al.* (2011) reported the existence of genetic diversity within *Rosa damascena* cultivated in Syria and recommended Almarahl and Bab Alnayrab accessions to be used to broaden the production of rose oil. On the other hand, Gichimu and Omondi (2010) reported that morphological characterization of five newly developed lines of arabica coffee as compared to commercial cultivars in Kenya. They reported low genetic variation among newly developed lines of arabica coffee as compared to commercial cultivars in Kenya and emphasizing the need to broaden the genetic base of Arabica coffee in Kenya. Knowledge of correlation coefficients is also an invaluable aid in selecting the breeding material for improving the complex traits (Teklewold *et al.*, 2000; Ismail *et al.*, 2001; Ullah *et al.*, 2011). However, this alone disregards interrelations among traits and do not show the cause and effect interrelationships. Hence, information obtained from the correlation coefficient can be enhanced by partitioning into direct and indirect effects for a set of a prior cause-effect relationships (Gravois and McNew, 1993; Teklewold *et al.*, 2000; Kozak *et al.*, 2007; Ullah *et al.*, 2011; Selvaraj and Nagarajan, 2011). Correlation and path analysis study in Ullah *et al.* (2011) and Ray and Debi (1999) showed that grain per panicle were most yield contributing trait in rice. This study was, therefore, executed with the objectives of assessing the extent and pattern of genetic variability and revealing the genetic correlations among agronomic traits and partition genetic correlation coefficients into direct and indirect effects.

MATERIALS AND METHODS

The experiment was conducted at Holetta (38°E and 9°N) Agricultural Research Center (HARC) in 2010 cropping season. Holetta is one of the representatives of oil seed *Brassica* growing areas in the central highlands of Ethiopia with its annual rainfall of 1100 mm, altitude of 2400 m a.s.l and temperatures of 22°C (maximum) and 6°C (minimum) (Alemayehu and Mesfin, 1994). Thirty six genotypes of Ethiopian mustard including the standard checks were used in the study. The genotypes were collected by formerly Institute of Plant Genetic Resource Conservation and Research, currently Institute of Biodiversity Conservation (IBC) from diverse geographical region of the country. Genotypes by origin are described in Table 1. The experiment was carried out using 6×6 simple lattice design with two replications and with a plot size of 3×1.8 m. Each genotype was planted in a plot consisting of six rows of 3 m long with spacing of 30 cm between rows. All recommended agronomic practices (Alemayehu and Mesfin, 1994) were followed to raise good crop.

Data were collected both on plot basis and plant basis for days to flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, number of pods

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

Acc. No.	Area of collection	Altitude (m)	Acc. No.	Area of collection	Altitude (m)	Acc. No.	Area of collection	Altitude (m)
PGRC/E 20052	West Shoa	2540	PGRC/E 208560	*	-	PGRC/E 21163	East Wolega	2340
PGRC/E 20059	West shoa	1630	PGRC/E 208571	*	-	PGRC/E 21266	South Wolo	2550
PGRC/E 20068	West shoa	2010	PGRC/E 208575	*	-	PGRC/E 21278	South Wolo	-
PGRC/E 20163	East Tigrai	2300	PGRC/E 208584	*	-	PGRC/E 213168	-	-
PGRC/E 20168	East Tigrai	-	PGRC/E 208585	East shoa	1600	PGRC/E 21369	Jimma	1720
PGRC/E 208419	West Gojam	2050	PGRC/E 208594	East Hararrgae	1750	PGRC/E 214620	North Omo	-
PGRC/E 208507	*	-	PGRC/E 208596	East Harargae	-	PGRC/E 215284	East Gojam	-
PGRC/E 208513	*	-	PGRC/E 208865	North Omo	1300	PGRC/E 215562	Gedeo	1820
PGRC/E 208523	*	-	PGRC/E 208961	East Wolega	2700	PGRC/E 215790	West Wolega	1950
PGRC/E 208530	*	-	PGRC/E 21057	East Gojam	-	YD	Check	2400
PGRC/E 208545	*	-	PGRC/E 21068	Bale	2500	S-67	Check	2400
PGRC/E 208558	*	-	PGRC/E 21069		-	H-1	Check	2400

*Donation by foundation for Agricultural Plant Breeding S.V.P. P.O. Box 117 Wageningen, The Netherlands, -Information not available, Acc. No. = Genotype accession number

per plant, number of seeds per pod, plant height, number of seeds per plant, 1000 seeds weight, seed yield per plot and oil yield per plot.

Data analysis: Data were subjected to analysis of variance using the procedures outlined by Gomez and Gomez (1984). Hierarchical clustering was performed by a serious of successive mergers (agglomerative) of groups of individuals using the procedure CLUSTER (ward's minimum) as described in SAS (1985). The most similar individuals were first grouped and these initial groups were merged according to their similarities.

Using PROC CANDISC procedure of SAS (1985), genetic divergence between clusters was calculated using the generalized Mahalanobis (1936) D2.

Principal component analysis was also done using the procedure PRINCOMP as described in SAS (1985) to clarify the relationships between two or more characters and to divide the total variance of the original characters into a limited number of uncorrelated new variables according to Wiley (1981).

Genotypic correlation coefficients (Pearson's correlation) were computed by the genotypic values of the traits determined as the method described by Zhu (1996) but assuming the interaction component as nil (Falconer, 1981).

The path analysis technique performed according to the method suggested by Dewey and Lu (1959) using the procedure PROC CALIS of the SAS software version 9.00 (SAS, 1985).

RESULTS AND DISCUSSION

The univariate analysis of variance (not presented) showed that there were significant differences among genotypes for all traits except number of pods per plant, secondary branches per plant and number of seeds per plant. This indicates the existence of considerable genetic variability for selection and breeding.

Clustering produced a clear grouping of the 36 genotypes into seven clusters, whereby the individuals within any one cluster are more closely related than are individuals in different clusters (Fig. 1). The acceptable limit for number of cluster was made based on pseudo F and t^2-statistics. Genotypes with the same geographic origin were grouped in the same cluster such as PGRC/E 21057, PGRC/E 215284, PGRC/E 208594, PGRC/E 208596, PGRC/E 208865 and PGRC/E 215562 in C5 and PGRC/E 208961 and PGRC/E 215790 in C1. This phenomenon might have resulted from their similar genetic background. On the other hand, there are also genotypes with same geographical origin but grouped in different clusters which might be due to difference in their genetic background. Besides, genotypes with different geographical origin were grouped in same cluster which might have been as a result of synchronization of selection differential applied on different components of various geographical areas. In general, the present investigation indicated that factors other than geographic diversity such as genetic drift, selection pressure, closeness in their pedigree and environment may be responsible for differential grouping of genotypes. Similarly, these situations have been reported by various authors (Teklewold *et al*., 2000; Verma and Sachan, 2000; Alemayehu and Becker, 2001; Iftekharuddaula *et al*., 2002; Jeena and Sheikh 2003; Keneni *et al*., 2005). On the other hand, Zhuang *et al*. (2011) reported that the clustering analysis done on Persian Wheat (*Triticum turgidum* ssp. *carthlicum*) accessions using EST-SSR markers suggested that most of the accessions with adjacent geographic origins had the tendency to cluster together.

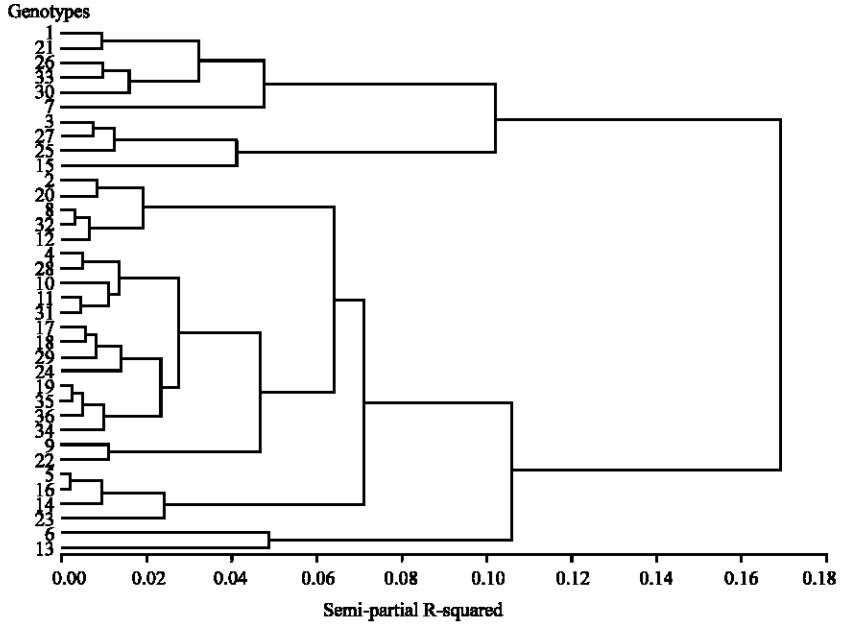

Fig. 1: Wards minimum variance dendrogram which shows the distribution of the 36 Ethiopian mustard genotypes based on morpho-agronomic traits

Solitary genotype in C2, such as PGRC/E 208507 was among donations which have been collected from Ethiopia as *Brassica carinata*. This Solitary genotype might have resulted from geographical barriers preventing gene flow or intensive natural and human selection for adaptive gene complexes which is in accordance to the other findings (Bhatt, 1973; Joshi and Singh, 1979; Teklewold *et al*., 2000). On the other hand, other donated materials were also grouped in different clusters such as C2, C3, C4, C5, C6 and C7 which may be inferred that they may genetically affiliate with their respective cluster's member. Similarly, the two unknown genotypes such as PGRC/E 21069 and PGRC/E 213168 were grouped in the same cluster which indicates that they may be closely related in their pedigree and/or the operation of similar forces of natural or artificial selection made them to be grouped together. By the same talk, S-67 and Holetta-1 grouped together in C1 but Yellow-Dodolla was identified in C4, which indicates that these varieties may have close pedigree relationships with the genotypes in their respective clusters.

In crop improvement venture, genetically distant parents are needed for crossing/hybridization. This is because the genetic diversity between genotypes indicates differences in gene frequencies which may result for heterotic group and/or transgressive segregants. The pairwise generalized squared distance (D^2) among the seven clusters is presented in Table 2. The distance among clusters ranged between 76.0 to 6328. The highest genetic distance was recorded between C2 and C4 (6328) followed by the cluster C3 and C4 (4468) and C2 and C7 (3744). The genetic divergences among other clusters were also highly significant. Parents may be selected from those clusters which had significant genetic distance for crossing in order to obtain genetic recombination and transgressive segregants in the subsequent generations. Likewise, Rohman *et al*. (2004) reported that high divergence between the clusters for 25 sorghum varieties which were grouped into four clusters.

Intra-class average and range of genetic divergence for traits measured is shown in Table 3. Genotypes in C3 showed earliness in days to flowering and maturity than other clusters. Similarly, high number of seeds per pod and seed yield per plot as well as high oil yield per plot and 1000 seeds weight were identified in C6 and C5, respectively.

In order to assess the patterns of variations, Principal Component Analysis (PCA) was done using 9 significant morpho-agronomic traits simultaneously (Table 4). Principal component analysis showed that 91.4% of the variation was contributed by the first five principal components. Days to flowering was the major positive contributor of the variation in the first principal component in which 40.6% of the variation revealed. Days to maturity and length of pod had relatively high positive weight. Number of seeds per pod, seed yield per plot and oil yield per plot had negative weight. It indicated that early varieties would be developed with improved seed and oil yield of the genotypes. The 21.1% additional variation in the second principal component was mainly observed

Table 2: Pairwise generalized squared distance (D2) among 36 genotypes of Ethiopian mustard in seven clusters based on their morpho-agronomic traits

Cluster	C1	C2	C3	C4	C5	C6	C7
C1	0	1230**	490.4**	2013**	76.0**	269.0**	724.0**
C2		0	192.7**	6328**	764.2**	2482**	3744**
C3			0	4468**	243.5**	1388**	2364**
C4				0	2709**	935.3**	354.5**
C5					0	501.9**	1138**
C6						0	143.8**
C7							0

**χ^2 test at p = 0.01 significance level, C: Cluster

Table 3: Intra-class average and range of genetic divergence in morpho-agronomic traits of the seven clusters of Ethiopian mustard genotypes

	Cluster												
	C1		C2		C3		C4		C5		C6		C7
Traits	R	M	R	M	R	M	R	M	R	M	R	M	M
DF	78.5-93	86.8	79		76.5-78.5	77.8	87.5-96	92.6	75-94.5	83.8	61-76.5	71.6	91
DM	171-182	177.1	178.5		154.5-167.5	163	174-180.5	179	162-180	174	160-176	168.8	177.5
PH	183.3-199.8	190	195		182.2-197.3	189.6	207-225.5	217.1	177.3-232.3	206.9	185-203.3	194.7	225.8
NPB	9-11	10.3	12		9-11	9.8	10-11	10.6	8-11	8.9	8-9	8.8	8.5
LP	4.2-4.7	4.5	3.8		3.94.9	4.5	4.3-5.4	4.8	148-275	186.3	3.5-4.4	4	4.7
SPPD	7-13	11	7		10-13	11.5	8-14	10.6	3.9-6	4.5	11-14	12.3	11
SYPP	388.5-749.7	568.4	539.8		547.5-875.8	748.6	775.7-1300.3	985.7	334.4-1016.6	9.3	668.7-1086.2	845.6	670.1
OYPP	161.3-322.3	247.9	220.6		244.3-395.1	335.2	331.9-584	428.8	334.4-1016.6	785.6	288.1-476.6	366	287.2
TSW	2.4-3.5	3.2	2.8		3.1-3.6	3.4	3.1-3.9	3.4	3.2-4.6	3.6	3.4-3.8	3.6	3.5

DF: Days to flowering, DM: Days to maturity, PH: Plant height, NPB: No. of primary branches per plant, LP: Length of pod, SPPD: No. of seeds per pod, SYPP: Seed yield per plot, OYPP: Oil yield per plot, TSW: 1000 seeds weight, C: Cluster, R: Range, M: Mean

Table 4: Component scores of the first six principal components of 36 genotypes of Ethiopian mustard

	Component score				
Traits	1	2	3	4	5
DF	0.442	0.202	-0.139	0.062	-0.301
DM	0.428	0.213	-0.148	-0.079	0.217
PH (cm)	0.297	0.402	0.183	-0.477	-0.297
NPB	0.081	0.325	-0.61	0.143	0.565
LP (cm)	0.319	0.233	0.165	0.74	-0.262
SPPD	-0.427	0.107	-0.133	0.394	-0.228
SYPP	-0.341	0.532	0.038	-0.086	-0.079
OYPP	-0.351	0.522	0.053	-0.085	-0.023
TSW (g)	0.06	0.158	0.71	0.154	0.572
Eigenvalue	3.60	1.90	1.40	0.70	0.50
Variance (%)	40.60	21.10	16.00	7.90	5.80
Cumulative (%)	40.60	61.70	77.70	85.60	91.40

DF: Days to flowering, DML: days to maturity, PH: plant height, NPB: No. of primary branches per plant, LP: length of pod, SPPD: No. of seeds per pod, SYPP: Seed yield per plot, OYPP: Oil yield per plot, TSW: 1000 seeds weight

through trait such as seed yield per plot and oil yield per plot. Plant height and number of primary branches per plant had relatively high positive coefficients in this principal component. The third principal component was accounted for another additional 16.0% of the variation in which 1000 seeds weight was the major contributor. Number of primary branches per plant had the highest negative weight. Principal component 4 and 5 contributed 7.9 and 5.8% additional variations respectively. Length of pod in principal component 4, number of primary branches per plant in principal component 5 was the major contributors. Plant height in principal component 4 and days to flowering in principal component 6 had the most negative weight. In this study, most of the traits individually contributed small effects (±0.06-0.44) to the total variation and, therefore, differential grouping of genotypes was mainly attributed by the cumulative effect of the individual traits.

Genotypic correlation coefficients (Table 5) revealed that seed yield per plot showed significant positive correlation with number of seeds per pod (0.583), number of seeds per plant (0.587) and

Table 5: Genotypic correlation coefficients among 12 agronomic traits in 36 Ethiopian mustard genotypes tested at Holetta, 2010/11

	DF	DM	PH	NPB	NSB	NPP	LP	SPPD	SPP	SYPP	OYPP	TSW
DF	1	0.8**	0.558**	0.259	-0.001	-0.0267	0.57**	-0.519	-0.492	-0.338	-0.364	-0.024*
DM		1	0.493**	0.347*	-0.05	-0.008	0.435**	-0.577**	-0.533**	-0.301	-0.33	0.069
PH			1	0.11	-0.128	-0.068	0.387*	-0.484**	-0.386*	0.039	0.02	0.236
NPB				1	0.514**	0.377*	0.122	0.013	0.079	0.135	0.136	-0.324
NSB					1	0.674**	0.044	0.227	0.536**	0.289	0.261	-0.23
NPP						1	-0.197	-0.129	0.400*	0.062	0.054	-0.274
LP							1	-0.317	-0.315	-0.183	-0.202	0.275
SPPD								1	0.757**	0.583**	0.584**	-0.17
SPP									1	0.587**	0.595**	0.085
SYPP										1	0.993**	0.077
OYPP											1	0.106
TSW												1

*, **Significant at p = 0.05 and p<0.01 significance level respectively. DF: Days to flowering, DM: Days to maturity, PH: Plant height, NPB: No. of primary branches per plant, NSB: No. of secondary branches per plant, NPP: No. of pods per plant, LP: Length of pod, SPPD: No. of seeds per pod, SPP: No. of seeds per plant, SYPP: Seed yield per plot, OYPP: Oil yield per plot, TSW: 1000 seeds weight

oil yield per plot (0.993) which indicates that considering number of seeds per pod and number of seeds per plant as selection criteria will be an effective way to increase both seed and oil yield. This result is in agreement with the findings of Aytac and Kinaci (2009), Engqvist and Becker (1993) and Jeromela *et al.* (2007) who reported positive correlation of seed yield per plot with oil yield per plot and seed yield per plant. Similarly, associations between the seed yield and the number of pods per plant, as well as number of seeds per pod and seed weight per pod was found positive (Shabana *et al.*, 1990; Thompson, 1983).

Correlation of days to flowering with days to maturity (0.8), plant height (0.558), length of pod (0.57) was found significant and positive whereas correlation between days to flowering and number of seeds per pod (-0.519), number of seeds per plant (-0.492), seed yield per plot (-0.338) and oil yield per plot (-0.364) was negative though it was insignificant. Similarly, days to maturity showed significant positive correlation with plant height (0.493), number of primary branches per plant (0.347) and length of pod (0.435), while highly significant but negative correlation was found with number of seeds per pod (-0.577) and number of seeds per plant (-0.533). This indicated that earliness with short stature and high yielding could be achieved in efforts of variety development. Days to flowering showed significant negative correlation with 1000 seeds weight (-0.024) which implies that earliness in flowering may be achieved at the expense of 1000 seeds weight. Result of positive correlation of days to flowering with days to maturity as well as negative correlation of these two traits with seed and oil yield are in agreement with the result of Delesa (2006).

Association of plant height with length of pod (0.387) was significant and positive, while association with number of seeds per pod (-0.484) and number of seeds per plant (-0.386) was found significant but negative. Number of primary branches per plant showed significant correlation with number of secondary branches per plant (0.514) and number of pods per plant (0.377). Likewise, correlation of number of secondary branches per plant with number of pods per plant (0.674) and number of seeds per plant (0.536) was highly significant and positive. Besides, number of pods per plant showed significant positive correlation with number of seeds per plant (0.4). These results indicate that the greater the number of branches per plant, higher will be the number of pods and number of seeds per plant and thus ultimately contributing positively towards yield. Basalma (2008), Khan and Rashid (1999), Guo *et al.* (1987) and Kumar *et al.* (1987) reported

similar findings of a positive and significant correlation between number of secondary branches per plant and number of pods per plant.

In the present investigation, relationship between 1000 seeds weight and seed yield per plot was low. This agrees with the result of Basalma (2008) and Jiang and Guan (1988). Relationship of number of seeds per pod with number of seeds per plant (0.757), seed yield per plot (0.583) and oil yield per plot (0.584) was significant and positive. Similarly, number of seeds per plant showed significant positive correlation with seed yield per plot (0.587) and oil yield per plot (0.595). Most of the correlation results of this study are in agreement with findings of Sheikh *et al.* (1999) who reported positive correlation of all yield components with seed yield. These results also substantiated the results of principal component analysis for instance, positive correlation of umber of seeds per pod with seed and oil yield per plot and negative correlation of days to flowering, days to maturity and length of pod with number of seeds per pod, seed yield per plot and oil yield per plot had been expressed in the study of pattern of variations too.

Cause and effect interrelationships analysis (Table 6) showed that number of seeds per plant and oil yield per plot showed positive direct effect on seed yield per plot, these traits also showed positive and significant correlation with seed yield per plot. Therefore, considering these traits as selection criteria will be advantageous in improvement of Ethiopian mustard genotypes. This result is inconformity with findings of Singh and Singh (1997) and Basalma (2008). Days to maturity showed positive direct effect on seed yield per plot, while they had negative correlation which may be as a result of its negative effects via other traits. Similarly, number of primary branches per plant and length of pod showed no direct effect on seed yield per plot, while they had correlated with seed yield in which their indirect effect via other traits might be the cause. On the other hand, days to flowering had negative direct effect on seed yield per plot which had also been negatively correlated with seed yield per plot which implies consideration of this trait in breeding work for achieving earliness in days to flowering is valuable. Number of seeds per pod revealed negative direct effect on seed yield per plot but its indirect effect through oil yield per plot was high and positive. Direct effect of 1000 seeds weight on seed yield per plot was negative, which indicates selection of this trait may be ineffective in improving the seed yield per plot, however, its effect via number of seeds per plant and oil yield per plot is helpful.

Table 6: Genotypic direct and indirect effects of agronomic traits on seed yield per plot tested at Holetta, 2010/11

	DF	DM	PH	NPB	NSB	NPP	LP	SPPD	SPP	OYPP	TSW	r_g
DF	**-0.018**	-0.014	0.011	-0.005	0.010	0.001	-0.010	0.009	0.009	0.006	0.001	-0.338
DM	0.010	**0.012**	-0.010	0.004	-0.001	0.002	0.015	-0.007	-0.006	-0.008	0.001	-0.301
PH	-0.002	-0.001	**-0.003**	0.000	0.003	0.005	-0.001	0.001	0.001	0.000	-0.001	0.039
NPB	0.000	0.000	0.000	**0.000**	0.002	0.008	0.000	0.000	0.000	0.000	0.000	0.135
NSB	0.000	0.001	-0.002	0.006	**0.012**	0.001	0.014	0.003	0.006	0.003	-0.003	0.289
NPP	0.001	0.000	0.013	-0.017	-0.031	**-0.046**	0.009	0.006	-0.018	-0.005	0.013	0.062
LP	0.000	0.000	0.000	0.000	0.000	0.000	**0.000**	0.000	-0.039	0.000	0.000	-0.183
SPPD	0.026	0.029	0.025	-0.001	-0.012	0.007	0.016	**-0.051**	0.000	-0.050	0.009	0.583**
SPP	-0.025	-0.017	-0.019	0.004	0.030	0.020	-0.016	0.038	**0.050**	0.060	0.004	0.587**
OYPP	-0.331	-0.309	0.031	0.135	0.270	0.056	-0.202	0.579	0.586	**1.050**	0.081	0.993**
TSW	0.001	-0.002	-0.007	0.009	0.006	0.008	-0.008	0.005	-0.002	-0.063	**-0.028**	0.077

Bold values show direct genotype. **Significant at $p<0.01$ significance level. DF: Days to flowering, DM: Days to maturity, PH: Plant height, NPB: No. of primary branches per plant, NSB: No. of secondary branches per plant, NPP: No. of pods per plant, LP: Length of pod, SPPD: No. of seeds per pod, SPP: No. of seeds per plant, OYPP: Oil yield per plot, TSW: 1000 seeds weight, r_g: Genotypic correlation coefficient

CONCLUSIONS

This study has shown the existence of considerable genetic variation among the genotypes considered which may help for further selection and breeding. Parents may be selected from those clusters which had significant genetic distance for crossing in order to obtain genetic recombination and transgressive segregants in the subsequent generations. However, it is also worthy, considering genotypes within a cluster with respect to a trait of interest. Traits association and cause and effect interrelationships have revealed that number of seeds per plant is the most important yield component. However, further study across location and years needs to be done in order to corroborate the result obtained in the present investigation.

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