academicJournals

Vol. 5(11), pp. 770-774, November 2013
DOI: 10.5897/IJBC2013.0626
ISSN 2141-243X © 2013 Academic Journals
http://www.academicjournals.org/IJBC

International Journal of Biodiversity and Conservation

Full Length Research Paper

Genetic divergence analysis of garden cress (*Lepidium sativum* L.)

Temesgen Bedassa[1,2], Mebeaselassie Andargie[2]* and Million Eshete[3]

[1]Department of Biology, Madawalabu University, P.O. Box 276, Robe, Ethiopia.
[2]Department of Biology, Haramaya University, P.O. Box 217, Dire Dawa, Ethiopia.
[3]Debrezeit Agricultural Research Center, P.O.Box 32, Deberezeit, Ethiopia.

Accepted 20 September, 2013

The D^2 analysis allowed the 49 garden cress accessions to be classified into seven distinct clusters. Cluster 1 included 16 accessions that mature and flower early. Cluster 2 contained 11 accessions, which had the higher mean values for both numbers of primary and secondary branches, harvest index and seed yield/plant. They also showed higher number of seeds per plant and per plot than the overall mean value. Cluster 3 had 15 accessions which had a relatively high biomass yield per plot. Cluster 4 included only one accession having longer height at flowering, high seed yield per plant and harvest index. Similarly, cluster 5 also had one accession which was characterized by late flowering, but very short in height at flowering. Cluster 6 also included a single accession, which is characterized by early flowering and maturity. The last cluster, cluster 7 had 3 accessions which had high seed yield per plant, harvest index and essential oils. The maximum inter-cluster distance (D^2 = 10.11) was observed between clusters 5 and 6 whereas the lowest value (D^2 = 3.07) was between cluster 2 and 4. Biomass yield per plot and number of seeds per plant contributed the maximum towards divergence in the existing germplasm.

Key words: Garden cress, genetic diversity, cluster analysis.

INTRODUCTION

Garden cress (*Lepidium sativum* L.) is a fast-growing, edible plant botanically related to watercress and mustard and share their peppery, tangy flavor and aroma (Bedassa et al., 2013). Though, the clear origin of garden cress is not known, it is possibly believed to have originated from North-East Africa, particularly Ethiopia, Eritrea, Egypt and South-West Asia, particularly Iran (Datta et al., 2011; Asfaw and Demissew, 2009). Garden cress is a plant that is well suited to all soils and climates, although it does not tolerate frosts. In temperate conditions, it has a very rapid growth rate. It grows sub spontaneously in areas transformed by humans, close to crops or human settlements (Bermejo and León, 1994). Vavilov (1926) considers its main centre of diversity to be Ethiopia, where he found the widest variability of the dominant forms of *L. sativum*. The Near East, central Asia and the Mediterranean are considered secondary centers. It is now naturalized in numerous parts of Europe, including the British Isles. Wild cress extends from the Sudan to the Himalayas. Most authors consider it to be a native of Western Asia, whence it passed very quickly to Europe and the rest of Asia as a secondary crop, probably associated with cultivars of flax (Bermejo and León, 1994).

L. sativum is classified in the category of neglected and under-utilized horticultural crops (Bermejo and León,

*Corresponding author. E-mail: mebhel@yahoo.com.

1994). It is one of the aromatic plant species of Ethiopia which contains considerable amount of essential (volatile) oil and is required for its medicinal values and other purposes (Asfaw and Demissew, 2009). The seeds contain edible oil which has medicinal properties as antiscorbutic, incites and stimulates the appetite (Shehzard et al., 2011). Getahun (1976) stated that seeds of the plant have several medical implications as a livestock drench for stomach-disorders, human skin-disorders, chapped lips and sunburn, for amoebic infection, as an insect-repellant, applied on the skin, soldiers use it to engender a feeling of warmth at night, and for stomach cramps.

The edible whole seed is known to have health promoting properties as it contains 25-39% of protein. It contains 33%carbohydrate, 2.4% crude fat, 7.6% crude fiber and 6.4% minerals having 0.723% phosphorous and hence it was assumed that these seed can serve as raw material for functional foods (Patel et al., 2010), sharing its peppery, tangy flavor and aroma (Roy et al., 2002). In addition, sprouts of garden cress are very popular ingredient of salads and sand-wiches in some regions of the world (Michalczyk et al., 2011).

Genetic diversity is an important factor in any crop improvement programme for obtaining high yielding variety. Multivariate analysis such as D^2 cluster and factor analysis have been proved to be useful in selecting accessions for hybridization. D^2 statistic (Mahalanobis, 1936) is one of the important biometrical techniques used for assessing genetic divergence present in a population. An understanding of nature and magnitude of variability among the existing garden cress germplasm is a prerequisite for its improvement. Divergence analysis is a useful tool in quantifying the degree of divergence between biological population of geographical level and to access in assessing relative contribution of different components to the total divergence both at intra and inter cluster levels (Jatasra and Paroda, 1978). Besides assisting in the selection of divergent parents for a breeding program, D^2 statistic is useful to determine the relative contribution of each component character to the total divergence. Precise information on the nature and degree of genetic divergence helps the plant breeder in choosing the diverse parents for purposeful hybridization (Arunachalam, 1981; Samsuddin, 1985). Since published work on garden cress is scanty, the present study has been undertaken on 49 garden cress accessions to understand the nature and magnitude of genetic divergence and the characters contributing to a genetic diversity by D^2 analysis.

MATERIALS AND METHODS

The field experiment was conducted at the Debre Zeit Agricultural Research Center (DZARC), Ethiopia during the main cropping season of the year of 2011. DZARC is located about 47 km South East of the capital Addis Ababa at 8°44'N and 38°58'E. Forty-nine garden cress accessions were obtained from the Institute of Biodiversity Conservation (IBC) of Ethiopia that were collected from diverse agro ecological locations of the country varying in altitude, rainfall, temperature and soil types. The experimental design and the layout of the experiment were conducted as it was explained by Bedassa et al. (2013).

Data were recorded as it was previously explained by Bedassa et al. (2013) on days to flowering initiation, days to 50% flowering, plant height, number of primary branch/plant, number of secondary branches/plant, days to maturity, biomass yield/plot, biomass yield /plant, number of seeds/plant, seed yield/plant, seed yield/ plot, 1000-seed weight, harvesting index, fatty oil content and essential oil content from five randomly selected plants of the middle two rows of each plot. Mahalanobis D^2 (Mahalanobis, 1936) was used to estimate the genotypic divergence between the clusters in the experimental population. All the accessions used were clustered into different groups based on D^2 statistics following Tocher's Methods (Rao, 1952).

RESULTS AND DISCUSSION

In this study, the forty nine accessions of garden cress were grouped into seven clusters based on the Mahalanobis D^2 values (Table 1). The distribution pattern indicate that the maximum number of genotypes were included in clusters 1 and 3 followed by cluster 2 and the minimum number of genotypes in cluster 4, 5 and 6, respectively (Figure 1). The different members within a cluster are assumed to be more closely related in terms of the trait under consideration with each other than those members in different clusters. Similarly, members in clusters with non-significant distance were assumed to have closer association with each other than those with significant distance clusters. This can mean that members in clusters with significant distance tend to be genetically more divergent than those having non-significant distance.

Cluster 1 contained sixteen genotypes with the characteristics of early flowering and maturity together with less value for thousand seed weight, seed yield per plant, harvest index and fatty oil content. However, it had intermediate number of both primary and secondary branches, and intermediate content of essential oil. Cluster 2 included 11 genotypes that exhibited high numbers of both primary and secondary branches, also high in seed yield per plant and harvest index, with higher number of seeds per plant and per plot than the overall mean value. Cluster 3 consisted of sixteen genotypes like cluster I which has a characteristic feature of requiring longer period of days to start flowering and maturation. Clusters 4, 5 and 6 contained only one genotype respect-tively. The genotype contained in cluster 7 has a characteristics of late flowering and maturing but have high seed yield per plant and harvest index while that of the genotype found in clusters 5 and 6 had a typical feature of having very high number of both primary and secondary branches and less number of both primary and secondary branches, respectively. The last cluster, group 7, consisted of three genotypes which were charac-

Table 1. Grouping 49 Ethiopian *L. sativum* accession into different clusters and collection regions.

Cluster	Total no. of accessions in the cluster	Lists of accessions in the cluster	Collection regions
C1	16 (32.65%)	GCAc90002 [1], GCAc208666 [11],GCAc202116[7], GCAc90023[6], GCAc231210 [44], GCAc208693[14], GCAc215808 [23], GCAc216886 [26], GCAc230524 [40], GCAc208669 [13], GCAc212852 [17], GCAc216815 [24], GCAc215807, [22] GCAc230831 [43], GCAc90022 [5], GCAc205141[8],	Oromia (East and West Harage,Jimma,West Wellega, Arsi), SNNP (Gurage) and Somali (Jigjiga)
C2	11 (22.45%)	GCAc90007 [2], GCAc90021 [4], GCAc229199 [32], GCAc233981 [47], GCAc216886 [31], GCAc230830 [42], GCAc208769 [15], GCAc216816 [25], GCAc90018 [3],GCAc233679 [46], GCAc216816 [27]	Arsi, East Hararge, North and Central Tigray, North and West Shewa, South Wello, Beneshangul and Gumuz,
C3	16 (32.65%)	GCAc207542 [9], GCAc208667 [12], GCAc219958 [28], GCAc233370 [45],GCAc233982[48], GCAc214243 [19], GCAc212852 [18], GCAc229204[36], GCAc219959[29], GCAc215713 [20], GCAc229799,[38], GCAc229798 [37], GCAc215714 [21], GCAc233983[49],GCAc229201 [34], GCAc219960 [30],	South Gonder, North Shewa, South Wello, West Harerge, Bale, West Wellega, North, West and Centeral Tigray
C4	1 (2.04%)	GCAc208030 [10]	Amhara (North Gonder)
C5	1 (2.04%)	GCAc229200 [33]	Amhara (North Shewa)
C6	1 (2.04%)	GCAc212628 [16]	Amhara (South Wello)
C7	3 (6.12%)	GCAc229203 [35], GCAc230523 [39], GCAc230829 [41]	Amhara (North Gonder) and Somali (Jigjiga)

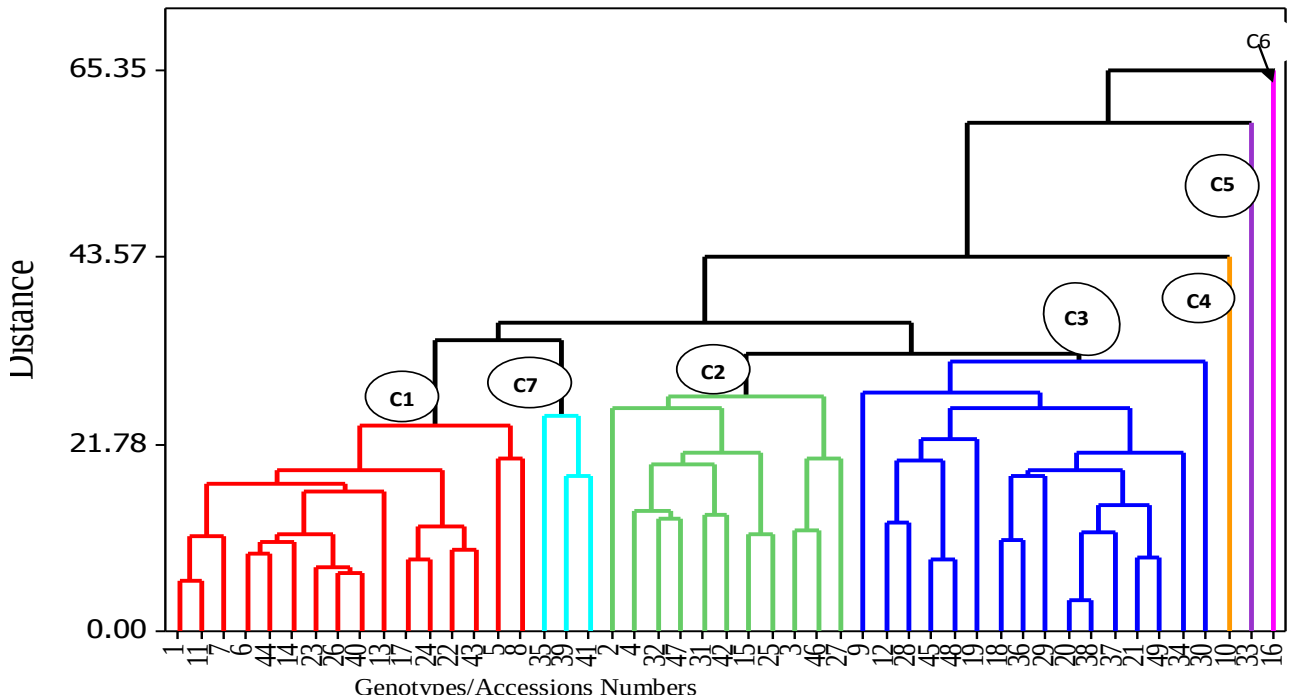

Figure 1. Dendrogram of 49 Ethiopian *L. sativum* L. accessions based on the average linkage cluster analysis. *C1 = Cluster 1, C2 = Cluster 2, C3 = Cluster 3, C4 = Cluster 4, C5 = Cluster 5, C6 = Cluster 6, and C7 = Cluster 7.

Table 2. Pair wise, average intra-cluster (the bold diagonal) and inter-cluster (off diagonal) distance (D^2) among the seven clusters of Ethiopian *L. sativum* accessions.

Clusters	C1	C2	C3	C4	C5	C6	C7
C1	**9.07**						
C2	3.81*	**5.24**					
C3	4.93*	5.29*	**27.48**				
C4	3.94*	3.07	3.57	**0**			
C5	6.88**	7.18**	9.49**	7.74**	**0**		
C6	7.63**	7.35**	6.73**	5.70*	10.11**	**0**	
C7	4.22*	4.54*	7.25**	5.31*	7.16**	8.56**	**13.87**

*, **Significant at 0.05 and 0.01 probability level, respectively.

characterized by having high number of primary branches, high number of seeds per plant, high seed yield per plant, high harvest index, high essential oils and intermediate in its fatty oil content.

Generally, the cluster analysis indicated that the geographic and genetic diversity are not necessarily related; *viz.* germplasm accessions collected from the same geographic region fell in different genetic clusters whereas those collected from different geographic regions tended to be grouped in the same cluster. Therefore, the difference in geographic origin cannot be used as indication of genetic diversity for parental selection. However, the existence of considerable genetic divergence can lead to suggest that there can be a wide span to bring about improvement through hybridization and selection by crossing accessions from different clusters. Latif et al. (1999) and Surek and Korkut (1996) also reported that geographical and genetic distributions did not follow the same trend. Mannan et al. (1993) and Singh and Singh (1979) reported similar results in pani kachu and okra, respectively.

It is worthy to note that in calculating cluster mean, the superiority of a particular accession with respect to a given character could get diluted by other accessions that are grouped in the same cluster but are inferior or intermediate for the character in question. Hence, apart from selecting genotypes from the clusters which have higher inter-cluster distance for hybridization, one can also think of selecting parents based on the extent of divergence with respect to a character of interest (Million, 2009).

The lines belonging to distinct characters could be used in hybridization program for obtaining a wide spectrum of variation among segregates. Based on the estimated pair wise squared distance (D^2) among the seven clusters, under this study, out of twenty one possible pairs of clusters, differences between eleven pairs were highly significant ($P<0.01$) and eight pairs were significant ($P<0.05$) while those between the rest (two pairs) clusters were non-significant (Table 2). The most divergent clusters were cluster five and six ($D^2=10.11$). Each of the two clusters consists of only one accession. Cluster five constitutes an accession from North Shewa, while cluster six constitutes a single accession from South Wello (Table 1). The second maximum inter-cluster distance was found between cluster three and five ($D^2 = 9.49$). Cluster three constitutes 16 accessions collected from South Gonder, North Shewa, South Wello, West Harerge, Bale, West Wellega, North, West and Centeral Tigray of Ethiopia. Similar results were also reported by Prasad (1995) in bush bean and Khan (2006) in pointed gourd.

On the other hand, intra-cluster genetic distance (the bold diagonal values in Table 2), was analyzed and estimated for the seven formed clusters. This can indicate that genotypes that were grouped into the same cluster most likely diverge slightly from one another as the combined characters are measured. Accordingly, among the seven clusters formed, cluster three (C3) showed the maximum intra-cluster value ($D^2 = 27.48$) followed by cluster seven ($D^2 = 13.87$), cluster one with ($D^2 = 9.07$) and cluster two ($D^2 = 5.24$). Nevertheless, cluster four, five and six were exclusive in that each of them contained a solitary accession; hence, the intra-cluster D^2 value for each of them was zero. Similarly, Parameshwarappa et al. (2011) reported grouping of 37 genotypes of niger *Guizotia abyssinica* (L.) Cass into seven clusters which indicates a wider genetic diversity in the germplasm collections of niger. Higher inter and intra-cluster distance indicates higher genetic variability among accessions between and within clusters, respectively. The minimum inter and intra-cluster distance indicates closeness among the accessions of two clusters and within the cluster also.

In general, the crosses involving parents belonging to the maximum divergent clusters were expected to manifest maximum heterosis and also wide variability in genetic architecture.

Ramanujam et al. (1974) and Mian and Bhal (1989) reported that parental clusters separated by medium D^2 values exhibited significant and positive heterosis for seed yield and some of its components in mungbean and chickpea, respectively. In the present study, therefore,

crossing of accessions from cluster five and six will give rise to maximum genetic segregation and would yield high heterotic hybrids.

ACKNOWLEDGEMENTS

The authors would like to express their gratitude to Ministry of Education of Ethiopia for providing fund for this research work. The support of Debre Zeit Agricultural Research Center, Holetta Agricultural Research Center and Wendogenet Agricultural Research Center staff members is highly appreciated.

REFERENCES

Arunachalam VA (1981). Genetic distances in plant breeding. Indian J. Genet. 4:226-236.

Asfaw N, Demissew S (2009). Aromatic Plants of Ethiopia. 1st edn, Shaama Books, Addis Ababa, Ethiopia. p. 257.

Bedassa T, Andargie M and Eshete M (2013). Genetic variability and association among yield, yield related traits and oil content in Ethiopian garden cress (*Lepidium sativum* L.) genotypes. J. Plant Breed. Crop Sci. 5(7):141-149.

Bermejo JEH, León J (1994). Neglected horticultural crops. Plant Production and Protection. FAO, Rome, Italy. p. 26

Datta PK, Diwakar BK, Viswanatha S, Murthy KN, Naidu KA (2011). Safety evaluation studies on Garden cress (*Lepidium sativum* L.) seeds in Wistar rats. Int. J. Appl. Res. Natural Prod. 4(1):37-43.

Getahun A (1976). Some Common Medicinal And Poisonous Plants Used in Ethiopian Folk Medicine**.** Faculty of Science, Addis Abeba University, Addis Ababa, Ethiopia.

Jatasra DS, Paroda RS (1978). Genetic divergence in wheat under different environmental conditions. Cereal Res. Comm. 6:307-317.

Khan AS (2006). Study of Genetic Diversity and Production Technology of Pointer gourd. Ph.D. Thesis, Bangladesh Agricultural Univ., Mymensingh, Bangladesh. pp. 77-93.

Latif A, Alam MS, Shamsuddin AKM (1999). Genetic divergence analysis in groundnut (*Arachis hypogaea* L.). J. Asiat. Soc. Bangladesh Sci. 25(2):293-298.

Mahalanobis PC (1936). On the generalized distance in statistics. Proc. Nat. Inst. Sci. Ind. 2:49-55.

Mannan MA, Ahmad MS, Rashid MM, Bhuiyan MKR, Gomes R (1993). Genetic diversity of *Colocasia esculenta* (L.) Schtt. Root Crops 19(2):95-99.

Mian MAK, Bhal PN (1989). Genetic divergence and hybrid performance in chickpea. Indian J. Genet. 49(1):119-129.

Michalczyk D, Drozdowicz A, Pintscher S, Plonka PM (2011). Mycetozoal bloom in a hydroponic culture of garden cress (Lepidium sativum L.). Int. J. Food. Microbiol. 145(1):336-341.

Million F (2009). Genetic Divergence for Morpho-physiological and Nodulation Traits and their Associations in Ethiopian Fenugreek (*Trigonella foenum-graecum* L.) Landraces. A Thesis Submitted to School of Graduate Studies Haramaya Univeristiy, Ethiopia.

Parameshwarappa SG, Shindhe GG (2011). Genetic Diversity Studies in Germplasm Collections of Niger (*Guizotia Abyssinica* (L.) Cass]. Plant Archives 11(2):1071-1074.

Patel R, Kumar S, Jaiswal R, Rai S, Sahu A, Dwivedi S (2010). Quantitative estimation of fixed oil obtained from seeds of *Lepidium sativum* Linn. Int. J. Chem. Analytical Sci. 1(1):6-9.

Prasad VSR (1995). Genetic divergence of yield and its component in bush bean. Indian J. Hort. 527(1):146-150.

Ramanujam S, Tiwary AS, Mehra RB (1974). Genetic divergence and hybrid performance in mungbean. Theor. Appl. Genet. 44(5):211-214.

Rao CR (1952). Advanced Statistical Methods in Biometrical Research. John Wiley and Sons, New York. pp.45-110.

Roy B, Wivay J, Remco W, Xander W (2002). Altering the taste of plants and vegetable. J. Lipids. 12:951-956.

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

Shehzad M, Tanveer A, Ayub M, Mubeen K, Sarwar N, Ibrahim M, Qadir I (2011). Effect of weed-crop competition on growth and yield of garden cress (*Lepidium sativum* L.) J. Med. Plants Res. 5(26):6169-6172.

Singh SP, Singh HN (1979). Genetic divergence in okra (*Abelmoschus esculentus* L. Moerch). Indian J. Hort. 36(2):166-170.

Surek H, Korkut KZ (1996). Heterosis for yield and yield components in rice (*Oryza sativa* L.) under temperate conditions. J. Bangladesh Plant Breed. Genet. 9(1&2):33-39.

Vavilov NI (1926). Center of origin of cultivatited plants. Trends Pract. Bot. Gener. Sel. 16:3-24.