Global Science Research Journals

ISSN: 2437-1874 Vol. 7 (2), pp. 1-8, August 2020.

http://www.globalscienceresearchjournals.org/

Global Journal of Plant Breeding and Genetics

Full Length Research Paper

Genetic variability, character association and path coefficient analysis in germplasm collections of garden cress (*Lepidium sativum* L.) genotypes

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Garden cress (*Lepidium sativum* L.) is one of the aromatic plant species of Ethiopia containing edible oil with several medicinal implications. Grain yield and oil content of garden cress are usually low, depending on genetic variability and other important characters with these traits. Hence, the objectives of this study were to investigate genetic variability and association among characters. Forty nine garden cress genotypes were tested using randomized complete block design at Debre Zeit Agricultural Research Center, Ethiopia during the main cropping season of 2011. The analysis of variance showed highly significant (p≤0.01) difference among the studied genotypes for all characters, except for fatty oil content, indicating the existence of variability and the potential for selection and improvement within characters. High phenotypic and genotypic variation was recorded for harvest index, seed yield per plant, biomass yield per plant and biomass yield per plot. Seed yield per plot had the highest heritability value. Path coefficient analysis at both phenotypic and genotypic levels showed that number of seeds per plant, days to flowering initiation, biomass yield per plant, harvest index and 1000 seed weight had strong direct effect on seed yield. This indicates that breeding programs should be based on these traits for further improvement of the crop.

Key words: Correlation coefficient, genetic advance, genetic divergence, heritability, medicinal plant, path coefficient

INTRODUCTION

Garden cress (*Lepidium sativum* L.) is an annual, aromatic erect herb that belongs to the family *Brassicaceae/Cruciferae* (Jonsell, 2000; Schlegel, 2009). Its common name can be one of the following English terms garden cress, common cress, pepper weed, garden pepperwort (Giacometti and Leon, 1994). The Brassicaceae family has about 370 genera and 3500 species, and this family holds plants that have a wide range of agronomic traits and economic importance. Species in this family have a worldwide distribution and have the highest diversity in the Mediterranean region, West and Central Asia and parts of North America (Jonsell, 2000). This popular herb is referred to as 'Feto' in Ethiopia. Because of the presence of four petals which are arranged in a cross-like appearance, botanically, this plant is a member of family "*Brassicaceae*" (formerly: "*Cruciferae*"). They are rich in their vitamin C content in addition of having vitamin A and B (DiCosta, 2011).

The greater or lesser cleft of the basal leaves serve as a character to show the degree of variability mainly in Africa, a character which is controlled by a single incompletely dominant gene. There are also red, yellow

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and black varieties of garden cress in terms of their seed color (Bermejo and Leon, 1994). As it was reported by Jurgen et al. (1985) Povalijaeva classified *L. sativum* into three types (subvar. *sativum*, subvar. *crispum* and *subvar*. *Latifolium)* based on the anatomical features of the leaf, stem and root. *Lepidium sativum* is classified in the category of neglected and under-utilized horticultural crops (Bermejo and León, 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 and have been used as a spicy condiment in addition to its medicinal properties (Shehzad et al., 2011). In addition, sprouts of garden cress are a very popular ingredient of salads and sand-witches in some regions of the world (Michalczyk et al., 2011). The seeds of *L. sativum* are also used as a livestock drench for stomach-disorders, as a cure for human skin-disorders, chapped lips and sunburn, and for amoebic infection, in addition it is also used as an insect-repellant (Getahun, 1976).

Though its cultivation and medicinal importance relates with the Ethiopian agriculture since long period of history, this medicinal plant is negligibly cultivated. Besides this, at present, the production of this crop species in terms of its yield per hectare is even not specifically known. One important factor restricting the production, utilization and development of better varieties of the plant type is very little information about its genetic diversity. The existence of genetic variability among population is the most important rationale for judicious selection and breeding of desired plant genotypes (Singh et al., 2005). Knowing the degree of genetic variability and its magnitude is a prerequisite to develop a sound crop improvement program in any plant (Welsh, 1990). Therefore, in order to sustainably and appropriately exploit this available neglected crop in the country detail evaluation of the accessions for different morphological, as well as agronomic traits like yield and oil content is necessary.

No apparent reports are available on genetic variability of garden cress either in Ethiopia or worldwide. Likewise there is only little information on the nature of inter-relationships among characters that help in formulating efficient scheme of multiple trait selection for this plant. Thus, this study has been initiated in view of filling such information gap in relation to its genetic variability, character association and path coefficient analysis in 49 germplasm collections of garden cress for 15 characters.

MATERIALS AND METHODS

Experimental site

The field experiment was carried out at Debre Zeit Agricultural Research Center, Ethiopia during the main cropping season of the year of 2011. The research center is found at an altitude of 1860 meter above sea level (m.a.s.l) and it receives an annual rainfall ranging from 452.8 to 934.2 mm with an annual mean of 691.5 mm. The mean annual temperature of this location is 19. 32°C and it has soil types of Vertisols, Mollisols and Alfisols.

Materials

For this study, forty nine garden cress germplasm collections were used. The accessions were collected by Institute of Biodiversity Conservation (IBC) of Ethiopia from diverse agro ecological locations of the country varying in altitude, rainfall, temperature and soil types. The list of the tested accessions is given along with their geographical origins in Table 1.

Design and procedures

Randomized complete block design (RCBD) with three replications was used. Each genotype was sown in 1.5 m^2 (1.5 m × 1 m) plots. Each plot contained four rows with inter-row spacing of 25 cm and seeds were thoroughly and almost thickly sown in the row, but later, 10 days after germination (at true leaf stage) the plants in each row of the plots was thinned out as it should have about 15 to 25 cm gap from each other. For each genotype 1.5 g of seed per plot was used. The distance between replications was 1.5 m. The layout and randomization were done as per the standard procedure set by Cochran and Cox (1957). Three weeding activities and two hoeing practices were carried out and no fertilizer and chemicals was applied. All pertinent crop management practices were implemented and the weeding activities were completed before 35 day after germination, because according to Shehzard et al. (2011) for obtaining higher yield of the garden cress, weeds may be controlled before 40 days after emergence as it was a critical period of competition.

Data collection

The following data were collected during the experimental time both from the whole plot and from the sample plants that were randomly selected from the middle two rows of each plot. Since there is no descriptor for *L. sativum* L., the descriptor of a related plant species of the same family *viz.* descriptor of *Brassica carnata* A. Braun was used.

On plant basis

Plant height at flowering (PHF): Height of five randomly taken plants during flowering period from each experimental unit was measured in centimeter from the ground to top of the plant and the average height was recorded.

Number of primary branches (NPB): Number of productive branches extending from the main stem was recorded on five randomly selected plants.

Number of secondary branches (NSB): Number of branches extending from the primary branches was recorded on the same plants used to determine the number of primary branches.

Number of seeds per plant (NSP): This was recorded as average total number of seed of five randomly taken plants from each experimental plot.

Seed yield per plant (SYP): The average weight in grams of seeds adjusted 7% moisture content was obtained from five randomly selected plants on each plot.

Table 1. Geographic origin of Ethiopian garden cress accessions by region, administrative Zone, district, altitude and locality.

S/N	Accessions	Region	Zone[1]	Woreda[2]	Altitude*	Locality
1	GCAc90002	Oromia	Bale	Dinsho	NA	Robe
2	GCAc90007	Beneshngul and Gumuz	Metekel	Wenbera	NA	Dawila
3	GCAc90018	Amara	south Wello	Debresina	2520	Mekane Selam
4	GCAc90021	Oromia	West Shewa	Chelya	2620	Delebi
5	GCAc90022	“	West Wellega	Dale Lalo	1480	Chanka
6	GCAc90023	“	Jimma	LimuSeka	NA	Getere Kebele
7	GCAc202116	SNNP	Shekicho	Ginbo	NA	Bonga
8	GCAc205141	SNNP	Gurage		1900	Gambelana kuturi
9	GCAc207542	Amara	South Gonder	Kemekem	NA	Tara Gedam
10	GCAc208030	“	North Gonder	Zuria	1930	Near Gonder
11	GCAc208666	Oromia	West Hararge	Mieso	1450	Beha
12	GCAc208667	“	“	Habro	1900	Gebo
13	GCAc208669	“	East Hararge	Kersa	2180	Werabele
14	GCAc208693	“	“	Gursum	NA	Kobele
15	GCAc208769	“	West Wellega	Sayo	1900	Ado
16	GCAc212628	Amara	South Wello	Kutaber	2400	Ambo
17	GCAc212852	Oromia	Bale	Goro	NA	Beliyu Burka
18	GCAc212853	“	“	“	NA	Beliyu Burka
19	GCAc214243	Amara	North Gonder	Debark	NA	Debark
20	GCAc215713	Amara	South Wello	Werebabu	2200	Gubisa
21	GCAc215714	Amara	South Wello	WereBabu	2200	Werekalu
22	GCAc215807	Oromia	West Wollega	Sayo	1720	Galano Mete
23	GCAc215808	Oromia	West Wollega	Sayo	1950	Ado Boro
24	GCAc216815	Somali	Jigjiga	Jigjiga	1910	Jijiga (market)
25	GCAc216816	Oromia	East Hararge	Gursum	NA	Fugnabira
26	GCAc216885	“	Arsi	Merti	1570	Abomsa
27	GCAc216886	“	“	“	1570	“
28	GCAc219958	Tigray	Central Tigray	Maychew	2130	Enda Yesus
29	GCAc219959	“	West Tigray	Zana	NA	Enda silse
30	GCAc219960	“	“	Koraro	1940	My Adrasha
31	GCAc219961	“	Central Tigray	Adawa	NA	Adawa
32	GCAc229199	Amara	North Shewa	Wayu	2220	Salaish
33	GCAc229200	“	“	Tach Bet	2150	Dale Debdibe
34	GCAc229201	“	“	“	2310	Embima
35	GCAc229203	“	“	“	2620	Wero gide
36	GCAc229204	“	“	“	2580	Jurir Belil
37	GCAc229798	“	East Gojam	Enese	2250	Ansharba Mariam
38	GCAc229799	Amara	East Gojam	Midir	2550	Yebsina
39	GCAc230523	Somali	Jigjiga	Jigjiga	NA	Kocher
40	GCAc230524	Oromia	East Hararge	Girawa	NA	Alemitu
41	GCAc230829	Somali	Jigjiga	Jigjiga	NA	Kocher
42	GCAc230830	Oromia	East Hararge	Jarso	2450	Eltoke
43	GCAc230831	“	“	Girawa	2050	Dogo Mudi
44	GCAc231210	Somali	Jigjiga	Jigjiga	1910	Sauradry
45	GCAc233370	Tigray	North Tigray		NA	Mendefera
46	GCAc233679	Tigray	North Tigray		NA	
47	GCAc233981	Tigray	East Tigray	Afeshum	2140	Tewahido
48	GCAc233982	“	Central Tigray	Adewa	2210	Seno
49	GCAc233983	“	“	WerieLehe	1950	Indabagerima

* Meter above sea level (m.a.s.l.), NA = Not available; [1]The second highest administrative level next to the region which can accommodate several woredas; [2]The next highest administrative level after Zone and is characterized by accommodating several Kebels or many peasants.

Biomass yield per plant (BYP): The above ground biomass yield at the time of harvesting was determined in grams from five randomly taken plants.

On the whole plot basis

Days to flowering initiation (DFI): Number of days from date of sowing to date of some plants in each plot starts to bloom was determined.

Days to 50% flowering (DF): Number of days from the date of planting to the date on which about 50% of the plants in each plot produce flower was taken.

Days to maturity (DM): The number of days from sowing to the date when the peduncles turned to yellow straw color was determined.

Seed yield per plot (SYPL): Moisture adjusted seed at 7% (dry seed yield) from the possible total harvestable rows of each experimental plot was recorded in grams

Seed yield per hectare (SYH): After the value of seed yield per plot converted into kg/ha.

Thousand seed weight (TSW): The weight in grams of 1000 was randomly taken and 7% moisture- adjusted seeds from each experimental plot

Essential oil content (EOC): The essential oil content in percentage was determined by hydro-distillation as per the standard procedure set by Guenther (1972).

Fatty oil content (FOC): Fatty oil content in percent (%) was determined from an oven dried 25 g composite seed samples. Then the Nuclear Magnetic Resonance Spectrometer reader (NMR) was used to measure the fatty oil content according to the International Organization for Standardization, number ISO 10565: 1992, (ISO, 2010)

Biomass yield per plot (BYPL): The above ground biomass yield at the time of harvesting was determined in grams from each experimental plot *viz.* from the net plot size

Harvest index (HI): The ratio of the moisture-adjusted seed yield per plant to the above ground biomass yield per plant was determined.

Data analysis

Analysis of variance (ANOVA)

The data collected for each quantitative trait were subjected to analysis of variance (ANOVA) as per the method of Gomez and Gomez (1984) using SAS computer Software program (SAS, 2002, Version 9.0). Homogenity test for the error variance was done before computing the analysis of variance. For significant difference among the treatments, mean separation was carried out using Duncan multiple range test (DMRT) at 5% levels of significance.

Estimation of variance components

The phenotypic, genotypic and environmental variances and coefficient of variation were estimated according to the methods suggested by Burton and Dorane (1953) as follows:

Estimation of heritability: Heritability (h^2) in broad sense for all characters was computed using the formula adopted by Allard (1960).

Estimation of expected genetic advance: Genetic advance as part of mean (GA) for each character, assuming selection of the superior 5% of the genotypes, was estimated using the formula adopted from Johnson et al. (1955).

Estimation of phenotypic and genotypic correlations: Phenotypic and genotypic correlations between yield and yield related traits were estimated using the method described by Miller et al. (1958).

Path coefficient analysis: Path coefficient analysis was worked out using the method suggested by Dewey and Lu (1959) using the phenotypic as well as genotypic correlation coefficients to determine the direct and indirect effect of yield related traits (yield components) on seed yield and oil contents of the seed based on the following relationship:

$$rij = pij + \Sigma rikpk$$

Where: rij = mutual association between the independent character (i) and dependent character *viz.* seed yield (j) as measured by the correlation coefficient. Pij = component of direct effects of independent character (i) and dependent character (j) as measured by the path coefficient and Σrikpkj = Summation of components of indirect effect of a given independent character (i) on the given dependent character (j) via all other independent character (k).

The contribution of the remaining unknown factors (effect) was measured as the residual effect (R_E) which is calculated as:

$$R_E = \sqrt{1 - R^2}, R^2 = \sum pijrij$$

The magnitude of R_E indicates how best the causal factors accounts for the variability of the dependent factor (Singh and Chaudhary, 1999). That is if the value of R_E is small (for instance near zero) the considered dependant character (for example seed yield) is fully explained by the variability of the considered independent character, whereas the higher R_E value indicates effects some other factors which have not been considered, but need to be included in the model to account fully for the variation in the dependent character. Four different types of yields as seed yield per plot, seed yield per plant, fatty oil content and essential oil content were used as dependent characters separately for path coefficient analysis and the remaining characters were used as independent variables as required.

RESULTS

From the 16 studied traits, 15 of them showed a highly significant variation among the forty-nine garden cress genotypes (Table 2). The observed highly significant values of the mean squares due to the genotypes for most of the traits indicate a sufficient genetic variability.

Variance components and coefficients of variation

Estimates of phenotypic, genotypic and environmental variances and phenotypic and genotypic coefficients of variation are given in Table 2. The genotypic coefficient

Table 2. Estimates of minimum, mean and maximum values, variance and coefficient of variation in percent at both phenotypic (σ^2P) and genotypic levels (σ^2g), heritability in broad sense (h^2 %), genetic advance in absolute (GA) and as mean (GAM) for the studied sixteen traits of Ethiopian *Lepidium sativum* genotypes.

Traits	Min	Mean	Max	σ^2g	σ^2e	σ^2P	GCV%	PCV%	h^2%	GA	GAM
DFI	32.0000	38.7333	46.3333	29.4721	5.1581	34.6311	14.0202	15.1867	85.1131	10.32	26.6665
DF	37.6714	44.7011	52.3333	22.6432	6.8276	29.4667	10.6321	12.1367	76.8191	8.6041	19.2514
PHF	48.8125	61.0367	68.6015	33.8267	8.0893	41.9154	9.5185	10.3723	80.6667	10.6821	17.4936
NPB	13.9333	17.4467	21.031	4.0703	1.6871	5.7567	11.5567	13.6412	70.6871	3.4653	19.8464
NSB	80.4011	107.8674	159.1345	262.0381	63.8743	325.9133	15.012	17.7814	80.4001	31.2861	29.000
DM	86.6723	92.2533	99.6667	30.3397	7.9115	38.2512	6.0562	6.7041	79.3169	10.1183	10.9679
BYPL	792.5021	1865.574	2920.533	218704.3	28623.63	247327.9	26.3667	28.0333	88.421	907.234	48.6191
BYP	31.0000	62.4231	105.1	311.8967	182.137	494.0333	28.2867	33.6123	63.1121	28.9406	46.3783
NSP	2268.532	3092.383	4032.602	134072.2	34858.22	168930.5	11.8356	13.2878	79.3361	672.907	21.7621
SYP	9.6667	20.402	32.6667	37.2432	5.2075	42.4457	30.8762	36.9667	87.7112	11.7912	57.7867
SYPL	253.6667	362.93	512.3333	4701.633	134.4769	4836.11	18.8873	19.1556	97.2313	139.4634	38.4333
SYH	1691.113	2419.611	3415.554	208942.6	6001.726	214944.3	10.9891	12.2221	97.2221	929.1665	38.4333
TSW	3.3000	4.0545	5.5025	0.55	0.2147	0.7667	18.3132	21.5181	72.4333	1.3021	32.1489
HI	19.5467	33.3467	53.8567	163.1133	23.4634	186.5767	37.1792	39.7667	87.4213	24.6234	71.6854
FOC	19.2031	22.2623	24.6667	1.1945	0.7647	1.9636	4.9141	6.1678	61.011	1.7642	7.9232
EOC	0.1133	0.133 3	0.1667	0.0003	0.0001	0.0004	13.3151	15.3763	75.0112	0.0331	23.800

Min and max stand for minimum and maximum respectively. DFI = Days to flowering initiation; DF = Days to 50% flowering; PHF = Plant height at flowering in centimeter; NPB = number of primary branch per plant NSB = Number of secondary branches per plant; DM = Days to maturity; BYPL= Biomass yield in gram per plot; BYP = Biomass yield in gram per plant NSP= Number of seeds per plant; SYP = seed yield in gram per plant; SYPL=Seed yield in gram per plot; SYH = Seed yield in kilo gram per Hectare; TSW = Thousand seed weight in gram; HI = Harvesting index in percentage; FOC = Fatty oil content in percentage; EOC = Essential oil content in percentage.

of variation ranged from 4.91% for fatty oil content to 37.18% for harvest index, whereas the phenotypic coefficient of variation varied from 6.17 to 39.77% for the same traits. However, two traits namely days to maturity (6.06%) and fatty oil content in percentage (4.91%) were accompanied with the relatively very low genotypic coefficients of variation (GCV).

Heritability and genetic advance

Estimate of heritability for the traits under study is given in Table 2. The magnitude of the estimated broad heritability in this study ranged from 61.01% for fatty oil content to 97. 23% for seed yield per plot. The existence of relatively high heritability in a given trait indicates the presence of more additive gene effects for possible improvement. Generally, high heritability was coupled with relatively high genetic coefficient of variation for almost all traits except for days to maturity and fatty oil contents.

The magnitude of genetic advance, at 5% selection intensity, along with the corresponding genetic advance as percent of mean was estimated and presented in Table 2. There was relatively high genetic advance for such traits as, seed yield per hectare, biomass yield per plot, number of seeds per plant, seed yield per plot, number secondary branches and biomass yield per plant. Therefore, selection based on these traits could predict the performance of the progenies.

Association among the traits

Since seed yield per hectare (SYH) was the derivative or direct conversion of seed yield per plot, correlation analysis was done only for 15 traits. Table 3 summarizes both genotypic and phenotypic correlation coefficients between all possible pairs of the fifteen traits based on the analyzed value for the studied Ethiopian *L. sativum*

Table 3. Phenotypic correlation coefficient (above the diagonal) and genotypic correlation coefficient (bellow the diagonal) of fifteen traits of *L. sativum* genotypes.

Traits	DFI	DF	PHF	NPB	NSB	DM	BYPL	BYP	NSP	SYP	SYPL	TSW	HI	FOC	EOC
DFI	1.00	0.94**	0.19*	0.17*	0.21*	0.69**	0.33**	0.39**	0.19*	0.22*	0.19*	0.10	0.18*	0.04	0.08
DF	0.96**	1.00	0.15*	0.14*	0.20*	0.63**	0.31**	0.36**	-0.09	-0.18*	-0.17*	-0.37**	-0.34**	0.04	0.10
PHF	0.24*	0.28*	1.00	-0.19*	-0.11	0.30**	-0.08	-0.09	-0.15*	-0.21*	-0.28**	-0.17*	-0.07	-0.33**	-0.16*
NPB	0.27*	0.12	-0.37**	1.00	0.42**	0.16*	0.38**	0.21*	0.29**	0.23*	0.24*	-0.07	0.16*	-0.12*	-0.14*
NSB	0.41**	0.14	-0.25*	0.46**	1.00	0.27**	0.41**	0.29**	0.36**	0.34**	0.34**	-0.18*	0.37**	-0.23*	-0.11
DM	0.82**	0.78**	0.25*	0.17	0.38**	1.00	0.39**	0.52**	0.32**	0.29**	0.31**	0.45**	0.26**	0.31**	0.16*
BYPL	0.45**	0.44**	-0.33*	0.42**	0.38**	0.44**	1.00	0.56**	0.35**	0.24*	0.43**	-0.39**	-0.07	-0.16*	-0.12*
BYP	0.52**	0.49**	-0.27*	0.40**	0.46**	0.65**	0.58**	1.00	0.28**	0.48**	0.39**	-0.29**	-0.48**	-0.35**	0.07
NSP	0.32*	-0.11	-0.07	0.48**	0.51**	0.37**	0.44**	0.31*	1.00	0.37**	0.46**	-0.10	0.16*	0.11	0.20*
SYP	0.34**	-0.28*	-0.43**	0.32*	0.39**	0.32*	0.42**	0.51**	0.41**	1.00	0.38**	0.28**	0.45**	0.23*	0.18*
SYPL	0.29*	-0.15	-0.41**	0.31*	0.36**	0.40**	0.52**	0.43**	0.47**	0.49**	1.00	0.38**	0.32**	0.18*	0.24*
TSW	0.12	-0.57**	-0.13	-0.43**	-0.21*	0.60**	-0.36**	-0.39**	-0.11	0.40**	0.45**	1.00	0.43**	0.40**	0.35**
HI	0.24*	-0.29*	-0.36*	0.26*	0.40**	0.36**	-0.25*	-0.38**	0.21*	0.57**	0.42**	0.48**	1.00	0.39**	0.28**
FOC	0.07	0.09	-0.31*	-0.38**	-0.25*	0.39**	-0.22*	-0.09	0.04	0.27*	0.29*	0.49**	0.43**	1.00	0.19*
EOC	0.11	0.14	-0.29*	-0.22*	-0.12	0.26*	-0.13	0.15	0.27*	0.37**	0.15	0.47**	0.40**	0.31*	1.00

*,**Significant at 0.05 and 0.01 probability level respectively. DFI = Days to flowering initiation; DF = Days to 50% flowering; PHF = Plant height at flowering in centimeter; NPB = number of primary branch per plant NSB = Number of secondary branches per plant; DM = Days to maturity; BYPL = Biomass yield in gram per plot; BYP = Biomass yield in gram per plant; NSP = Number of seeds per plant; SYP = seed yield in gram per plant; SYPL = Seed yield in gram per plot; SYH = Seed yield in kilo gram per Hectare; TSW = Thousand seed weight in gram; HI = Harvesting index in percentage; FOC = Fatty oil content in percentage; EOC = Essential oil content in percentage.

L. genotypes.

Seed yield had positive and highly significant genotypic association with number of seeds per plant, harvesting index, number of secondary branches, days to maturity, thousand seed weight, biomass yield per plant, and biomass yield per plot. It also exhibited positive and significant genotypic associations with days to flowering initiation and number of primary branches whereas it had negative and highly significant genotypic correlation with plant height at flowering.

The phenotypic correlation revealed that seed yield showed positive and highly significant association with number of seed per plant, number of secondary branches, days to maturity, thousand seed weight, harvesting index, biomass yield. It has also shown positive and significant phenotypic correlation with number of primary branches and days to flowering initiation. But it had shown negative and significant association with days to flowering.

The genotypic correlation among other traits showed days to flowering to have positive genotypic and highly significant association with days to maturity, biomass yield per plot, and biomass yield per plant, and showed positively significant correlation with plant height at flowering. This suggests that dwarf plants were early in flowering. It had negative and highly significant correlation with thousand seed weight and exhibited negative and significant correlation with harvesting index. Plant height at flowering did not show any positive genotypic association at 1% probability level, but it showed positive genotypic association with days to maturity. It showed negative genotypic correlation at 5% probability level, with number secondary branches, biomass yield per plot and biomass yield per plant.

Path coefficient analysis

The genotypic direct and indirect effect of different traits on seed yield is presented on Table 4. Seed yield per plant, biomass yield per plant and harvest index exerted positive and highly significant direct effect on seed yield. In addition, biomass yield per plot followed by days to maturity, fatty oil content, numbers of primary branches, number of seeds per plant, days to flowering initiation, and thousand seed weight also

Table 4. Estimates of direct (bold-diagonal) and indirect effects (off-diagonal) of fourteen traits on seed yield per plot, SYPL, at genotypic level in *L. sativum* genotypes.

Var.	DFI	DF	PHF	NPB	NSB	DM	BYPL	BYP	NSP	SYP	TSW	HI	FOC	EOC	ɤg
DFI	**0.142**	-0.087	-0.030	0.039	0.007	0.213	0.204	0.503	0.047	0.330	0.006	0.212	0.018	0.005	0.29*
DF	-0.136	**-0.091**	-0.036	0.019	0.002	0.202	0.198	0.474	-0.017	-0.279	-0.032	-0.258	0.024	0.007	-0.15
PHF	-0.034	-0.025	**-0.127**	-0.059	-0.005	0.065	-0.149	-0.262	-0.010	-0.429	-0.007	-0.320	-0.081	-0.014	-0.41*
NPB	-0.038	-0.011	0.047	**0.161**	0.008	0.044	0.189	0.387	0.071	0.320	-0.023	0.229	-0.096	0.011	0.31*
NSB	-0.058	-0.012	0.032	0.074	**0.017**	0.098	0.172	0.445	0.075	0.389	-0.011	-0.353	-0.063	-0.006	0.36*
DM	-0.116	-0.071	0.032	0.027	0.006	**0.259**	0.199	0.629	0.054	0.319	0.032	0.319	0.099	0.013	0.40**
BYPL	0.064	-0.041	-0.042	0.067	0.007	0.114	**0.452**	0.561	0.065	0.419	0.019	0.221	0.055	0.006	0.52**
BYP	0.074	-0.045	-0.034	-0.064	0.008	0.168	0.262	**0.968**	0.046	0.509	0.021	0.336	-0.023	0.008	0.43**
NSP	0.045	0.010	0.009	0.077	0.009	0.096	0.198	0.300	**0.147**	0.409	-0.006	0.185	0.010	0.013	0.47**
SYP	0.047	0.025	0.055	0.052	0.007	0.083	0.189	0.494	0.061	**0.999**	0.021	0.503	0.068	0.018	0.49**
TSW	0.017	0.052	-0.017	-0.007	-0.004	0.155	-0.163	0.377	-0.016	0.399	**0.053**	0.424	0.124	0.023	0.45**
HI	0.034	0.026	0.046	0.042	0.007	0.091	0.113	0.367	0.031	0.569	0.025	**0.883**	0.108	0.019	0.42**
FOC	0.009	-0.008	0.039	-0.062	-0.004	0.101	-0.099	-0.087	0.006	0.269	0.252	0.382	**0.252**	0.015	0.29*
EOC	0.016	-0.013	-0.037	-0.035	-0.002	0.067	0.059	0.145	0.039	0.369	0.325	0.353	0.078	**0.049**	0.15

Rg = 0.48; DFI = Days to flowering initiation, DF = Days to 50% flowering, PHF = Plant height at flowering in centimeter, NPB = number of primary branch per plant, NSB = Number of secondary branches per plant, DM = days to maturity, BYPL= Biomass yield in gram per plot, BYP = Biomass yield in gram per pl ant, NSP = Number of seeds per plant, SYP= Seed yield in gram per plant, TSW = Thousand seed weight in gram, HI= Harvesting index in percentage, FOC = fatty oil content in percentage, EOC = Essential oil content in percentage. Var = variables. ɤg = genotypic correlation coefficient, Rg = residual effect at genotypic level.

showed relatively high positive genotypic direct effect on seed yield.

Seed yield per plant, thousand seed weight and fatty oil content on seed yield per plot exerted an effect *via* harvest index. Harvest index by itself, in turn along with essential oil content and number of seeds per plant exerted strong effect on seed yield per plot through seed yield per plant. In the same way, biomass yield per plot, days to maturity, number of primary and secondary branches exhibited the maximum positive indirect influence passing through biomass yield per plant.

Then again, there was negative direct genotypic path effect exerted by the trait plant height at flowering and days to flowering on seed yield per plot; as the two traits had negative correlation coefficient values with seed yield per plant (Table 3). The residual effect value (Rg = 0.48) indicates that characters included in the genotypic path analysis explained 52% of the total variation in seed yield which indicates that there may be some more components that are contributing to seed yield.

DISCUSSION

Generally, in this study, for all traits the values of phenotypic variance (σ^2p) exceeded that of genotypic variance (σ^2g), though the difference is small. This indicates that environmental variance (σ^2e) had its own contribution on the performance of the traits in addition to genotypic variance. In line with this Mengesha and Alemaw (2010) reported a higher value of genotypic coefficient of variability for most of the traits in Ethiopian coriander accessions except for days to maturity, 100-seed weight and plant height. Petros (2008) also reported a wide range of variability among niger (*Guizotia abyssinica)* particularly from those that were collected from Wello and Hararge for days to maturity, plant height, days to 50% flowering and days to flowering initiation. They also found oil content and seed weight to have narrow range of variability.

From the result it is possible to conclude that the variability in this study was mainly due to genotypic variance. Genetic coefficient of variation together with heritability estimates would give the best indication of the amount of gain due to selection. Therefore, there could be a better chance for improvement of the above traits with the relatively highest value genotypic coefficient of variation.

Genetic coefficient of variation provides information on the genetic variability present in various quantitative characters, but it is not possible to determine the amount of the variation that was heritable from only the genotypic coefficient of variation. It is the indication of the effectiveness with which selection of genotypes can be based on the phenotypic performance (Johnson et al., 1955).

According to Dabholkar (1992) heritability estimates are classified as low (5-10%), medium (10-30%), high (30-70%) and the highest for the value greater than this. An estimate of heritability is essential for applying optimum breeding strategy. In this study traits like seed yield per plot, seed yield per plant, harvesting index, days to flowering initiation, biomass yield in gram per plot, plant height at flowering, numbers of secondary branches, number of seeds per plant, days to maturity, essential oil content, thousand seed weight and number of primary branches had very high heritability. Similar result was reported in 49 Ethiopian coriander accessions in which broad sense heritability of more than 50% was obtained for most of the studied quantitative traits (Mengesha and Alemaw, 2010). In the study carried out on *Brassica carinata* by Delesa (2006) heritability estimates were high for days to maturity, days to flowering, 1000-seed weight, plant height, biomass per plot, seed yield per plot and oil yield per plot. For the traits with highest heritability that is close to 1 phenotype is a good index of genotypic merit, so genetic gain can be made easily through selection (Johnson and Frey, 1967). Therefore heritability determines the effectiveness of selection, though the effectiveness of selection for a given trait depending on relative importance of both genetic and environmental factors in the expression of phenotypic differences among genotypes in a population.

According to Delesa (2006) a relatively high genetic advance was obtained for seed yield per plot and biomass yield per plot in Ethiopian mustard, which partially supports the result of our study. Similarly, Major and Singh (1996) studied *B. carinata* and had found relatively high genetic advance for plant height and seed yield. But, relatively low genetic advance was observed for number of primary branch (3.465), thousand seed weight (1.302), fatty oil content (1.764), and essential oil content (0.031). This low estimate of genetic advance as a percent mean arises from low estimate of phenotypic variance and heritability.

The existence of a strong positive correlation between seed yield and different traits can help to identify traits that could be used for indirect selection of the accessions with higher yield. Obtaining high yield is one of the breeding objectives in all breeding programs. However, yield is regarded as a complex character which is influenced by many component traits contributing in both positive and negative directions. Hence direct selection for yield is not sufficiently effective due to its low heritability; thus, it is desirable to select indirectly for improved yield.

Seed yield had positive and significant phenotypic and genotypic correlation with both fatty oil and essential oil content in this study, indicating simultaneous improvement of these traits is possible. The present study is consistent with the results reported by Delesa (2006) where oil yield was observed to have positive and highly significant correlation with seed yield in Ethiopian mustard. Diederichesen (1996) also obtained positive correlation between essential oil and foliage of the plant in coriander. Generally, traits significantly correlated with seed yield may be important yield predictors in garden cress breeding.

Generally, the existence of genotypic positive association at 1% probability level for fatty and essential oil contents with such other traits as harvesting index, thousand seeds weight, and days to maturity indicates that the higher the seed yield, the heavier the seed and the more the matured seed respectively are genetically heritable to the next progenies and give higher oil content. Therefore, these traits are genetically heritable and selection to these traits will lead to finding high yield of oil content.

The positive association between plant height at flowering and days to physiological maturity in both genotypic and phenotypic cases can indicate that the longer the germplasm collection, in height, at flowering period, the more it can get into earlier maturation period. However, the negative association between this trait and other yield and yield component characters can specify that the increase in size of the plant causes the decrease in yield. Therefore, selection for this trait cannot escort to yield improvement. In addition negative and highly significant genotypic and phenotypic correlations were exhibited by harvest index with biomass yield per plant. It also showed negative significant genotypic association with biomass yield per plot. This negative association between characters indicates simultaneous selection of traits is difficult; hence an independent selection has to be used for the improvement of such traits.

The genotypic direct and indirect effect of different traits on seed yield which was observed by the path coefficient analysis assures that these characters will be considered as most important components for selection in breeding program for higher seed yield, since a slight increase in one of the above traits may directly contribute to seed yield. In a study carried out by Uddin et al. (1995), on Indian mustard, 1000-seed weight and primary branches were found to have high positive direct effects on seed yield per plant; which supports the result of the current study.

The result of genetic variability, character association and path coefficient analysis confirmed that the characters harvest index, days to maturity, thousand seed weight and biological yield were important in respect of genetic variability, correlation and path coefficient analysis. The greater variability in these

characters could give a prime scope for the development of high yielding plants through selection in the segregating generation.

According to this study about 2400 kg of garden cress seed can be harvested from one hectare on average; which highly exceeds the yield of linseed (flax) and other oil crops in Ethiopia and the seeds contain considerable amount of edible oil, though it is somewhat spicy and pungent. Therefore, garden cress will have the most significant contribution in the area of increasing edible oil supply; if future studies give emphases on its seed oil content and DNA/gene of the plant that determine its pungency.

Conclusion

From the present study, it is clear that considerable genetic differences existed in the analyzed garden cress genotypes. The study revealed that seed yield per plant had strong and positive genotypic correlation with biomass yield per plant, harvest index and days to maturity with maximum direct effects. These three traits were the key contributors to yield per plant suggesting the need of more emphasis on these components for increasing the grain yield in garden cress. In addition, both correlation and path analysis confirmed that 1000 seed weight is the most prominent trait for the improvement of the two yields, fatty oil and essential oil contents of the garden cress seeds. Improvement in seed yield in garden cress could be brought through selection of component characters directly concerned with final yield like number of secondary branches, 1000 seed weight, biomass yield and harvest index which showed positive direct effects.

ACKNOWLEDGMENT

The authors would like to express their gratitude to Ministry of Education of Ethiopia for providing funding 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

Allard RW (1960). Principles of Plant Breeding. John Willey and Sons, Inc., New York. P. 485.

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

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

Cochran WG, Cox M (1957). Experimental Designs. John Wiley and Sons, Inc. NewYork.

Dabholkar AR (1992). Elements of biometrical genetics. Concept publishing Company, New Delhi 110059.

Delesa A (2006). Genetic Variability and Association Among Seed Yield and Yield Related Traits in Ethiopian Mustard (*Brassica Carinata* A. Braun). Msc. Thesis, Haramaya University, Ethiopia.

Dewey DR, Lu KH (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. Agron. J. 57:515-518.

Dicosta A (2011). Family *Brassicaceae.* Available at http://www.helium.com. [Accessed on February 23, 2012].

Diederichesen A (1996). Coriander (*Corianderum sativum* L.). Promoting the conservation and use of underutilized and neglicated crops. 3. Institute of Plant Genetics and Crop plant Research, Gatersleben, IPGRI, and Rome. P. 83.

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

Giacometti DC, Leon J (1994). Neglected Crops: 1492 from a Different Perspective. In: Plant Production and Protection. Hernando-Bermejo, J.E. and J. Leon (Eds.). FAO, ISBN: 9251032173. Rome, Italy. pp. 253-258.

Gomez AK, Gomez AA (1984). Statistical procedures for agricultural research. 2nd ed. Wilney Int. Sci., New York, P. 680.

Guenther E (1972). The Essential Oils." New York: Robert E. Krieger Publishing Company 1:3-225.

ISO (2010). Oilseeds methods and tests used to measure quality. Canadian Grain Commission, Canada.

Johnson HW, Robinson HF, Comstooc RE (1955). Estimates of genetic and environmental variability in soybeans. Agron. J. 47:314-318.

Johnson GR, Frey KJ (1967). Heritabilities of quantitative attributes of Oats at varying levels of environmental stess. Crop Sci. 7(1-6):43-46.

Jonsell B (2000). *Brassicaceae* In: Flora of Ethiopia and Eritrea: Magnoliaceae to Flacourtiaceae. Edwards S, Tadesse M, Demissew S, Hedberg I, (Eds.). National Herbarium, Addis Ababa. Univ. USA. 2:121-154.

Jurgen S, Reinhard F, Karl H, Peter H, Jaochim K, Harald O, Klaus P (1985).Taxonomy and evolution of cultivated plants: Lierature review 1983/1984. Kulturpllanze 33:307-124.

Mengesha B, Alemaw G (2010): Variability in Ethiopian Coriander accessions for agronomic and quality trait. Afr. Crop Sci. J. 18(2): 43-49.

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):336-41.

Miller PA, Williams C, Robinson HF, Comstock RE (1958). Estimates of genotypic and Environmental variances and co-variances in upland cotton and their implications in selection. Agron. J. 50:126-131.

Petros Y (2008). Genetic Diversity and Oil Quality of *Guizotia* Cass. (Asteraceae). [PhD. Thesis.] Swedish University of Agricultural Sciences, Sweden.

SAS (2002). SAS /STAT guide for personal Computer, Proprietary software Version 9. SAS Institute Inc., Cary. NC. USA.

Schlegel RHJ (2009). Dictionary of Plant Breeding. 2nd Edn., CRC Press, New York, ISBN: 9781439802427. P. 571.

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 RK, Chaudhary BD (1999). Biometrical Methods in Quantitative Genetics Analysis. Kalyani Publishers, New Delhi, India, P. 318.

Singh SP, Katiyar RS, Rai SK, Triphathi SM, Srivastva JP (2005). Genetic divergence and its implication in breeding of desired plant types in coriander (C*oriandrum sativum*L.). Genetika 37:155-163.

Uddin MJ, Chowdhury MAZ, Mia MFU (1995). Genetic variability, character association and path analysis in Indian mustard (*Brassica juncea* L.). Ann. Bangladesh Agric. 5:51-54.

Welsh RJ (1990). Fundamentals of Plant Genetics and Breeding. John Wiley and Sons, New York.