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RESEARCH ARTICLE

Genetic variation in garden cress (*Lepidium sativum* L.) germplasm as assessed by some morphological traits

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Abstract The morphological variation of 81 garden cress including 77 accessions of Genebank Department of Leibniz Institute of Plant Genetics and Crop Plant Research in Gatersleben, Germany and four ancient varieties collected from different geographical and bioclimatic areas of Iran were assessed based on 19 morphological traits. The genotypes were grown according to simple lattice design with four replications across 2 years (2012 and 2013). Significant differences among accessions were revealed for the majority of traits. The coefficient of variation varied from 18.05 (number of seeds per silique of lateral branches) to 52.79 % (biological yield) in the first year and varied from 9.12 (number of seeds of silique per plant) to 36.05 % (biological yield) in the second year. The first four factors explained 83.92 % of the total variation at year 2012 while the first four factors explained 76.93 % of the total variation at year 2013 among 81 of garden cress accessions. At both years, days to flowering, days to maturing, height of first branch and height of first silique, number of silique per lateral branches and number of siliques per plant were the most important traits contributing to the first two factors. This indicates that breeding programs should be based on these traits for improvement of garden cress. The regions of origin of the accessions were dispersed in ten sub-units which the first factor axis was much more important than the second one in separating the regions of origin of the accessions and separated sub-units five from four other sub-units, but this factor axis could not separate accessions of sub-unit I. Based on the observed structures of variation, it is concluded that the magnitude of morphological variation in the material studied is high and the implications of the results for plant breeding programs are discussed. The results of the present study can be used for breeding and improvement of garden cress for various desired traits through hybridization in future.

Keywords Classification · Garden cress · Genetic variation · *Lepidium sativum* · Morphological traits

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Introduction

The genus garden cress (*Lepidium sativum* L., belongs to the Brassicaceae family) is an important vegetable crop cultivated in temperate and cold climates. It is believed to have originated in Southwest Asia (perhaps Iran, Parsa 1960) and its cultivation spread many centuries ago to Europe and it was one of the vegetables most widely eaten in the sixteenth century, some attempts were made to introduce it into America (Bermejo and Leon 1994). The garden cress is

cultivated and used in the form of vegetable in North Africa, west and central Asia, but at present, the cultivation of cress is very occasional in North America and Europe except United Kingdom. It is an exceptionally rich source of antioxidants (Souri et al. 2004), and contains glucosinolates that are non-nutritive constituents present in crucifers associated with substantial health benefits (Li et al. 2010). Since ancient times, the seeds of garden cress have been used in traditional medicine because they are claimed to possess varied medicinal components such as galactogogue which are given as a tonic for general weakness in young girls and after child birth to increase breast milk (Sharma and Agarwal 2011). The galactogogue is a substance that promotes lactation in humans and may be synthetic, plant-derived, or endogenous (Gabay 2002). Edible oil of garden cress (up to 58 % of seed weight) can be used for lighting (Sumeet et al. 2010).

The genus *Lepidium* is made up of about 150 species and specie *L. sativum* L. (garden cress) has been divided into three botanical varieties as: *vulgare, crispum* and *latifolium* based on the morphology of the leaf, stem and root (Povalyaeva 1981; Majeed et al. 2010). Most of the genetic improvement programs on garden cress had been carried out in the Russia, with little or no work being done at present in the Europe (Bermejo and Leon 1994). First studies on the genetic variation and breeding of new cultivars of garden cress are being carried out in Russia, where there is a good collection of plant materials. The mentioned plant materials are being used as the basis of other breeding programs due to good performance in production potential and quality of Russian cultivars (Bermejo and Leon 1994). New cultivars have also been produced in Europe, Turkey and Japan in the last decades (Dayal and Singh 1985; Sat et al. 2013). Some accessions collected during an expedition to Southwest Asia, central Asia and other regions are now stored in IPK (Leibniz Institute of Plant Genetics and Crop Plant Research, Gatersleben) in Germany (Bermejo and Leon 1994). Most of the collected garden cress accessions were landraces which are highly adapted to specific environmental conditions and are useful sources of genetic variation.

Efficient evaluation and utilization of the genetic materials needs detailed knowledge about the collections including characterization and classification (Nooryazdan et al. 2010). Bansal et al. (2012) assessed

genetic diversity of 18 Chandrasur (*L. sativum*) genotypes using RAPD molecular marker and divided them into two main clusters and the dendrogram revealed 23–66 % genetic relatedness among genotypes. Bedassa et al. (2013b) classified 49 Ethiopian accessions into seven distinct groups, mainly based upon morphologic traits. Such similar classification is simple, reliable and aids to evaluate not only the patterns of genetic variation but also the paths of developing target traits such as yield (Szamosi et al. 2010; Hegay et al. 2014). Multivariate methods are useful for characterization and classification of genetic resources when a number of accessions are to be evaluated for several agronomical traits and physiological importance. The usefulness of multivariate statistical procedures for evaluation morphological variation in collections of accessions has been demonstrated in many crops (Trimech et al. 2013; Hegay et al. 2014; Sabaghnia et al. 2014). The obtained information can be useful to identify groups of accessions that have desirable traits for different targets including crossing, planning germplasm collecting efforts, establishing core collections, revealing the structure of variation and studying some aspects of crop evolution.

With regard to morphological variation of the international garden cress germplasm, some few studies have been done in the past (Bedassa et al. 2013b). The objective of the present investigation was to determine the extent and patterns of distribution of morphological and phenotypic variation for 19 traits in 81 accessions of garden cress germplasm obtained from IPK's genebank had been collected from different geographical and bioclimatic areas and to identify groups of accessions with similar traits using multivariate statistical methods.

Materials and methods

The small samples (about 200 seeds) of experimental seed materials (77 accessions) were obtained from Genebank Department of Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) in Gatersleben, Germany. These samples were propagated in growing season 2010–2011 and their name and origin are given in Table 1. The mentioned accessions and four ancient varieties (Birjand, Tabriz, Kerman and Shiraz) earlier collected from different geographical

Table 1 The name and origin of 77 garden cress accessions of IPK and four local Iranian landraces

Code	Accession number	Botanical variety	Local name	Donor country	Code	Accession number	Botanical variety	Local name	Donor country
A1	LEP-1	var. *sativum*	–	Afghanistan	A42	LEP-59	var. *latifolium* DC.	–	Georgia
A2	LEP-2	var. *latifolium* DC.	–	Afghanistan	A43	LEP-60	var. *latifolium* DC.	–	Georgia
A3	LEP-3	var. *sativum*	–	Greece	A44	LEP-61	var. *latifolium* DC.	Armjanskaja	Tajikistan
A4	LEP-4	var. *sativum*	Gewöhnliche	Germany	A45	LEP-62	var. *latifolium* DC.	–	Georgia
A5	LEP-5	var. *crispum* (Medik.) DC.	Grüne Krause	Germany	A46	LEP-63	var. *latifolium* DC.	–	Georgia
A6	LEP-8	var. *sativum*	–	Unknown	A47	LEP-64	var. *sativum*	–	Georgia
A7	LEP-9	var. *sativum*	–	Unknown	A48	LEP-65	var. *sativum*	Burpee's Curlieress	USSR
A8	LEP-12	var. *crispum* (Medik.) DC.	–	Unknown	A49	LEP-66	var. *sativum*	Gartenkresse	Germany
A9	LEP-14	var. *crispum* (Medik.) DC.	–	Unknown	A50	LEP-67	var. *sativum*	Gartenkresse	Germany
A10	LEP-15	var. *crispum* (Medik.) DC.	–	Unknown	A51	LEP-68	var. *sativum*	Gartenkresse	Germany
A11	LEP-16	var. *latifolium* DC.	–	Afghanistan	A52	LEP-69	var. *sativum*	Gartenkresse	Germany
A12	LEP-18	var. *latifolium* DC.	–	Unknown	A53	LEP-70	var. *sativum*	Gartenkresse	Germany
A13	LEP-19	var. *crispum* (Medik.) DC.	–	Unknown	A54	LEP-72	var. *sativum*	Gartenkresse	Germany
A14	LEP-21	var. *latifolium* DC.	–	Georgia	A55	LEP-73	var. *sativum*	Gartenkresse	Germany
A15	LEP-22	var. *latifolium* DC.	–	Germany	A56	LEP-74	var. *sativum*	–	Yemen (Al-Hilf)
A16	LEP-23	var. *sativum*	–	Armenia	A57	LEP-75	var. *latifolium* DC.	Gartenkresse	Azerbaijan
A17	LEP-24	var. *latifolium* DC.	–	Armenia	A58	LEP-76	var. *latifolium* DC.	Gartenkresse	Germany
A18	LEP-25	var. *sativum*	Nastruzio	Italy	A59	LEP-78	var. *sativum*	Gartenkresse	Germany

Table 1 continued

Code	Accession number	Botanical variety	Local name	Donor country	Code	Accession number	Botanical variety	Local name	Donor country
A19	LEP-26	var. *latifolium* DC.	–	Georgia	A60	LEP-86	–	–	Unknown
A20	LEP-27	var. *latifolium* DC.	–	Georgia	A61	LEP-102	–	–	Unknown
A21	LEP-28	var. *latifolium* DC.	–	Georgia	A62	LEP-103	var. *sativum*	–	Austria
A22	LEP-30	var. *latifolium* DC.	–	Georgia	A63	LEP-104	–	–	Belarus
A23	LEP-31	var. *latifolium* DC.	–	Georgia	A64	LEP-105	–	–	Georgia
A24	LEP-32	var. *latifolium* DC.	–	Georgia	A65	LEP-106	–	–	Azerbaijan
A25	LEP-33	var. *sativum*	–	Libya	A66	LEP-107	–	–	Russia
A26	LEP-34	var. *latifolium* DC.	–	Georgia	A67	LEP-108	–	–	Armenia
A27	LEP-36	var. *latifolium* DC.	–	Georgia	A68	LEP-110	–	–	Russia
A28	LEP-40	var. *sativum*	–	Iraq	A69	LEP-111	–	–	Georgia
A29	LEP-42	var. *sativum*	–	Iraq	A70	LEP-114	var. *sativum*	–	Hindukusch
A30	LEP-43	var. *latifolium* DC.	–	Georgia	A71	LEP-115	–	–	Unknown
A31	LEP-44	var. *sativum*	–	Georgia	A72	LEP-116	var. *crispum* (Medik.) DC.	–	Unknown
A32	LEP-45	var. *latifolium* DC.	–	Georgia	A73	LEP-117	var. *sativum*	–	Unknown
A33	LEP-46	var. *sativum*	Riccio	Italy	A74	LEP-118	var. *sativum*	–	Unknown
A34	LEP-47	var. *latifolium* DC.	–	Ukraine	A75	LEP-119	var. *latifolium* DC.	–	Unknown
A35	LEP-48	var. *sativum*	–	Georgia	A76	LEP-120	var. *latifolium* DC.	–	USSR
A36	LEP-49	var. *latifolium* DC.	–	Georgia	A77	LEP-126	–	CAF	USSR
A37	LEP-50	var. *sativum*	–	Korea	A78	–	–	–	Iran (Birjand)
A38	LEP-51	var. *latifolium* DC.	–	Georgia	A79	–	–	–	Iran (Kerman)

Table 1 continued

Code	Accession number	Botanical variety	Local name	Donor country	Code	Accession number	Botanical variety	Local name	Donor country
A39	LEP-53	var. *latifolium* DC.	cicmati	Georgia	A80	–	–	–	Iran (Tabriz)
A40	LEP-55	var. *latifolium* DC.	–	Georgia	A81	–	–	–	Iran (Shiraz)
A41	LEP-57	var. *latifolium* DC.	–	Georgia					

CAF cresson alenoise frise

and bioclimatic areas of Iran were grown in two subsequent growing seasons 2011–2012 (with 258.3 mm annual precipitation) and 2012–2013 (with 201.3 mm annual precipitation) in the experimental field of University of Maragheh. Plots were established using replicated 9 × 9 simple lattice design with four replications. Sowing was done at the bottom of a furrow in a 30 cm between rows system in the spring (the first week of May) which is the optimal sowing time for garden cress in the trial area. There were six rows 2 m long and 0.30 m apart, plot size was 3.6 m^2. Plots were overplanted and thinned to a distance between plants in the row of 15 cm for an established plant density of about 22 plants m^{-2}. Irrigation was selectively applied six times during rainfall shortages (about 10 days' intervals). The amount of irrigation water was calculated to restore water content in the root zone to field capacity. Fertilizers were hand broadcast to the soil before sowing. A uniform basal dose of potassium (60 kg K ha^{-1}), nitrogen (120 kg K ha^{-1}) and phosphorus (30 kg K ha^{-1}) were applied to all the plots. The sources of K, N and P were the muriate of potash (KCI), urea (46 % N), and single super phosphate, respectively. Weeds were controlled by hand as needed. The soil was clay loam (25.6 % sand, 38.8 % silt and 35.6 % clay) with neutral reaction pH 7.3.

Nineteen traits of garden cress were measured on 81 accessions cross 2 years (Table 2). Eleven traits were measured evaluated on ten randomly selected plants as vying samples in the four mid-rows of plots: height of first branch (HFB), height of first silique (HFS), main axis length (MAL), number of lateral branches (NLB),

Table 2 Measured traits and their abbreviation for 81 garden cress accessions

Abb.	Measured traits	Scale
DE	Days to emergence	day
EP	Emergence percentage	%
DF	Days to flowering	day
FP	Flowering period	day
DM	Days to maturing	day
HFB	Height of first branch	cm
HFS	Height of first silique	No.
MAL	Main axis length	cm
NLB	Number of lateral branches	No.
NSL	Number of silique per lateral branches	No.
NSM	Number of siliques per main axis	No.
NSP	Number of siliques per plant	No.
SLB	Number of seeds per silique of lateral branches	No.
SMA	Number of seeds per silique of main axis	No.
NSSP	Number of seeds of silique per plant	No.
PH	Plant height	cm
SY	Seed yield	kg
TSW	Thousand-seeds weight	g
BY	Biological yield	kg

Abb. abbreviation

number of silique per lateral branches (NSL), number of siliques per main axis (NSM), number of siliques per plant (NSP), number of seeds per silique of lateral branches (SLB), number of seeds per silique of main axis (SMA), number of seeds of silique per plant (NSSP) and plant height (PH). Also, days to emergence (DE), emergence percentage (EP), days to flowering (DF), flowering period (FP) and days to maturing (DM) were

recorded as was as possible. The thousand-seeds weight (TSW) was measured on a sub-sample of seed harvested from each plot. Only the middle four rows were harvested and weighed to determine biological yield and the area harvested was 1.8 m^2. Seed yield (SY) was measured at physiological maturity and was adjusted to 12.5 % seed moisture content.

The datasets were first tested for normality by the Anderson–Darling normality test using Minitab version 17 (2014) statistical software. Data from each trial were subjected to analysis of variance (ANOVA) using appropriate models. For each trait, ANOVA based on lattice design (Snedecor and Cochran 1981) was performed using PROC LATTICE of SAS version 9.1 (SAS 2004). If the relative efficiency of the lattice design was <105 % for a variable, the data could be analyzed according to a randomized complete block design and so there is no need for using of adjusted treatments and blocks within replications. In other words, the differences among blocks of each replication, are not consirdbale and significant and they could be ignored. Duncan's New Multiple Range Test was used to provide significant differences between averages of traits. The general divergence among accessions was estimated using factor analysis based on

principal component analysis (PCA) which was performed via correlation matrix to define the patterns of variation according to all measured traits. The factor analysis consisted of the reduction of a large number of correlated variables to a much smaller number called factors. After extraction, the matrix of factor loading was submitted to a varimax orthogonal rotation. The array of communality, the amount of variance of a variable accounted by the common factors together, was estimated by the highest correlation coefficient in each array as suggested.

Results

Table 3 shows some of the descriptive statistics (the minimum and maximum values, arithmetic mean, range, and coefficient of variation) for all estimated traits of garden cress. The coefficient of variation (CV) of measured traits varied from 18.05 (SLB) to 52.79 % (biological yield) in the first year (2012) while CV of studied traits varied from 9.12 (NSSP) to 36.05 % (biological yield) in the second year (2013). It seems that, the environmental condition of the second year is less variable than the first year and so the CV of the

Table 3 Descriptive statistics of the 19 measured traits in 81 garden cress accessions

Traits	Year 2012				Year 2013			
	Mean	Min.	Max.	CV	Mean	Min.	Max.	CV
DE	17.15	8.50	26.00	20.17	14.68	6.00	18.75	14.85
EP	68.92	33.75	90.75	18.83	72.43	36.00	88.25	11.23
DF	48.09	24.25	75.75	22.52	50.02	23.75	64.25	14.14
FP	15.38	7.50	21.50	24.80	17.87	11.25	22.50	13.47
DM	86.89	45.00	110.75	18.12	91.44	47.00	102.75	10.52
HFB	10.89	2.22	21.77	35.81	12.56	7.23	31.20	26.64
HFS	20.68	8.27	48.10	28.63	23.20	15.30	37.24	15.83
MAL	9.24	4.07	19.12	29.34	11.48	7.52	16.56	16.18
NLB	12.07	6.00	29.75	29.91	10.46	3.00	19.50	22.57
NSL	33.14	12.50	55.75	29.97	30.96	13.50	47.50	22.73
NSM	23.55	11.25	40.00	26.89	20.68	10.75	29.00	18.90
NSP	518.89	193.50	899.00	28.06	466.27	145.75	685.50	20.75
SLB	1.92	1.00	2.75	18.05	2.65	1.50	3.50	10.55
SMA	2.54	1.25	4.00	23.46	2.71	1.25	3.75	15.37
NSSP	2.04	1.00	3.00	21.61	2.77	1.75	3.00	9.12
PH	33.02	0.00	78.89	36.60	36.13	13.47	59.70	25.35
SY	631.03	220.88	1,431.45	36.32	675.78	262.55	1,360.58	24.34
TSW	2.00	0.91	2.86	21.54	2.04	0.96	2.63	13.68
BY	7,831.99	2,027.26	25,632.96	52.79	8,223.37	2,862.87	22,025.21	36.05

measured traits in the second year are relatively lower than the first year. The most variable traits included HFB (35.81 % at 2012 and 26.64 % at 2013), PH (36.60 % at 2012 and 25.35 % at 2013) and SY (36.32 % at 2012 and 24.34 % at 2013). The traits with less variation included SLB (18.05 %) as mentioned above, EP (18.83 %) and DM (18.12 %) in the year 2012 (Table 3). Also, the traits with less variation included NSSP (9.12 %) as mentioned above, SLB (10.55 %) and DM (10.52 %) in the year 2013 (Table 3).

The analysis of variance revealed significant differences for the examined traits among of garden cress accessions (results are not shown). The first four factors, with eigenvalues greater than unity, explained 83.92 % of the total variation of year 2012 while the first four factors explained 76.93 % of the total variation of year 2013 (Table 4). At first year, the first factor accounted for 56.11 % of the total variation and including DE, DF, DM, HFB and HFS were the most important traits contributing to the first factor. In the second factor which accounted for 13.57 % of the total variation, NSL and NSP had important contribution in the first year (Table 4). In the third factor (with accounting for 8.56 % of the total variation), SY and biological yield indicated importance in year 2012 while, in the fourth factor (with accounting for 5.67 %

of the total variation), MAL and flowering period were important in this year (Table 4).

In the second year (2013), the position of important traits of the first and second factor is changed to each other. In other words, NSL and NSP were the most important traits contributing to the first factor which accounted for 46.15 % of the total variation (Table 4). Also, DE, DF, DM, HFB and HFS were the most important traits contributing to the second factor which accounted for 13.27 % of the total variation (Table 4). Similar to first year, in the third factor (with accounting for 10.88 % of the total variation), SY and biological yield were the most important traits and in the fourth factor (with accounting for 6.63 % of the total variation), MAL and flowering period were the most important traits (Table 4).

To better understand the relationships among the measured traits they are graphically displayed as a plot of Factor 1 versus Factor 2. In plot of first year (Fig. 1), five distinct groups are determined: Group I consist on PH, BY, MAL, SY and FP; Group II consist on EP, DM, DF, DE and HFS; Group III consist on NSSP, TSW, SMA, NLB and SLB; Group IV consist on NSL, NSM, NSP; and Group V consist on HFB. In plot of second year (Fig. 2), nearly similar groups were determined. Regarding this similar pattern for both years, the mean values of 2 years were used for factor

Fig. 1 Plot of two first factor analysis of 19 traits for the 81 garden cress accessions at first year (2012). For abbreviation of traits refer to Table 2
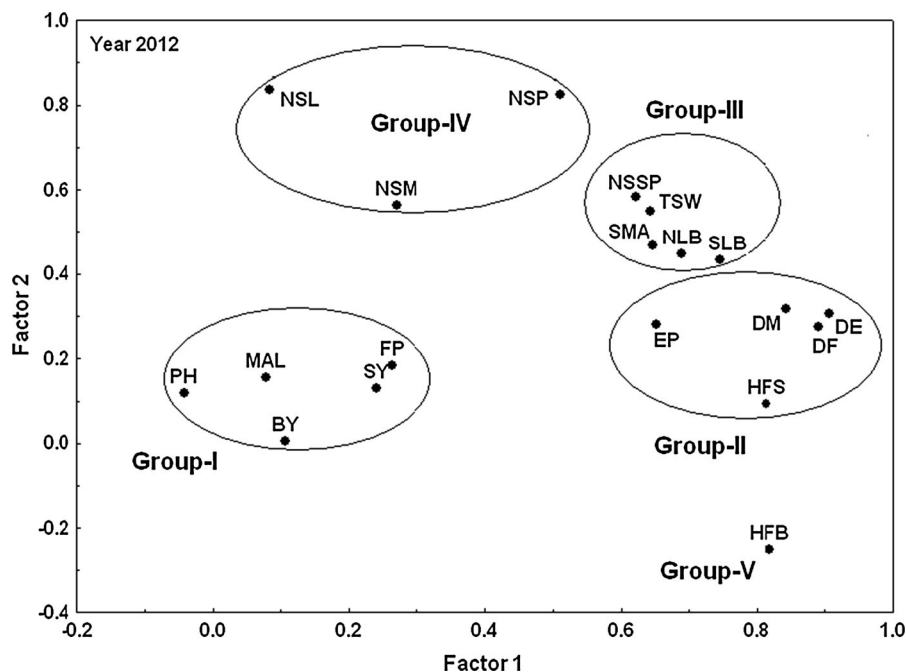
Fig. 2 Plot of two first factor analysis of 19 traits for the 81 garden cress accessions at second year (2013). For abbreviation of traits refer to Table 2
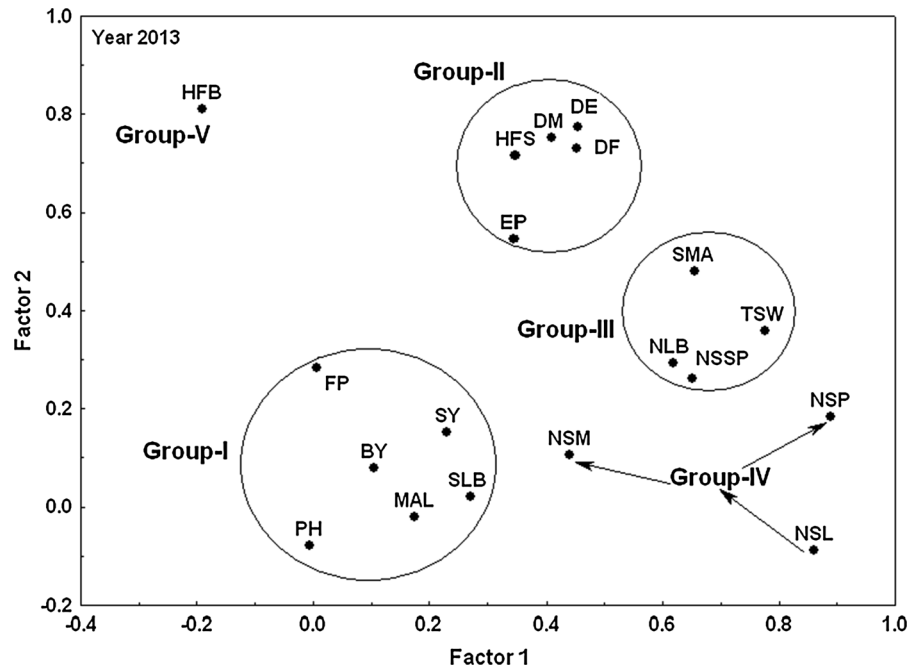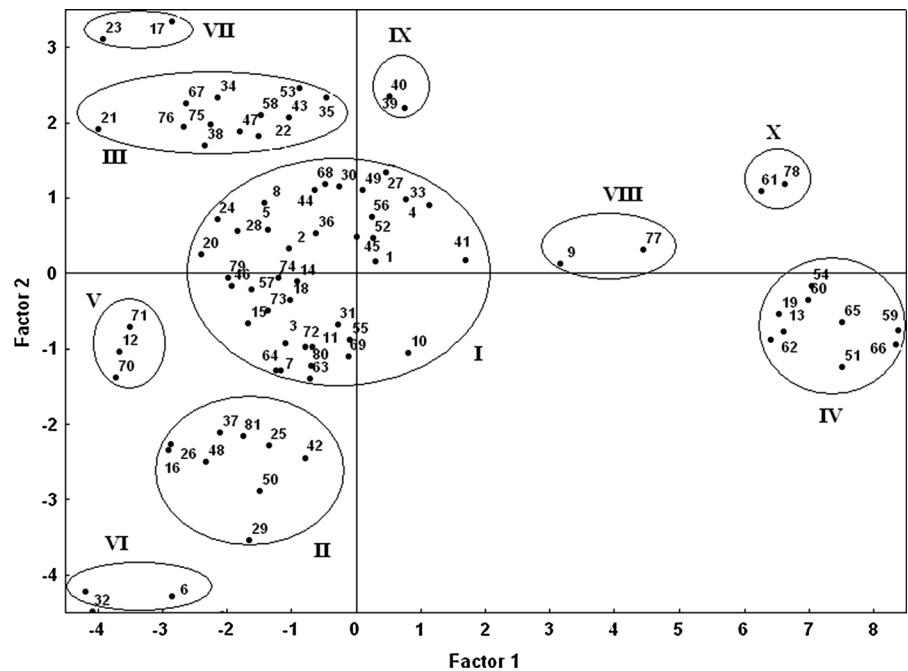

Fig. 3 Factor analysis plot according to axes 1 and 2 based on all analyzed traits for all accessions based on mean values of two experimental years

analysis of in order to study the regional pattern of variation. The analysis was effective in that the first two factors accounted for 65 % of the total variation (52 and 13 % for Factor 1 and Factor 2, respectively). Figure 3 shows the distribution of the 81 regions of

origin of the accessions along the first two axes of the factor analysis. The regions of origin of the accessions were dispersed in ten sub-units (Fig. 3). The first factor axis separated sub-units III, VII, VIII, IX and X from sub-units II, IV, V and VI and the second factor

Table 4 Factor components loadings of 19 traits obtained from 81 garden cress accessions

Measured traits	Year 2012					Year 2013				
	F1	F2	F3	F4	Comm.[†]	F1	F2	F3	F4	Comm.
DE	**0.897**	0.296	0.095	0.162	1.45	0.440	**0.765**	0.199	0.051	1.46
EP	0.652	0.282	0.550	0.357	1.84	0.346	0.546	0.656	0.280	1.83
DF	**0.891**	0.274	0.082	−0.048	1.20	0.452	**0.732**	0.123	−0.124	1.18
FP	0.263	0.185	0.168	**0.753**	1.37	0.007	0.282	0.360	**0.645**	1.29
DM	**0.844**	0.317	0.148	0.323	1.63	0.409	**0.752**	0.269	0.210	1.64
HFB	**0.819**	−0.250	0.063	0.185	0.82	−0.191	**0.812**	0.007	0.074	0.70
HFS	**0.814**	0.095	0.057	0.234	1.20	0.347	**0.717**	−0.053	0.135	1.15
MAL	0.078	0.155	0.265	**0.827**	1.33	0.174	−0.020	0.182	**0.844**	1.18
NLB	0.688	0.448	0.003	−0.168	0.97	0.612	0.294	0.122	−0.144	0.88
NSL	0.083	**0.837**	0.100	0.343	1.36	**0.861**	−0.088	−0.071	0.326	1.03
NSM	0.269	0.564	0.224	0.602	1.66	0.439	0.107	0.137	0.640	1.32
NSP	0.511	**0.826**	0.078	0.148	1.56	**0.889**	0.184	0.066	0.125	1.26
SLB	0.745	0.433	0.161	0.348	1.69	0.271	0.022	−0.027	0.450	0.72
SMA	0.646	0.467	0.298	0.079	1.49	0.655	0.481	0.339	0.110	1.59
NSSP	0.631	0.573	0.141	0.356	1.70	0.650	0.262	0.266	0.208	1.39
PH	−0.042	0.119	0.735	0.261	1.07	−0.006	−0.079	0.794	0.212	0.92
SY	0.239	0.129	**0.934**	0.129	1.43	0.231	0.154	**0.923**	0.146	1.45
TSW	0.643	0.551	0.434	0.181	1.81	0.777	0.358	0.415	0.176	1.73
BY	0.106	0.005	**0.964**	0.098	1.17	0.104	0.080	**0.949**	0.123	1.26
Eigenvalues	10.66	2.58	1.63	1.08		8.77	2.52	2.07	1.26	
% of Variance	56.11	13.57	8.56	5.67		46.15	13.27	10.88	6.63	
% Cumulative	56.11	69.68	78.25	83.92		46.15	59.42	70.30	76.93	
% KMO[‡]	80.43					69.63				

[†] Communality

[‡] Kaiser–Meyer–Olkin measure of sampling adequacy

The bold numbers are the highest loadings for each factor

axis separated sub-units III and VII from sub-units VIII, IX and X as well as separated sub-units II, IV and V from sub-unit VI (Fig. 3).

The mean values of the measured traits for each of ten identified sub-units are given in Table 5. The accessions of sub-units IV and X were low in the most of the measured charters and so are good candidates for improving earlier maturity in garden cress due to low amounts of DF, flowering period and DM (Table 5). Also, the mentioned accessions have a few numbers of DE which would be regarded in cold regions. The accessions of sub-units II, V, VI and VII were high in EP, NSP, NSSP, TSW and other similar yield components traits and can be introduced as good source for improving yield components of garden cress (Table 5). The accessions of sub-units I and IX can be regarded from good potential for EP and biological yield. The accessions of sub-unit VIII had moderate values for the most of the measured characteristics and can be used for improving these traits of garden cress regarding targets of breeder (Table 5).

Discussion and conclusions

Morphological and molecular markers have been used extensively to describe the variability of different crops landraces but such investigations have not been performed properly for garden cress germplasm. Most of these investigations showed a high variation of measured traits among accessions of various geographical regions (Nooryazdan et al. 2010; Szamosi

Table 5 The mean values of the measured traits for each of ten identified sectors of Fig. 3

	DE	EP	DF	FP	DM	HFB	HFS	MAL	NLB	NSL	NSM	NSP	SLB	SMA	NSP	PH	SY	TSW	BY
Analysis of variance																			
BC	50.22[a]	678.09	453.75	37.95	1,079.03	38.85	90.24	15.62	38.70	204.11	109.28	76,260.76	0.38	1.23	0.55	449.31	190,001	0.71	61,690,656
WC	0.79	11.53	15.31	3.52	7.36	6.18	8.06	2.28	2.95	39.81	9.11	3,918.64	0.02	0.07	0.02	45.22	10,118	0.02	3,204,705
Mean values of clusters																			
I	16.57	73.52	50.56	17.56	92.84	11.87	22.32	10.57	11.34	32.94	22.88	505.33	2.34	2.67	2.44	35.91	652.0	2.04	7,796
II	15.96	77.51	47.18	19.01	91.50	11.59	21.79	12.95	11.04	35.76	24.99	521.71	2.40	2.81	2.53	46.54	831.1	2.19	11,213
III	18.14	72.21	57.72	15.39	96.75	13.01	23.77	9.45	14.64	34.64	23.60	596.25	2.35	2.90	2.59	27.88	622.5	2.23	6,902
IV	10.06	49.99	32.65	12.06	60.99	7.38	14.69	8.20	7.35	24.33	14.57	307.78	1.78	1.85	1.83	27.88	472.8	1.42	5,927
V	17.21	80.83	52.04	18.17	95.96	13.84	25.43	12.38	11.79	39.88	28.88	577.63	2.46	2.88	2.67	36.81	887.8	2.42	11,982
VI	16.13	83.06	47.31	19.63	92.75	10.83	21.84	11.22	11.38	28.94	24.81	476.94	2.31	3.25	2.63	55.98	1,228.0	2.41	19,911
VII	18.75	68.50	57.13	16.56	98.13	11.50	32.86	10.16	14.25	41.13	23.69	670.88	2.63	3.44	2.88	23.93	483.7	2.42	4,366
VIII	13.63	62.31	42.50	15.63	80.06	10.20	20.37	9.49	8.56	19.19	17.44	316.19	2.25	2.00	2.25	32.23	462.2	1.52	5,289
IX	17.50	71.75	57.56	14.75	95.81	20.05	23.97	8.76	11.63	22.94	16.63	406.56	2.31	2.31	2.31	30.40	593.4	1.88	6,994
X	12.00	51.63	37.88	13.75	70.00	12.35	20.48	8.60	6.81	22.00	15.50	301.00	1.81	1.88	1.88	18.11	372.7	1.42	3,925

The maximum and minimum values are underlined

BC between clusters, *WC* within clusters

[a] All of the between clusters were significant at 0.01 probability level

et al. 2010; Cheema et al. 2011) and we found relatively high variation in our plant materials. A total of nineteen qualitative and quantitative traits were used to assess the variation of garden cress landraces. A high variation was observed for the HFB, PH, SY and biological yield traits. Also, a moderate variation was observed for DF, flowering period, HFS, MAL, NLB, NSL, NSM and NSP and TSW traits. The traits DE, DF, DM, HFB, HFS, NSL and NSP are the main traits contributing to the total variation among accessions based on factor analysis. Although, we found that NSL (not per main axis) had important contribution to total variation, but in rapeseed (*Brassica napus* L.), from Brassicaceae family, the number of silique -per main axis is very important in contribution to total variation as well as SY potential (Sabaghnia et al. 2010). However, it seems the length of main axis in these two genera is not comparable and it is very short in garden cress. Height to the first lateral branch and height to the first silique are important traits not only in garden cress but also in all genera of Brassicaceae, especially during harvesting, which makes plant breeders eager to develop high yielding genotypes with desirable plant architecture (Marjanovic-Jeromela et al. 2008). With regard to the mentioned traits, breeding for garden cress with high values of above traits could also be useful at harvest (Table 5).

In a study carried out by Bedassa et al. (2013a), SY of garden cress had positive and significant association with number of seeds per plant, number of secondary branches, biological yield while we found SY is related to PH, biological yield, MAL, and flowering period. Similar reports have been made by Ozer et al. (1999) and Ivanovska et al. (2007) in rapeseed (*Brassica napus* L.) and by Uddin et al. (1995), on Indian mustard (*Brassica juncea* L. Czerno). These authors emphasized that suitable flowering period types are the most suitable for lowland areas of semi-arid regions, where rainfall is limited and the growing season is short. The result of this investigation confirmed that the traits DE, DF, DM, HFB, HFS, MAL and NSL were important in respect of genetic variability. The greater variability in the mentioned traits could give a prime scope for the development of high yielding cultivars through selection in the segregating generation. According to our results about 630 kg ha^{-1} of garden cress (with maximum 1430 kg ha^{-1}) seed can be harvested on average; which is good potential as future source of edible oil in

some areas of world. Bedassa et al. (2013a) have estimated 60 % more potential for Ethiopian garden cress accessions and compared this potential with linseed (flax). However, it seems that the most contribution in the area of increasing edible oil supply will have in future increasing investigations mainly on its seed oil content as breeding target.

Our results suggest that the pattern of morphological variation in the garden cress accessions studied is not influenced by environmental factors due to similar structure of two experimental years' dataset. The factor analysis plot based on all measured traits allowed distinction among accessions from their properties. Regarding the supposed origin of garden cress (Iran), we expected the ancient Iranian garden cress genotypes indicate high variation which is verified by assigning them (Birjand, Tabriz, Kerman and Shiraz) to the different sub-units with different properties. In other words, the studied accessions did not cluster separately from their origin, suggesting the mixing of the different landraces. In general, the garden cress accessions are highly variable being grouped over ten sub-units that are significantly different from each other. Similarly, Bedassa et al. (2013b) stated that the geographic and genetic diversity are not necessarily in garden cress germplasm and indicated different garden cress accessions collected from the same geographic area fell in different genetic groups whereas those collected from different geographic areas tended to be grouped in the same group. Thus, the difference in geographic origin cannot be used as indication of genetic diversity for parental selection in some crops and it may be useful for some crops as indicated by Trimech et al. (2013) in melon. This might be migration of the garden cress materials from one region to another in collection sites through farmer to farmer exchange of seeds. Although, garden cress has been identified as an autogamous plant, some evidence raises the possibility of natural out-crossing due to self-compatible and self-incompatible forms as well as with various degrees of tolerance to prolonged autogamy (Povalyaeva 1981; Bermejo Leon 1994). Similarly, Bandila et al. (2011) used the cluster analysis of some Indian sesame genotypes and concluded that geographical origins did not separate the sesame germplasm. Although, determining origin of plant materials from different geographic regions are important, but there are gradual changes between populations from different geographic regions

(Lanner-Herrera et al. 1996). In fact, geographic variation in distribution is nearly impossible to separate from genetically determined variation (Rao and Hodgkin 2002).

More importantly, the mentioned ten groups of garden cress accessions are characterized by many traits especially in early flowering, early maturity, high EP, good potential in yield components like number of siliques and biological yield. Early maturity and good yield potential types of garden cress are widely found among this collection and this is also the main reason for introducing this germplasm for other areas of world. However, the existence of remarkable genetic divergence suggest that there can be a wide span to exploit through breeding via hybridization and selection by crossing accessions from different ten groups of garden cress accessions. It is essential to note that in calculating mean of each group of garden cress accessions, the superiority of a particular accession with respect to a given trait could get diluted by other accessions that are grouped in the same group but are inferior or moderate for the trait in question. Therefore, apart from selecting candidate accessions from the groups which have higher inter-group distance for hybridization, one can also think of selecting accessions based on the extent of divergence with respect to a trait of interest (Million 2011).

In the present study, partitioning and interpretation of the accession × trait two-way dataset pattern was based on the factor analysis technique while the univariate methods had shown certain deficiencies for determining and explaining two-way dataset patterns because they attempt to define them by one parameter; however the multivariate two-way dataset pattern is far too complex to be summarized by one parameter. Multivariate statistical methods such as factor analysis have been introduced to explore multidirectionality aspects and attempt to extract more information from two-way dataset pattern. Trimech et al. (2013) showed the advantages of principal component analysis in identifying useful germplasm particularly by including reference varieties and we found that using factor analysis with varimax rotation could be proper in similar investigations. Factor analysis appears to be able to extract a large portion of the total variation and is thus more efficient in analyzing two-way dataset pattern in different crops.

No such extensive work has ever been reported for such international garden cress accessions. The analysis of molecular markers should be conducted to deepen the assessment of the genetic variation and the classification of accessions to suggest more efficient conservation strategy. Such molecular marker investigations will reveal whether accessions that share similarities of traits are genetically different.

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