Genet Resour Crop Evol (2017) 64:7–22
DOI 10.1007/s10722-015-0329-0

RESEARCH ARTICLE

Morphological characterization of snake melon (*Cucumis melo* var. *flexuosus*) populations from Palestine

Mohammed S. Ali-Shtayeh · Rana M. Jamous · Munqez J. Shtaya · Omar B. Mallah · Imad S. Eid · Salam Y. Abu Zaitoun

Received: 5 May 2015 / Accepted: 28 September 2015 / Published online: 9 October 2015

Abstract Genetic diversity in 50 snake melon accessions collected from Palestine (West Bank) was assessed by examining variation in 17 phenotypic characters. These accessions belonged to four important landraces of *Cucumis melo* var. *flexuosus*: Green "Baladi" (GB), white Baladi (WB), green Sahouri (GS), and white Sahouri (WS). Principal component analysis (PCA) and a dendrogram were performed to determine relationships among populations and to obtain information on the usefulness of those characters for the definition of cultivars. PCA revealed that secondary fruit skin color, flesh color, primary fruit skin color, and secondary skin color pattern were the principal characters to discriminate melon accessions examined in the present study. According to the scatter diagram and dendrogram, landraces of *C. melo* var. *flexuosus*: GB, WB, GS, and WS formed different clusters. However, based on Euclidean genetic coefficient distances, GB and WB had the least degree of relatedness with GS and WS, indicating distantly related landraces (Baladi and Sahouri). On the other hand, the highest degree of relatedness was detected between WS on one hand, and both GS and WB on the other indicating closely related cultivars. Fruit traits variability among the different snake melon landraces was evaluated and discussed in this study. This evaluation of fruit trait variability can assist geneticists and breeders to identify populations with desirable characteristics for inclusion in cultivars breeding programs.

Keywords *Cucumis melo* var. *flexuosus* · Fakous · Palestine · Phenotypic diversity · Snake melon

M. S. Ali-Shtayeh (✉) · R. M. Jamous ·
M. J. Shtaya · O. B. Mallah · I. S. Eid · S. Y. A. Zaitoun
Biodiversity and Environmental Research Center, BERC, Til, Nablus, Palestine
e-mail: msshtayeh@yahoo.com

M. J. Shtaya
Department of Plant Production and Protection, Faculty of Agriculture and Veterinary Medicine, An-Najah N. University, Nablus, Palestine

Introduction

Melon (*Cucumis melo* L., family Cucurbitaceae) is a morphologically diverse crop with very polymorphic fruit types (Fanourakis et al. 2000; Forouzandeh et al. 2010). The classification of the crop was discussed by Hammer and Galdis (2014), they cited 18 groups belonging to 2 subspecies: subsp. *agrestis* (Naud.) Pangalo and subsp. *melo* (Hammer and Gladis 2014), 10 in subspecies *agrestis* (var. *acidulus* Naud., var. *agrestis* Naud., var. *chate* (Hasselq.) Sageret, var. *chito* (Morren) Naud. var. *conomon* (Thunb.) Makino, var. *dudaim* (L.) Naud., var. *momordica* (Roxb.) Duthie et Fuller, var. *texanus* Naud., var. *makuwa* Makino), and 8 in subspecies *melo* L. (var. *flexuosus* (L.) Naud., var. *inodorus* H. Jacq., var. *cantalupensis*

Naud. (var. *cantalupo* Ser.), var. *reticulatus* Ser., var. *adana* Pangalo, var. *ameri* Pangalo, var. *chandalak* Pangalo, and var. *tibish* Mohamed).

The snake melon *C. melo* L. var. *flexuosus* (L.) Naud., is one of the ancient horticultural crops in many parts of the world including Palestine (Grebenshchikov 1986; Walters and Thieret 1993). Landraces of var. *flexuosus* (known locally as "Fakous Baladi", in Arabic) have earned their common name "snake melon" from their slender and almost bent and twisted fruits (Pitrat et al. 2000). They are traditionally cultivated in the Mediterranean area, and are an important horticultural, mainly rain-fed, crop in Palestine, with particular relevance for the economy of the rural communities of Palestine (PCBS 2009).

Landraces and their wild relatives represent genetic resources, essential for crop breeding. They harbor precious genetic variation that constitutes a "safety valve" against evolving diseases, pests and climatic changes, maintaining long-term food security and sustainability of plant production (Simmonds 1993). Landraces of "Fakous Baladi" snake melon are grown in the open field on significant scale in Palestinian villages, where they exhibit considerable genetic variation for traits with economic importance, e.g., yield, fruit characteristics, good climatic adaptation, pest reaction, maturity, and some stress tolerance which allow their survival and adaptation to harsh conditions and low input cultivation (Dhillon et al. 2007; Mohammed 2009; Fergany et al. 2011). In Palestine; four sub-cultivars of *C. melo* var. *flexuosus* are grown "White Baladi" (WB), Arabic: "Baladi Abiadh", "Green Baladi" (GB), Arabic: "Baladi Akhder", and "White Sahouri" (WS), Arabic: "Sahouri Abiadh", and "Green Sahouri" (GS), Arabic: "Sahouri Akhder" (Fig. 1) (PCBS 2010). However, local melon genetic resources are currently being lost due to severe genetic erosion caused by the replacement of local varieties by improved varieties and improper management.

The diversity of *C. melo* has been analyzed using several morphological traits and molecular markers (Nhi et al. 2010; Fergany et al. 2011; Nasrabadi et al. 2012; Trimech et al. 2013). Molecular markers provide complete morphological and pomological data because they are plentiful, free of tissue and environmental factors and allow for cultivar identification in the early stages of development (Kaçar et al. 2012). In 1977 Esquinas-Alcazar conducted preliminary study to determine genetic relationships of melon using isozymes (McCreight et al. 2004), following in 1996, Katzir et al. (1996) developed the first simple sequence repeats (SSR) markers in melons. The molecular characterization of melons was performed using techniques including cleaved amplified polymorphic sequences (Zheng et al. 1999), amplified fragment length polymorphism (AFLP) (Yashiro et al. 2005), random amplified polymorphic DNA (RAPD) (Stepansky et al. 1999; Mliki et al. 2001; Staub et al. 2004; Nakata et al. 2005; Sensoy et al. 2007; Tanaka et al. 2007; Soltani et al. 2010) and SSR (Tzitzikas et al. 2009; Kaçar et al. 2012). Several studies were conducted to compare between different types of molecular markers to determine the genetic diversity of melons. Silberstein et al. (1999) revealed molecular variation by restriction fragment length polymorphism (RFLP) and RAPD, Stepansky et al. (1999) used RAPD and inter-simple sequence repeat for intraspecific classification; while López-Sesé et al. (2002) assessed between and within accession variation in Spanish melon germplasm by RAPD and SSR.

No systematic work has been undertaken until now to collect, describe and evaluate native snake melon germplasm in Palestine and the loss of snake melon landraces is an ever present danger. To increase the usefulness of snake melon germplasm for melon conservationists, breeders and growers, the morphological and molecular characterizations of snake melon are required. Therefore, a survey of the genetic diversity is necessary to encourage rational management and selection programs involving the local snake melon germplasm. The aim of the present study was to determine the agro-morphological variation in four local varieties of snake melon to provide useful information to facilitate the choice of genitors for snake melon breeding program.

Materials and methods

Plant material and descriptors

The study was performed on 50 accessions of *C. melo* (Fakous Baladi) collected from Palestine between April–July, 2014 (Tables 1, 2; Fig. 2). Data were collected on morphological (both qualitative and quantitative) characters of snake melon which included flower, stem, fruit and seed. A descriptor list

Fig. 1 Representative fruits of snake melon accessions **A** "Green Baladi" (GB), **B** "White Baladi" (WB), **C** "White Sahouri" (WS), **D** "Green Sahouri" (GS)

Table 1 Geographic distribution of sampled melon fields and varieties in the West Bank—2014

Variety	Districts								
	Jenin	Tubas	Tulkarem	Qalaqilia	Nablus	Salfit	Ramallah	Hebron	Bethlehem
Green Baladi	0	0	6	6	4	0	0	0	0
White Baladi	8	0	0	0	1	3	0	0	0
White Sahouri	0	1	0	0	1	0	9	7	0
Green Sahouri	0	0	0	0	0	0	0	0	5
Total fields	8	1	6	6	6	3	9	7	5

with a set of predefined morphological characters was adopted from Stepansky et al. (1999), International Plant Genetic Resources Institute (IPGRI) (2003) and Soltani et al. (2010) and was refined and used in characterization. In total, 17 traits including 5 quantitative and 12 qualitative characters were recorded (Table 3).

Morphological characters were recorded using ten plants in each field. Ten immature fruits were harvested from each field, where the following traits were scored: fruit shape, fruit length from stem end to blossom, width at the broadest point, predominant and secondary skin color and pattern which covers the primary and secondary largest surface area of the fruit, skin texture, fruit flesh color (FC) and taste, fruit weight and presence or absence of fruit hair. For flower characterization five plants from each field were evaluated for flower size, sex type, and ovary shape and pubescence length. For stem characterization the hair density and stem thickness at fifth node of the main stem was measured. The genotypes were also harvested upon maturity; seeds were extracted from the ten mature fruits from ten plants and evaluated for hundred seed weight.

Finally, with the aim to compare together qualitative and quantitative data, a numerical transformation was applied to traits such as fruit shape, predominant and secondary skin color and pattern, skin texture, fruit flesh, color and taste (sweet, non-sweet), presence or absence of fruit hair, sex type, ovary shape and hair

Table 2 Details of snake melon accessions used in the present study

SL no.	Fields	Collection site	District	Variety	Cluster
10	BERC-TA12	Anabta	Tulkarm	GB	III
11	BERC-TA13	Anabta	Tulkarm	GB	III
12	BERC-TA14	Anabta	Tulkarm	GB	III
13	BERC-TB15	Beat Lead	Tulkarm	GB	III
14	BERC-TB16	Beat Lead	Tulkarm	GB	III
15	BERC-TK17	Kour	Tulkarm	GB	III
16	BERC-QH18	Hajjah	Qalqilia	GB	III
17	BERC-QH19	Hajjah	Qalqilia	GB	III
18	BERC-QH20	Hajjah	Qalqilia	GB	III
19	BERC-QJ21	Jeat	Qalqilia	GB	III
20	BERC-QJ22	Jeat	Qalqilia	GB	III
21	BERC-QG23	Gensafoot	Qalqilia	GB	III
22	BERC-NT24	Til	Nablus	GB	III
23	BERC-NT25	Til	Nablus	GB	III
24	BERC-NT26	Til	Nablus	GB	III
27	BERC-NF29	Sabastiah	Nablus	GB	III
1	BERC-JB01	Bear al-basha	Jenin	WB	II
2	BERC-JZ03	Zababdeh	Jenin	WB	II
3	BERC-JZ04	Zababdeh	Jenin	WB	II
4	BERC-JM05	Meslyeh	Jenin	WB	II
5	BERC-JM06	Meslyeh	Jenin	WB	II
6	BERC-JA07	Mythaloon	Jenin	WB	II
7	BERC-JA09	Mythaloon	Jenin	WB	II
8	BERC-JA10	Mythaloon	Jenin	WB	II
25	BERC-NF27	Al-Fara'a	Nablus	WB	II
28	BERC-SD30	Dear Baloot	Salfit	WB	II
29	BERC-SD31	Dear Baloot	Salfit	WB	II
30	BERC-SD32	Dear Baloot	Salfit	WB	II
9	BERC-UA11	Aqqaba	Tubas	WS	I
26	BERC-NF28	Al-Fara'a	Nablus	WS	I
31	BERC-RT33	Trmosayah	Ramallah	WS	I
32	BERC-RT34	Trmosayah	Ramallah	WS	I
33	BERC-RS35	Senjel	Ramallah	WS	I
34	BERC-RS36	Senjel	Ramallah	WS	I
35	BERC-RB37	Batonia	Ramallah	WS	I
36	BERC-RB38	Batonia	Ramallah	WS	I
37	BERC-RA39	Dear Ammar	Ramallah	WS	I
38	BERC-RA40	Dear Ammar	Ramallah	WS	I
39	BERC-RA41	Dear Ammar	Ramallah	WS	I
40	BERC-HB47	Beat Kahel	Hebron	WS	I
41	BERC-HO48	Beat Ola	Hebron	WS	I
42	BERC-HH49	Halhol	Hebron	WS	I
43	BERC-HH50	Halhol	Hebron	WS	I
44	BERC-HD51	Dora	Hebron	WS	I
45	BERC-HD52	Dora	Hebron	WS	I
46	BERC-BT53	Taqoa'a	Bethlehem	GS	I

Table 2 Details of snake melon accessions used in the present study

SL no.	Fields	Collection site	District	Variety	Cluster
47	BERC-BT54	Taqoa'a	Bethlehem	GS	I
48	BERC-BB55	Beit Sahour	Bethlehem	GS	I
49	BERC-BB56	Beit Sahour	Bethlehem	GS	I
50	BERC-BB57	Beit Sahour	Bethlehem	GS	I

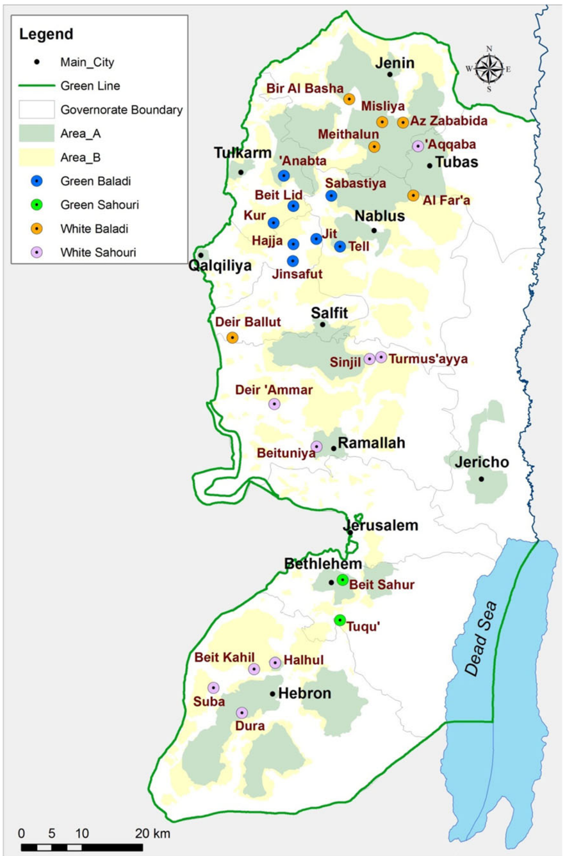

Fig. 2 Sampling sites in the West Bank

density (Table 3). In particular, a numerical value, ranging from 1 to k (k equal to number of classes), was assigned to each phenotypic class established, detecting different degrees of trait expression.

Data analysis of vegetative and horticultural traits

The Shannon–Weaver diversity index (H′) for qualitative and quantitative traits was estimated as follows (Hutchenson 1970):

$$H' = \sum_{i=1}^{n} (p_i \log_e p_i)$$

where, p_i is the proportion of individuals in the ith class of n–class trait and n is the number of phenotypic classes for a given trait. The estimates of diversity index values for each trait (H′) was divided by logen for standardization of values of H′ within 0 to 1 interval. An Euclidean distance Matrix was generated from morphological data and used as input data for cluster analysis based on unweighted pairgroup method of arithmetic average (UPGMA). All the original data were transformed into standardized data to eliminate the difference in the variance of each character. Principal component analysis (PCA) was performed to generate a cluster diagram. Eigenvalue and contribution percentage of each principal component axis were calculated using the correlation matrix among 9 characters for 50 accessions. All computations were performed using the Unscrambler 10 software (CAMO) and SPSS 16.0.

Results

Morphological traits variation

Out of the 17 traits studied in this work, seven were monomorphic and ten polymorphic. The monomorphic phenotypic classes were observed in fruit shape, skin texture, fruit hair, sex type, ovary shape and pubescence length and hair density. All collected fruits were elongated with wrinkled hairy skin. Also, all accessions possess flowers with ovaries covered with short pubescence, and stems with medium hair density. In addition, all accessions possess flowers with ovaries covered with short pubescence, and stems with medium hair density. The frequency distribution of polymorphic phenotypic classes for the five

Table 3 Morphological characters measured in snake melon collections

Character no.	Character code	Character and descriptive value	References
1	PFSC	Predominant fruit skin color: 1 (white), 2 (green)	IPGRI (2003)
2	SFSC	Secondary fruit skin color: 1 (white), 2 (pale green), 3 (green)	IPGRI (2003)
3	SSCP	Secondary skin color pattern: 1 (no secondary skin color), 2 (striped)	IPGRI (2003)
4	FC	Flesh color: 1(white), 2 (pale green)	Stepansky (1999)
5	T	Taste: 1 (insipid (non-sweet)), 2 (sweet (low))	Stepansky (1999)
6	STH	Stem thickness: 1 (<7.5 mm), 2 (7.6–9 mm), 3 (9.1–10.5 mm)	Stepansky (1999)
7	MFS	Male flower size: 1 (<20 mm), 2 (20.1–25 mm), 3 (25.1–30 mm)	Stepansky (1999)
8	FS	Fruit size: 1 (<100 g), 2 (100.1–150 g), 3 (150.1–200 g)	IPGRI (2003)
9	FLWR	Fruit length/width ratio- Fruit length/width ratio [L/W]: 1 (<5), 2 (5.1–7.0), 3 (7.1–9)	IPGRI (2003)
10	FSH	Fruit shape: 1 (oblate), 2 (elongate)	IPGRI (2003)
11	ST	Skin texture: 1 (wrinkled) 2 (ribbed)	Stepansky (1999)
12	FH	Fruit hairs: 1 (presence), 2 (absence)	Soltani 2010
13	STY	Sex type: 1(monoecious, plant bears staminate and pistillate flowers), 2 (andromonoecious, with staminate and perfect flower)	Stepansky (1999)
14	OS	Ovary shape: 1 (flat), 2 (round), 3 (long), 4 (very long)	IPGRI (2003)
15	OPL	Ovary pubescence length: 1 [short (<1 cm)] 2 [intermediate (1–5 cm)], 3 [long (>5 cm)]	IPGRI (2003)
16	HD	Hair density: 1 (sparse), 2 (medium), 3 (dense)	Stepansky (1999)
17	SW	Seeds weight: 1 (2.5–3.25 g), 2 (3.3–4.0 g), 3 (4.1–4.8 g)	Stepansky (1999)

qualitative traits is shown in Fig. 3. These qualitative traits showed marked differences in their distribution and the amount of variation.

Two phenotypic classes were recognized for each of the following traits: predominant fruit skin color (PFSC), secondary skin color pattern (SSCP), FC, fruit taste (FT); the sweet FT, the white PFSC, the white FC, and without SSCP were more predominant among all genotypes (Fig. 3).

Three classes of the secondary fruit skin color (SFSC) were found within the snake melon collection: white, pale green, and green. The white SFSC was rare. The pale green was dominant reaching 44 % of all accessions, followed by the green (32 % and white (24 % SFSC. Overall, the polymorphic qualitative traits showed considerably high diversity indices (H′) ranging from 0.97 for SFSC to 0.99 for SSCP.

Distribution of quantitative traits

For each quantitative trait evaluated, the descriptive statistics including mean, maximum and minimum and coefficient of variation (CV) values are summarized in Table 4. Among all quantitative traits recorded, stem thickness, male flower size (MFS), fruit size, fruit length/width ratio, and hundred mature seed weight (SW) showed relatively low CV values ranging from 13.6 to 32.9. About 52 % of the accessions had medium stem thickness and fruit length/width ratio. Accessions differed in fruit size from large size (20 %, to medium (48 %, 24), to small size (32 %), with the fruit length/width ratio ranging from 3 to 9 among all genotypes. Also, accessions differed in seed weight from large (23 %) to medium (44 %) to small weight (33 %). All quantitative traits showed high diversity index ranging from 0.78 for MFS and 0.97 for SW.

Principal component analysis (PCA)

The current study assessed the diversity of 50 snake melon populations collected in the West Bank, Palestine, using 10 selected qualitative and quantities characters (Table 3). A large genetic variability was observed in the *Cucumis* genotypes with respect to fruit skin and FC (Fig. 4). PCA was used to evaluate and describe the variation in snake melon accessions. The percentages of variation explained by the first

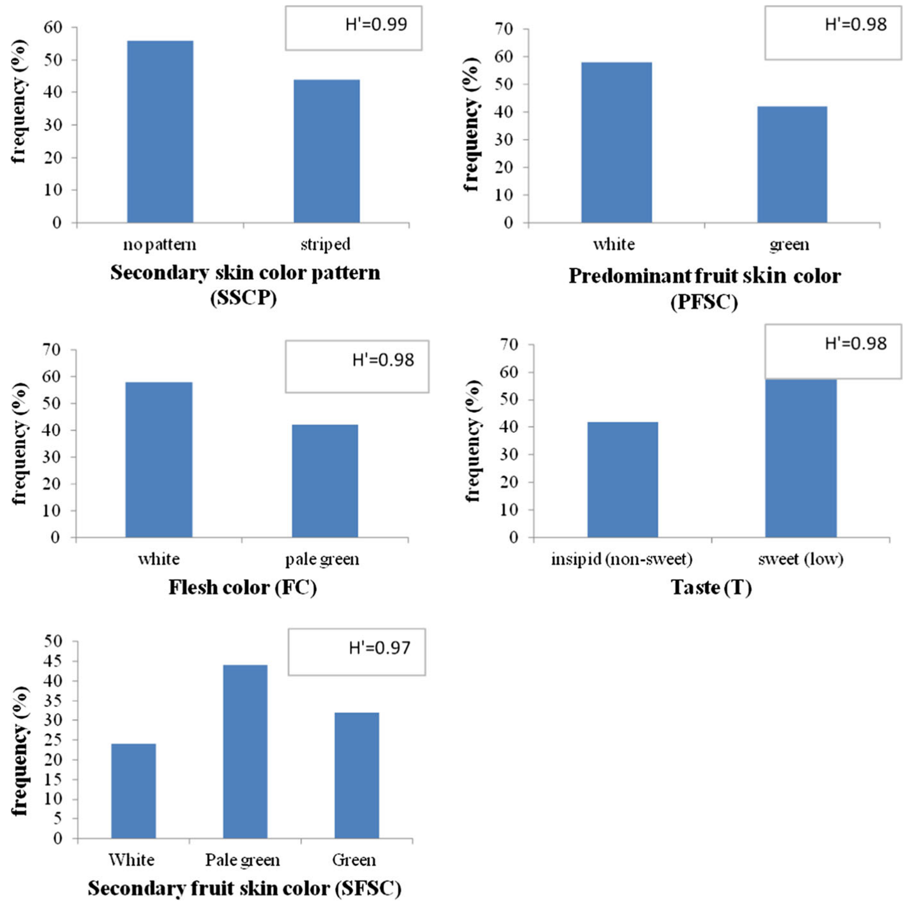

Fig. 3 Diversity indices and frequencies for polymorphic qualitative fruit-related traits recorded from the 50 *Cucumis melo* var. *flexuses* accessions from Palestine. H′, diversity index

three components were 33.41, 22.02, and 11.54 %, respectively. The principal characters with higher Eigenvectors that delineated the accessions into separate groups in the first two components included SFSC, FC, PFSC, SW, T, and FLWR (Table 5).

Figure 4 shows the scattering of 50 snake melon accessions and component scores of the first and the second principle components. The formed clusters are mainly related to variation in PFSC, SFSC, FC, SW (with H′ 0.98, 0.97, 0.98 and 0.97, respectively) in principal component 1, and SSCP, T, and FLWR (with H′ 0.99, 0.98, and 0.91, respectively) in principal component 2 (Table 5). From Fig. 4, it was clear that three clusters were formed from snake melon accessions. By these components, accessions from WS and GS varieties which have striped pale green secondary skin pattern; grouped in cluster I. Also, accessions from WB local landrace with white PFSC, SFSC, FC and have no SSCP clustered in cluster II. Cluster III comprised accessions from GB variety with green PFSC, and SFSC, pale green FC and have no SSCP.

A detailed description of the snake melon fruits used in the present study is provided in Table 6. The range of variability of phenotypic characters in terms of maximum, minimum and mean values are presented in Table 7. The results depicted some variation in phenotypic traits among the four snake melon cultivars (GB, WB, GS, and WS). Fruit size (g) and fruit length/width ratio were larger in WB (131.5, 7.3) and GB (115.56, 6.0) compared to WS (108.9, 4.8) and GS (104, 4.2) varieties.

Clustering analysis

Based on the Euclidean genetic distances to estimate the level of relatedness between

Table 4 Measured characteristics, range of variability, means and coefficient of variability and frequency distribution of the 50 snake melon accessions from Palestine

Variables	Min. values	Mean	Max. values	CV %	Frequency of traits distribution			H′
					Small	Medium	Large	
Stem thickness (mm)	5	8.32	11	14.04	0.34	0.52	0.14	0.89
Male flower size (mm)	15	23.06	31	13.61	0.12	0.66	0.22	0.78
Fruit size (g)	53	115.96	201	32.99	0.32	0.48	0.2	0.93
Fruit length/width ratio	3	5.74	9	23.03	0.3	0.52	0.18	0.91
Seed weight (g)	2.6	3.6	4.80	15.6	0.33	0.44	0.23	0.97

H′ High diversity index

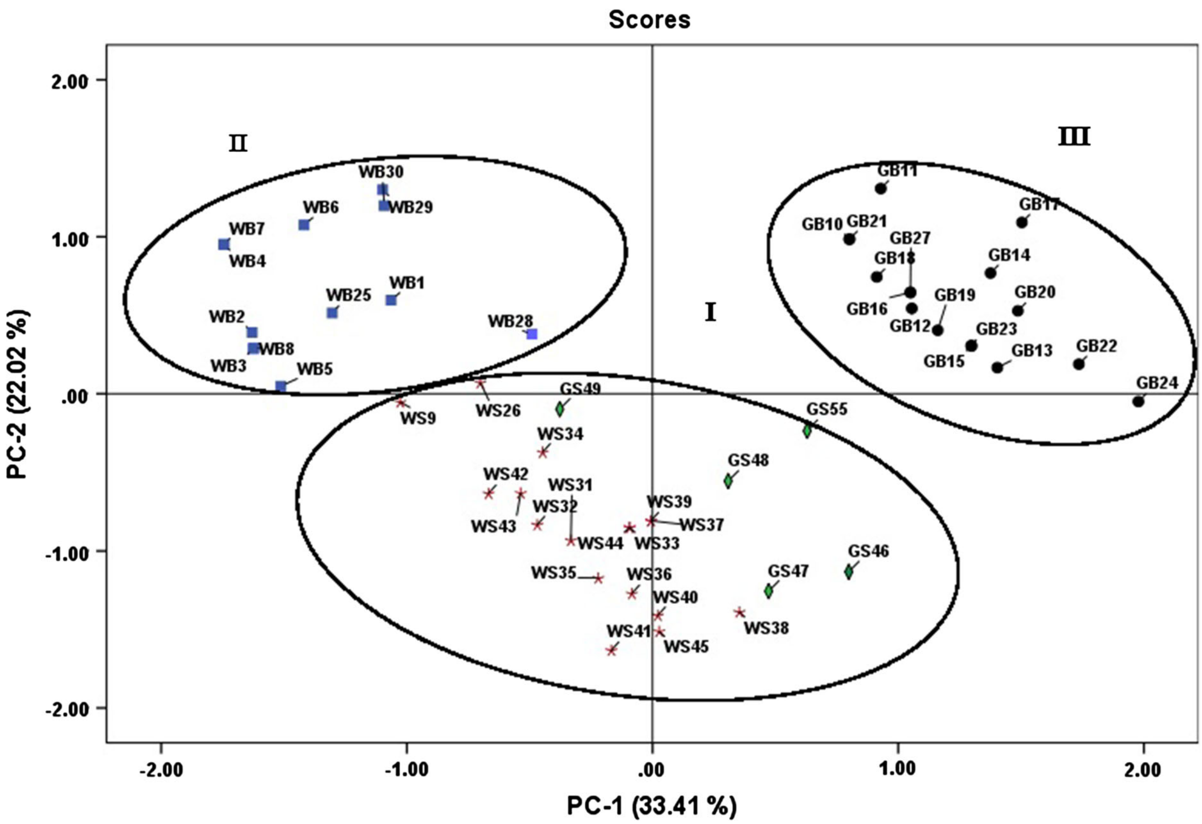

Fig. 4 Cluster diagram constructed on the basis of the two principle components axes, which contain 55 % of total variation

accessions, pair-wise Euclidean distances ranged from 0 to 4.2 among all accessions (Table 8). WB3 and WB8; WB4 and WB7; GB10 and GB21; GB15 and GB23; GB16 and GB27; and WS33 and WS44 accessions were the most genetically related genotypes (distance = 0). On the other hand GB24 and WS31; GB17 and WS40; WS41 and GB18-20; GS46 and WB4,5, WB7,8, and WB30; GS47, and WB30, and WB6; GS48, and WB2, and WB29; GS49, and WB1, and WB28; and GS50, and WB29,and WB35 were the least genetically related genotypes (distance = 4.2).

Table 5 Contribution percentage and major characters associated with the three first principal components of 50 melon accessions and their Eigenvectors

X loadings	PC-1	PC-2	PC-3
Explained proportion of variation (%)	33.41	22.02	11.54
Cumulative proportion of variation (%)	33.34	55.36	66.90
Traits[a]	Eigenvectors		
SFSC	0.910*	−0.066	0.153
FC	0.905*	0.252	0.210
PFSC	0.881*	0.275	0.242
SSCP	−0.232	−0.833*	0.281
FLWR	−0.111	0.794*	−0.464
T	−0.179	0.552*	0.334
STH	−0.371	0.005	0.583*
FS	−0.184	0.381	0.486
MFS	−0.382	0.479	0.171
SW	0.644*	−0.252	−0.152

* Significant factor loading (values above 0.5)

[a] As in Table 3

The generated UPGMA dendrogram has discriminated the collected accessions into three main clusters (cluster I, II, and III) (Fig. 5). The first main cluster (I) contained accessions that mainly collected from the southern Palestine (Fig. 2). It was divided into two sub-clusters (Ia and Ib). Ia comprised accessions from WS with distance coefficient ranging between 0 and 3.7. Subcluster Ib contained accessions from GS with distance coefficient ranging between 1.4 and 2.4. The second and third main clusters (II, and III) comprised accessions that were mainly collected from northern Palestine with distance coefficient ranging between 0 and 3.2. All accessions from WB, and GB were discriminated in separate clusters, II, and III, respectively.

Discussion

Palestinian snake melon landraces are cultivars of domesticated agricultural plant species *C. melo* var. *flexuosus* which have developed over a long period of time and as a result have adapted to the local natural environment in which they live. It has been a widespread practice of Palestinian snake melon growers to save seeds from their crops annually for the following year's cultivation. The seeds would come from selected plants that were best suited to the local conditions and over generations of selective breeding, a few cultivars have been developed with different traits across the country (Ali-Shtayeh and Jamous 2005, 2006).

In this study, seventeen quantitative and qualitative well defined traits were selected in order to characterize snake melon cultivars grown Palestine (Stepansky et al. 1999; IPGRI 2003; Soltani et al. 2010). All snake melon cultivars fruits share the elongated shape, hairy skin and wrinkled skin texture. They also possess flowers with ovaries covered with short pubescence, and stem with medium hair density. Morphological differences and similarities in fruit, flower, seed, and stem among the four cultivars were detected. The GB and GS accessions share the green PFSC and pale green FC, whereas accessions of WB and WS share the white PFSC and FC. Also accessions belonging to the GB and WB genotypes share the absence of SSCP compared with WS and GS accessions which have striped SSCP. Overall, all selected quantitative traits, and polymorphic qualitative traits revealed intermediate to high diversity index (H′) ranging from between 0.78 for MFS and 0.97 for SW. These relatively high diversity indices are mainly contributed to either the presence of more than two phenotypic classes or the even distribution of the classes of the individual traits. The variation in Palestinian snake melon populations reflects the heterogeneous and heterozygous nature of snake melon landraces compared to commercial varieties. Obvious differences were observed in fruit shape and dimensions and fruits color and shape. Similarly, genetic variability among *flexuosus* accessions from Greece (Staub et al. 2004), and Jordan (Abdel-Ghani and Mahadeen 2014) was previously reported.

Table 6 Morphological characters of snake melon accessions evaluated

SL no.	Variety	Cluster	Predominant fruit skin color	Secondary fruit skin color	Secondary skin color pattern	Flesh color	Taste	Stem thickness (mm)	Male flower size (mm)	Fruit size (g)	Fruit length/ width ratio	Seed weight (g)
9	WS	I	White	Pale green	Striped	White	Insipid (non-sweet)	9	22	169	5	3
26	WS	I	White	Pale green	Striped	White	Insipid (non-sweet)	8	24	183	6	3.5
31	WS	I	White	Pale green	Striped	White	Insipid (non-sweet)	8	22	124	5	3.3
32	WS	I	White	Pale green	Striped	White	Sweet (low)	8	21	156	5	3.8
33	WS	I	White	Pale green	Striped	White	Sweet (low)	8	25	85	6	3.6
34	WS	I	White	Pale green	Striped	White	Insipid (non-sweet)	9	27	76	6	3.2
35	WS	I	White	Pale green	Striped	White	Sweet (low)	8	20	131	4	4.3
36	WS	I	White	Pale green	Striped	White	Insipid (non-sweet)	9	23	67	4	4.1
37	WS	I	White	Pale green	Striped	White	Insipid (non-sweet)	5	21	104	4	3.9
38	WS	I	White	Pale green	Striped	White	Sweet (low)	6	23	53	4	3.4
39	WS	I	White	Pale green	Striped	White	Insipid (non-sweet)	7	24	107	5	3.8
40	WS	I	White	Pale green	Striped	White	Sweet (low)	8	19	125	4	2.8
41	WS	I	White	Pale green	Striped	White	Insipid (non-sweet)	9	15	93	4	3.9
42	WS	I	White	Pale green	Striped	White	Sweet (low)	9	23	106	5	3.6
43	WS	I	White	Pale green	Striped	White	Insipid (non-sweet)	11	16	121	6	3.2
44	WS	I	White	Pale green	Striped	White	Sweet (low)	8	23	73	5	2.8
45	WS	I	White	Pale green	Striped	White	Sweet (low)	9	21	78	4	4.6
46	GS	I	Green	Pale green	Striped	Pale green	Sweet (low)	8	22	61	3	3.6
47	GS	I	Green	Pale green	Striped	Pale green	Sweet (low)	10	23	65	4	3.8
48	GS	I	Green	Pale green	Striped	Pale green	Sweet (low)	9	26	124	5	3.6
49	GS	I	Green	Pale green	Striped	Pale green	Insipid (non-sweet)	9	27	166	5	3.6
50	GS	I	Green	Pale green	Striped	Pale green	Sweet (low)	9	25	104	4	3.5
1	WB	II	White	White	No pattern	White	Sweet (low)	8	21	120	7	4.4
2	WB	II	White	White	No pattern	White	Insipid (non-sweet)	9	25	161	6	3
3	WB	II	White	White	No pattern	White	Insipid (non-sweet)	10	26	110	6	2.9
4	WB	II	White	White	No pattern	White	Insipid (non-sweet)	10	25	112	7	3.4
5	WB	II	White	White	No pattern	White	Sweet (low)	10	26	108	7	3.2
6	WB	II	White	White	No pattern	White	Insipid (non-sweet)	9	28	140	9	3.3
7	WB	II	White	White	No pattern	White	Insipid (non-sweet)	9	30	124	8	2.7
8	WB	II	White	White	No pattern	White	Insipid (non-sweet)	10	31	102	7	2.8
25	WB	II	White	White	No pattern	White	Insipid (non-sweet)	9	23	197	7	2.6

Table 6 continued

SL no.	Variety	Cluster	Predominant fruit skin color	Secondary fruit skin color	Secondary skin color pattern	Flesh color	Taste	Stem thickness (mm)	Male flower size (mm)	Fruit size (g)	Fruit length/ width ratio	Seed weight (g)
28	WB	II	White	White	No pattern	White	Sweet (low)	6	24	96	8	2.9
29	WB	II	White	White	No pattern	White	Insipid (non-sweet)	7	23	183	8	2.9
30	WB	II	White	White	No pattern	White	Insipid (non-sweet)	7	26	125	8	3.2
10	GB	III	Green	Green	No pattern	Pale green	Insipid (non-sweet)	8	21	184	6	4.1
11	GB	III	Green	Green	No pattern	Pale green	Insipid (non-sweet)	8	23	100	7	3.9
12	GB	III	Green	Green	No pattern	Pale green	Insipid (non-sweet)	9	28	78	6	2.9
13	GB	III	Green	Green	No pattern	Pale green	Sweet (low)	9	19	111	6	4.1
14	GB	III	Green	Green	No pattern	Pale green	Insipid (non-sweet)	7	21	113	6	4.2
15	GB	III	Green	Green	No pattern	Pale green	Insipid (non-sweet)	9	21	62	5	4.8
16	GB	III	Green	Green	No pattern	Pale green	Insipid (non-sweet)	9	25	136	6	3.8
17	GB	III	Green	Green	No pattern	Pale green	Insipid (non-sweet)	7	23	68	7	4.3
18	GB	III	Green	Green	No pattern	Pale green	Sweet (low)	8	22	176	6	3.5
19	GB	III	Green	Green	No pattern	Pale green	Sweet (low)	8	24	129	6	4.1
20	GB	III	Green	Green	No pattern	Pale green	Sweet (low)	7	21	113	6	4.6
21	GB	III	Green	Green	No pattern	Pale green	Insipid (non-sweet)	8	23	201	5	3.9
22	GB	III	Green	Green	No pattern	Pale green	Sweet (low)	7	20	66	7	3.8
23	GB	III	Green	Green	No pattern	Pale green	Insipid (non-sweet)	9	23	99	6	4
24	GB	III	Green	Green	No pattern	Pale green	Sweet (low)	7	18	90	5	3.6
27	GB	III	Green	Green	No pattern	Pale green	Insipid (non-sweet)	8	21	123	6	3

Table 7 Variability in some quantitative traits of Palestinian snake melon local landraces

Trait[a]	Green Baladi			White Baladi			White Sahouri			Green Sahouri		
	Min. values	Max. values	Mean ± SD	Min. values	Max. values	Mean ± SD	Min. values	Max. values	Mean ± SD	Min. values	Max. values	Mean ± SD
STH	7	9	8.0 ± 0.8	7	10	8.7 ± 1.4	5	11	8.2 ± 1.3	8	10	9 ± 0.7
MFS	18	28	22.06 ± 2.4	21	31	25.7 ± 2.9	15	27	21.7 ± 3.2	22	27	24.6 ± 2
FS	62	201	115.56 ± 42.0	96	197	131.5 ± 32.5	53	183	108.9 ± 36	61	166	104.0 ± 43.6
FLWR	5	7	6 ± 0.6	6	9	7.3 ± 0.9	4	6	4.8 ± 0.8	3	5	4.2 ± 0.8
SW	2.6	4.8	3.83 ± 0.6	2.7	4.4	3.15 ± 0.5	2.8	4.6	3.5 ± 0.5	3.5	3.8	3.62 ± 0.1

[a] As in Table 3

Morphological and pomological traits considered in this study showed a large variability for the Palestinian snake melon cultivars. Results of the PCA based on 5 qualitative and 4 quantitative traits showed that 67 % of the total variability is accounted by the first three PCs. The fruit traits including FLWR, PFSC, SFSC, SSCP, T, 100-seed weight, and FC were of high discriminating level and were consistent in their contribution in the first two components and therefore could be used for snake melon characterization. The SFSC and FC were the most discriminative traits among the morphological traits used (Eigenvectors = 0.9 in the PC 1). On the other hand, STH and FS traits were consistently present in the third and fourth components and therefore contributed less to the total genetic variation present among snake melon genotype. Studies based on morphological and pomological traits conducted for snake melon in Jordan, Tunisia, and Turkey found, respectively, 39.9 % (Abdel-Ghani and Mahadeen 2014), 89.8 % (Trimech et al. 2013), and 44 % (Sensoy et al. 2007) of the total variability. Characters related to fruits were powerful for studying the genetic diversity of local landraces of snake melon in Palestine. Results showed that, among these characters, some were good criteria for discriminating between cultivars (PFSC, SFSC, FC SSCP, T, and FLWR). Similar results were reported by Abdel-Ghani and Mahadeen 2014 in snake melon collection in Jordan and by Henane et al. (2013) in snake melon collection in Tunisia.

In the dendrogram generated by morphological characters, similar accessions in terms of fruit color characteristics have positioned in similar clusters. All accessions from GB genotype were separated from the other genotypes mainly based on SFSC. Besides green PFSC, pale green FC, and absence of SSCP contributed to discriminate GB from other landraces. The white SFSC trait clustered WB genotype accessions together. Similarly, WS and GS landraces clustered together based mainly on pale green SFSC and striped SSCP. GS genotype was discriminated from WS forming two subclusters (Ia and Ib) based mainly on its green PFSC and pale green FC.

The cluster analysis showed high degree of diversity in the germplasm of Palestinian snake melon. Among the cultivars with the same names, there is a similarity between WS and GS (av distance coefficient = 3.1) and between WB and GB. However, the levels of similarity observed were not high enough to

Table 8 Snake melon accession with minimum and maximum relatedness based on their Euclidean distances

Distance coefficient	Pairwise accessions	Site of collection	District	Cluster
0	WS33	Senjel	Ramallah	I
	WS44	Dura	Hebron	
0	WS37	Deir Ammar	Ramallah	I
	WS39			
0	GB16	Hajja	Qalqilia	III
	GB27	Sebastia	Nablus	
0	GB15	Kour	Tulkarm	III
	GB23	Til	Nablus	
0	GB10	Anabta	Tulkarm	III
	GB21	Jeensafout	Qalqilia	
0	WB3	Zababdeh	Jenin	II
	WB8	Maithaloun		
0	WB4	meslyeh	Jenin	II
	WB7	Maithaloun		
4.2	WS40	Beit Kahel	Hebron	I
	GB17	Hajja	Qalqilia	III
4.2	WS41	Beit Ola	Hebron	I
	GB18	Hajja	Qalqilia	III
	GB19	Jeet	Qalqilia	III
	GB20	Jeet	Qalqilia	III
	GS46	Taqoa'a	Bethlehem	I
4.2	WB4	Meslyeh	Jenin	II
	WB5	Meslyeh	Jenin	II
	WB7	Maithaloun	Jenin	II
	WB8	Maithaloun	Jenin	II
	WB30	Deir BalLout	Salfit	II
4.2	GS47	Taqoa'a	Bethlehem	I
	WB30	Deir BalLou	Salfit	II
	WB6	Maithaloun	Jenin	II
4.2	GS48	Beit Sahour	Bethlehem	I
	WB2	Zababdeh	Jenin	II
	WB29	Deir BalLou	Salfit	II
4.2	GS49	Beit Sahour	Bethlehem	I
	WB1	Bear al-basha	Jenin	II
	WB28	Deir BalLou	Salfit	II
4.2	GS50	Beit Sahour	Bethlehem	I
	WB29	Deir BalLou	Salfit	II
	WB35	Petonia	Ramallah	II

believe that they are synonymous. WB vs GS and WB vs GS are the most genetically distant cultivars. On the other hand, WS vs WB, and GS vs GB and WS have shown to be the most genetically related cultivars. Both cultivars WS and WB have almost the same characteristics of the PFSC, and differed mainly by the fruit secondary skin color and SSCP, Both cultivars GS and GB have a similarity in terms of the PFSC and

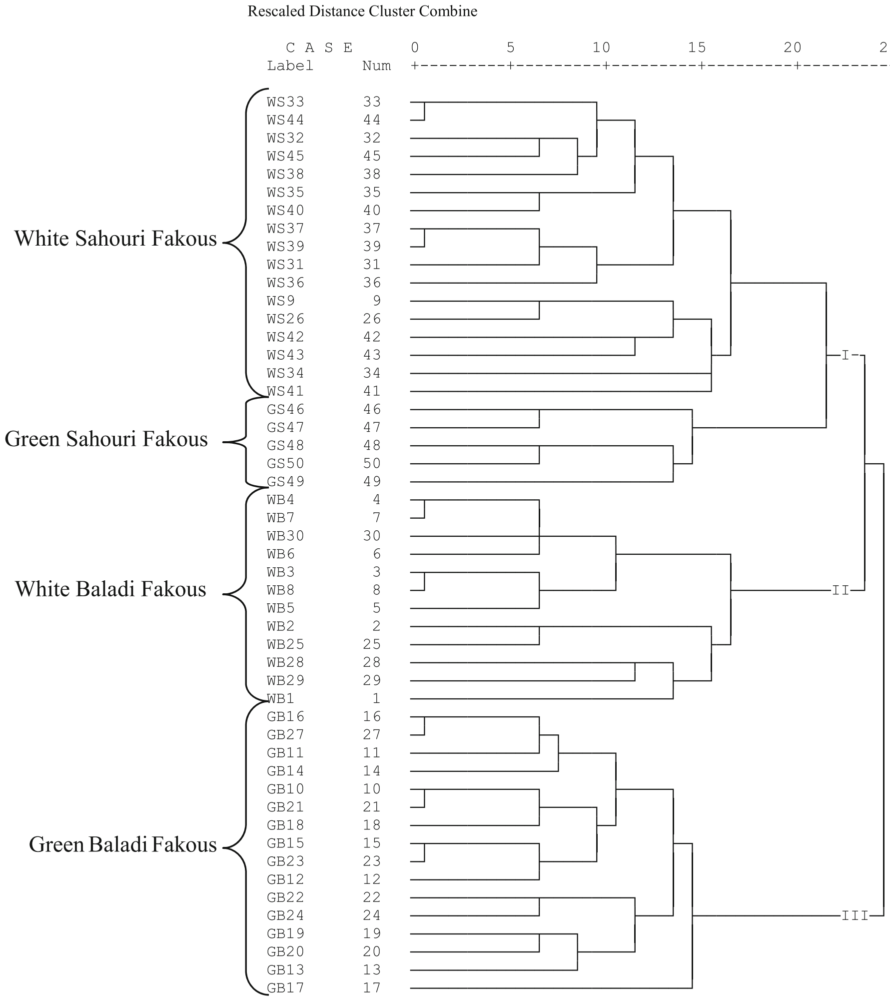

Fig. 5 UPGMA dendrogram (based on squared Euclidian distance) of 50 snake melon accessions performed using morphological and pomological characters

FC, and differed mainly by the PFSC and FC. This suggests that WS may have evolved from WB, and GS from GB.

Thus, it has become obvious that the method of seed-saving practiced by local farmers has maintained genetically diverse crops cultivars namely GB, WB, GS, and WS that are particularly suited to growing in their local environment under rain-fed agriculture. These plants have now become a valuable genetic resource for future generations. This practice of seed collecting has been largely maintained in Palestine, since highly modified crop varieties have been unhelpful, and were generally not well adapted to the local environment and rain-fed agriculture.

Most traits screened in this study are with economic interest especially those related to the fruit quality that serve as target traits for plant breeders and snake melon growers and consumers in addition to their importance in snake melon characterization (Decker-Walters et al. 2002; Kristkova et al. 2003; Jose et al. 2005).

Some desirable phenotypic classes recognized in the immature fruit included straight shape, sweet taste, skin colors, and crispy or soft texture are critical for fresh snake melon consumption and consumers' preferences (Stepansky et al. 1999). Marketable fruit shape, dimensions, and weight are the most important characters that attract growers and meet their interests and also of great importance in packing and transportation. Based on the results, it would be possible to select favorable fruit shape index and weight that meets consumers' needs (Stepansky et al. 1999). The immature fruit shape index (FLWR) and fruit weight (FS) varied among the studied snake melon accessions. Fruits of accessions from GS and WS landraces have relatively short, straight, stout, crispy textured fruits with light yellow color or light green skin. Such traits are favorable to consumers and traders because of their importance in packing, transportation, food processing (e.g., pickling, stuffing… etc.), and longer shelf-life. Therefore, priority was given for collection, evaluation and conservation of these landraces, a situation which may threaten the biodiversity among the local cultivated landraces of snake melon. Presence of pubescence might be associated with plant resistance to insects in plant species; more pubescence is less preferred for egg laying (Gillman et al. 1999).

The characters adopted in this study could be used to establish a catalog of local snake melon cultivars. The concordance between the results of PCA and cluster analysis showed that morphological and pomological analysis can provide reliable information on the variability in snake melon. The overall analysis of all traits brings out a wide diversity in plant material that may have important implications for genetic resources management. This diversity could be due to the antiquity of the culture in this region and particular cultural practices (e.g., rain-fed agriculture, self-saving of seeds) (Ali-Shtayeh and Jamous 2006). More interest has been focused on the diversity since it was known that the domestication of snake melon occurred independently in different areas especially around the edge of the Mediterranean. Thus, it is very interesting to conduct the proper management of these genetic resources. This can be addressed by different tools such as the establishment of ex situ collections. The on-farm conservation can ensure the sustainability of these resources. It is also possible to explore the techniques of tissue culture as an alternative as future protocols for in vitro micropropagation and even cell-cultured snake melon can be developed. Further studies are needed involving chemical, biochemical, and molecular markers (Raman et al. 2011; Kaçar et al. 2012). They would clarify the genetic variation at the molecular level in these cultivars.

Acknowledgments This research was funded by MIDDLE EAST REGIONAL COOPERATION Program (MERC)-USAID, Grant No. M32-016. Authors are grateful to Mr. Issa Zboun, Applied Research Institute, Beithlehem, Palestine, for help with map preparation.

References

Abdel-Ghani AH, Mahadeen A (2014) Genetic Variation in Snake Melon (*Cucumis melo* var. *flexuosus*) populations from Jordan using morphological traits and RAPDs. Jordan J Agric Sci 10(1):96–119

Ali-Shtayeh MS, Jamous RM (2005) Establishing a community seed bank for semi-arid agriculture in Palestine: structure, management, and function. Biodivers Environ Sci Stud Ser 3: 1–42 ISSN: 1818-3751

Ali-Shtayeh MS, Jamous RM (2006) Field guide on the production and storage techniques of seeds of indigenous (baladi) varieties of vegetables. Til, Nablus: Biodiversity and Environmental Research Center (BERC)

Decker-Walters DS, Chung SM, Staub JE, Quemada HD, López-Sesé AI (2002) The origin and genetic affinities of wild of wild populations of melon (*Cucumis melo*, Cucurbitaceae) in North America. Plant Syst Evol 223:183–197

Dhillon NPS, Ranjana R, Singh K, Eduardo I, Monforte AJ, Pitrat M, Dhillon NK, Singh PP (2007) Diversity among landraces of Indian snapmelon (*Cucumis melo* var. *momordica*). Genet Resour Crop Evol 54:1267–1283

Fanourakis N, Nanou E, Tsekoura Z (2000) Morphological characteristics and powdery mildew resistance of *Cucumis melo* landraces in Greece. Acta Hortic 510:241–245

Fergany M, Kaur B, Monforte AJ, Pitrat M, Rys C, Lecoq H, Dhillon NPS, Dhaliwal SS (2011) Variation in melon (*Cucumis melo*) landraces adapted to the humid tropics of southern India. Genet Resour Crop Evol 58:225–243

Forouzandeh S, Akashi Y, Kashi A, Zamani Z, Mostofi Y, Kato K (2010) Characterization of Iranian melon landraces of *Cucumis melo* L. Groups flexuosus and Dudaim by analysis of morphological characters and random amplified polymorphic DNA. Breed Sci 60:34–45

Gillman JH, Dirr MA, Braman SK (1999) Gradients in susceptibility and resistance mechanisms of *Buddleia* L. Taxa to the two-spotted spider mite (*Tetranychus urticae* Koch). J Am Soc Hortic Sci 124:114–121

Grebenshchikov I (1986) Cucurbitaceae. In: Schultze-Motel J (ed) Rudolf Mansfelds Verzeichnis landwirtschaftlicher und gärtnerischer Kulturpflanzen. Akademie-Verlag, Berlin, pp 914–951

Hammer K, Gladis T (2014) Notes on infraspecific nomenclature and classifications of cultivated plants in Compositae, Cruciferae, Cucurbitaceae, Gramineae (with a remark on *Triticum dicoccon* Schrank) and Leguminosae. Genet Resour Crop Evol 61:1455–1467

Henane I, Mezghani N, Tlili I, Rhim Th, Ghezal I, Arfaou K, Jebari H (2013). Agro-morphological characterization and assessment of variability in local germoplasm of Cucumis melo L. in Tunisia. JBES 3(12):198–207

Hutchenson K (1970) A test for comparing diversities based on the Shannon formula. J Theor Biol 29:151–154

International Plant Genetic Resources Institute (IPGRI) (2003) Descriptors for Melon (*Cucumis melo* L.). Rome. ISBN 92-9043-597-7

Jose MA, Iban E, Silvia A, Pere A (2005) Inheritance mode of fruit traits in melon: heterosis for fruit shape and its correlation with genetic distance. Euphytica 144:31–38

Kaçar YA, Simsek O, Solmaz I, Sari N, Mendi YY (2012) Genetic diversity among melon accessions (*Cucumis melo*) from Turkey based on SSR markers. Genet Mol Res 11(4):4622–4631

Katzir N, Danin-Poleg Y, Tzuri G, Karchi Z et al. (1996) Length polymorphism and homologies of microsatellites in several *Cucurbitaceae* species. Theor Appl Genet 93:1282–1290

Kristkova E, Lebeda A, Vinter V, Blahousek O (2003) Genetic resources of the genus Cucumisand their morphological description (English-Czech version). Hortic Sci 30:14–42

López-Sesé AI, Staub JE, Katzir N, Gómez-Guillamón ML (2002) Estimation of between and within accessions variation in selected Spanish melon germplasm using RAPD and SSR markers to assess strategies for large collection evaluation. Euphytica 127:41–51

McCreight JD, Staub JE, López-Sesé AI, Chung S (2004) Isozyme variation in Indian and Chinese melon (*Cucumis melo* L.) germplasm collection. J Am Soc Hortic Sci 129:811–818

Mliki A, Staub JE, Sun Z, Ghorbel A (2001). Genetic diversity in melon (Cucumis melo L.): An evaluation of African germplasm. Genet Res Crop Evol 48:587–597

Mohammed AM (2009) Genetic studies on resistance to powdery mildew disease in snake melon (*Cucumis melo* L. var. *flexuosus*). M.Sc. thesis, Sudan Academy of Science, Khartoum, Sudan

Nakata E, Staub JE, López-Sesé AI, Katzir N (2005). Genetic diversity of Japanese melon cultivars (Cucumis melo L.) as assessed by random amplified polymorphic DNA and simple sequence repeat markers. Genet Resour Crop Evol 52:405–419

Nasrabadi HN, Nemati H, Sobhani A, Sharifi M (2012) Study on morphologic variation of different Iranian melon cultivars (*Cucumis melo* L.). Afr J Agric Res 7(18):2764–2769

Nhi PTP, Akashi Y, Hang TTM, Tanaka K, Aierken Y, Yamamoto T, Nishida H, Long C, Kato K (2010) Genetic diversity in Vietnamese melon landraces revealed by the analyses of morphological traits and nuclear and cytoplasmic molecular markers. Breed Sci 60:255–266

Palestinian Central Bureau of Statistics (PCBS) (2009) Agricultural statistics, 2008/2009. Ramallah—Palestine: PCBS

Palestinian Central Bureau of Statistics (PCBS) (2010) Agricultural statistics, 2008/2009. Ramallah—Palestine: PCBS

Pitrat M, Hanelt P, Hammer K (2000) Some comments on infraspecific classification of cultivars of melon. Acta Hortic 510:29–36

Raman H, Raman R, Nelson MN, Aslam MN, Rajasekaran R, Wratten N, Cowling W A, Kilian A, Sharpe A G, Schondelmaier J (2011) Diversity array technology markers: genetic diversity analyses and linkage map construction in rapeseed (*Brassica napus* L.). DNA Res 1–15

Sensoy S, Bϋyϋkalaca S, Abak K (2007) Evaluation of genetic diversity in Turkish melon (*Cucumis melo* L.) based on phenotypic characters and RAPD markers. Genet Resour Crop Evol 54:1351–1365

Silberstein L, Kovalski I, Huang R, Anagnostou K et al. (1999) Molecular variation in melon (*Cucumis melo* L.) as revealed by RFLP and RAPD markers. Sci Hortic 79:101–111

Simmonds NW (1993) Introgression and incorporation strategies for the use of crop genetic resources. Biol Rev 68(539):562

Soltani F, Akashi Y, Kashi A, Zamani Z, Mostofi Y, Kato K (2010) Characterization of Iranian melon landraces of *Cucumis melo* L. Groups *Flexuosus* and *Dudaim* by analysis of morphological characters and random amplified polymorphic DNA. Breed Sci 60:34–45

Staub JE, López-Sesé AI, Fanourakis N (2004) Diversity among melon landraces (*Cucumis melo* L.) from Greece and their genetic relationship with other melon germplasm of diverse origin. Euphytica 136:151–166

Stepansky A, Kovalski I, Perl-Treves R (1999) Intraspecific classification of melons (*Cucumis melo* L.) in view of their phenotypic and molecular variation. Plant Syst Evol 217:313–333

Tanaka K, Nishitani A, Akashi Y, Nishida H et al. (2007). Molecular characterization of South and East Asian melon, *Cucumis melo* L., and the origin of group conomon var. *makuwa* and var. conomon revealed by RAPD analysis. Euphytica 153:233–247

Trimech R, Zaouali Y, Boulila A, Chabchoub L, Ghezal I, Boussaid M (2013) Genetic variation in Tunisian melon (*Cucumis melo*.L) germplasm as assessed by morphological traits. Genet Resour Crop Evol 60:1621–1628

Tzitzikas NE, Monforte AJ, Fatihi A, Kypriotakis Z et al. (2009). Genetic diversity and population structure of traditional Greek and Cypriot melon cultigens (Cucumis melo L) based on simple sequence repeat variability. HortScience 44:1820–1824

Walters TW, Thieret JW (1993) The snake melon (*Cucumis melo*; Cucurbitaceae). Econ Bot 47:99–100

Yashiro K, Iwata H, Akashi Y, Tomita K, Kuzuya M, Tsumura Y, Kato K (2005) Genetic relationship among East and South Asian melon (*Cucumis melo* L.) revealed by AFLP analysis. Breed Sci 55:197–206

Zheng XY, Wolff DW, Baudracco-Arnas S, Pitrat M (1999) Development and utility of cleaved amplified polymorphic sequences (CAPS) and restriction fragment length polymorphisms (RFLPs) linked to the Fom-2 Fusarium wilt resistance gene in melon (*Cucumis melo* L.). Theor Appl Genet 99:453–463