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Genetic Relationships Among Various Sihke Melon Landraces

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Abstract: Landraces and older varieties face with extinction in modern agriculture. Therefore, the preservation of diversity becomes vital for future breeding efforts because landraces and older varieties might contain genes that current varieties do not. The present study aimed to determine genetic relationships among various Sihke melon landraces for phenotypic traits. The main materials of the study were 15 Sihke melon genotypes collected from various parts at Van province of Turkey. Moreover, 2 foreign standard melon genotypes (Sembol F_1 and Sempati F_1) and 13 local melon genotypes that previously have not been characterized were included into the phenotypic characterization. Total 63 measurements or observations were used to define the genetic similarity among the studied melon genotypes by dendrograms or two- and three-dimensional scaling obtained from Euclidian distance matrix. With this study, the phenotypic traits of Sihke melon landrace of Van and some other local and foreign melon genotypes were determined. Moreover, the genetic relatedness among Sihke melon populations and other local and foreign genotypes were examined. Based on the molecular Euclidean distance matrix, Sihke melon landraces were different from the others and tended to be grouped together. Among the studied genotypes, the most distinct genotype was Genotype 30 called Semame. The remaining genotypes were divided into three main groups.

Key words: Characterization, Melon, Phenotypic, Sihke.

Farklı Sıhke Yerel Kavun Genotipleri Arasındaki Genetik İlişkiler

Özet: Yerel ve eski çeşitler, modern tarımda yok olma tehdidi ile karşı karşıya bulunmaktadır. Bu nedenle, yerel ve eski çeşitler mevcut çeşitlerin sahip olmadığı genleri içerebileceğinden dolayı, çeşitliliğin korunması ıslah çalışmaları için hayati önem taşımaktadır. Mevcut çalışma, Sıhke kavun yerel çeşidi arasındaki genetik ilişkileri fenotipik özellikler ile belirlemek amacıyla yürütülmüştür. Çalışmanın ana materyalini, Türkiye'nin Van ilinde çeşitli yerlerden toplanmış 15 Sıhke Kavun genotipi oluşturmuştur. Ayrıca, 2 yabancı standart kavun genotipi (Sembol F_1 ve Sempati F_1) ve daha önce karakterize edilmemiş 13 yerel kavun genotipi, fenotipik karakterizasyona dahil edilmiştir. Fenotipik karakterizasyonda kullanılmak üzere, kavun genotiplerine ait toplam 63 adet ölçüm veya gözlemden yararlanılmıştır. Kavun genotipleri arasındaki genetik akrabalık dereceleri, fenotipik veriler kullanılarak elde edilen Öklid matrislerinden dendrogramlar, 2 ve 3 boyutlu ölçeklemeler oluşturularak incelenmiştir. Bu çalışma ile, Van yöresi Sıhke kavun yerel çeşidi ve bazı yabancı ve yerli genotiplerin fenotipik özellikleri belirlenmiştir. Bununla birlikte Sıhke yerel kavun çeşidinin kendi içerisindeki ve diğer yerli ve yabancı genotiplerle aralarındaki genetik ilişkiler ortaya çıkartılmıştır. Moleküler Öklid matrisine göre, Sıhke yerel kavun çeşidi, diğer genotiplerden farklı çıkmış ve kendi aralarında grup oluşturma eğilim göstermiştir. Çalışılan genotipler içerisinde, Genotip 30-Şemame en farklı genotip olarak bulunmuştur. Geri kalan genotipler iki ana gruba ayrılmışlardır.

Anahtar kelimeler: Fenotipik, Karakterizisyon, Kavun, Sıhke

Introduction

Melon (*Cucumis melo* L.) is an important vegetable both worldwide and in Turkey with a 24 million tons and 1.61 million tons of production on 1.07 million and 95 thousands ha area, respectively (Anonymous 2010). Moreover, Turkey is located in the secondary genetic diversity center, from Minor Asia to Japan (Pitrat et al. 1999; Jeffrey 2001; Sensoy et al. 2007a). Although the domestication origins of melons are

disputed, it is agreed that initial domestication probably occurred in the Middle East (Robinson and Decker-Walters 1997; Jeffrey 2001; Luan et al. 2008).

The local melon genotypes in Turkey are rich in diversity and group cantalupensis type melons spread to Europe from the Eastern part of Turkey, especially from Van province (Zhukovsky 1951; Günay 1993; Sensoy et al. 2007a; Sari et al. 2008; Szamosi et al. 2010; Yildiz et al. 2011). Thus, Turkish local melon genotypes have been collected for use in breeding programs where reasonable collection of germplasm exist at Aegean Agricultural Research Institute-Izmir, Turkey, Cukurova University Faculty of Agriculture, Department of Horticulture-Adana, Turkey and Yuzuncu Yil University Faculty of Agriculture, Department of Horticulture-Van, Turkey (Küçük et al. 2002; Sensoy et al. 2007a and b; Sari et al. 2008; Yildiz et al. 2011).
A comparison of the plant phenotype is the simplest approach for the detection of mislabeled genotypes and the assessment of genetic diversity. In the present study, we employed phenotypic traits; (1) to initially define genetic similarity among 15 Sihke melon genotypes collected from various parts in Van province of Turkey; (2) to compare them with other foreign and local accessions.

Material and Methods

Plant material

The majority of plant material employed in the study was collected from various parts in Van province of Turkey. The province of Van is located between 37°55′ and 39°24′ north longitude and 42°05′ and 44°22′ east latitude and at an altitude of 1720 m above sea level. Moreover, 2 foreign standard cantaloupe (*Cucumis melo* L. subsp. *melo* var. *cantalupensis* Naudin) melon genotypes (Sembol F_1 and Sempati F_1) and 13 local melon genotypes which had not been characterized before were included into the phenotypic characterization (Table 1, 2 and Figure 1).

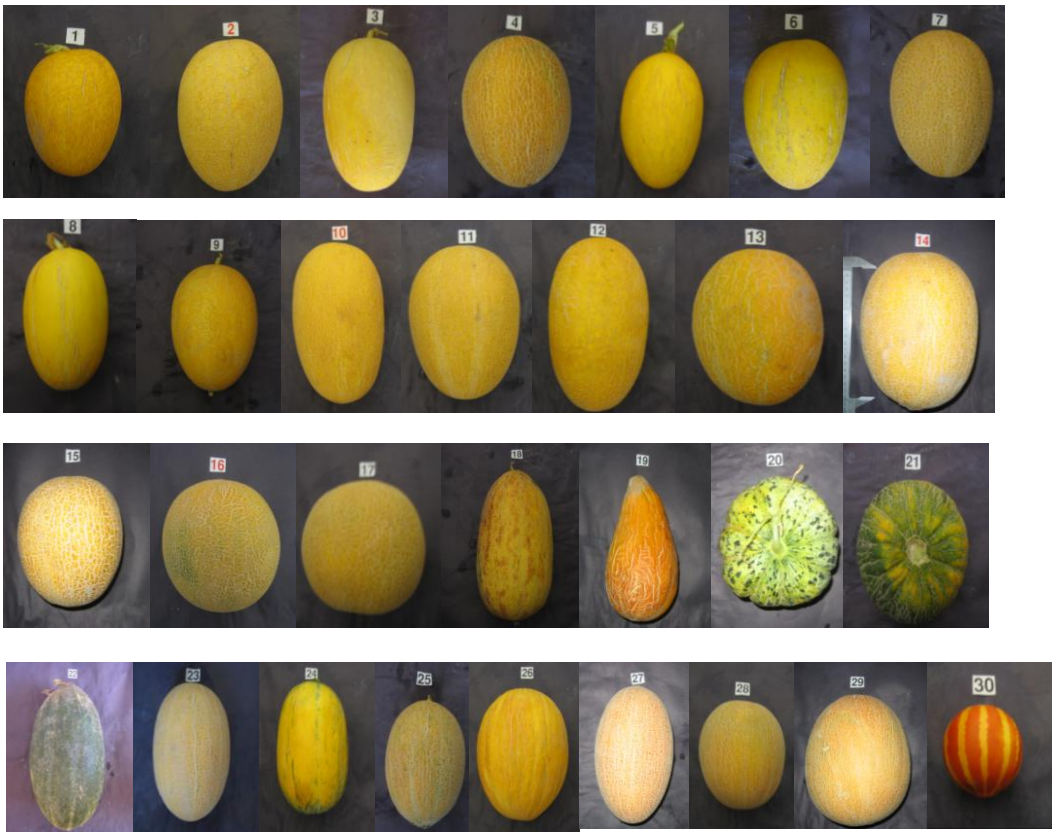

Figure 1. Mature fruit from the examined melon (*Cucumis melo* L.) genotypes.

Table 1. Origins and donors of melon accessions used for examination of genetic relationships.

Genotype	Origin	Donor
Genotype-1	Van-Sihke-Kiratli	Mesut Tunc
Genotype-2	Van-Sihke-Kiratli	Mesut Tunc
Genotype-3	Van-Sihke-Kiratli	Mesut Tunc
Genotype-4	Van-Sihke-Kiratli	Mesut Tunc
Genotype-5	Van-Sihke-Kiratli	Mesut Tunc
Genotype-6	Van-Sihke-Kiratli	Mesut Tunc
Genotype-7	Van-Sihke	Sükrü Akar
Genotype-8	Van-Sihke	Sükrü Akar
Genotype-9	Van-Sihke	Sükrü Akar
Genotype-10	Van-Sihke	Ismail Akbas
Genotype-11	Van-Sihke-Kiratli	Mesut Tunc
Genotype-12	Van-Sihke-Kiratli	Mesut Tunc
Genotype-13	Van-Sihke-Kiratli	Mesut Tunc
Genotype-14	Van-Sihke-Kiratli	Mesut Tunc
Genotype-15	Van-Sihke-Kiratli	Mesut Tunc
Genotype-16	Foreign-Sembol F_1	Seto Seed
Genotype-17	Foreign-Sempati F_1	Seto Seed
Genotype-18	Van-Cakirbey	Rifat Saginc
Genotype-19	Van-Muradiye-Unseli	Refik Bulut
Genotype-20	Van-Muradiye-Unseli	Sadik Alatas
Genotype-21	Van-Muradiye-Unseli	Sadık Alatas
Genotype-22	Van-Ercis	Mustafa Keles
Genotype-23	Van-Ercek-Irgatli	Mehmet Avinc
Genotype-24	Van-Ercek-Irgatli	Mehmet Avinc
Genotype-25	Van-Ercek-Irgatli	Rami Buyukkaya
Genotype-26	Van-Ercek-Irgatli	Rami Buyukkaya
Genotype-27	Van-Ercek-Irgatli	Rami Buyukkaya
Genotype-28	Van-Ercek-Irgatli	Rami Buyukkaya
Genotype-29	Van-Ercek-Irgatli	Yilmaz Avinc
Genotype-30	Van-Ercek-Irgatli	Rami Buyukkaya

Phenotypic evaluation

Seeds were sown in pots in a greenhouse and then twenty-four plants of each genotype (in a randomized block experimental design with three replications) transplanted into open field at the Experimental Area of the Horticulture Department of Yuzuncu Yil University, Van-Turkey. Plants were furrow irrigated and fertilized with 100 kg N and 50 kg P_2O_5 ha^{-1}. Phenotypic descriptions of genotypes were determined at two stages: flowering and fruit maturation. At harvesting, mature fruits were described and photographed. In all 63 phenotypic traits were scored and quantitative traits were converted into 3-5 discrete classes (as in Stepansky et al. 1999; Sensoy et al. 2007a).

Traits used in the phenotypic evaluation are: *01- Length of nodes on branches* = (1): 5 cm ≥, (2): 5-10cm, (3): 10 cm ≤; *02- Number of nodes on main stem* = (1): 15 ≥, (2): 15-25 (3):25 ≤; *03- Number of branches* = (1): 3 ≥, (2): 3-5 (3):5 ≤; *04- Length of nodes on main stem* = (1): 5 cm ≥, (2): 5-10 cm, (3): 10 cm ≤; *05- Main stem thickness (at fifth node)* = (1): 9 mm ≥, (2): 9-12 mm, (3): 12 mm ≤; *06- Hair density (on fifth node)* = (1): sparse, (2): medium, (3): dense; *07- Size of leaf blade* = (1): 9 cm ≥, (2): 9-12 cm, (3): 12 cm ≤; *08- Lobes in leaf* = 1): no lobe, (2): 3-lobes, (3): 5-lobes, (4): deep 3-lobes, (5): deep 5-lobes; *09- Green color of leaf blade* = 1): light, (2): middle, (3): dark; *10- Development of lobes in a leaf blade* = (1): poor, (2): middle, (3): strong; *11- Length of terminal lobe in a leaf blade* = 1): short, (2): middle, (3): long; *12- Dentations of margin in a leaf blade* = (1): poor, (2): middle, (3): strong; *13-*

Undulation of margin in a leaf blade = (1): poor, (2): middle, (3): strong; *14- Blistering in a leaf blade* = (1): poor, (2): middle, (3): strong; *15- Petiole attitude (at 3-leaf-stage)* = (1): vertical, (2): semi-vertical, (3): horizontal; *16- Petiole length* = (1): 9 cm ≥, (2): 9-12 cm, (3): 12 cm ≤; *17- Male flower density* = (1): none, (2): slight, (3): medium, (4): dense; *18- Male flower diameter* = (1): 25 mm ≥, (2): 25-35 mm, (3): 35 mm ≤; *19- Female flower density* = (1): none, (2): slight, (3): medium, (4): dense; *20- Ovary width* = (1): 6 mm ≥, (2): 6-10 mm, (3): 10 mm ≤; *21- Ovary length* = (1): 10 mm ≥, (2): 10-20 mm, (3): 20 mm ≤; *22- Ovary shape* = (1): short (ratio of ovary length: width 1.20 ≥), (2): medium (1.20-2.10),(3): long (2.10-3.00), (4): very long (3.00 ≤); *23- Time of ripening (50 % of plants with at least one ripe fruit)* = (1): 126 day ≥, (2): 126-156 day, (3): 156 day ≤; *24- Ground color of fruit skin before maturity* = (1): white, (2): yellow, (3): green, (4): grey-green; *25- Intensity of ground color (before maturity)* = (1): light, (2): middle, (3): dark; *26- Position of maximum width in fruit* = (1): towards blossom end, (2): center, (3): towards stalk; *27- Splitting in fruit* = (0): absent, (1): present; *28-External aroma in fruit* = (0): absent, (1): present; *29- Color of fruit skin at maturity* = (1): yellow/orange, (2): cream, (3): yellow-green, (4): green; *30- Color intensity of fruit skin at maturity* = (1): light, (2): middle, (3): dark; *31- Design color (secondary colors of skin)* = (1): yellow, (2): brown, (3): green; *32- Distribution of design color* = (1): absent, (2):speckled (3): spotted, (4): streaked, (5): striped; *33- Abscission of peduncle* = (0): absent, (1): present; *34- Shape of fruit base* = (1): sharp tip, (2): round, (3): flat; *35- Shape of fruit apex* = (1): sharp, (2): round, (3): flat; *36- Size of pistil scar* = (1): 4 mm ≥, (2): 4-12 mm, (3): 12-20 mm, (4): 20-38 mm, (5): 28 mm ≤; *37- Grooves on fruit* = (0): absent, (1): present; *38- Grooves depth* = (1): sligth, (2): medium, (2): deep; *39- Cork formation on fruit* = (0): absent, (1): present; *40- Creasing of fruit surface* = (0): absent, (1): present; *41- Main color of fruit flesh* = (1): white, (2): green, (3): cream-yellow, (4): orange; *42- Main color intensity of fruit flesh* = (1): light, (2): middle, (3): dark; *43- Color of flesh of outer layer* = (1): cream, (2): green, (3): orange; *44- Thickness of fruit flesh* = (1): 10 mm ≥, (2): 10-20 mm, (3): 20-30 mm, (4): 30-40 mm, (5):40 mm ≤; *45- Thickness of fruit skin* = (1): 2 mm ≥, (2): 2-4 mm, (3): 4-6 mm, (4): 6-8 mm, (5): 8 mm ≤; *46- Peduncle length* = (1): 10 mm ≥, (2): 10-20 mm, (3): 20-30 mm, (4): 30-40 mm, (5): 40 mm ≤; *47- Thickness of peduncle 1 cm from fruit* = (1): 4 mm ≥, (2): 4-5 mm, (3): 5-6 mm, (4): 6-7 mm, (5): 7 mm ≤; *48- Fruit length* = (1): 9 cm ≥, (2): 9-15 cm, (3): 15-21 cm, (4): 21-27 cm, (5): 27 cm ≤; *49- Fruit width* = (1): 6 cm ≥, (2): 6-9 cm, (3): 9-12 cm, (4): 12-15 cm, (5): 15cm ≤; *50- Fruit length/width ratio* = (1): 1.0 ≥, (2): 1.0-1.5, (3): 1.5-2.5, (4): 2.5-5.0 cm, (5): 5.0 ≤; *51- Fruit shape* = (1): round, (2):oval, (3):pear, (4):flat, (5):long, (6):very long; *52- Fruit weight* = (1): 100 g ≥, (2): 100-500 g, (3): 500-1000 g, (4): 1000-2000 g, (5): 2000 g ≤; *53- Shape at hiilum end of seed* = (1):sharp tip, (2):blunt tip; *54- Shape of cross section of seed* = (1): narrow elliptic, (2): elliptic; *55- Seed weight* = (1): 15 mg ≥, (2): 15-30 mg, (3): 30-50 mg, (4): 50-65 mg, (5): 65 mg ≤; *56- Seed color* = (1):white, cream, (2): yellow, (3): tan, (4): brown; *57- Amount of seed* = (1): little, (2): medium, (3): many; *58- Taste* = (0): sour-bitter, (1): insipid, non-sweet, (2): mildly sweet, (3): sweet, (4): very sweet; *59- Soluble solid content (^{o} Brix):* = (1): 4 ≥, (2): 4-6, (3): 6-8, (4): 8-10, (5): 10 ≤; *60- pH* = (1): 5 ≥, (2): 5-6, (3): 6 ≤; *61- Length of main stem* = (1): 50 cm ≥, (2): 50-100 cm, (3): 100 cm ≤; *62 – First male flowering* = (1): 70 day ≥, (2): 70-90 day, (3): 90 day ≤; *63 – First female flowering* = (1): 70 day ≥, (2): 70-90 day, (3): 90 day ≤. Moreover, it was also observed that all melon genotypes had an andromonoic sex expression and short and appressed hairs for ovary pubescence.

Table2. Sixty-three phenotypic traits scored in 30 melon genotypes

	Phenotypic data*
	000000000111111111122222222223333333333444444444455555555556666
Genotypes	123456789012345678901234567890123456789012345678901234567890123
Genotype-1	212123321113221333122323231012101233011042124352321311333332222
Genotype-2	111133321113221223122323231012101223011031134253322211523232133
Genotype-3	211223321112232223111223231011101233010032123353322321423333133
Genotype-4	211233321113221223122323231012101233011031133353322312523333222
Genotype-5	111233321113231323122323131012101232010042123352322312443221223
Genotype-6	212133321113231223122323230131101233111042223352322321423322233
Genotype-7	211133321113231223122323231012101233011032124352322321423453222
Genotype-8	111133321112231222113232311311002321100321233434223215232321333
Genotype-9	211133321112321213111323231012100232011041124352322311443232133
Genotype-10	211233321113231333212323230012101233011043123353332322323322222
Genotype-11	211233321113331233222323231011101233111031123353322322423322222
Genotype-12	212233321113331233222423230012101233011041133353435422443322222
Genotype-13	212233321113331333222323220012101232011042234352322321423232222
Genotype-14	211233321113331333222323131012101223011033134353422312423332222
Genotype-15	212233321113321233222323131012101223011042133352322321423342222
Genotype-16	222113333221321333222323320112321333011032353252311411331553222
Genotype-17	222222333221212333222213320112101333011031253253411412341543222
Genotype-18	212223223112121233322323310112221223011032123344435412442443222
Genotype-19	212222223113321233222323311111313131301013222335443342252233322
Genotype-20	212223322112222232222323120033321312130242233343511422541552222
Genotype-21	212222322111121333222323320133121334120043132252314322442452223
Genotype-22	212222323112221333322333320033121232120032243355536412443442222
Genotype-23	212222223112221333322324320012101332011042233434432412432443222
Genotype-24	212222333212321233122323310112321223121043233443425421422332223
Genotype-25	212212212113221233221324330112121233111042224243332311443453223
Genotype-26	211222322112221223121323330112101314010143234353425322333442233
Genotype-27	212222313111211223222323320113101213011032133354335312432443223
Genotype-28	211222312111121233322324220112321334011032142352322421343452222
Genotype-29	211222312112221323112323131112321335011043232433422322323442223
Genotype-30	111111253331212212111123320113231311110032111221211211241131133

* described in the materials and method section

Modified descriptions of the UPOV (The International Union for the Protection of New Varieties of Plants) criteria were followed in the present study. At least three mature fruits from each genotype were harvested, measured, and analyzed. The length measurements were performed by a ruler or a caliper compass; total soluble solids (TSS) was analyzed by a hand refractometer (Atago N1); pH was analyzed by a pH-meter (Hach 50050).

Results and Discussion

Based on the phenotypic Euclidean distance matrix, the most similar genotypes were G13-G15, G14-G15, and G4-G11 (3.316E+14) genotype pairs; the most dissimilar ones were G22 and G30 (1.273E+15) followed by G12 and G30 (1.249E+15) and by G14-G30 genotype pairs (1.170E+15). Of all evaluated genotypes, the most distinct ones were G30, G20 and G22 while the least distinct ones were G15, G4, and G14 (Figure 2, 3, 4). According to the phenotypic dendrograms, 2D and 3D scalings, G30 was the most distant genotype. Genotypes 16, 17, 20, 21, and 22 had also very distinctive positions. There was a definite clustering among Sihke melon genotypes. Based on the molecular Euclidean distance matrix, Sihke melon landraces were different from the others and tended to be grouped together. Among the studied genotypes, the most distinct genotype was Genotype 30 called Semame belonging to *Cucumis melo* L. subsp. *melo* var. *dudaim* (L.) Naudin. The remaining genotypes were divided into three main groups belonging to two informal subgroups, cantalupensis (*Cucumis melo* L. subsp. *melo* var. *cantalupensis* Naudin) and inodorus (*Cucumis melo* L. subsp. *melo* var. *inodorus* H. Jacq.).

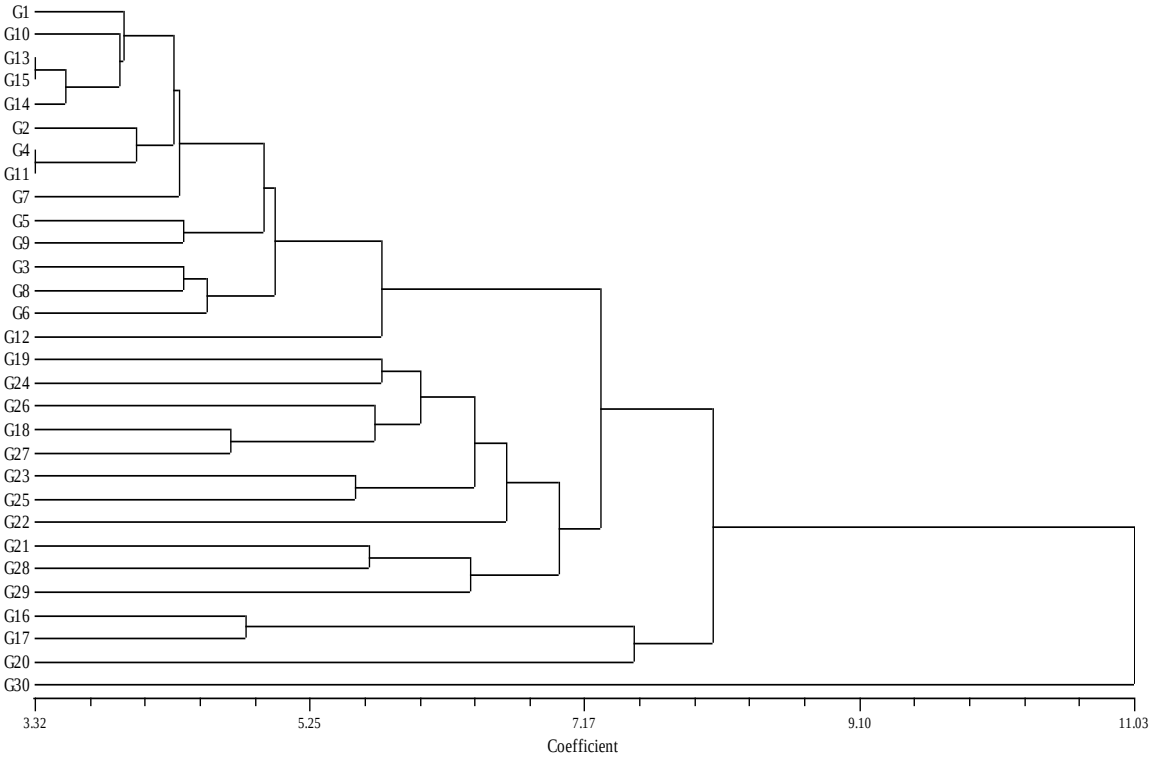

Figure 2. Associations among melon genotypes revealed by UPGMA clustering analysis on the basis of the phenotypic Euclidean distance values.

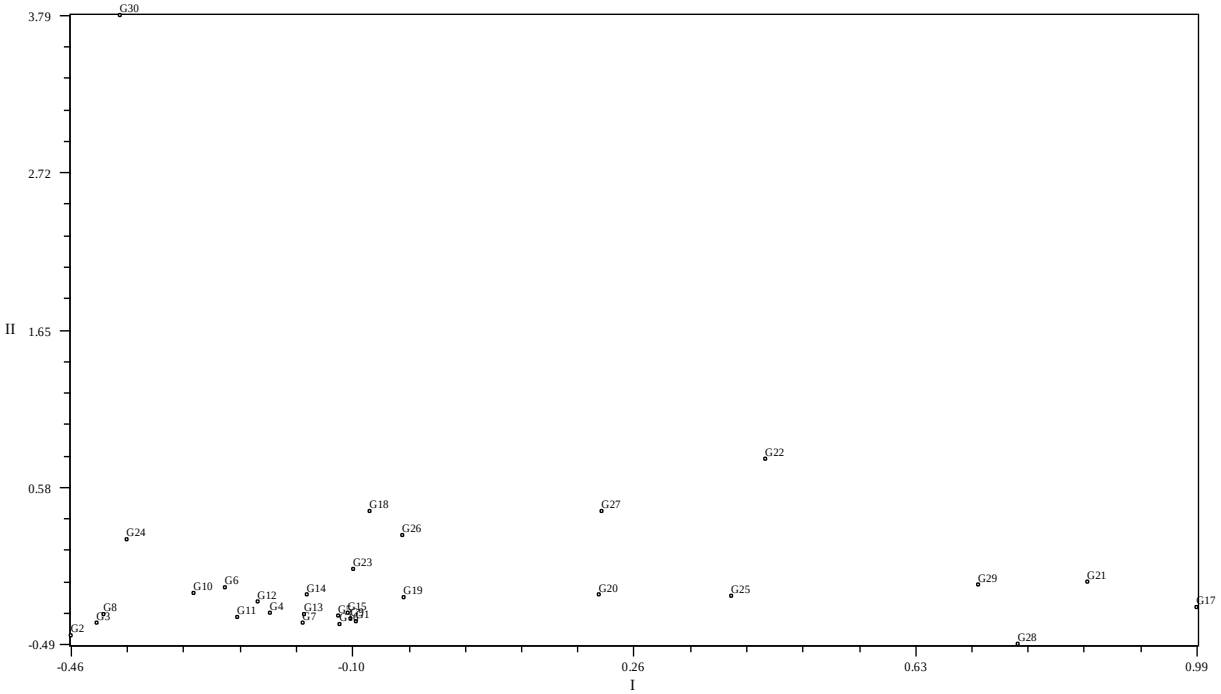

Figure 3. Associations among melon genotypes revealed by 2D scaling analysis on the basis of the phenotypicEuclidean distance values.

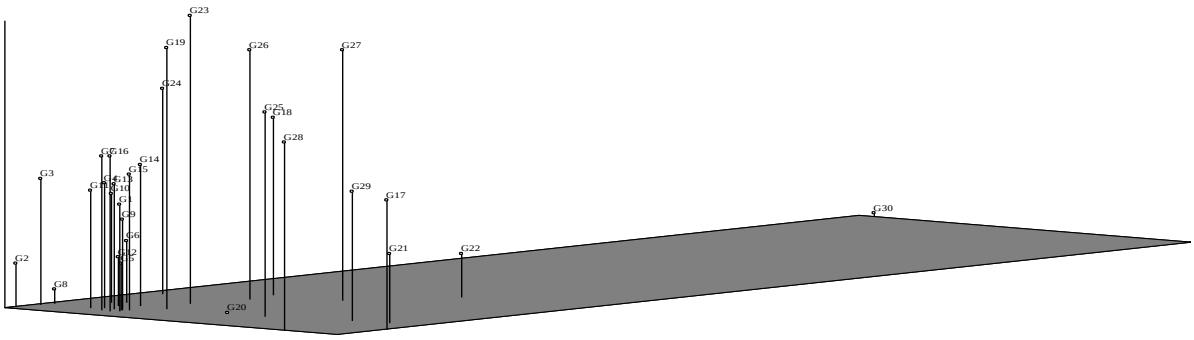

Figure 4. Associations among melon genotypes revealed by 3D scaling analysis on the basis of the phenotypicEuclidean distance values.

Phenotypic markers have been used to discriminate genotypes in various plant species and positive results have been obtained (Rabbani et al. 1998a and b; Piergiovanni et al. 2000; Acampora et al. 2007; Yetisir et al. 2008). Staub et al. (1997) stated that the minimum markers number was to be 35 in genetic discrimination studies. Therefore, the number of markers in the present study (63) was considered to be enough.

Although there has been high phenotypic variation among modern commercial melon cultivars, the genotypic variation among them found to be lower than expected (Stepansky et al. 1999; Silberstein et al. 1999). Therefore, it is wise to search for greater variation among local melon genotypes or wild relatives.

It was observed that the phenotypic data obtained in the present study was fitting to most of the data obtained from the other studies (Stepansky et al. 1999; Türkmen et al. 2005; Sensoy et al. 2007a). Presence of group dudaim, cantalupensis, and inodorus genotypes in Turkey has also long been known (Silberstein et al. 1999; Stepansky et al. 1999; Jeffrey 2001; Sensoy et al. 2007a).

One of the reasons of large variation in melon was the inevitable out-crossing among melon genotypes in Lake Van Basin. Intermediate forms might have been formed among group inodorus and group cantalupensis due the old farming practices employed by some local small-scale melon producers for centuries. Several melon genotypes grow together in Lake Van Basin and introgression of genotypes occurs naturally.

Local varieties and old varieties are faced with extinction in modern agriculture practices. Local varieties and old varieties may contain genes which are not present in their modern contemporaries. Therefore, biodiversity conservation will be essential in cultivar development efforts. Sihke melon landrace is specific to Lake Van Basin, but began to disappear for several reasons. In the world there is an increasing interest to collect local melon landraces. For example Laghetti et al. (2008) continue to collect, to characterize, and to long storage facilities in "Meloncella" traditional melon landrace in Italy.

In conclusion, with this study, the phenotypic traits of Sihke melon landrace of Van and some other local and foreign melon genotypes were determined. Moreover, the genetic relatedness among Sihke melon populations and other local and foreign genotypes were examined. Lake Van Basin is still a secondary diversity centre for melons (Sensoy et al. 2007a,b) but new cultivars progressively replace the traditional landraces; therefore, an intensive continuation of the collecting and evaluation work is necessary in the future.

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