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Diversity of Cucumber Accessions in Oman

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ABSTRACT

Twenty-four local accessions of cucumber were collected from the four regions of Oman, to evaluate genetic diversity based on morphological traits. The Shannon-Weaver diversity index analysis revealed the presence of genetic diversity based on morphological traits among the accessions both rationally and regions. The diversity index for agronomic, fruit and seed characters showed that Omani cucumber accessions had higher diversity (H) for all characters. Two main clusters were obtained. One group was further sub-divided into five sub-groups. The results showed significant genetic diversity in Omani cucumber accessions collected from different regions of Oman. This diverse indigenous cucumber gene pool may signify the potential for future cucumber crop improvement in Oman.

Key Words: Cucumber; Genetic diversity; Cluster analysis; Variability

INTRODUCTION

Cultivated cucumbers are widely distributed in Asia and Australia (Sebastian *et al*., 2010). In Oman, there are many local germplasm landraces for different crops such as forages, cereals, vegetables and fruits (Al-Maskri *et al*., 2003). Among vegetable crops, many local landraces of garlic (*Allium sativa*), onion (*Allium cepa*), carrot (*Daucus carrota*), sweet potato (*Ipomoea batatas*), cucumber (*Cucumis sativaus* L. var. *sativus*) and melons (*Cucumis melo*) are usually cultivated and kept for future use by the local framers.

Local Omani cucumber is one of the important traditional vegetable crops grown in the Sultanate of Oman. It has been grown in different regions of Oman for many years and through time, different names such as Samail, Bahla and Nizwa were given to local types resulting in about 24 different accessions of local cucumber. Omani cucumber is an open pollinated crop with male and female flowers and sex ratio of flowers is influenced by genetic make up of accessions, growing environment, cultural practices and nutrient level of the plants. The increased consumer demand for cucumber in recent years has resulted in an increasing area of production and the introduction of new hybrid cultivars.

Increased greenhouse production and use of new hybrid cultivars has resulted in the abandonment of some marginal cultivation sites in remote mountain villages. Local landraces of cucumber and other plant genetic resources such as wheat are increasingly at risk (Akhtar, 1981; Toll & Moss, 1995; Al-Khanjari *et al.*, 2005). However, despite the widespread of hybrid cultivars, because of their suitability for both open field and greenhouse cultivation with higher yields, some farmers continue to grow local Omani cucumbers particularly in remote regions on a small scale. This practice is threatened by rural land use and other sociological changes in Oman. Hence, it is essential to conserve and evaluate the available genetic diversity in cucumber.

Morphological characterization has been used successfully in genetic evaluation (Belay *et al.*, 1994; Maxted *et al*., 1997; Hamid *et al.*, 2002). In addition, length, diameter and fruit color have been used as economically important traits (Kennard & Havey, 1995; Ahmed *et al.*, 2004). There is an urgent need to investigate diversity among these accessions before initiating breeding programs for conservation of local cucumber. In the absence of requisite information on indigenous landraces of cucumber in Oman, the present study was initiated to evaluate the vegetative and reproductive diversity among local cucumber accessions in Oman.

MATERIALS AND METHODS

Plant material: Seeds of twenty-four cucumber accessions were collected from different regions of Oman (Table I; Fig. 1) and kept under cool dry conditions until use. Seed of each accession was multiplied by bulk seed production and each plant was treated as single plant.

Methods adapted: The experiment was conducted at

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Directorate General of Agriculture and Livestock Research, Rumais, Sultanate of Oman. Soil and water samples were taken for the determination of electrical conductivity and acidity using a wet paste (1:5) from two depths i.e., 0-30 cm and 31-60 cm. Samples of water used for irrigation were taken for analysis at different intervals during course of investigations.

Twenty-four cucumber accessions were randomly numbered 1 to 24. Plot size was 4 m^2 (2×2m). The seeds of each accession were directly seeded in the field with four seeds on each hill. Plants were spaced 50 cm apart. Two weeks after sowing, the plants were thinned to five plants per plot for each accession. The seedlings were covered directly after germination with agryl to prevent against pests and to prevent pollination between accessions at the time of flowering. A drip irrigation system was used and plants were irrigated for ten minutes per day and increased or decreased according. Fertilization and protection programs were followed as per local recommendations. First harvest for all accessions was made after seven weeks of sowing and fruits were harvested weekly up to three weeks thereafter. Observations were collected at various growth stages on ten plants per accession.

Data collection: The data were recorded on the following traits: plant length, leaf length and width, flower number and tendril length. Fruit characteristics included fruit number and weight per plant, fruit length and diameter and 100 seed weight.

Statistical analysis: Cluster analysis was performed using MINITAB. Each of the 13 quantitative characters were recorded and analyzed using the Shannon-Weaver diversity index (Shannon & Weaver, 1949) as defined by Jain *et al.* (1975) to calculate phenotypical variation for each accession:

$$H = - \sum_{i=1}^{n} pi \ln pi / H_{max}$$

Where n is the number of phenotypic classes for a character and Pi is the genotype frequency or the proportion of the total number of entries in the I class.

H was standardized by converting to a relative phenotypic diversity index (H').

RESULTS

Morphological diversity: Analysis of the genetic diversity index (H) for different morpho-agronomic characters for all regions combined ranged from 0.32 to 0.88. Tendril lobe length had highest diversity index (0.85) followed by large leaf length (0.83) and male flowers-2 (0.78). Similarly, diversity index for plant length after 60 days, male flower-1, female flower-1 and female flower-2 was 0.71, 0.75, 0.74 and 0.71, respectively. However, the lowest H value was for large leaf width (0.32), indicating low diversity of the trait. The overall average for all characters was 0.68. In general, morpho-agronomic characters showed high variation of diversity among the landraces germplasm of Omani cucumber (Table II).

Table I: Twenty-four cucumber accessions collected from four regions of Oman

Accessions	Code	Regions	Villages
1	MCT1	Muscat	Rusail
2	MCT3	Muscat	Jahlut
3	BTH2	Batinah	Abyadh
4	BTH3	Batinah	Hoqain
5	BTH4	Batinah	Alaaya
6	SH2	Sharqiya	Ghayan
7	SH3	Sharqiya	Ghubairaa
8	SH4	Sharqiya	Ghubairaa
9	SH5	Sharqiya	Ghubairaa
10	SH6	Sharqiya	Ghubairaa
11	SH7	Sharqiya	Ghubairaa
12	SH8	Sharqiya	Ghubairaa
13	SH9	Sharqiya	Ghubairaa
14	SH10	Sharqiya	Hamam
15	SH12	Sharqiya	Haima
16	DKH1	Dakhilia	Mutamar
17	DKH2	Dakhilia	Mutamar
18	DKH3	Dakhilia	Sufaihaa
19	DKH4	Dakhilia	Izz
20	DKH5	Dakhilia	Izz
21	DKH6	Dakhilia	Habub
22	DKH7	Dakhilia	Habub
23	DKH10	Dakhilia	fankh
24	DKH11	Dakhilia	Ndaab

Fig. 1: Seed of cucumber accessions collected from different regions of Oman

Batinah: 1. Alhooqain, 2. Alaaya, 3. Alabyadh; **Muscat:** 1. Alrusail, 2. Gahlot; **Dakhilia:** 1. Nidab, 2. Falaj, Almarag, 3. AL Fankh, 4. Habob, 5. Almoatamer, 6. Alsfiha; **Sharqiah:** 1. Alghayan, 2. Alghubairaa, 3. AlHamam

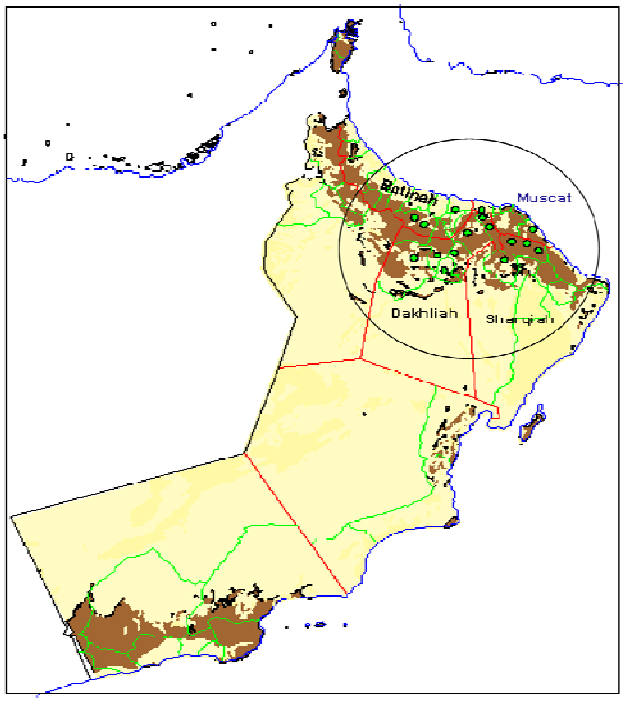


Table II: Genetic diversity (H) of morpho-agronomic characters according to Shannon-Weaver for cucumber landraces accessions for all regions combined and for four individual regions of Oman

Characters	All Regions	DKH	SH	BTH	MCT
Plant Length (cm) 60 days	0.71	0.80	0.81	0.63	0.61
Small Leaf Length (cm)	0.68	0.70	0.66	0.70	0.65
Small Leaf Width (cm)	0.62	0.62	0.66	0.74	0.47
Medium Leaf Length (cm)	0.61	0.54	0.66	0.60	0.64
Medium Leaf Width (cm)	0.56	0.55	0.65	0.49	0.56
Large Leaf Length (cm)	0.83	0.83	0.85	0.80	0.82
Large Leaf Width (cm)	0.31	0.30	0.32	0.20	0.42
Number of male flowers (1)	0.75	0.78	0.91	0.71	0.61
Number of male flowers (2)	0.78	0.82	0.78	0.81	0.71
Number of Female flowers (1)	0.74	0.82	0.83	0.71	0.61
Number of Female flowers (2)	0.71	0.81	0.77	0.69	0.58
Stem Thickness (cm	0.75	0.71	0.75	0.83	0.71
Tendril lobe length (cm)	0.85	0.83	0.83	0.87	0.86
Total	**9.44**	**9.11**	**9.48**	**8.78**	**8.25**
Average	**0.68**	**0.70**	**0.73**	**0.68**	**0.63**

Table III: Genetic diversity (H) of Fruit and seeds characters according to Shannon-Weaver for cucumber landraces accessions for all Regions combined and from four individual regions of Oman

Characters	All regions	DKH	SH	BTH	MCT
Fruit Length (cm)	0.50	0.55	0.48	0.54	0.41
Fruit Diameter (cm)	0.72	0.76	0.66	0.79	0.68
Fruit number /plant (H1)	0.80	0.87	0.82	0.81	0.72
Fruit weight kg/plant(H1)	0.77	0.81	0.83	0.75	0.69
Fruit number /plant (H2)	0.81	0.86	0.80	0.74	0.83
Fruit weight kg/plant (H2)	0.63	0.66	0.64	0.67	0.56
100 Seeds weight in (g)	0.35	0.59	0.37	0.23	0.23
Total	**4.93**	**5.1**	**4.60**	**4.53**	**4.12**
Average	**0.65**	**0.73**	**0.66**	**0.65**	**0.59**

The diversity index (H) between regions varied from 0.63 to 0.73. Sharqiah region having the highest H value (0.73) followed by Dakhilia (0.70), Batinah (0.68) and Muscat region (0.63) respevtively (Table II). The variation in diversity index between the regions could be due to specific characters of population of landraces collected in each region.

Within the regions, the diversity index ranged from 0.30 to 0.83 for Dakhilia with an overall average of 0.70. Large leaf length and tendril lobe length characters recorded the highest H value (0.83), while large leaf width was the lowest character (0.30). In Sharqiah region, the diversity index varied from 0.32 to 0.91 with an overall average of 0.73. Number of male flowers in the first samples gave the highest H value (0.91) followed by large leaf length (0.85), whereas large leaf width was the lowest in H value (0.32). In Batinah region, the H value ranged from 0.20 for leaf width to 0.87 from tendril lobe length, with an overall average of 0.68. The highest H values were recorded for tendril lobe length as compared to stem thickness. With respect to Muscat region, the H value ranged from 0.42 for leaf width to 0.86 for tendril lobe length, with an over all average of 0.63 (Table II).

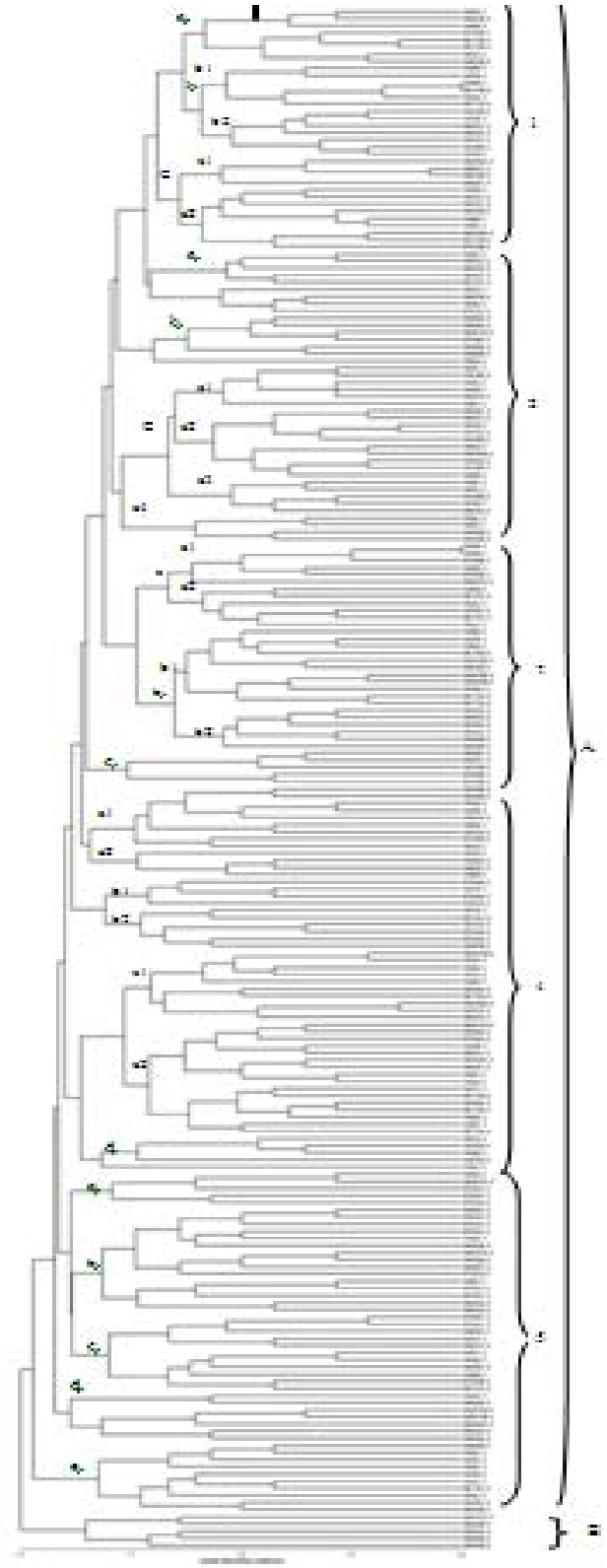
From the comparison within the characters in all regions combined, it can be seen that all the characters have high diversity index except large leaf width in which diversity index was 0.31. These results agree with the results of a previous study by Maliki *et al.* (2003) in African cucumber, where diversity varied from region to region. Batinah region gave the lowest diversity in this character (0.20), while Muscat region gave the highest (0.42). This could be due to the fact that the leaf had reached its final stage of maturity. Number of male flowers and stem thickness in Sharqiya and Batinah region were higher in diversity index (0.91 & 0.83, respectively) when compared to other regions.

Cluster analysis of simple matching coefficients of quantitative characters for all regions combined revealed the presence of two major populations (A & B) within the Oman cucumber accessions (Fig. 2). The first group of cluster A consisted of five subgroups and several sub-subgroups scattered with accessions from different regions. Sub-subgroup cluster (1b1) showed similarity to each other although were from diferent regions, i.e., SH9B-2 and MCT1B-3. Similarly, first group A1 at sub-subgroup (c1) the accessions DKH10C-3, DKH1C-2, DKH3B-1 and DKH2C-1 and accessions DKH3A-2,DKH3A-3, DKH5A-2, DKH3C-1, DKH4B-1 and DKH4B-3, SH7A-2, SH10A-1, SH6B-2, SH12A-3 and SH6C-1 and accession DKH11B-1, DKH11B-3, DKH10C-1, DKH3A-1 and DKH5A-3 at sub-subgroups b2, 4d and 5d2 of sub group A3, A4 and A5 were clustered in one group although they were from different villages. This showed that these phenotypes probably have similar genetic backgrounds. Accessions SH5B-1 and SH8B-1 clustered in a sub-subgroup (a1) of the subgroup A3 showed similarity. This could be because they were from the same village (Alghubairaa in the Sharqiya region). Accessions DKH11C-1, DKH2B-1, DKH1A-3 DKH5B-1 and DKH5B-2 were clustered together in group B, all from the same locality in Dakhilia region.

Fruit quality attributes: Genetic diversity index for cucumber fruit quality and seeds for all regions combined ranged from 0.5 to 0.81. Fruit number (H1) trait gave the highest diversity index (H=0.81) followed by fruit number at harvest (H2) (H=0.80). Fruit length (cm) recorded the lowest H value (0.50) with an overall average diversity of index H=0.65 (Table III).

On a regional basis, a low diversity index (H=0.23 to 0.59) for hundred seed weight. A high diversity index (H=0.72 to 0.87 for fruit number character) were obtained among all the seven characters from all four regions (Table III). Dakhilia region recorded the highest diversity index (H) on an overall average basis among all characters examined while it was lowest in Muscat. Genetic diversity index ranged from 0.55 to 0.87 in Dakhilia with an over all average H value of 0.73. Similarly, the fruit length character recorded lowest diversity index (H=0.55), while the fruit number character gave the highest value (H=0.87).

Fig. 2: Dendrogram of 13 quantitative characters of Oman cucumber accessions showing their relationship using simple matching coefficient of a cluster analysis for all regions combined



In Sharqiya region, H varied from 0.37 to 0.83 with an overall of diversity index of 0.66. Hundred seed weight gave the lowest (H=0.37) and fruit weight at first harvest (H1) recorded the highest (H=0.83). In Batinah region diversity index, H ranged from 0.23 for 100 Seed weight to 0.81 for fruit number at harvest one (H1) character with an over all of 0.65. For Muscat region, the diversity index varied from 0.23 to 0.83. Fruit number at harvest two (H2) recorded the highest (H=0.83), whereas seeds weight gave a low H value (0.23) with an overall values of 0.59. The overall diversity index (H) between regions varied from 0.59 to 0.73. However, Dakhilia region recorded the highest H value of 0.73 followed by Sharqiya (0.66) and Batinah regions (0.65), while the diversity index (0.59) was lower for Muscat region (Table III).

DISCUSSION

In general, analysis of genetic diversity index (H) for different morphological characters of cucumber ranged from 0.31 to 0.85 for leaf width and tendril lobe length among all characters. Tendril lobe length had highest diversity index (H=0.88), which indicated high diversity of the trait among accessions, while leaf width had a low H value (0.31) indicating low diversity of the trait with an overall average of diversity index (H=0.68). Low diversity for leaf width could be explained by no variations in leaf width as the leaf width was recorded at the maturity stage in all accessions. In general morpho-agronomic characters showed high variation among the landrace germplasm of Omani cucumber. Maliki *et al.* (2003) for African cucumbers and Staub et al. (1999) for Chinese cucumber could exist over a relatively limited geographical range, which also stand fast for Omani cucumber.

The overall diversity index (H) between regions varied from 0.63 to 0.73. Sharqiya region recorded the highest polymorphic diversity values (0.73) and the least was given by Muscat region (0.63). The variations in diversity index (H) between the regions could be due to differences in environmental conditions in each region.

Within the regions, diversity index values between characters showed differences like male flowers gave high H values (0.91) in Sharqiya, which indicated high genetic dissimilarity in accessions. Additionally in most of the cucurbits, sex expression is controlled by genetic and environmental factors (Malepszy & Niemirowicz-Szczytt, 1991). Either a single gene (*Cucurbita pepo*) or two or more genes (*Cucumis melo* & *Cucumis sativus*) with three or more alleles for each gene (Luffa sp.) control sex expression (Robinson & Decker-Walters, 1997). Leaf width observed in this study showed low diversity index in all four regions with variations in their values. Similar results obtained in all regions combined and this could be due to the fact that leaves had already reached maturity at the time of sampling.

Comparison in overall values of genetic diversity index (H) between combined analysis of all regions and the

four regions separately indicated that there were no significant polymorphic differences especially between Dakhilia and Sharqiah regions (H=0.70 & 0.73, respectively). The results showed that Oman cucumber accessions had high morphological genetic diversity as reported for *C. hardwickii* where polymorphism level was higher than in *C. sativus* (Dijkhuizen *et al.,* 1996; Meglic *et al.,* 1996; Horejsi & Staub, 1999). In addition, López-Sese *et al.* (2003) indicated that genetic diversity was highest in accessions of African origin, while it was lower in accessions of Spanish origin. On the other hand, some studies have indicated that the diversity of cucumber (*Cucumis sativus*) was relatively low (Knerr *et al.,* 1989; Meglic *et al.,* 1996; Staub *et al.,* 1997). Most cultivated cucurbits are similar in shoot characteristics and root habit. They are extremely diverse for fruit shape and other fruit characteristics resulting in the variety of uses (Bisognin, 2002). The results of the present study revealed that Omani cucumber accessions have high similarities for some morpho-agronomic traits.

Generally in cucurbits and particularly in cucumber fruits quality attributes are of economic importance. Many breeding efforts have been focused on improving fruit quality and disease resistance, which do not reflect yield but are important to determine the cultivar quality. Important quality characteristics include shape, color, spine type (coarse or fine), spine color (white or black), fruit length/diameter ratio, skin thickness and surface warts. A range of methods could be used to improve disease resistance, yield, fruit appearance and other fruit quality characteristics (Lower & Edwards, 1986). In the present study, on average the diversity index (H) ranged from 0.50 for fruit length to 0.80 for fruit number at first harvest in all regions combined. Similar results were found in four regions except for hundred seed weight in Sharqiya, Batinah and Muscat regions, where low diversity was observed. Fruit number, in general, showed high diversity in all regions combined and in the four regions individually. This could be because most plants produce more than one branch that is reflected in the total number of fruits. Additionally the fruit number character is a character with high heritability. Smith *et al.* (1978) found that fruit number was comparatively more heritable (0.17) than fruit weight (0.02). Cramer and Wehner (2000) reported that the number of branches per plant was positively correlated with total fruit number per plant in a pickling cucumber population. In the current study fruit length showed the lowest diversity for all regions combined and in the Dakhilia region. Serguen *et al*. (1997) suggested that the number of QTL controlling fruit dimension in cucumber is relatively low, hence fruit length and diameter in cucumber can be manipulated by phenotypic selection strategies. Seed weight however, gave the lowest diversity index in Sharqiya, Batinah and Muscat regions. This could be explained by the similarity of the fruit length values and weight values of the seeds between the accessions in both cases. Seed weight diversity varied from 0.23 in Muscat (low diversity) to 0.59 in Dakhilia (high diversity). The Dakhilia region recorded a high diversity index as compared to the other three regions.

The dendogram described the relationship among the landraces which were divided into two main groups (A & B) for all regions (combined) and four regions individually. From all regions (combined) the first group of cluster A was consisted of five subgroups and several subgroups were mixed with accessions from different regions. In Cluster analysis of four regions (Sharqiya, Dakhilia, Batinah, Muscat) accessions were divided into two groups (A & B), several subgroups and sub-sub groups within each region. The accessions SH9B-2 and MCT 1B-3 from subgroup cluster 1b1 and accessions SH5B-1 and SH8B-1 cluster is a subgroup (3a1) of the subgroup A3 from the Alghubairaa in Sharqiya region showed similarity. The similarity of these accessions could be result of trade activities/exchange of landraces material within the farmers of same village or region/ regions of Oman. Staub *et al.* (1999) revealed that certain accessions acquired by collectors in one region but originated in another region of China. Meglic *et al.* (1996) showed that accessions within China and Turkey were genetically similar. In the present study, Accessions (DK10C-3, DKH1C-2, DKH3B-1 & DK H2C-1), (DKH3A-2, DKH3A-3, DKH5A-2, DKH3C-1, DKH4B-1 & DKH4B-3), (SH7A-2, SH10A-1, SH6B-2, SH12A-3, SH6C-1) and (DKH11B-1, DKH11B-3, DKH10C-1, DKH3A-1 & DKH5A-3), sub-groups c1, b2, 4d and 5d2 of subgroup A1, A3, A4 and A5, respectively were clustered in one group although they were from different villages of the related regions. Results suggested that these accessions have same morphological characters and genetically closely related or referred to the same genotypes possibly due to exchange of material within the growers. A similar pattern was recorded in accessions from Dakhilia region (DKH11C-1, DKH2B-1, DKH1A-3, DKH5B-1, DKH5B-2) clustered together in-group B.

For instance, accessions (SH5B-1 & SH8B-1) of subgroup cluster 2A from Sharqiya region, accessions (DKH10A-3 & DKH7A-2) and (DKH1C-2 & DKH3B-1) of subgroup, 1 and 2 of group A cluster in sub- subgroup 1b and 2d2 from Dakhilia region, accessions (BTH4C-2 & BTH4C-3) of subgroup cluster 4A of group A from Batinah region and accessions (MCT3B-1 & MCT3B-3) of subgroup 1 of group A cluster in sub-subgroup 1a from Muscat region showed similarity suggesting that these accessions referred to similar genotype. This behavior strengthens the earlier results that the distribution of plant material occurred in close proximity or at longer distance in regions. Staub *et al.* (1997) showed that genetic similarities exist among cucumber landraces in India at moderate distances (i.e., 15 to 20 Km), while land races collection site might be different. Meglic *et al.* (1996) indicated genetic similarities among accessions from the countries of closed geographic proximity (China, Japan & Korea). Bramardi *et al.* (2005) showed that the two accessions the same cultivar

and seed lot (V4-V6 & V38-V390) confirmed their genetic uniformity, whereas those belong to the same cultivar but different seed lots (V8-V12 & V33-34) showed minimal differences. The ccessions (SH4C-2) from Alghubairaa village in Sharqiya region was isolated in one group B. It is unclear that why this accession was isolated alone, while it came from the same village Alghubairaa of the other accessions (SH3 to SH9). However, the only explanation could that this accession might be a derivative from the one of the regions or through the exchange of landraces between growers, reached at Sharqiya region. Staub *et al.* (1999) argued the possibility that the accessions 22311 (Changchun Mi Ci), 22318 (Xintai Mi Ci) and 23745 (Xintai Mi Ci) are similar landraces or cultivars although they were collected from different region.

Cluster analysis between all regions (combined) and four regions (individually) indicated that there were no significant differences between accessions in terms of morphological quantitative characters although the diversity was high within the germplasm in both cases which suggested that they are genetically related.

Knerr (1989) indicated that the limited number of accessions in the cucumber collection does not allow for a comprehensive analysis of germplasm diversity within this species. However, within the constraints of analysis it did provide information on diversity within the collection and can provide a basis for further evaluation and documentation.

Overall results indicated diversity for all regions, and the four regions separately for both vegetative and reproductive characters among different Omani cucumber accessions having a high diversity (H). This diverse cucumber germplasm could be used in future breeding and crop improvement program. Clusters with superior morphological types have been identified. This can be exploited for their genetic potential and desirable gene transformation.

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