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# Genetic diversity in local Palestinian watermelon (*Citrullus lanatus*) accessions

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The genetic diversity of 14 watermelon [*Citrullus lanatus* (Thunb.)] accessions collected from Palestine were morphologically characterized using 37 descriptors. Data were analyzed considering the genotypes, years and year\*genotype interactions for the two years 2014 and 2015. The statistical uncertainty of resulting hierarchical cluster groups was determined by calculating approximately unbiased p-values using Genstat program. Cluster analysis indicated that 14 accessions divided into three major clusters. A maximum genetic similarity was observed between accession numbers 9 from Arabeah and 17 from Meithalon, which revealed a high degree of similarity to the extent of 95% existing between them. Whereas, a minimum genetic similarity was observed between accession number 7 and 15 from Meithalon, which showed 60% similarity. The results also showed that, based on agronomic measurements significant variation ( $P > 0.05$ ) among accession were found for fruit yield, number of seeds per fruit. Accession number 3 was the highest for fruit yield and accession number 20 have the highest number of seeds per fruit. This information on variation and relationships among the morphological traits will be helpful for selection strategies in local and international breeding programs.

**Key words:** Watermelon, characterization, breeding, genetic similarity.

## INTRODUCTION

Watermelon (*Citrullus lanatus*) is one the most important and widely cultivated crop in the world. China is considered the leading country in production of watermelon followed by Turkey (FAOSTAT 2014). It is believed to have originated in Africa but is now widely spread throughout the tropics and the Mediterranean (Gichimu et al, 2009). Watermelon was an important crop in Palestinian and it was cultivated in large areas. Currently, watermelon production was seriously reduced due to its infection by soil born disease where the crop is grown continuously (Ministry of Agriculture, 2012). The soil born disease caused by *Fusarium* is one of the major factors limiting watermelon production worldwide (Zhang et al, 2005). Production of high quality watermelon fruit consider traits of firmness, full red color, high soluble

solids, and perceived shelf life in field and market (Hassell et al. 2014). Local watermelon genotypes considered a valuable source for enhancing disease and pest resistance in new watermelon cultivars. Characterization of local watermelon genotypes would help to prescreen watermelons to a biotic and biotic stress in order to accelerate breeding programs. Breeding efforts in watermelon have largely concentrated on fruit quality and morphological characteristics include fruit size and shape, sugar content (Brix), flesh color, and rind patterns (Wehner, 2008). These characteristics influenced by 62 genes (Wehner, 2012). Breeding strategies that incorporate gene pools from local cultivars are necessary for utilization the diversity (Hwang et al, 2011). The objective of this study is to determine the genetic

**Table 1.** Name and source of watermelon accessions

no	Accession number*	Species	Local Name	Collection site
1	3	<i>C. lanatus</i>	Gadoi	Meithalun
2	5	<i>C. lanatus</i>	Baladi	Yabed
3	7	<i>C. lanatus</i>	Baladi	Meithalun
4	8	<i>C. lanatus</i>	Baladi	Beer el Basha
5	9	<i>C. lanatus</i>	Gadoi	Arabeh
6	10	<i>C. lanatus</i>	Gadoi	Seer
7	11	<i>C. lanatus</i>	Gadoi	Seer
8	12	<i>C. lanatus</i>	Gadoi	Meithalun
9	13	<i>C. lanatus</i>	Baladi	Anza
10	15	<i>C. lanatus</i>	Zend Abd	Meithalun
11	16	<i>C. lanatus</i>	Teliani	Meithalun
12	17	<i>C. lanatus</i>	Gadoi	Meithalun
13	20	<i>C. lanatus</i>	Malali	NARC
14	21	<i>C. lanatus</i>	Gadoi	NARC

\*Accession number at NARC genetic resource unit

diversity of Palestinian watermelon germplasm which could be used in breeding programs.

## MATERIALS AND METHODS

The experiment was carried out at Qabatia research station belongs to the National Agricultural Research Center, NARC. The station is located close to Jenin city in West Bank-Palestine. Jenin is located at about 175 m above the sea level. The area receives annual rainfall of 450 mm with the rainy season extended from October to April. The mean annual temperature is 30 °C with the hottest period occurring between July and August.

Fourteen local watermelon (*Citrullus lanatus*) accessions (Table 1) obtained from the watermelon local collection at NARC Genetic Resources Unit were evaluated. The seeds were sown in peat moss and perlite mixture (2:1) into plug trays in mid March. Three weeks later, one hundred seedlings of each watermelon accession were transplanted to the open field at a spacing of 1.5 m between plants and 1.5 m within row using the completely randomized block design with three replications under rain fed conditions.

A descriptor list with morphological characters was adopted from Diez et al. (2005) and Jarret and Griffin (2007) and used in the characterization (Table 2).

The qualitative traits were used for the development of the dendogram and calculations of the similarity. The experiment was conducted in two growing season: during 15 March 2014 to 1 July 2014 and during 17 March 2015 to 1 July 2015. Organic manure and compound fertilizer (17 %N:17% P: 17% K) were applied before sowing at the recommended rate of 30 t/ha and 100 Kg/ha, respectively. Data were analyzed using Genstat program (GenStat 12th Edition, considering the genotypes, years and year\*genotype interactions) for the two years 2014 & 2015. The statistical

uncertainty of resulting hierarchical cluster groups was determined by calculating approximately unbiased p-values using Genstat program. Descriptive statistics (mean, and coefficient of variation), were generated using general analysis of variance (ANOVA) procedure and Least Significant Difference (LSD5%) was used to separate the means.

## RESULTS

The statistical analysis of the **quantitative traits** revealed significant variation ( $P > 0.05$ ) among the accessions between the two years and revealed significant variation ( $P > 0.05$ ) for thickness of rind and days for male flower (Table 3).

The statistical analysis of the **agronomic traits** revealed significant variation ( $P > 0.05$ ) among the accessions for fruit yield and number of seeds per fruit (Table 4).

The highest fruit yield was taken from accession number 3 followed by accession 7 and 5. Those accessions could be used in breeding high yield watermelon genotypes. The number of seeds per fruit was the highest for accession 20. The thickness rind was determined in accession 17. Days for male flowering was longest with 66 days for accession 20 (Table 5).

Significant negative correlation was found for width of strips and length of peduncle (-0.5) and days to male flowers and length of the main vine (-0.7) the vegetative meristems gradually become floral (Guner and Wehner 2004). Positive correlation were found for days to male flowers and days to female flowers (0.75), node number and size of insertion (0.57), leaf width and number of vines (0.68) and leaf width and leaf length (0.77) (Table 6).

Results of the principle component analyses for the 14 agronomic and quantitative traits indicated that the first

**Table 2.** Morphological traits, descriptors and measurements of the traits

Trait	Number	Descriptor	Unit	Measurements
Quantitative traits	1	Length of main vine	cm	At the final growing stage
	2	Number of vines per plant		At the final growing stage
	3	Width of strips on fruit	cm	Means for the fruits/replicate
	4	Rind thickness	cm	Means for the fruits/replicate
	5	Length of peduncle	cm	Means for the fruits/replicate
	6	size of insertion of peduncle	cm	Means for the fruits/replicate
	7	Days to male flower initiation	Day	Means for the first three flowers/replicate
	8	Days to female flower initiation,	Day	Means for the first three flowers/replicate
	9	Number of nodes per plant		Means for the plants/replicate
	10	Leaf length and width	cm	Means for the three leaves/replicate
	11	Petiole length	cm	Means for the three petiole /replicate
Agronomic traits	1	Fruit yield	kg/m <sup>2</sup>	All fruits/ replicate
	2	Number of seeds per fruit		Means for the three fruits /replicate
Qualitative traits	1	Flower sex		Three measurements for verification
	2	Ovary size		Three measurements for verification
	3	Petal size		Three measurements for verification
	4	Secondary color of testa (for seed)		Three measurements for verification
	5	Type of distribution of secondary color of testa (for seed)		Three measurements for verification
	6	Area of secondary color in relation to that of ground color (for seed)		Three measurements for verification
	7	Patches at hilum (for seed)		Three measurements for verification
	8	Pathes at margin (for seed)		Three measurements for verification
	9	Seed size		Three measurements for verification
	10	Fruit shape of longitudinal section		Three measurements for verification
	11	Fruit ground color of skin		Three measurements for verification
	12	Fruit intensity of green color of skin		Three measurements for verification
	13	Fruit shape of basal part		Three measurements for verification
	14	Fruit depression of base		Three measurements for verification
	15	Fruit shape of apical part		Three measurements for verification
	16	fruit depression of apex		Three measurements for verification
	17	Fruit grooves		Three measurements for verification
	18	Fruit stripes		Three measurements for verification
	19	Fruit intensity of green color of stripes		Three measurements for verification
	20	Fruit marbling		Three measurements for verification
	21	Fruit intensity of marbling		Three measurements for verification
	22	Fruit main color of flesh		Three measurements for verification
	23	Fruit intensity of main color of flesh		Three measurements for verification
	24	Fruit firmness of flesh		Three measurements for verification

**Table 3.** Analysis of variance for quantitative traits of the watermelon accession

source of variation	Days to male flower	Number of nodes	Days to Female flower	Rind thickness	Main vine length	Number of vines	Length of peduncle	Size of insertion of peduncle
Year (Y)	103.3**	13.2**	41.2**	2.1*	537312.8**	107.4**	8.2**	3.2**
Accessions(A)	0.9*	0.3	0.6	0.2**	507.6	1.5	0.8	0.05
A.Y	4.5	2.4	9.8	0.08	503.1	1.8	3.2	0.1

**Table 4.** Analysis of variance for the agronomic traits of watermelon accession

Source of variation	Fruit yield	Number of seeds per fruit
Year (Y)	32.7**	28.2
Accessions (A)	1.26**	20495**
A.Y	0.26	

**Table 5.** Mean, least significant differences and coefficients of variation for agronomic and quantitative traits of watermelon accessions evaluated during 2014-2015 seasons

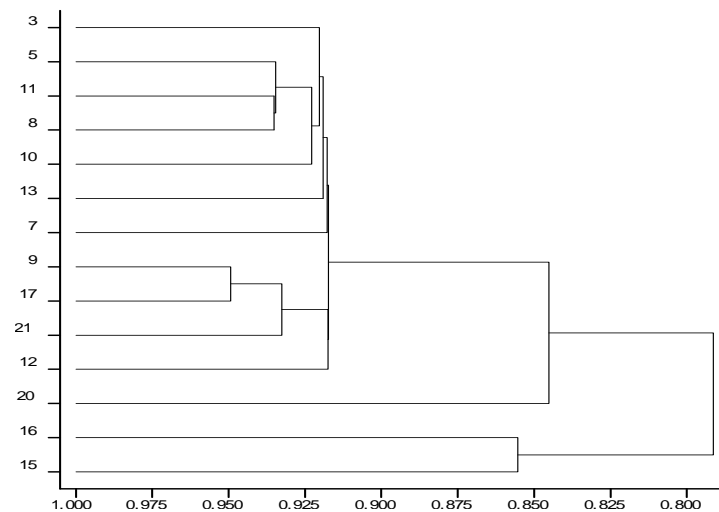
Aa\	Fruit yield (kg per m <sup>2</sup> )	Main vine length (cm)	Number of vines per plant	Length of peduncle (cm)	Size of insertion of peduncle (cm)	Width of strips (cm)	Rind thickness (cm)	No of Seeds per fruit	Days to first male flower	Days to first female flower	Node number	Petiole length (cm)	Leaf length (cm)	Leaf width (cm)
3	2.5	83.0	5.9	4.0	1.2	0.5	1.3	203.3	54.3	61.3	7.7	8.5	13.9	14.5
5	2.1	85.5	6.3	3.5	1.3	0.6	1.2	207.3	61.3	65.7	9.7	7.6	14.8	15.1
7	2.3	78.2	6.8	4.5	1.4	0.4	1.4	148.7	59.8	66.3	12.7	7.1	14.2	15.3
8	1.9	97.7	6.1	4.6	1.3	0.4	1.1	132.0	52.8	62.0	9.3	6.4	14.8	14.4
9	1.8	77.7	6.6	4.1	1.2	0.5	1.2	95.7	64.7	64.7	10.0	6.8	13.6	12.9
10	1.3	85.3	6.2	4.3	1.1	0.6	1.1	148.3	53.8	60.7	8.7	6.2	14.0	14.4
11	1.4	94.6	5.4	4.4	1.2	0.6	0.9	131.6	61.0	64.0	10.0	7.3	14.0	13.3
12	1.5	95.9	5.3	4.6	1.4	0.4	1.1	140.0	52.5	60.3	11.3	8.1	13.4	12.3
13	1.3	83.9	5.8	4.2	1.3	0.5	1.2	251.1	59.5	62.3	10.0	7.2	14.8	14.6
15	1.5	64.1	5.1	4.2	1.2	0.4	1.2	162.0	65.2	65.0	10.0	5.4	11.3	12.1
16	1.3	76.7	6.3	4.1	1.3	0.8	1.1	76.7	60.4	60.0	14.5			
17	1.0	77.3	5.8	4.7	1.2	0.5	1.5	121.7	61.2	64.3	10.7			
20	1.6	75.5	6.3	4.3	1.2	0.4	1.2	289.5	66.0	69.0	9.0			
21	1.1	76.6	6.6	4.9	1.0	0.3	0.7	185.0	59.0	63.0	9.0			
LSD	0.59	20.6	1.2	1.2	0.2	0.2	0.3	80.2	2.4	1.1	1.7	1.2	1.9	1.7
CV	16.2	3.1	3.5	3.3	8	6.1	9.7	18.9	3.6	5	15.8	12	10	9.1

**Table 6.** Correlations matrix for the agronomic and quantitative traits

	Fruit weight	Length of the main vine	No of vines	Length of peduncle	Size of insertion	Width of strips	Rind thickness	No of seeds	Days to mail flowers	Days to female flowers	Node no	Petiole	Leaf length
Main vine	0.13												
No of vines	0.26	-0.16											
Length of Peduncle	-0.48	0.11	-0.04										
Size of insertion	0.42	0.33	-0.12	-0.22									
Width of Strips	-0.09	0.09	0.00	-0.50*	0.13								
Rind thickness	0.36	-0.25	0.00	-0.26	0.48	0.08							
No of seeds	0.15	-0.12	0.01	-0.19	-0.11	-0.37	0.02						
Days to mail flowers	-0.15	-0.70**	0.10	-0.25	-0.16	0.03	0.14	0.17					
Days to female flowers	0.20	-0.42	0.24	-0.12	-0.02	-0.35	0.27	0.45	0.75**				
Node no	-0.16	-0.13	0.11	0.05	0.57*	0.41	0.17	-0.53	0.15	-0.13			
Petiole	0.44	0.47	0.05	-0.19	0.38	0.16	0.12	0.30	-0.38	-0.26	-0.04		
Leaf length	0.22	0.64	0.55	-0.10	0.26	0.37	-0.02	0.27	-0.40	-0.13	-0.07	0.45	
Leaf width	0.49	0.17	0.68*	-0.28	0.16	0.29	0.42	0.47	-0.24	0.14	-0.07	0.25	0.77**

**Table 7.** The first two principle components (PC) of the quantitative characters

No	Variable	PC1	PC2
1	Days to female date	-0.00373	-0.12522
2	Days to first male flower date	-0.00452	-0.35128
3	Length of peduncle	-0.00324	0.01043
4	Main vine length	-0.02783	0.92376
5	Node number	-0.00732	-0.01654
6	Number of vines	-0.00139	-0.00344
7	Fruit weight	0.00107	-0.00421
8	Leaf length	0.00647	0.0649
9	Leaf width	0.01179	0.02412
10	Number of seeds per fruit	0.99945	0.02263
11	Petiole length	0.00598	0.04287
12	Size of insertion of peduncle	0.00027	0.00165
13	Thickness of outer layer of percurp	0.00128	-0.00549
14	Width of strips	0.00029	0.00187

**Figure 1:** External and interior structure of the fruits for Gadoi watermelon (accession number 3).**Figure 2:** Cluster dendrogram for the 14<sup>th</sup> watermelon accessions

two PCs explained 94.03% and 5.18% of the total variation (Table 7). All quantitative characteristics contributed almost equally to PC1 except number of seeds per fruit. On the other hand, main vine length had the biggest contribution to PC2.

## DISCUSSION

Most of watermelons genotypes traits are qualitative traits affected by a single or a few gene mutations (Rhodes and Dane, 1999; Rhodes and Zhang, 1995). Low variation in

qualitative traits (Figure 1) among watermelon accessions were found which may attributed to their narrow genetic background as reported by Gichimu et al. 2009, Levi et al. (2001a) and Levi et al. (2001b). It is commonly assumed that intensive selection within a population leads to reduction in genetic variability and ultimately to erosion of the basis for further selection responses (Berg 1993). Cluster analysis (Figure 2) indicated that 14 genotypes could be divided into three major clusters. Cluster I included two accessions (accession 15 and 16 from Meithalun), cluster II included accession number 20 (the control), cluster III was the largest and included 11 accessions and it is divided in six sub clusters. In this group we can observe that the accession 5 from Yabed, 11 from Seer and 8 from Beer el Basha are the most related accessions which suggest their close similarity. These three are linked to accession 10 from Seer meaning that the four accessions may have common ancestry. The accessions 7 from Meithalun and 9 from Arabeh are almost related accessions and linked to accession 21 NARC collections. A maximum genetic similarity was observed between accession numbers 9 from Arabeh and 17 from Meithalun, which revealed a high degree of similarity to the extent of 95% existing between them. Whereas, a minimum genetic similarity was observed between accession 7 and 15 from Meithalun, which showed 60% similarity.

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### Conflict of interests

The authors declare that they have no conflicting interests

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