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CHANGES IN ION (K, Ca AND Na) REGULATION, ANTIOXIDANT ENZYME ACTIVITY AND PHOTOSYNTHETIC PIGMENT CONTENT IN MELON GENOTYPES SUBJECTED TO SALT STRESS – A MIXTURE MODELING ANALYSIS

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ABSTRACT

The present study aimed to identify the response of melon accessions and cultivars to salt stress in terms of ion exchange, enzyme activity, lipid peroxidation and photosynthetic pigment contents by mixture modelling. In mixture modeling, it is expected that the data set demonstrates a heterogeneous structure. This heterogeneity is characterized as unobservable heterogeneity. The data set's heterogeneity produces severe deviations in the parameter assessments and the standard deviations. Heterogeneity is overcome when the data set separates itself into homogeneous sub-populations. Mixture modeling was performed using the Mclust mixture cluster program of the statistical software package R 5.2.3. Sub-populations were constructed by evaluating genotypes according to studied traits and correlation analysis was performed using the SPSS software package. The seedlings of 13 melon genotypes were harvested two weeks after salt application (0 mM or 50 mM NaCl) when symptoms of salt stress were observed. Nutrient contents and ratios (K, Ca, Na, K : Na and Ca : Na); superoxide dismutase (SOD), catalase (CAT) and ascorbate peroxidase (APX) activities malondialdehyde (MDA) chlorophyll *a*, chlorophyll *b*, total chlorophyll and carotenoid contents were measured. Mixture modeling and correlation analysis were used in evaluating the experimental data sets. Differences in responses to salt application were observed among genotypes. While all genotypes exhibited negative responses in terms of K : Na ratio, which is an important parameter of salt tolerance, the smallest decreases in K : Na ratios were observed in the YYU-11 (–57.09%) and YYU-4 (–58.78%) genotypes, indicating them to be the most tolerant to salt stress. In general, enzyme activity decreased in response to salt application, although the responses varied among genotypes, especially with regard to CAT and APX activity. The YYU-29 genotype was notable as the genotype with the highest K : Na ratio (1.79) as well as the smallest change in MDA content under salt stress.

Key words: chlorophyll, melon genotypes, nutritional variation, salinity, susceptibility, tolerance

INTRODUCTION

Salinity is one of the most important abiotic stress factors to affect yield, especially in semi-arid and arid regions [Ashraf and Harris 2004, Dasgan and Koç 2009, Yildiz and Balkaya 2016]. About 800 million hectares of agricultural land – representing 6% of the world's total agricultural area, and including 230 million hectares of irrigated land – suffer from salinity problems [Munns and Tester 2008, Peleg et al. 2012]. Plants exposed to salt may experience water deficit stress due to the low osmotic potential of the soil solution and ion toxicity due to ion imbalances caused by intake of ions such as Na^+ and Cl^-

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[Ashraf and Harris 2004, Kusvuran et al. 2008, Aktas et al. 2009]. High concentrations of salt in the soil may also slow or even shut down many plant physiological and biochemical processes, such as photosynthesis and nutrient uptake [Carillo et al. 2011]. In addition, salt stress, especially stress caused by Na^+ and Cl^- ion uptake, can impair both the function and structure of plant proteins [Tuteja et al. 2012].

The amount and type of salt applied and the duration of exposure affect how plants respond to salt stress [Çulha and Çakirlar 2011]. Genotypic differences also play a role in the level of tolerance/sensitivity that plants exhibit towards the toxic effects of salt accumulation; however, the genetic basis by which plants respond to salt stress and how this tolerance mechanism operates in the context of actual environmental conditions is not yet fully understood [Carillo et al. 2011, Çulha and Çakirlar 2011]. Zhu [2001] describes three different types of tolerance mechanisms, namely homeostasis (i.e. ion homeostasis and osmotic balance), damage control (i.e. repair and detoxification), and growth regulation. In addition to tolerance, plants may use strategies of escape and avoidance to cope with the negative effects of salt stress [Peleg et al. 2012].

Although various cultural practices may help protect against salt stress, the available measures represent neither economical nor long-term solutions; rather, the development of tolerant plant cultivars is considered to be the most effective solution to the problem of salt stress [Mendlinger and Pasternak 1992, Franco et al. 1997]. Melon is considered to be a species with a medium-level of tolerance to salt stress; however, the degree of tolerance varies among melon genotypes [Mendlinger and Pasternak 1992, Shani and Dudley 2001, Damianos and Savvas 2016]. The development of melon cultivars that can achieve high yields under saline conditions is especially important in the arid and semi-arid regions where melon cultivation is carried out.

Melon is one of the most important vegetables for Turkey, which ranks second in the world in terms of production, with 1 699 550 tons produced annually [Faostat 2013]. Although melon has its origins in East Africa [Pitrat 2008], Turkey is a micro-gene center for cucurbits in general and melon in particular [Sensoy et al. 2007]. Preliminary studies have been conducted to classify and evaluate a/biotic stress response of melon germplasm grown in the Lake Van Basin, an area rich in melon genetic diversity [Sensoy et al. 2005, Türkmen et al. 2008, Sensoy et al. 2012]. The limited numbers of selection and breeding programs aimed at the development of high-yielding commercial cultivars have led to a reduction in genetic diversity, which leads to a lower tolerance of cultivar varieties to abiotic stress conditions. By conducting studies to screen local accessions, it may be possible to identify stress-resistant genotypes for use in future breeding trials aimed at restoring genetic diversity and improving plant resistance to abiotic stress factors.

The need for new models to evaluate experimental data sets is being increasingly recognized, with many disciplines turning to a Gaussian-mixture model for analysis of normally distributed data [Yeşilova et al. 2010, 2016]. Mixture modeling aims to identify previously unobserved homogenous sub-populations comprising a seemingly heterogenous data set [Wang et al. 1996, Dalrymple et al. 2003, Martinez et al. 2009] using Akaike's data criteria (AIC) and Bayesian data criteria (BIC) [Yeşilova et al. 2010] to define and separate sub-populations. Therefore, the present study applied mixture modeling to investigate changes in ion regulation, enzyme activity and photosynthetic pigment content of melon genotypes under salt stress. Mixture model is a novel approach and has two important advantages compared to the cluster and factor analysis [Muthén and Muthén 2014]. The first, for each observation, mixture modeling is resolved according to the probability of inclusion within the subgroup categories. The second, mixture model gives the parameter estimates for each subgroup [Mao et al. 2013].

MATERIALS AND METHODS

Materials. Seventeen melon genotypes (13 local accessions-collected from different areas of the Van Lake Basin in eastern Turkey, 3 hybrid cultivars and 1 standard foreign melon cultivar) were used to investigate the response of melon genotypes to salt stress (tab. 1).

Table 1. Passport information of melon accessions and cultivars used in the study

Acc.#	Location	Cultivar	Location
YYU-1	Van-Sihke-Kiratlı	Kirkagac F_1	Yüksel Seed
YYU-4	Van-Sihke-Kiratlı	Lokum F_1	Yüksel Seed
YYU-6	Van-Sihke-Kiratlı	Napolyon F_1	Yüksel Seed
YYU-10	Van-Sihke	Galia	Standard
YYU-11	Van-Sihke-Kiratlı		
YYU-12	Van-Sihke-Kiratlı		
YYU-15	Van-Sihke-Kiratlı		
YYU-18	Van-Cakirbey		
YYU-20	Van-Unseli		
YYU-21	Van-Unseli		
YYU-22	Van-Ercis		
YYU-23	Van-Ercek-Irgatli		
YYU-29	Van-Ercek-Irgatli		

Salt application. The study was conducted using a completely randomized experimental design with 3 replications of 5 plants each. Seeds were sown into 1-liter pots without drainage and containing a 2 : 1 mixture of sterile peat : perlite. All seedlings were irrigated with Hoagland nutrient solution before and after salt application [Aktas et al. 2009]. For salt applications, a 50 mM concentration of NaCl dissolved in distilled water was applied gradually over 2 days starting when the seedlings reached the two-true-leaf stage.

Determination of shoot nutrient contents. After drying at 65°C for 48 hours, whole shoot samples were burnt at 550°C, the obtained ash was dissolved in 3.3% HCl, and an atomic absorption device (Thermo Scientific, ICE 3000) was used to measure Na, K and Ca contents [Aktas et al. 2009, Kuşvuran 2012].

Chlorophyll content analysis. Extracts were obtained by homogenizing and filtering 0.25 g leaf samples in 80% acetone and 20% of water under dim, indirect light. Acetone was added to obtain 25 ml of extract, the optical density (OD) of samples were measured spectrophotometrically at wavelengths of 663, 645 and 470 nm, and photosynthetic pigments were calculated, as follows [Lichtenthaler and Wellburn 1983, Zengin 2007, Amira 2011].

$$\text{Chlorophyll } a \text{ (mg g}^{-1}) = \\ = (12.7 \times OD_{663}) - (2.69 \times OD_{645}) \times V/W \times 1000$$

$$\text{Chlorophyll } b \text{ (mg g}^{-1}) = \\ = (22.91 \times OD_{645}) - (4.68 \times OD_{663}) \times V/W \times 1000$$

$$\text{Total chlorophyll (mg g}^{-1}) = \\ = (20.2 \times OD_{645} + 8.02 \times OD_{663}) \times V/W \times 1000$$

$$\text{Carotenoids } (\mu\text{g ml}^{-1}) = \\ = 1000 \times OD_{470} - 3.27 \times Chl_a - 104 \times Chl_b/227$$

Determination of enzyme amount. The enzyme activities were expressed on the base of FW. Frozen leaf samples were homogenized with a 5 ml mixture of cold 50 mM potassium phosphate and 0.1 mM Na-EDTA (pH: 7.6), the homogenate was centrifuged at 709 g for 30 minutes at 4°C, and enzyme extraction was also performed at 4°C.

Catalase (CAT) activity was identified by the disappearance of H_2O_2 at 240 nm according to Cakmak and Marschner [1992]. Superoxide dismutase (SOD) activity was identified by the 50% inhibition of nitro blue tetrazolium (NBT) salt at 560 nm and SOD activity (units per milligram protein) was calculated [Jebara et al. 2005]. Ascorbate peroxidase (APX) activity was determined by the reduction of ascorbic-acid-bound H_2O_2 at 290 nm, with the amount of activity defined as the amount of enzyme required to

consume 1 μmol of ascorbate per minute [Cakmak and Marschner 1992].

Determinaton of malondialdehyde (MDA) content. A 0.5 g frozen leaf sample was homogenized with 0.1% trichloroacetic acid (TCA), the homogenate was centrifuged at 492 g for 15 minutes, and 1 ml of the supernatant was dissolved in 2 ml of 20% TCA containing 0.5% thiobarbituric acid (TBA). After resting at 95°C for 30 minutes, the mixture was submerged in an ice bath and then centrifuged at 219 g for 10 minutes. Absorbance of the supernatant at 532 and 600 nm was measured and MDA content calculated using an absorption coefficient of 155 mM^{-1} cm^{-1} [Heath and Packer 1968].

Statistical analysis. Mixture modeling was performed using the Mclust mixture cluster program of the statistical software package R 5.2.3. Sub-populations were constructed by evaluating genotypes according to nutrient contents (K, Ca, and Na) and ratios (K : Na and Ca : Na), antioxidant enzyme activities (CAT, SOD, and APX) and MDA content, and photosynthetic pigment (chlorophyll *a*, chlorophyll *b*, total chlorophyll and carotenoid) contents, and correlation analysis was performed using the SPSS software package to identify relations between variables.

RESULTS AND DISCUSSION

This study examined the response of different melon genotypes to salt stress in terms of nutrient characteristics, enzyme activity, MDA content and photosynthetic pigment content. A Gaussian mixture model was used to construct 3 homogenous sub-populations for genotype nutrient characteristics and 4 homogenous sub-populations for enzyme activity/MDA content by using the smallest AIC and BIC criteria (tabs 3 and 4, figs 1–6). No sub-populations were formed for photosynthetic pigment content due to the similarity of data for this criterion.

Effect of salinity on K, Ca and Na contents. Changes in K, Ca, Na contents and K : Na, Ca : Na ratios of melon genotypes subjected to salt stress are given in Table 2. Potassium (K) content decreased with salt application in all genotypes except for the YYU29 genotype, which showed an increase of 7.74% (tab. 2). The YYU29 genotype also had the highest K intake under saline conditions of all the genotypes tested. The Kirkagac variety was most affected by salt stress, with K content 38.89% lower for the 50 mM salt application when compared to the salt-free control (tab. 2). The genotype with the second-largest reduction (–36.22%) in K content with salt stress was the YYU15 genotype, which was also the genotype with the highest K intake in the absence of salt stress. Potassium plays a vital role in plant growth, stoma movement, osmoregulation and enzyme activation [Wu et al. 1996]. Previous studies have reported high K contents to increase the salt tolerance of plants, although high levels of salinity have also been reported to trigger a reduction in plant potassium levels [Hagin et al. 1990, Catalan et al. 1994, Naido 1994].

The present study also found salt application to reduce plant Ca intake. With the exception of the YYU29, Lokum and YYU4 genotypes, Ca levels of plants subjected to 50 mM salt application were lower than control plants for all genotypes. Ca intake in the YYU18, YYU15 and YYU21 genotypes was lower by 36.02%, 33.76% and 26.27%, respectively; in plants exposed to 50 mM NaCl when compared to control plants (tab. 2). As with K intake, the YYU29 genotype also had the highest Ca intake (11.38%) under saline conditions of all the genotypes tested (tab. 2). Previous studies have reported increases in soil Na levels to cause reductions in plant Ca, K and Mg levels, although the toxic effect of soil Na has been shown to be mitigated by the presence of sufficient soil Ca [Grattan 1993, Marschner 1995, Gomez et al. 1999]. Moreover, Na ions accumulate in the cell wall apoplast, disrupting the functional structure of the cell wall and negatively affecting cell Ca contents [Çulha and Çakirlar 2011].

Na content in plants increased with salt application in all genotypes, with the YYU29 genotype showing the largest increase (394.55%) and the YYU11 genotype the smallest increase (88.71%). The relatively large difference in Na ratios observed between the salt-stressed and control applications in the YYU29 genotype, which had one of the lowest levels of Na of any of the genotypes following salt application, can be explained by the fact that it also had the lowest Na content in the salt-free control application.

Table 2. Nutrition contents of melon accessions and cultivars with/without salt application

Acc.#	K (%)			Ca (%)			Na (%)			K : Na			Ca : Na		
	0 mM	50 mM	change (%)	0 mM	50 mM	change (%)	0 mM	50 mM	change (%)	0 mM	50 mM	change (%)	0 mM	50 mM	change (%)
YYU1	5.14 ±0.35	4.18 ±0.31	–18.68	4.56 ±0.27	3.71 ±1.19	–18.64	1.50 ±0.08	3.50±0.68	133.33	3.43 ±0.43	1.23 ±0.29	–64.14	3.05 ±0.36	1.04 ±0.19	–65.90
YYU4	4.65 ±0.21	3.70 ±0.27	–20.43	4.20 ±0.54	4.32 ±0.77	2.86	1.92 ±0.22	3.74±0.56	94.79	2.45 ±0.38	1.01 ±0.20	–58.78	2.22 ±0.49	1.19 ±0.36	–46.40
YYU6	5.47 ±0.19	4.26 ±0.61	–22.12	5.11 ±0.61	4.12 ±0.42	–19.37	1.31 ±0.24	3.61±0.42	175.57	4.27 ±0.70	1.18 ±0.05	–72.37	4.06 ±1.25	1.14 ±0.05	–71.92
YYU10	5.40 ±0.26	4.30 ±0.41	–20.37	4.71 ±0.51	4.05 ±0.51	–14.01	1.52 ±0.40	3.73±0.70	145.39	3.71 ±0.96	1.17 ±0.15	–68.46	3.27 ±1.03	1.10 ±0.21	–66.36
YYU11	4.62 ±0.68	3.94 ±0.83	–14.72	4.48 ±0.98	4.24 ±0.79	–5.36	1.86 ±0.57	3.51±0.39	88.71	2.68 ±1.14	1.15 ±0.35	–57.09	2.64 ±1.18	1.20 ±0.09	–54.55
YYU12	4.45 ±0.60	3.39 ±0.08	–23.82	4.52 ±0.36	3.57 ±0.75	–21.02	1.93 ±0.46	3.79±0.74	96.37	2.35 ±0.33	0.91 ±0.15	–61.28	2.47 ±0.87	0.99 ±0.35	–59.92
YYU15	5.55 ±0.16	3.54 ±0.66	–36.22	4.68 ±0.44	3.10 ±0.21	–33.76	1.33 ±0.15	3.85±0.56	189.47	4.20 ±0.36	0.92 ±0.05	–78.10	3.53 ±0.33	0.81 ±0.09	–77.05
YYU18	5.02 ±0.06	3.79 ±0.31	–24.50	4.22 ±0.38	2.70 ±0.36	–36.02	0.98 ±0.13	3.53±0.69	260.20	5.18 ±0.75	1.09 ±0.12	–78.96	4.41 ±1.10	0.79 ±0.23	–82.09
YYU20	4.67 ±0.68	3.37 ±0.31	–27.84	4.41 ±0.41	3.83 ±0.38	–13.15	1.39 ±0.26	3.48±0.48	150.36	3.43 ±0.65	0.98 ±0.09	–71.43	3.28 ±0.88	1.11 ±0.14	–66.16
YYU21	4.35 ±0.34	4.28 ±0.17	–1.61	4.72 ±0.34	3.48 ±0.88	–26.27	1.13 ±0.12	3.53±0.43	212.39	3.89 ±0.69	1.22 ±0.12	–68.64	4.23 ±0.66	1.00 ±0.28	–76.36
YYU22	4.94 ±0.24	3.55 ±0.18	–28.14	4.34 ±0.61	4.02 ±0.64	–7.37	1.17 ±0.72	3.62±0.55	209.40	6.99 ±0.79	0.99 ±0.13	–85.84	6.46 ±0.78	1.11 ±0.13	–82.82
YYU23	5.02 ±0.42	4.35 ±0.34	–13.35	4.64 ±0.47	3.81 ±0.61	–17.89	0.73 ±0.60	2.62±0.79	258.90	9.77 ±5.29	1.77 ±0.60	–81.88	9.43 ±5.79	1.51 ±0.36	–83.99
YYU29	4.52 ±0.33	4.87 ±0.42	7.74	4.13 ±0.03	4.60 ±0.29	11.38	0.55 ±0.17	2.72±0.27	394.55	9.02 ±4.15	1.79 ±0.09	–80.16	8.10 ±3.07	1.70 ±0.12	–79.01
Galia	5.23 ±0.23	3.63 ±0.41	–30.59	4.57 ±0.21	3.49 ±0.61	–23.63	1.20 ±0.26	3.59±0.81	199.17	4.45 ±0.71	1.05 ±0.30	–76.40	3.91 ±0.80	0.98 ±0.14	–74.94
Kirkagac F_1	4.50 ±0.69	2.75 ±0.22	–38.89	4.16 ±1.22	3.65 ±0.46	–12.26	1.35 ±0.18	3.25±0.64	140.74	3.37 ±0.67	0.86 ±0.10	–74.48	3.06 ±0.68	1.16 ±0.34	–62.09
Lokum F_1	4.45 ±1.13	3.37 ±0.13	–24.27	3.51 ±0.21	3.73 ±0.92	6.27	1.51 ±0.35	3.35±0.26	121.85	3.06 ±1.19	1.01 ±0.11	–66.99	2.41 ±0.63	1.13 ±0.35	–53.11
Napolyon F_1	4.32 ±0.38	2.85 ±0.28	–34.03	3.74 ±0.59	3.25 ±0.23	–13.10	1.56 ±0.32	3.50±0.40	124.36	2.86 ±0.69	0.82 ±0.06	–71.33	2.49 ±0.74	0.93 ±0.12	-62.65

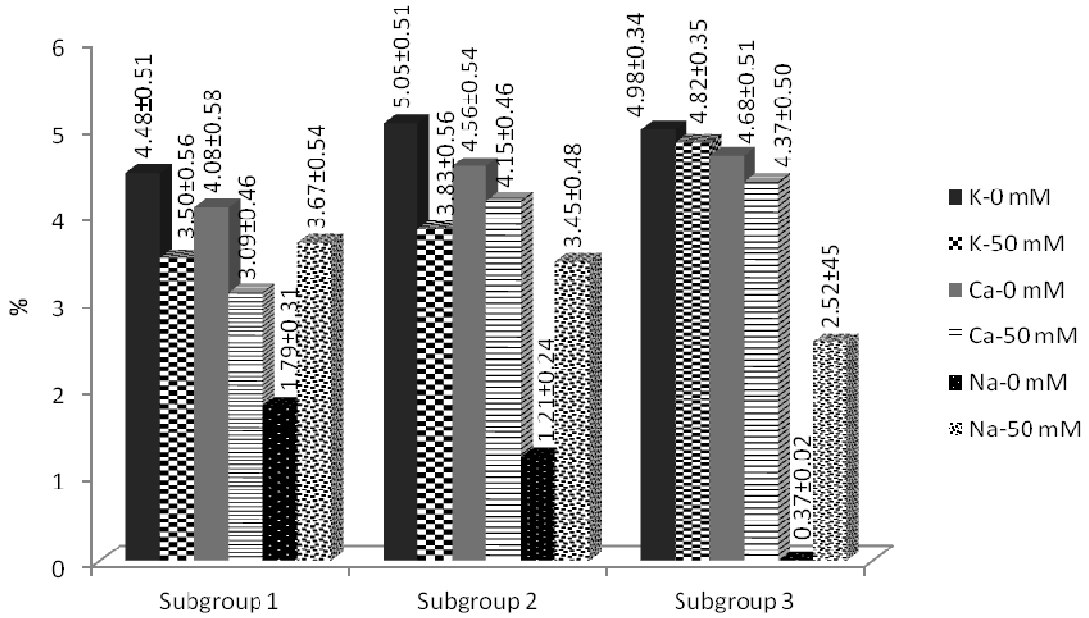

Fig. 1. Estimated means of variables for model with three sub-population for K, Ca and Na contents at 0 mM and 50 mM salt applications in melon genotypes

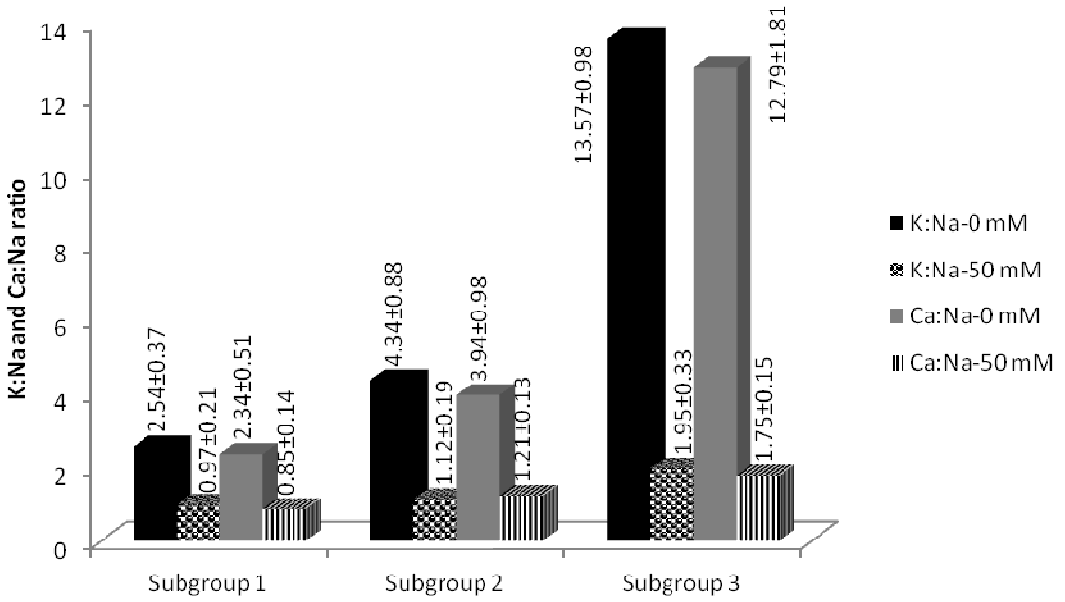

Fig. 2. Estimated means of variables for model with three sub-population for K : Na and Ca : Na ratio at 0 mM and 50 mM salt applications in melon genotypes

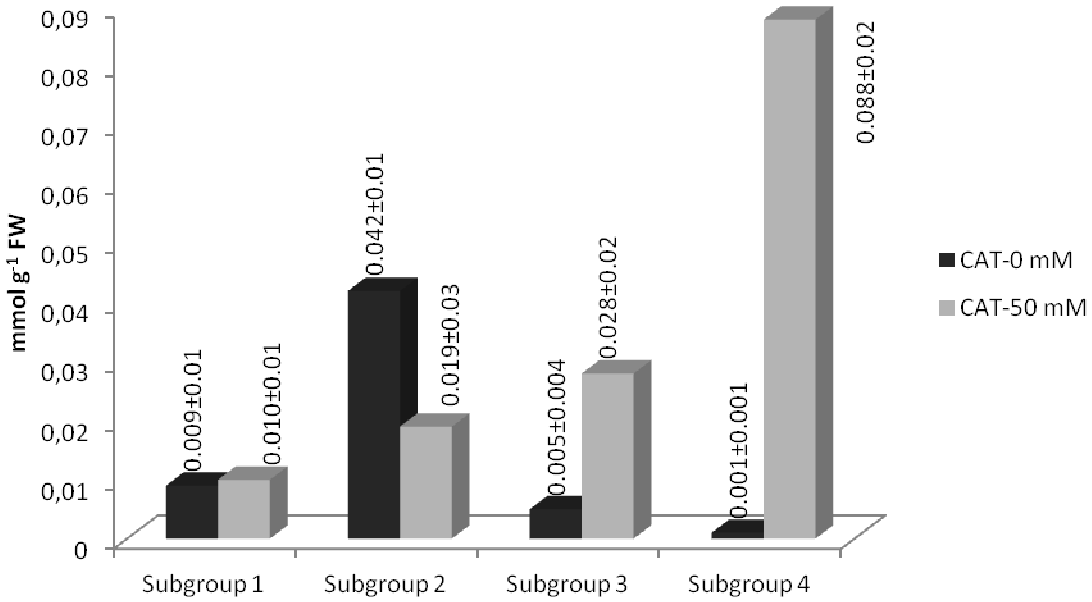

Fig. 3. Estimated means of variables for model with four sub-population for CAT enzyme activity at 0 mM and 50 mM salt applications in melon genotypes

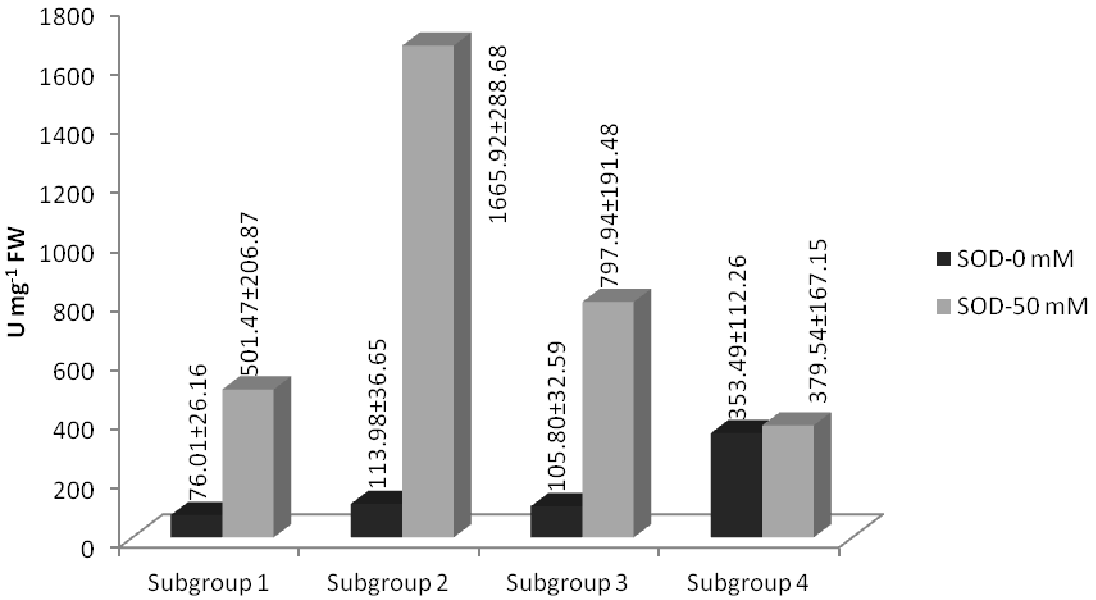

Fig. 4. Estimated means of variables for model with four sub-populations for SOD enzyme activity at 0 mM and 50 mM salt applications in melon genotypes

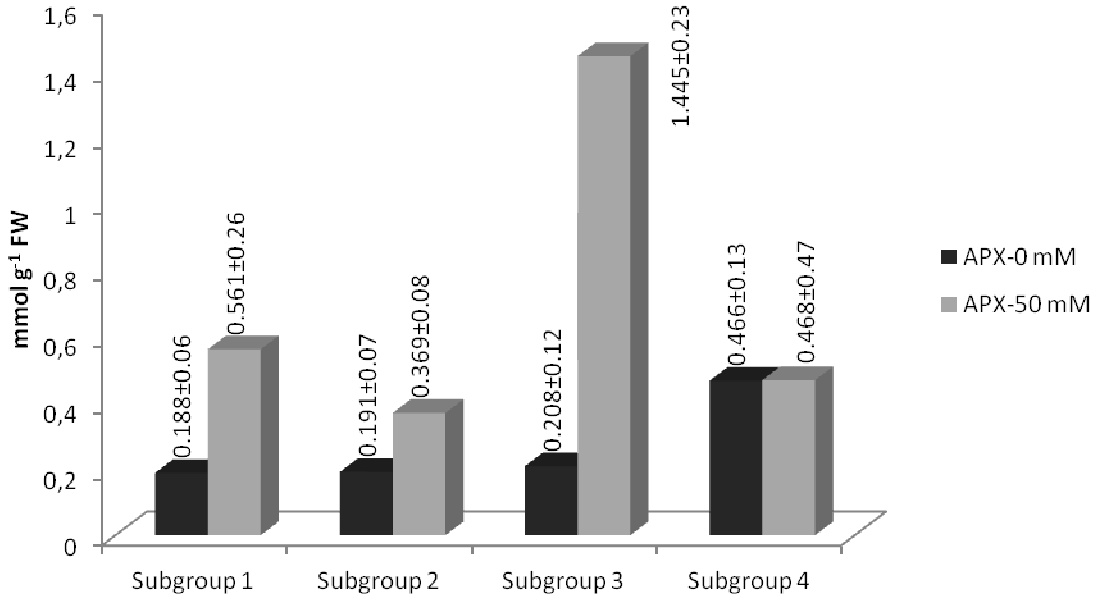

Fig. 5. Estimated means of variables for model with four sub-population for APX enzyme activity at 0 mM and 50 mM salt applications in melon genotypes

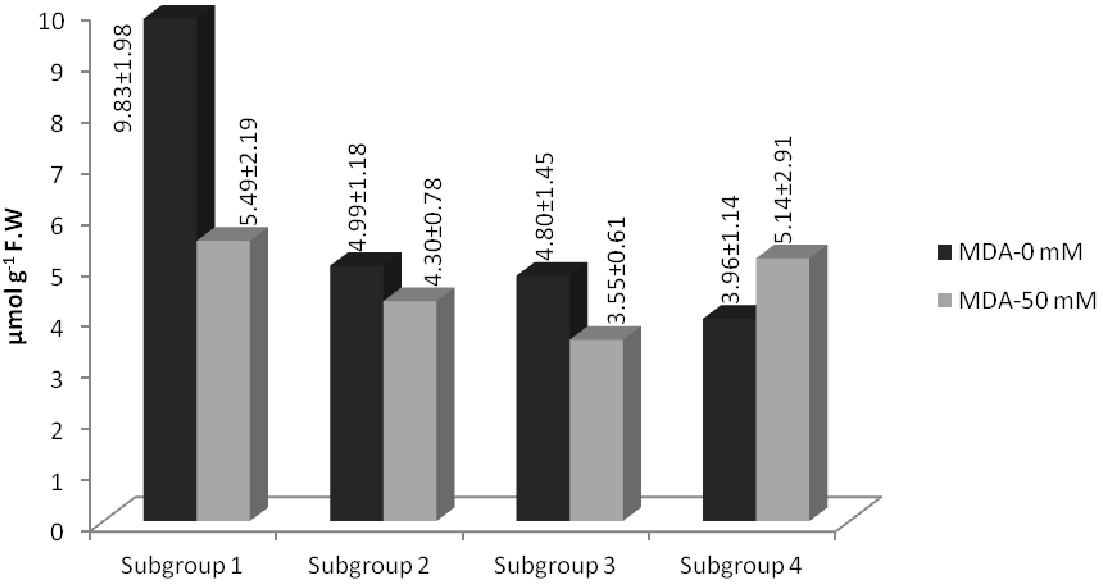

Fig. 6. Estimated means of variables for model with four sub-population for MDA content at 0 mM and 50 mM salt applications in melon genotypes

Table 3. Sub-populations according to model selection criteria for nutrition composition

Subgroups	Model selection criteria*					
	0 mM			50 mM		
	BIC	AIC	entropy	BIC	AIC	entropy
Model with one sub-population	435.83	426.13	–	441.04	437.82	–
Model with two sub-populations	422.07	417.92	0.94	430.13	424.53	0.97
Model with three sub-populations	413.02	409.42	0.98	418.51	411.43	0.99
Model with four sub-populations	420.85	416.61	0.95	431.56	426.18	0.96

* Lowest BIC and AIC values explain the best model

K : Na ratios play a role in determining salt tolerance. The YYU29 genotype was found to have the highest K : Na ratio under saline conditions (1.79), and the YYU23 genotype had the highest K : Na ratio among the salt-free control applications (9.77). All genotypes tested showed reductions in K : Na ratios following salt application, with the greatest reduction observed in the YYU22 genotype and the smallest reduction observed in the YYU11 genotype (–85.84% and –57.09% respectively).

The regularity of ion transport in plant cells is closely related to the equilibrium between monovalent (K^+ and $Na^{+)}$ and divalent (Ca^{+2} and Mg^{+2}) cations. When the competitive intake between Na^+ and K^+ that occurs in all plants (Tester and Davenport 2003, Yilmaz et al. 2011) swings in favor of the K^+ cations, the subsequent rise in K : Na helps plants to protect themselves against salt stress [Yoshida 2002, Rubio et al. 2002]. Rates of Na^+ and K^+ absorption have been reported to vary among plant genotypes, resulting in different K : Na ratios and thus differences in salinity tolerance [Heimler et al. 1995, Lopez and Satti 1996, Yu et al. 1998, Dasgan et al. 2002].

Similar to the findings for K : Na ratios, Ca : Na ratios under saline conditions were highest in the YYU29 genotype (1.70), whereas Ca : Na ratios under non-saline (control) conditions were highest in the YYU23 genotype (9.43). The YYU18 genotype was found to have the lowest Ca : Na ratio following salt application (0.79). Decreases in Ca : Na ratios that occur under saline conditions have been reported to increase cell-membrane permeability, leading to further salt uptake, and, thus, greater toxicity [Davenport et al. 1997, Villora et al. 2000].

Using mixture modeling, three homogenous sub-populations were formed to classify melon genotypes by nutrient contents for both 50 mM NaCl salt and 0 mM NaCl control applications (tab. 5, figs 1 and 2). The model with the smallest AIC and BIC is defined as the best model (tab. 3) [Wang and Putterman 1996]. The accuracy rate of the sub-population entropy classification by nutrition content were 98% and 99% for 0 mM NaCl and 50 mM NaCl salt using Table 3, respectively [Muthén and Muthén 2014, Yesilova et al. 2016].

For both the control (0 mM NaCl) and salt stress (50 mM NaCl) applications, Sub-population 3 had the highest mean Ca and K contents and K : Na and Ca : Na ratios and the lowest mean Na content (Figures 1 and 2), whereas Sub-population 1 had the lowest mean Ca and K contents and K : Na and Ca : Na ratios and the highest mean Na content (figs 1 and 2). In other words, the genotypes in Sub-population 3 showed greater tolerance to salt stress, whereas the genotypes in Sub-population 1 showed greater susceptibility to salt stress.

The classification of genotype by Sub-population varied somewhat according to salt application. For example, with salt application, the only genotypes to be included in Sub-population 3 were the YYU29 and YYU23 genotypes, whereas with the control application, Sub-population 3 included other genotypes as well. Furthermore, the YYU15, Galia and YYU18 genotypes fell into Sub-population 2 of the control classifications, but into Sub-population 1 of the salt-stress classifications (tab. 3).

Table 4. Sub-populations according to model selection criteria for antioxidant enzyme/MDA activity

Subgroups	Model selection criteria*					
	0 mM			50 mM		
	BIC	AIC	entropy	BIC	AIC	entropy
Model with one sub-population	451.91	437.82	–	594.89	582.45	–
Model with two sub-populations	415.04	392.14	0.96	589.01	568.79	0.95
Model with three sub-populations	402.88	371.18	0.95	583.97	555.98	0.96
Model with four sub-populations	394.42	353.92	0.97	582.95	547.17	0.98
Model with five sub-populations	424.13	374.81	0.96	582.96	539.41	0.95

* Lowest BIC and AIC values explain the best model

Table 5. Mixture model results for nutrition composition, with correct classification values for three accession sub-populations

Acc.#	0 mM			50 mM		
	sub-population 1	sub-population 2	sub-population 3	sub-population 1	sub-population 2	sub-population 3
YYU-1	0.002	0.998*	0	0.005	0.995	0
YYU-1	0.444	0.556	0	0.999	0.001	0
YYU-1	0.86	0.14	0	0	1	0
YYU-4	1	0	0	0	1	0
YYU-4	1	0	0	0	1	0
YYU-4	0.967	0.033	0	0.999	0.001	0
YYU-6	0	1	0	0.001	0.999	0
YYU-6	0.003	0.997	0	0.031	0.969	0
YYU-6	0.004	0.996	0	0	1	0
YYU-10	0	1	0	0	1	0
YYU-10	1	0	0	0.728	0.272	0
YYU-10	0	1	0	0.021	0.979	0
YYU-11	1	0	0	0.011	0.989	0
YYU-11	1	0	0	0.001	0.999	0
YYU-11	0.001	0.999	0	0	1	0
YYU-12	0.887	0.113	0	0.015	0.985	0
YYU-12	1	0	0	0.003	0.997	0
YYU-12	1	0	0	1	0	0
YYU-15	0.001	0.999	0	0.995	0.005	0
YYU-15	0.002	0.998	0	1	0	0
YYU-15	0	1	0	1	0	0
YYU-18	0	1	0	1	0	0
YYU-18	0	1	0	0.878	0.122	0
YYU-18	0	1	0	1	0	0
YYU-20	0.001	0.999	0	0.001	0.999	0

YYU-20	0.992	0.008	0	0.488	0.512	0
YYU-20	0.035	0.965	0	0.589	0.411	0
YYU-21	0.004	0.996	0	0	1	0
YYU-21	0.091	0.909	0	0.051	0.949	0
YYU-21	0	1	0	1	0	0
YYU-22	0.994	0.006	0	0.886	0.114	0
YYU-22	0.743	0.257	0	0	1	0
YYU-22	0	0	1	0.016	0.984	0
YYU-23	0	0	1	0	0.986	0.014
YYU-23	0	0	1	0	0	1
YYU-23	0.051	0.949	0	0	1	0
YYU-29	0	1	0	0	0	1
YYU-29	0	0	1	0	0	1
YYU-29	0	1	0	0	0.002	0.998
Galia	0.025	0.975	0	0.989	0.011	0
Galia	0	1	0	0.039	0.961	0
Galia	0	1	0	0.955	0.045	0
Kirkagac F_1	0.051	0.949	0	0.934	0.066	0
Kirkagac F_1	0.005	0.995	0	0	1	0
Kirkagac F_1	0.999	0.001	0	0.993	0.007	0
Lokum F_1	1	0	0	0.001	0.999	0
Lokum F_1	0.001	0.999	0	0	1	0
Lokum F_1	1	0	0	1	0	0
Napolyon F_1	0.099	0.901	0	0.999	0.001	0
Napolyon F_1	0.996	0.004	0	0.772	0.228	0
Napolyon F_1	1	0	0	1	0	0
Total Acc. #	18	29	4	21	26	4

* The higher the number, the higher the probability to be in that sub-population

Enzyme activity and lipid peroxidation. When plants are subjected to stress factors like salinity, drought, high temperature, high light intensity, herbicide application and mineral deficiency, reactive oxygen species (ROS) thrive and cause oxidative damage [Ashraf and Harris 2004, Kusvuran et al. 2016]. Antioxidant enzymes such as SOD, CAT and APX improve a plant's ability to detoxify ROS [Shi and Zhu 2008] overproduction, and their activity has been shown to be higher in plant genotypes with greater tolerance to salt stress when compared to less tolerant genotypes [Ahmad et al. 2012].

The findings of this study regarding changes in enzyme activity and MDA content of melon genotypes with salt stress are given in Table 6. According to these findings, sensitivity to salt resulted in decreased CAT and APX enzyme activities for some genotypes, but no decrease in SOD activity could be identified. In general, CAT activity of melon genotypes varied with salt stress, with the YYU6 genotype showing the greatest increase in comparison to the control (4100.00%), and the YYU23 genotype showing the greatest decrease (–88.24%) in comparison to the control (Table 6). With regard to APX activity, the YYU6 genotype had the highest amount of APX enzyme activity (0.589 mmol g^{-1} FW) in the control application, whereas the YYU4 genotype had the lowest APX enzyme activity (0.125 mmol g^{-1} FW) in

Table 6. Enzyme activity and MDA content of melon accessions and cultivars with/without salt application

Acc.#	CAT (mmol g^{-1} FW)			SOD (U mg^{-1} FW)			APX (mmol g^{-1} FW)			MDA (µmol g^{-1} FW)		
	0 mM	50 mM	change (%)	0 mM	50 mM	change (%)	0 mM	50 mM	change (%)	0 mM	50 mM	change (%)
YYU1	0.013 ±0.020	0.027 ±0.035	107.69	229.72 ±234.24	1290.00 ±710.00	461.55	0.256 ±0.13	0.375 ±0.05	46.48	3.74 ±1.23	5.10 ±0.09	36.36
YYU4	0.008 ±0.007	0.012 ±0.009	50.00	89.38 ±31.24	650.98 ±326.52	628.33	0.125 ±0.06	1.208 ±0.39	866.40	6.92 ±4.95	5.85 ±2.36	–15.46
YYU6	0.001 ±0.000	0.042 ±0.055	4100.00	333.33 ±0.00	425.83 ±3.88	27.75	0.589 ±0.00	0.057 ±0.00	–90.32	4.30 ±0.54	6.19 ±0.00	43.95
YYU10	0.003 ±0.004	0.013 ±0.000	333.33	140.56 ±78.26	750.00 ±0.00	433.58	0.304 ±0.08	0.714 ±0.00	134.87	4.26 ±1.64	7.48 ±0.00	75.59
YYU11	0.003 ±0.001	0.034 ±0.009	1033.33	155.56 ±100.46	503.50 ±59.34	223.67	0.363 ±0.22	0.581 ±0.08	60.06	5.25 ±3.17	7.61 ±2.96	44.95
YYU12	0.003 ±0.003	0.049 ±0.028	1533.33	244.38 ±222.12	598.29 ±0.00	144.82	0.268 ±0.08	0.786 ±0.61	193.28	5.98 ±1.55	3.48 ±0.51	–41.81
YYU15	0.006 ±0.009	0.003 ±0.001	–50.00	111.04 ±25.52	861.11 ±638.88	675.50	0.137 ±0.04	0.464 ±0.00	238.69	3.40 ±0.64	3.48 ±0.00	2.35
YYU18	0.013 ±0.018	0.018 ±0.008	38.46	125.25 ±44.16	629.63 ±390.20	402.70	0.220 ±0.12	0.768 ±0.05	249.09	5.68 ±1.59	4.09 ±0.25	–27.99
YYU20	0.005 ±0.002	0.040 ±0.056	700.00	95.78 ±27.12	360.50 ±37.43	276.38	0.196 ±0.11	0.417 ±0.05	112.76	4.00 ±1.15	5.68 ±1.54	42.00
YYU21	0.005 ±0.006	0.025 ±0.037	400.00	71.87 ±10.57	364.01 ±157.62	406.48	0.226 ±0.18	0.387 ±0.15	71.24	5.08 ±0.15	4.00 ±0.90	–21.26
YYU22	0.053 ±0.007	0.020 ±0.032	–62.26	127.36 ±32.18	610.39 ±221.54	379.26	0.178 ±0.00	0.405 ±0.06	127.53	4.90 ±1.92	2.80 ±0.63	–42.86
YYU23	0.017 ±0.014	0.002 ±0.001	–88.24	101.17 ±38.53	767.86 ±634.61	658.98	0.321 ±0.20	0.304 ±0.00	–5.30	6.37 ±3.49	3.91 ±2.28	–38.62
YYU29	0.006 ±0.003	0.004 ±0.000	–33.33	105.52 ±37.33	564.94 ±292.20	435.39	0.143 ±0.08	0.929 ±0.53	549.65	6.71 ±2.00	4.00 ±1.64	–40.39
Galia	0.004 ±0.004	0.046 ±0.017	1050.00	185.45 ±83.16	490.64 ±144.63	164.57	0.208 ±0.16	1.491 ±0.31	616.83	4.65 ±2.47	3.29 ±0.63	–29.25
Kirkagac F_1	0.003 ±0.002	0.004 ±0.005	33.33	120.30 ±29.55	545.45 ±0.00	353.41	0.226 ±0.05	0.673 ±0.34	197.79	5.03 ±2.07	3.18 ±0.72	–36.78
Lokum F_1	0.029 ±0.028	0.101 ±0.025	248.28	79.00 ±2.94	270.84 ±147.31	242.84	0.149 ±0.06	1.179 ±0.59	691.28	4.77 ±0.82	4.65 ±2.90	–2.52
Napolyon F_1	0.028 ±0.021	0.016 ±0.008	–42.86	78.21 ±10.02	424.24 ±212.12	442.44	0.215 ±0.05	0.524 ±0.28	143.72	5.48 ±2.82	5.89 ±3.20	7.48

Table 7. Mixture model results for antioxidant enzyme/MDA activity, with correct classification values for four accession sub-populations

Acc.#	0 mM				50 mM			
	sub-population 1	sub-population 2	sub-population 3	sub-population 4	sub-population 1	sub-population 2	sub-population 3	sub-population 4
YYU-1	0	0	0	1*	1	0	0	0
YYU-1	0	0	1	0	0	1	0	0
YYU-1	0	1	0	0	–	–	–	–
YYU-4	0	0	1	0	0.997	0	0.003	0
YYU-4	1	0	0	0	0.993	0	0.007	0
YYU-4	0	0	1	0	0	0	1	0
YYU-6	0	0	0	1	1	0	0	0
YYU-6	0	0	0	1	0	0	0	1
YYU-10	0	0	0.434	0.566	0.997	0	0.003	0
YYU-10	0	0	1	0	0.997	0	0.003	0
YYU-11	0	0	0.001	0.999	–	–	–	–
YYU-11	0.912	0	0.088	0	0.994	0	0.001	0.005
YYU-11	0	0	1	0	1	0	0	0
YYU-12	0	0	0	1	–	–	–	–
YYU-12	0.111	0	0.889	0	0	0	0	1
YYU-15	0	0	1	0	0	1	0	0
YYU-15	0	0	1	0	1	0	0	0
YYU-18	0	0	1	0	–	–	–	–
YYU-18	0.017	0	0.983	0	–	–	–	-
YYU-18	0	1	0	0	0.743	0.003	0.253	0
YYU-20	0	0	1	0	1	0	0	0
YYU-20	0.002	0	0.998	0	0	0	0	1
YYU-20	0	0	1	0	–	–	–	-
YYU-21	0	0	1	0	0.001	0	0	0.999
YYU-21	0	0	1	0	1	0	0	0
YYU-21	0.001	0	0.999	0	1	0	0	0
YYU-22	0	1	0	0	0.999	0	0.001	0
YYU-22	0	1	0	0	1	0	0	0
YYU-23	0	0	1	0	–	–	–	-
YYU-23	0	0.967	0.033	0	1	0	0	0
YYU-23	0.999	0	0	0	0	1	0	0
YYU-29	0.553	0	0.447	0	0.058	0	0.942	0
YYU-29	0.001	0	0.999	0	1	0	0	0
Galia	0	0	0.012	0.988	–	–	–	-
Galia	0	0	1	0	0.003	0	0.995	0.002
Galia	0.11	0	0.89	0	0.001	0	0.999	0
Kirkagac F_1	0	0	1	0	–	–	–	–
Kirkagac F_1	0	0	1	0	1	0	0	0
Kirkagac F_1	0.087	0	0.913	0	0.977	0	0.023	0
Lokum F_1	0	1	0	0	0	0	0	1
Lokum F_1	0	0	1	0	0	0	0	1
Napolyon F_1	–	–	–	–	1	0	0	0
Napolyon F_1	0	1	0	0	1	0	0	0
Napolyon F_1	0.294	0	0.706	0	1	0	0	0
Total Acc.	4	7	25	7	22	3	4	6

* The higher the number, the higher the probability to be in that sub-population

the control application (tab. 6). The greatest increase in APX activity with salt application was observed in the YYU4 genotype, which had an increase in APX activity of 866.40% with salt application. All melon genotypes showed an increase in APX activity with salt stress except for the YYU6 and YYU23 genotypes, which showed decreases of 90.32% and 5.30%, respectively, in APX activity (tab. 6). In terms of SOD activity in response to salt stress, YYU15 was the genotype with the highest rate of change (675.50%) whereas the YYU6 genotype, which had the highest amount of SOD activity under the control application (333.33 U mg^{-1} FW), had the lowest rate of change (27.75%) in response to salt application (tab. 6).

Previous studies have reported SOD activity in melon to be affected by salt stress [Keling et al. 2013, Kusvuran et al. 2007a]. However, not all genotypes show the same response to salt in terms of SOD activity; therefore, it has been suggested that CAT activity might be a better indicator of genotypic tolerance/sensitivity to salt stress [Kusvuran et al. 2007a]. A study by De Azevedo Neto et al. [2006] reported both CAT and APX to play important roles in H_2O_2 detoxification.

MDA contents also varied between the salt and control applications, with 41% of melon genotypes showing increases in MDA content in response to salt stress and the remaining 59% of genotypes showing decreases in MDA content in response to salt stress (tab. 6). The highest rate of increase in MDA content (75.59%) was observed in the YYU10 genotype, followed by the YYU11 genotype (44.95%), which had the highest total amount of MDA, whereas the highest rates of decrease in MDA content (42.86%) were observed in the YYU22 genotype, followed by the YYU12 (41.81%) and YYU29 (40.39%) genotypes (tab. 6).

MDA is produced by the oxidation of lipids from cell membranes damaged by environmental stress and may provide information about how plants respond to salt stress [Bharti et al. 2016], which varies among species as well as among genotypes. While studies conducted with bean [Yasar et al. 2008] pumpkin [Sevengor et al. 2011] as well as melon [Keling et al. 2013] reported all genotypes to show increases in MDA content with salt application, studies by Kuşvuran et al. [2007b, 2008] found some melon genotypes to exhibit decreases in MDA content with salt application.

In the present study, mixture modeling was able to classify melon genotypes into four homogenous sub-populations according to antioxidant enzyme activity/MDA content for both the 50 mM NaCl salt and 0 mM NaCl control applications (tabs 4 and 7, figs 3–6). The accuracy rate of this sub-population entropy classification by enzyme activity/MDA content were 97% and 98% for 0 mM NaCl and 50 mM NaCl salt using Table 4, respectively [Muthén and Muthén 2014, Yesilova et al. 2016]. Under salt-free (control) conditions, sub-population 2 showed the highest CAT activity (mean: 0.042 mmol g^{-1} FW), whereas sub-population 4 showed the highest SOD (mean: 353.491 U mg^{-1} FW) and APX (mean: 0.466 mmol g^{-1} FW) activity as well as the lowest MDA content (figs 3–6). By contrast, under saline conditions, sub-population 4 showed the highest CAT activity (0.088 mmol g^{-1} FW), sub-population 2 showed the highest SOD activity (1665.92 U mg^{-1} FW), and sub-population 3 showed the highest APX activity (3.548 μmol g^{-1} FW) as well as the lowest MDA content (1.445 mmol g^{-1} FW). In response to salt application, CAT activity increased in sub-populations 1, 3 and 4, whereas CAT activity decreased in sub-population 2 (figs 3–6). Moreover, whereas most genotypes fell into sub-population 1 under saline conditions, under salt-free conditions, most genotypes fell into sub-population 3 (tab. 7). In contrast to the distribution of genotypes for nutrient content (tab. 5), the distribution of genotypes with regard to enzyme activity showed less clear results, indicating that greater variations in enzyme activity occur in response to salt application and, therefore, enzyme activity alone is not a good indicator of salt tolerance/sensitivity of melon genotypes (tab. 7).

Photosynthetic content

Chlorophyll (*a*, *b*, total) and carotenoid contents of melon genotypes under saline and salt-free (control) conditions are given in Table 6. In general, pho-

Table 8. Photosynthetic pigment content of melon accessions and cultivars with/without salt application

Acc.#	Chlorophyll *a*			Chlorophyll *b*			Total chlorophyll			Carotenoid		
	0 mM	50 mM	change (%)	0 mM	50 mM	change (%)	0 mM	50 mM	change (%)	0 mM	50 mM	change (%)
YYU1	0.603 ±0.20	0.590 ±0.07	–2.16	0.133 ±0.08	0.175 ±0.01	31.58	0.740 ±0.29	0.770 ±0.09	4.05	0.900 ±0.53	0.990 ±0.24	10.00
YYU4	0.450 ±0.16	0.490 ±0.22	8.89	0.140 ±0.05	0.190 ±0.10	35.71	0.540 ±0.25	0.677 ±0.30	25.37	0.723 ±0.40	0.750 ±0.37	3.73
YYU6	0.323 ±0.18	0.420 ±0.00	30.03	0.057 ±0.07	0.130 ±0.01	128.07	0.387 ±0.24	0.545 ±0.01	40.83	0.440 ±0.33	0.645 ±0.05	46.59
YYU10	0.380 ±0.14	0.880 ±0.00	131.58	0.163 ±0.13	0.260 ±0.00	59.51	0.537 ±0.15	1.140 ±0.00	112.29	0.447 ±0.35	0.138 ±0.00	–69.13
YYU11	0.533 ±0.15	0.820 ±0.32	53.85	0.110 ±0.05	0.245 ±0.09	122.73	0.573 ±0.18	1.055 ±0.41	84.12	0.863 ±0.45	1.280 ±0.42	48.32
YYU12	0.570 ±0.07	0.660 ±0.27	15.79	0.203 ±0.22	0.267 ±0.07	31.53	0.773 ±0.28	0.927 ±0.32	19.92	0.757 ±0.08	0.887 ±0.46	17.17
YYU15	0.540 ±0.12	0.680 ±0.00	25.93	0.175 ±0.02	0.190 ±0.00	8.57	0.720 ±0.15	0.870 ±0.00	20.83	0.620 ±0.49	1.170 ±0.00	88.71
YYU18	0.477 ±0.09	0.750 ±0.25	57.23	0.043 ±0.05	0.213 ±0.04	395.35	0.523 ±0.10	0.963 ±0.22	84.13	0.663 ±0.23	1.167 ±0.25	76.02
YYU20	0.787 ±0.18	0.490 ±0.01	–37.74	0.200 ±0.11	0.090 ±0.07	–55.00	0.910 ±0.34	0.575 ±0.06	–36.81	1.280 ±0.32	0.940 ±0.11	–26.56
YYU21	0.523 ±0.17	0.647 ±0.32	23.71	0.095 ±0.02	0.147 ±0.04	54.74	0.580 ±0.11	0.797 ±0.36	37.41	0.707 ±0.37	1.033 ±0.42	46.11
YYU22	0.563 ±0.08	0.540 ±0.32	–4.09	0.105 ±0.06	0.137 ±0.07	30.48	0.617 ±0.08	0.673 ±0.39	9.08	0.890 ±0.50	0.903 ±0.59	1.46
YYU23	0.653 ±0.24	0.775 ±0.02	18.68	0.097 ±0.06	0.165 ±0.06	70.10	0.750 ±0.20	0.940 ±0.09	25.33	0.937 ±0.44	1.210 ±0.05	29.14
YYU29	0.760 ±0.25	1.220 ±0.24	60.53	0.080 ±0.00	0.160 ±0.01	100.00	0.800 ±0.29	1.380 ±0.23	72.50	1.335 ±0.73	1.900 ±0.20	42.32
Galia	0.423 ±0.06	0.723 ±0.18	70.92	0.085 ±0.09	0.230 ±0.02	170.59	0.457 ±0.12	0.957 ±0.20	109.41	0.537 ±0.10	1.110 ±0.20	106.70
Kirkagac F_1	0.827 ±0.25	0.630 ±0.22	–23.82	0.107 ±0.22	0.291 ±0.00	171.96	0.937 ±0.30	0.713 ±0.40	–23.91	1.263 ±0.55	1.253 ±0.27	–0.79
Lokum F_1	0.673 ±0.28	0.780 ±0.08	15.90	0.063 ±0.06	0.330 ±0.22	423.81	0.733 ±0.27	1.113 ±0.14	51.84	0.973 ±0.70	1.337 ±0.32	37.41
Napolyon F_1	0.750 ±0.15	0.913 ±0.36	21.73	0.015 ±0.00	0.107 ±0.07	613.33	0.775 ±0.14	1.017 ±0.29	31.23	1.220 ±0.46	1.387 ±0.57	13.69

tosynthetic content increased with salt exposure, with the YYU10 genotype showing the highest rate of increase in both chlorophyll *a* and total chlorophyll contents (131.58% and 112.29%, respectively), the Napolyon cultivar showing the highest rate of increase in chlorophyll *b* content (613.33%), and the Galia cultivar showing some increase in carotenoid content (106.70%) (tab. 8). In contrast, the YYU20 genotype had the highest rates of decrease in chlorophyll *a* (37.74%), chlorophyll *b* (55.00%) and total chlorophyll (36.81%) contents with salt exposure (tab. 8).

The increase in photosynthetic pigments with salt stress can be attributed to the increase in antioxidant enzyme activity. This is in line with Sevengor et al. [2011], who reported antioxidant enzyme activity to inhibit chlorophyll degradation. Generally, chlorophyll content is more affected in the early stages of salt stress: Kuşvuran et al. [2008] reported decreases in chlorophyll content of seedling leaves after 8 days of salt application, whereas Amira and Qados [2011] reported increases in chlorophyll content in pea plants after 15 days of salt application. In the present study, chlorophyll data was obtained at the end of 18 days of salt application.

Correlation analysis examining changes in nutrient composition, enzyme activity/MDA content and photosynthetic pigments of melon genotypes in response to salt application are presented in Table 9. Significant negative relationships ($p < 0.01$) were found between K : Na ratio and Na content ($r = –0.718$) and between Ca : Na ratio and Na content ($r = –0.679$). This is in line with previous studies showing K and Ca to play a role in protecting plants against salt stress [Hagin et al. 1990, Grattan 1993, Catalan et al. 1994, Naido 1994, Gomez et al. 1999, Kipçak and Erdinç 2016].

A significant negative relationship ($p < 0.01$) was also found between K : Na ratio and MDA content ($r = –0.136$). This suggests that the replacement of Na with K observed to occur with salt exposure may be limited by the production of MDA, which is believed to occur under stress conditions as a result of peroxidation of essential membrane lipids in plasmalemma or intracellular organelles [Esfandieri et al. 2007].

A statistically significant positive correlation was found among the contents of different photosynthetic pigments, whereas a significant negative correlation was found between SOD and CAT activity. This may be due, in particular, to a decrease in CAT activity in some genotypes and an increase in SOD activity with salt stress in all genotypes. This is in line with Kusvuran et al. [2007a], who also reported that CAT enzyme activity gave more sensitive results under salt stress.

Table 9. Correlations among parameters evaluating salt stress

	K	Ca	Na	K : Na	Ca : Na	Chl *a*	Chl *b*	Total chl	Carotenoid	CAT	SOD	APX	MDA
K	1	0.225	–0.120	0.728**	0.298*	0.098	–0.040	0.087	0.079	–0.143	0.101	–0.139	0.048
Ca		1	–0.007	0.142	0.701	0.257	0.134	0.230	0.251	–0.140	–0.156	0.034	0.193
Na			1	–0.718**	–0.679**	0.092	0.220	0.126	0.125	0.143	–0.217	0.049	0.191
K : Na				1	0.671	0.018	–0.161	–0.013	0.001	–0.194	0.274*	–0.102	–0.136**
Ca : Na					1	0.107	–0.072	0.062	0.097	–0.219	0.057	0.012	0.040
Chl *a*						1	0.893**	0.994**	0.991**	–0.054	0.289**	–0.018	0.039
Chl *b*							1	0.929**	0.889**	0.098	0.267**	0.073	–0.028
Total Chl								1	0.985**	–0.007	0.290**	0.001	0.027
Carotenoid									1	–0.047	0.299*	–0.023	0.033
CAT										1	–0.164*	0.127	0.075
SOD											1	–0.071	–0.135
APX												1	–0.062
MDA													1

* $p < 0.05$, ** $p < 0.01$

CONCLUSIONS

Mixture model is a novel approach having important advantages compared to the cluster and factor analysis; it is resolved according to the probability of inclusion within the subgroup categories and gives the parameter estimates for each subgroup. The present study, employing mixture model in identification the response of melon accessions and cultivars to salt stress in terms of ion exchange, enzyme activity, and lipid peroxidation and photosynthetic pigment contents, found variations in how melon genotypes responded to salt stress, with local genotypes performing better than the commercial varieties examined. Whereas K and Ca intake tended to decrease with exposure to salt, enzyme activation, MDA content and photosynthetic pigment content tended to increase. These findings support the importance of genetic diversity and the emphasis developing more tolerant varieties able to cope with the problem of increasing soil salinity occurring throughout the world.

The mixture modeling utilized in the present study had entropy classification accuracy rates of 97% for nutrition-content sub-populations and 98% and for antioxidant-enzyme activity/MDA content sub-populations, indicating the successful classification of observed values.

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REFERENCES

Ahmad, P., Hakeem, K.R., Kumar, A., Ashraf, M., Akram, N.A. (2012). Salt-induced changes in photosynthetic activity and oxidative defense system of three cultivars of mustard (*Brassica juncea* L.). Afr. J. Biotechnol., 11, 2694–2703.

Aktas, H., Dasgan, H.Y., Yetisir, H., Sari, N., Koc, S., Ekici, B., Solmaz, I., Unlu, H., Aloni, B. (2009). Variations in the response of different lines and hybrids of melon (*Cucumis melo* var. *cantaloupensis*) under salt stress. Am.-Eurasian J. Agric. Environ. Sci., 5, 485–493.

Amira, M.S., Qados, A. (2011). Effect of salt stress on plant growth and metabolism of bean plant *Vicia faba* (L.). J. Saudi Soc. Agric. Sci., 10, 7–15

Ashraf, M., Harris, P.J.C. (2004). Potential biochemical indictors of salinity tolerance in plants. Plant Sci., 166, 3–16.

Bharti, N., Pandey, S.S., Barnawal, D., Patel, V.K., Kalra, A. (2016). Plant growth promoting rhizobacteria *Dietzia natronolimnaea* modulates the expression of stress responsive genes providing protection of wheat from salinity stress. Sci. Rep., 6, 1–15.

Cakmak, I., Marschner, H. (1992). Magnesium deficiency and high light intensity enhance activities of superoxide dismutase, ascorbate peroxidase, and glutathione reductase in bean leaves. Plant Physiol., 98, 1222–1227.

Carillo, P., Annunziata, M.G., Pontecorvo, G., Fuggi, A., Woodrow, P. (2011). Salinity stress and salt tolerance. In: Abiotic stress in plants-mechanisms and adaptations, Shanker, A.K., Venkateswarlu, B.B. (eds.). InTech, Croatia, 21–38.

Catalan, L., Bazlarini, Z., Talesnik, E., Serono, R., Karlin, U. (1994). Effect of salinity on germination and seedling growht of *Prosopis flexuosa*. For. Ecil. Mang., 63, 347–357.

Çulha, Ş., Çakirlar, H. (2011). The effect of salinity on plants and salt tolerance mechanisms. AKU J. Sci., 11, 11–34.

Dalrymple, M.L., Hudson, I.L., Ford, R.P.K. (2003). Finite mixture, zero-inflated poisson and hurdle models with application to SIDS. Comput. Stat. Data An., 41, 491–504.

Damianos, N., Savvas, D. (2016). NaCl accumulation and macronutrient uptake by a melon crop in a closed hydroponic system in relation to water uptake. Agric. Water Manageric., 165, 22–32.

Dasgan, H.Y., Aktaş, H., Abak, K., Çakmak, İ. (2002). Determination of screening techniques to salinity tolerance in tomatoes and investigation of genotype responses. Plant Sci., 163, 695–703.

Dasgan, H.Y., Koc, S. (2009). Evaluation of salt tolerance in common bean genotypes by ion regulation and searching for screening parameters. J. Food Agric. Environ., 7, 363–372.

Davenport, R.J., Reid, R.J., Smith, F.A. (1997). Sodium-calcium interaction in two wheat species differing in salinity tolerance. Physiol. Plant., 99, 323–327.

De Azevedo Neto, A.D., Prisco, J.T., Eneas-Filho, J., De Abreu, C.E.B., Gomes-Filho, E. (2006). Effect of salt stress on antioxidative enzymes and lipid peroxidation in leaves and roots of salt-tolerant and salt-sensitive maize genotypes. Environ. Exp. Bot., 56, 87–94.

Esfandieri, E., Shekari, F., Shekari, F., Esfandieri, M. (2007). The effect of salt stress on antıoxidant enzymes activity and lipid peroxidation on the wheat seedling. Not. Bot. Horti. Agrobot. Cluj-Napoca, 35, 48–56.

Faostat, (2013). Statistic Database. http://faostat.fao.org/ [date of access: 16.06.2017].

Franco, J.A., Fernandez, J.A., Banon, S., Gonzalez, A. (1997). Relationship between the effects of salinity on seedling leaf area and fruit yield of six muskmelon cultivars. Hortic. Sci., 32, 642–644.

Gomez, J.M, Hernandez, J.A., Jimenez, A, Del Rio, L.A., Sevilla, F. (1999). Differential response of antioxidative enzymes of chloroplast and mitochondria to long term NaCl stress of pea plants. Free Radic. Res., 31, 11–18.

Grattan, S.R. (1993). Plant response to salinity and crop tolerance. In: Agricultural salinity and drainage, Hanson, B.R, Grattan, S.R., Fulton A. (eds). University of California, Davis, 11–37.

Hagin, J., Olsen, S.R., Shaviv, A. (1990). Review of interaction of ammonium nitrate an potassium nutrition of crops. J. Plant Nutr., 13, 1211–1226.

Heath, R.L., Packer, L. (1968). Photoperoxidation in isolated chloroplasts: I. Kinetics and stoichiometry of fatty acid peroxidation. Arch. Biochem. Biophys., 125, 189–198.

Heimler, D., Tattini, M., Ticci, S., Coradeshi, M.A., Traversi, M.L. (1995). Growth, ion accumulation, and lipid composition of two olive genotypes under salinity. J. Plant Nutr., 18, 1723–1734.

Jebara, S., Jebara, M., Limam, F., Aouani, M.E. (2005). Changes in ascorbate peroxidase, catalase, guaiacol peroxidase and superoxide dismutase activities in common bean (*Phaseolus vulgaris*) nodules under salt stress. J. Plant Physiol., 162, 929–936.

Keling, H., Ling, Z., Jitao, W., Yang, Y. (2013). Influence of selenium on growth, lipid peroxidation and antioxidative enzyme activity in melon (*Cucumis melo* L.) seedlings under salt stress. Acta Soc. Bot. Pol., 82, 193–197.

Kipçak, S., Erdinç, Ç. (2016). Determination of salt tolerance levels of common bean (*Phaseolus vulgaris* L.) genotypes grown in Van Lake Basin. YYU J. Agric. Sci., 26(3), 421–429 (in Turkish).

Kusvuran, Ş., Ellialtioglu, S., Yasar, F., Abak, K. (2007a). Effects of salt stress on ion accumulation and activity of some antioxidant enzymes in melon (*Cucumis melo* L.). J. Food Agric. Environ., 5, 351–354.

Kuşvuran, Ş., Ellialtioğlu, S., Abak, K., Yaşar, F. (2007b). Response of some melon (*Cucumis* sp.) genotypes to salt stress. Ankara Univ. J. Agric. Sci., 13, 395–404.

Kuşvuran, Ş., Yaşar, F., Abak, K., Ellialtioğlu, Ş. (2008). Changes occur in lipid peroxidation, chloropyll and ion contents of some salt tolerant and sensitive *Cucumis* sp. genotypes grown under salinity stress. Y.Y.U. J. Agric. Sci., 18, 11–18.

Kuşvuran, S. (2012). Ion regulation in different organs of melon (*Cucumis melo*) genotypes under salt stress. Int. J. Agric. Biol., 14, 141–144.

Kuşvuran, Ş., Ellialtioğlu, Ş., Daşgan, H.Y., Abak, K. (2012). Salt tolerance some native melon accessions. Turk. J. Sci. Rev., 5, 151–153 (in Turkish).

Kusvuran, S., Kiran, S., Ellialtioglu, S.S. (2016). Antioxidant enzyme activities and abiotic stress tolerance relationship in vegetable crops. In: Abiotic and biotic stress in plants – recent advances and future perspectives, Shanker, A., Shanker, C., (eds). InTech, Croatia, 481–503.

Lichtenthaler, H.K., Wellburn, A.R. (1983). Determinations of total carotenoids and chlorophylls a and b of leaf extracts in different solvents. Biochem. Soc. Trans., 11, 591–592.

Lopez, M.V., Satti, S.M.E. (1996). Calcium and potassium-enhanced growth and yield of tomato under sodium chloride stress. Plant Sci., 114, 19–27.

Mao, C.X., Yang, N., Zhong, J. (2013). On population size estimators in the poisson mixture model. Biometrics, 69, 758–765.

Marschner, H. (1995). Mineral nutrition of higher plants. Academic Press, London, 657–680.

Martinez, M.J., Lavergne, C., Trottier, C. (2009). A mixture model-based approach to the clustering of exponential repeated data. J. Multivar. Anal., 100, 1938–1951.

Mendlinger, S., Pasternak, D. (1992). Screening for salt tolerance in melons. Hortic. Sci., 27, 905–907.

Munns, R., Tester, M. (2008). Mechanisms of salinity tolerance. Annu. Rev. Plant Biol., 59, 651–681.

Muthén, L.K., Muthén, B. (2014). Mplus: User's guide. Muthén & Muthén, Los Angeles, CA.

Naido, G. (1994). Growth water and ion relations in the coastal halophytes *Trilochin bulbosa* and *T. striata*. Environ Expl. Bot., 34, 419–426.

Peleg, Z., Walia, H., Blumwald, E. (2012). Integrating genomics and genetics to accelerate development of

drought and salinity tolerant crops. In: Plant biotechnology and agriculture: Prospects for the 21st Century, Altman, A., Hasegawa, P.M. (eds). Academic Press, Elsevier, Amsterdam–Boston, 271–285.

Pitrat, M. (2008). Melon. In: Vegetables I, Asteraceae, Brassicaceae, Chenopodiaceae and Cucurbitaceae, Prohens, J., Nuez, F. (eds). Springer Science, Business Media, LLC, New York, 283–316.

Rubio, C., Hadisson, A., Martin, R.E., Baez, A., Martin, M.M., Álvarez, R. (2002). Mineral composition of the red and green pepper (*Capsicum annuum*) from Tenerife Island. Eur. Food Res. Technol., 214, 501–504.

Sensoy, S., Turkmen, O., Kabay, T., Erdinc, C., Turan, M., Yildiz, M. (2005). Determination of salinity tolerance of melon genotypes collected from Lake Van Basin. J. Bio-Sci., 5, 637–642.

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

Sensoy, S., Demir, S., Turkmen, O., Erdinc, C., Durak Demirer, E. (2012). Variation in the reaction of Lake Van Basin melon genotypes to *Fusarium oxysporum* f. sp. *melonis*. Int. J. Agric. Biol., 14, 1024–1026.

Sevengor, S., Yasar, F., Kusvuran, S., Ellialtioglu, S. (2011). The effect of salt stress on growth, chlorophyll content, lipid peroxidation and antioxidative enzymes of pumpkin seedling. Afr. J. Agric. Res., 6, 4920–4924.

Shani, U., Dudley, L.M. (2001). Field studies of crop response to water and salt stress. Soil Sci. Soc. Am. J., 65, 1522–1528.

Shi, Q.H., Zhu, Z.J. (2008) Effects of exogenous salicylic acid on manganese toxicity, element contents and antioxidative system in cucumber. Environ. Exp. Bot., 63, 317–326.

Tester, M., Davenport, R. (2003). Na+ tolerance and Na+ transport in higher plants. Ann. Bot., 91, 503–527.

Tuteja, N., Singh, L.P., Gill, S.S., Gill, R., Tuteja, R. (2012). Salinity stress: A major constraint in crop production. In: Improving crop resistance to abiotic stress, Tuteja, N., Gill, S.S., Tiburcio, A.F., Tuteja, R. (eds). Wiley-Blackwell, Weinheim, 71–96.

Türkmen, Ö., Şensoy, S., Erdinç, Ç. (2008). Determination of yield and related traits of melon genotypes collected from Lake Van Basin. Selcuk J. Agric. Food Sci., 22, 64–70. (in Turkish).

Villora, G., Moreno, A., Pulgar, G., Romero, L. (2000). Yield improvement in zucchini under salt stress: determining micronutrient balance. Sci. Hortic. (Amsterdam), 86, 175–183.

Wang, P, Puterman, M.L., Cockburn, I.M., Le, N. (1996). Mixed poisson regression models with covariate dependent rates. Biometrics, 52, 381–400.

Wu, S.J., Ding, L., Zhu, J.K. (1996). SOS1, a genetic locus essential for salt tolerance and potassium acquisition. Plant Cell, 8, 617–627.

Yasar, F., Ellialtioglu, S., Yildiz, K. (2008). Effect of salt stress on antioxidant defense systems, lipid peroxidation and chlorophyll content in green bean. Russ. J. Plant Physiol., 55, 782–786.

Yeşilova, A., Özrenk, K., Kaki, B., Almali, M.N., Balta, F. (2010). Locational classification of walnut (*Juglans Regia* L.) genotypes collected from Lake Van Basin by using mixture modeling. Afr. J. Agric. Res., 5, 1509–1514.

Yeşilova, A., Yilmaz, A., Ser, G., Kaki, B. (2016). Modeling with Gaussian mixture regression for lactation milk yield in Anatolian buffaloes. Indian J. Anim. Res., 50, 989–994.

Yildiz, S., Balkaya, A. (2016). The hypocotyls traits of salt tolerant winter squash and pumpkin rootstocks and the determination of grafting compatibility with cucumber. YYU J. Agric. Sci., 26, 538–546.

Yilmaz, E., Tuna, A.L., Bürün, B. (2011). Tolerance strategies developed by plants to the effects of salt stress. C.B.U. J. Sci., 7, 47–66.

Yoshida, K. (2002). Plant biotechnology: Genetic engineering to enhance plant salt tolerance. J. Biosci. Bioeng., 94, 585–590.

Yu, B., Gong, H., Liu, Y. (1998). Effects of calcium on lipid composition and function of plasma membrane and tonoplast vesicle isolated from roots of barley seedlings under salt stress. J. Plant Nutr., 21, 1589–1600.

Zengin, F.K. (2007). Effects of some heavy metals on pigment content in bean (*Phaseolus vulgaris* L. cv. Strike) seedlings. KSU J. Sci. Engin., 10, 6–12.

Zhu, J.K. (2001). Plant salt tolerance. Trends Plant Sci., 6, 66–71.