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Article

Population parameters of *Tetranychus turkestani* (Acari: Prostigmata: Tetranychidae) on fourteen melon genotypes

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Abstract

The antixenosis effects of Galia, CMD-158, CMC-132, CMI-157, CMI-167, CMI-175, Ananasi, Yellow Canary, Samsoori, Honey Dew, Bargney, CM-170, Khaghani and Garmsari, and the life table parameters of *T. turkestani* on CMC-132, CMI-167, Ananasi, Samsoori, Honey Dew and Bargney, were examined at 28 ± 1°C, 65 ± 10 % RH and a photoperiod of 16:8 L:D. In free-choice assay, the lowest preferences by adults were observed on CMI-167, Samsoori and Ananasi opposed to Honey Dew and Bargney were preferred the highest by adults of *T. turkestani*. The longest developmental times for both sexes were observed on CMC-132 and Ananasi, while the shortest developmental times were obtained on Honey Dew, Samsoori for females. The lowest total fecundity was observed on CMC-132 whereas the maximum was on Honey Dew. In addition, the highest value of intrinsic rate of increase (r_m), net reproductive rate (R_0), finite rate of increase (λ) of *T. turkestani* were observed on the Honey Dew. The Weibull and Enkegaard models were used to fit survivorship (l_x) and age specific fecundity (m_x) data, respectively. The comparison and cluster analysis of biological parameters of *T. turkestani* on different melon genotypes demonstrated that CMC-132, Ananasi and CMI-167 were the most resistant genotypes to this pest.

Key words: intrinsic rate of increase, life history, reproduction, plant resistance, host plant.

Introduction

Different arthropods and diseases cause important Melon's (*Cucumis melo* L.; Cucurbitaceae) crop losses and among them *Tetranychus turkestani* Ugarov & Nikolski is one of the most important pests. Its population has increased extremely in melon-producing areas of Iran and under appropriate conditions this spider mite can produce nearly 20 generations a year (Khanjani & Hadad Irani-Nejad 2009). This mite infests both sides of the leaves specially underside where it produces much webbing and it causes yellow chlorotic spots on the leaves. Heavy infestation causes leaves to turn brown and die, lowering yields and weakening plants (Martinez–Ferrer *et al*. 2006).

As in many other agricultural areas in the world, control of spider mite in Iran relies on acaricide application. The short life span, high fecundity, irregular treatments acaricides and its ability to develop resistance to many acaricides have made chemical control of this mite particularly difficult (Lee *et al.* 2003). Recently, the rising awareness of environment issues, the side-effects of pesticide toxicity to human beings, and pesticide resistance have motivated researchers to find alternative control methods. The most important alternative control methods against the Acarina are integrated pest management (IPM) using host plants genetically based on plant resistance (Lorenzen *et al*. 2001). The first step in identifying a pest resistant genotype is to understand sources and mechanisms of host plant resistance to specific pest species (Jyoti *et al*. 2001). The mechanism of plant resistance against a pest can be caused by antixenosis, antibiosis and tolerance or some combinations of them (Painter 1951; Kogan & Ortman 1978).

Currently host–plant resistance to spider mites has been reported in different crops such as melon lines, water melon and soybean (Mansour *et al*. 1987; Fadel *et al*. 1994; Lopez *et al*. 2005; Sedaratian *et al*. 2009).

Although the general life history of *T. turkestani* has been documented on some crops, there is a critical need for more detailed information on the basic biology of this mite, specially on newly produced genotypes of melon. The objective of the present study is to determine the effect of different melon varieties on biological and demographic parameters of *T. turkestani* using detached leaves in order to develop future IPM programs.

Material and methods

Planting the plants

The fourteen melon genotypes including: Galia, CMD-158, CMC-132, CMI-157, CMI-167, CMI-175, Ananasi, Yellow Canary, Samsoori, Honey Dew, Bargney, CM-170, Khaghani, Garmsari were used. All genotypes were supplied from the Seed and Plant Improvement Institute (SPII) of Karaj, Alborz province, Iran. Each genotype was planted in air conditioned glasshouses at 28 ± 2°C and with a light intensity of 500lux at leaf sample height [as measured with aLI-I 8513 photometer; LI-COR, Lincoln, Nebr.] and a photoperiod of L:D 16:8 h.

Rearing of mites

Mites were collected from infested weeds, Agricultural College campus of Bu-Ali Sina University and then, were reared on bean plants (*Phaseulos vulgaris* L. cv. Khomein) in a growth chamber at 26 ± 1°C, 60 ± 5 % RH and a photoperiod of L:D 16:8 h.

Free-choice assay (antixenosis)

A free-choice assay was carried out in order to assess the genotype preferences of *T. turkestani*. The assay was set up in a test device consisting of a white cylindrical plastic cage (1 m in diameter and 15 cm height). Fourteen potted plants with similar vegetative growth were randomly selected per each cultivar. These pots laid on the circumference of a 50-cm-radius circle which was set beside the device. One apical leaf of these plants was introduced in cylinder making it possible for all genotypes to be compared. For each replicate, twenty female mites were placed in the center of the device bottom. During the assay, the device top was covered by a thin plastic lid in order to limit mite's movement due to air currents. The assay lasted 48 hrs and was

carried out at 16 L: 8 D photoperiod, 300 lux of light intensity on the leaf surface, and 28 ± 1°C. Then, the apical leaves of the potted plants were examined under a dissecting stereomicroscope and the mites were counted for each tested plant. This assay, following a complete random design, was replicated ten times for each genotype and each plant represented a replicate.

Life table experiment

To accomplish the experiments, the leaf disc method was used. Based on free-choice assay, the developmental time and life table of *T. turkestani* were studied on six melon genotypes including: CMC-132, CMI-167, Ananasi, Samsoori, Honey Dew and Bargney at 28 ± 1°C, RH of 60 ± 5% and a photoperiod of L:D 16:8 h. At the first step, five pairs of adults were transferred from bean plants to leaf disks of different melon genotypes with a tiny hair brush (000). In order to collect the same age eggs, the adults of *T. turkestani* were removed after 6 h and then the eggs were individually transferred to the leaf disks (one egg per leaf disk). A total of 50 leaf discs of each genotype were prepared. All eggs and subsequent stages were checked and recorded at 8:00 AM and 4:00 PM until the emergence of adults; thereafter a pair of male and female mites were transferred to each melon genotype's leaf disk. After emergence of the adults, duration of pre-oviposition, oviposition and post-oviposition periods as well as longevity, daily fecundity and total fecundity were also recorded.

Statistical analysis

Free-choice assay

Data of free choice assay were carried out according to a complete random design. All data were subjected to a one-way Analysis of Variance (ANOVA) using the Proc GLM procedure of SAS (2003), after their normal distribution and equal variance verification. Means were compared using the Tukey's multiple range tests at $P < 0.05$.

Life table analysis

The life history raw data of all individuals were analyzed based on the age-stage, two-sex life table theories (Chi & Liu 1985; Chi 1988) using the TWOSEX-MSChart program. The means and standard errors of the population parameters were estimated using the Bootstrap method. The age-stage specific survival rate (s_{xj}) (where x is the age and j is the stage), age-stage specific fecundity (f_{xj}), age-specific survival rate (l_x), age-specific fecundity (m_x), and population parameters including: intrinsic rate of increase (r_m); net reproduction rate (R_0); and the mean generation time (T) calculated accordingly. The intrinsic rate of increase is estimated using iterative bisection method:

$$\sum_{x=0}^{\infty} e^{-r(x+1)} l_x m_x = 1 \qquad [1]$$

With age indexed from 0 (Goodman 1982). To take stage differences into consideration, the l_x and m_x were calculated by the use of the following formulae:

$$l_x = \sum_{j=1}^{k} s_{xj} \qquad [2]$$

and

$$m_x = \frac{\sum_{j=1}^{k} s_{xj} f_{xj}}{\sum_{j=1}^{k} s_{xj}} \quad [3]$$

Where k is the number of stages (Chi & Liu 1985). As calculating life table is extremely time consuming and replication is impractical, we used the Bootstrap method to calculate the means and standard errors of the life table parameters. The mean generation time is defined as the time length that a population needs to increase to R_0-fold of its size (i.e., $e^{rT} = R_0$ or $\lambda^T = R_0$) at the stable age–stage distribution. The mean generation time is calculated as $T = \text{In}R_0/r$. The TWOSEX–MS Chart program is available at http://140.120.197.172/ecology (Chi 2008).

Survival models

The age-specific survival rate (l_x) of the adult was fitted to Weibull frequency distribution:

$$l(x) = e^{-\left(\frac{x}{b}\right)^c} \quad [4]$$

Where x is the age, b is the scale parameter that is inversely related to the mortality rate, and c is the shape parameter that allows the model to produce survival distributions of different forms, from exponential to an extreme inverted S shape (Kontodimas *et al*. 2007).

Age–specific fecundity model

An age-specific fecundity model (m_x) was fitted to Enkegaard (1993), where x is the female age (day) and a, b, c and d are model parameters (Pinder *et al*. 1978; Enkegaard 1993).

$$M(x) = (a+bx) \text{ Exp } [-(c+dx)] \quad [5]$$

Estimates of the model parameters were accomplished using nonlinear platform of JMP version 8.2 (SAS Institute 2007). All graphs were produced by Sigma Plot version 11.0 (Systat Software Inc. 2008).

Both Weibull and Enkegaard models are used for finding curves that come closed to the points. In order to study, two criteria were used to select the best fitted curve. In this study, sum of square (SSE) and Akaike information criterion (AIC) were used to appraise goodness-of-fit of nonlinear models (Akaike 1974; Draper & Smith 1998). AIC is defined as AIC = $n$ln (SSE/n) $2p$, in which n is the number of observations, p is the number of model parameters and SSE is the sum of squares for the model error term. The model that has the smallest value of AIC is considered the best. The lowest value of SSE is the best curve fitting.

Results

In the antixenosis assay, there was some variation among melon genotypes with respect to *T. turkestani* adult density on leaves (Fig. 1). In the preliminary antixenosis assay, CMI-167, Samsoori and Ananasi were significantly ($F_{13, 126} = 11.18$, $P < 0.0001$) the least preferred by adults of *T. turkestani*, while adults strongly preferred the Honey Dew and Bargney (Fig. 1). The other genotypes showed intermediate performance (Fig. 2).

Developmental time & adult longevity

The male developmental time were significantly longer on CMC-132 and Ananasi ($F_{5, 144}$ = 18.27, P < 0.0001) (Table 1). The shortest adult longevity of males were recorded on CMI–167, and the longest on Honey Dew and Ananasi genotypes ($F_{5, 144}$ = 8.23, P < 0.0001) (Table 2). The longest and shortest males total longevity were observed on Ananasi and CMI–167 ($F_{5, 144}$= 8.23, P < 0.0001), respectively (Table 2).

Table 1. The mean (±SE) duration of different development stages of *Tetranychus turkestani* (male & female) on different melon genotypes.

Stages/Genotypes	CMI- 167	Bargney	CMC- 132	Honey Dew	Samsoori	Ananasi
			Male			
Incubation	3.94±0.12ab	3.74±0.09b	3.96±0.06ab	3.72± 0.05b	3.72± 0.07b	4.16± 0.07a
Larval	1.24±0.10b	0.94±0.07c	1.50±0.1a	1.04±0.06bc	0.96±0.07c	1.48±0.08a
Protochrysalis	0.62±0.04bc	0.74±0.05ab	0.80±0.05a	0.58±0.03c	0.66± .04abc	0.68±0.04abc
Protonymph	0.94±0.03a	0.64±0.04c	0.96±0.08a	0.74±0.05c	0.76±0.05bc	0.92±0.08ab
Deutochry-salis	0.60±0.04bc	0.54±0.02bc	0.74±0.06a	0.51±0.0c	0.58±0.03bc	0.66±0.04ab
Deutonymph	0.58±0.03b	0.70±0.05ab	0.84±0.04a	0.70±0.05ab	0.74± 0.05ab	0.74± .07ab
Teliochrysalis	1.16±0.0a	0.96±0.04b	0.80±0.05c	0.82± .04bc	0.78± 0.05c	0.92± .031bc
Immature time	9.08±0.20b	8.26±0.16c	9.60±0.21a	8.11±0.05c	8.21±0.11c	9.56±0.17a
			Female			
Incubation	4.06± 0.07a	3.74± 0.08b	3.9± 0.08ab	3.82± 0.06b	3.78± 0.08 b	3.90±0.05ab
Larval	1.22± 0.06ab	1.11± 0.07b	1.38± 0.09a	1.12± 0.09b	1.06± 0.06b	1.46±0.11a
Protochrysalis	0.74±0.05a	0.78±0.06a	0.70±0.05a	0.68±0.05a	0.66±0.04a	0.62±0.05a
Protonymph	0.92± 0.03abc	0.88± 0.05abc	1.04±0.05ab	0.76± 0.05c	0.82±0.05bc	1.06±0.13a
Deutochrysalis	0.64± 0.05a	0.60± 0.04a	0.70± 0.06a	0.70± 0.05a	0.58±0.03a	0.72±0.05a
Deutonymph	0.78± 0.05bc	0.98± 0.08ab	1.04±0.08a	0.72±0.05c	0.88±0.05abc	0.78±0.06bc
Teliochrysalis	1.00±0.05a	0.94± 0.06ab	1.02± 0.06a	0.82± 0.04b	0.84±0.04b	1.02±0.05a
Immature time	9.36±0.17ab	9.02±0.14bc	9.78±0.20a	8.62±0.12c	8.62±0.10c	9.56±0.25a

Means in each column followed by the same letter are not significantly different (P < 0.05, Tukey)

There was no significant difference among the developmental time of female protochrysalis ($F_{5, 144}$ = 1.02, P = 0.4087) and deutochrysalis ($F_{5, 144}$ = 1.28, P = 0.2759), but the durations of other female developmental stages were affected by melon genotypes. The longest female developmental time was observed on CMI–132 and Ananasi ($F_{5, 144}$ = 7.57, P < 0.0001) (Table 1). The longest total longevity was observed on Bargney ($F_{5, 144}$ = 2.75, P = 0.0208) while the shortest female longevity was obtained on CMC–132 and Samsoori ($F_{5, 144}$= 3.69, P = 0.0036) (Table 2).

Mortality

Mortality was observed in developmental stages of *T. turkestani* on all genotypes, and it was obtained as: 10.0, 8.0, 8.0, 6.0, 4.0 and 2.0% on Ananasi, CMI-167, CMI-132, Samsoori, Bargney and Honey Dew, respectively.

Oviposition period and fecundity

The pre-oviposition ($F_{5, 144}$ = 1.12, P = 0.3531) and post-oviposition ($F_{5, 144}$= 0.91, P = 0.4768) of *T. turkestani* were not significantly affected by different melon genotypes, but the oviposition period of this mite was significantly different among all melon genotypes ($F_{5, 144}$ = 7.27, P < 0.0001). It was significantly longer on Bargney and Honey Dew genotypes than other genotypes tested (Table 2). The spider mites spent a larger percentage of its longevity in oviposition period and a smaller part of its longevity in pre-oviposition time. Female fecundity as a function of melon genotypes was summarized in Table 2. The total fecundity was significantly higher on Bargney and Honey Dew than other varieties ($F_{5, 144}$ = 10.29, P < 0.0001) (Table 2).

Table 2. The mean (±SE) pre- and post-oviposition periods and fecundity of *Tetranychus turkestani* reared on different melon genotypes.

Genotypes	CMI- 167	Bargney	CMC- 132	Honey Dew	Samsoori	Ananasi
Pre-oviposition period (days)	1.40±0.16a	0.86±0.09a	1.18±0.12a	0.92±0.06a	0.96±0.12a	1.48±0.54a
Oviposition period	5.84±0.52b	10.00±0.70a	5.54±0.73b	9.68±0.80a	6.58±0.77b	5.96±0.90b
Post-oviposition period (days)	1.42±0.30a	0.96±0.12a	1.18±0.30a	1.34±0.27a	1.30±0.24a	1.92±0.58a
Adult longevity (♀)	8.64±0.52b	11.82±0.71a	7.90±0.82b	11.94±0.84a	8.84±0.75b	9.36±1.42ab
Total longevity (♀)	18±0.53bc	20.84±0.76a	17.68±0.83c	20.56±0.82ab	17.46±0.72c	18.92±1.40ab
Daily fecundity	5.91±0.46b	7.80±0.62a	5.37±0.47b	9.48±0.50a	8.02±0.74a	5.75±0.58b
Total fecundity	37.76±4.91b	80.28±8.14a	32.8±5.00b	93.04±9.35a	54.96±9.21b	41.28±8.21b
Adult longevity (♂)	7.96±0.86d	15.70±1.37ab	12.38±1.54bc	16.58±1.29a	10.76±1.23cd	16.42±0.90a
Total longevity (♂)	17.04±0.82d	23.96±1.41ab	21.98±1.47bc	24.68±1.28ab	18.96±1.22cd	25.98±0.91a

Means in each column followed by the same letter are not significantly different ($P < 0.05$, Tukey)

Age-stage survival rate (s_{xj})

The age-stage survival rates (s_{xj}) of *T. turkestani* on different genotypes are shown in Fig. 2. It shows the probability that an egg will survival to age x while in stage j, as the age-stage, two-sex life table takes the variable developmental rate among individuals into consideration, so significant stage overlapping could be observed. Acquisition of this result from our experiment, was an important outcome of our research, because it showed us that susceptibility to pesticide and vulnerability to natural enemies are stage-dependent, and adults could emerge at different ages, and it disproves the possibility of survival rate based on "female adult age".

Age-specific survival rate (l_x) and age specific fecundity (m_x)

When individuals of different stages are pooled together, we obtain the age-specific survival rate (l_x). The curve l_x is the simplified version of s_{xj}. The important information of stage differentiation cannot be observed in l_x. Distribution of the age-specific survival rate was fitted to the Weibull frequency distribution (Fig. 4). The estimated Weibull parameters are listed in Table 4. The survival curve of *T. turkestani* on different melon genotypes was type I because all parameters c > 1 (Tingle & Copland 1989). Furthermore, the survival rate (l_x) is more affected on the CMI-167 genotype with the highest slope. The fitted Weibull of CMC-132 and Bargney genotypes were fitted better than other genotypes, because these genotypes had the lowest value of AIC.

The female age-stage specific fecundity (f_{x8}) is plotted in Fig. 3. It is the mean fecundity of female adults at age x. The age-specific fecundity (m_x) and the age-specific maternity ($l_x m_x$) are also displayed in Fig. 3. The summation of the age-specific maternity over all ages produces the net reproductive rate (R_0). The f_{x8} is plotted with age indexed from egg stage. Thus, it is the correct fecundity curve. Chi & Su (2006) pointed out the problem of construction fecundity curve based on “adult” age.

Our data of age-specific fecundity (m_x) are compatible with Enkegaard model. The highest observed value of the daily age specific fecundity (m_x) of *T. turkestani* in the different melon genotypes was observed in the Honey Dew genotype compared to the lowest value on CMC-132 genotype (Fig. 5).

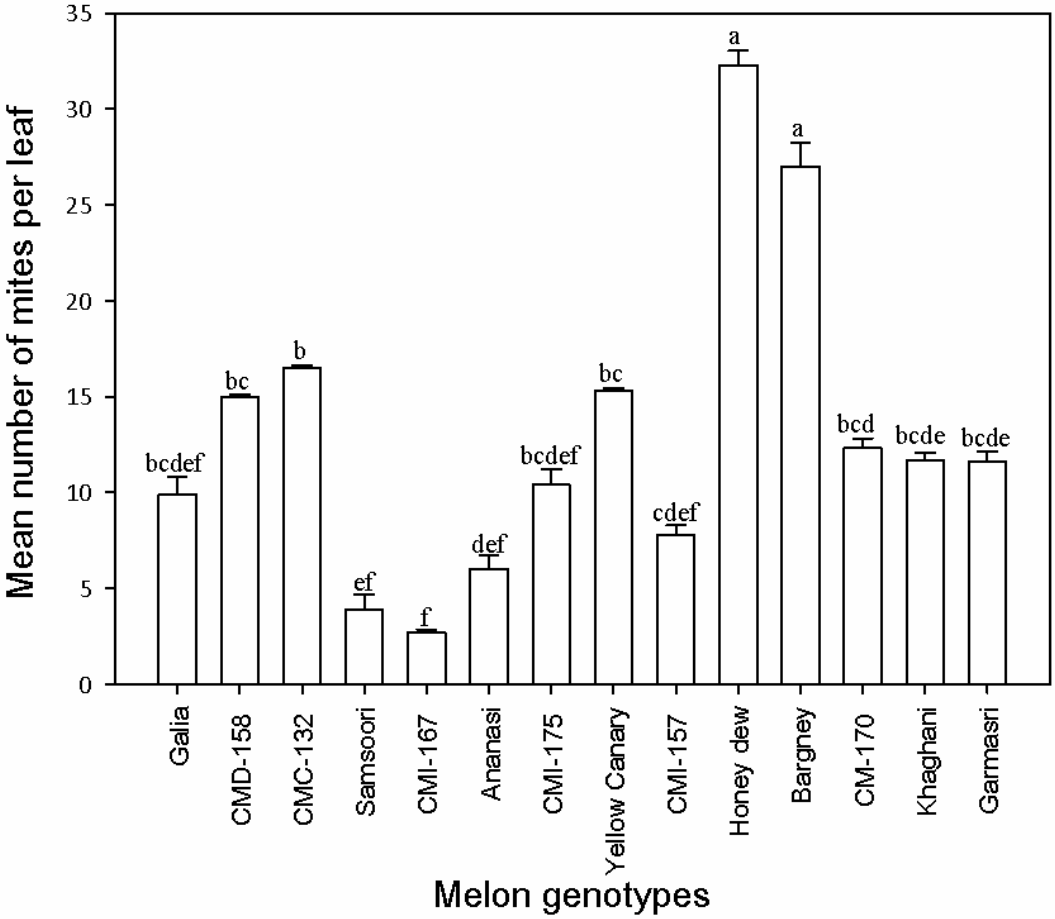

Figure 1. Mean number (±SE) of *Tetranychus turkestani* adult mites counted on the exposed leaves of 14 melon genotypes in the antixenosis assay. Means in a column followed by the same letter do not differ significantly at $P < 0.05$ level (Tukey's test).

The net reproductive rate (R_0) was significantly higher on Honey Dew and Bargney than other genotypes. The intrinsic rate of increase (r_m) showed the highest value on the Honey Dew. The mean generation time (T) parameter had a significantly difference in various melon genotypes and Bargney was observed to have the highest value, and concerning the highest finite rate of increase (λ),was observed on Honey Dew (Table 3).

Melon genotypes, regarding some biological parameters of *T. turkestani* (both sexes together), were grouped in three distinct groups by Ward's method (Ward 1963) using SPSS (2004). The cluster A included CMI-167, CMC-132 and Ananasi genotypes (resistant group); the mean developmental time in this cluster was more than the total mean of all genotypes, but the mean total fecundity, oviposition period, adult longevity and whole total longevity in this cluster were less than total mean of these parameters among all genotypes. The cluster C consisted of Bargney and Honey Dew (susceptible group) and the mean of the above mentioned parameters in this cluster was more than total mean of them between all genotypes. The Samsoori genotype had intermediate status and grouped in cluster B. (Fig. 6).

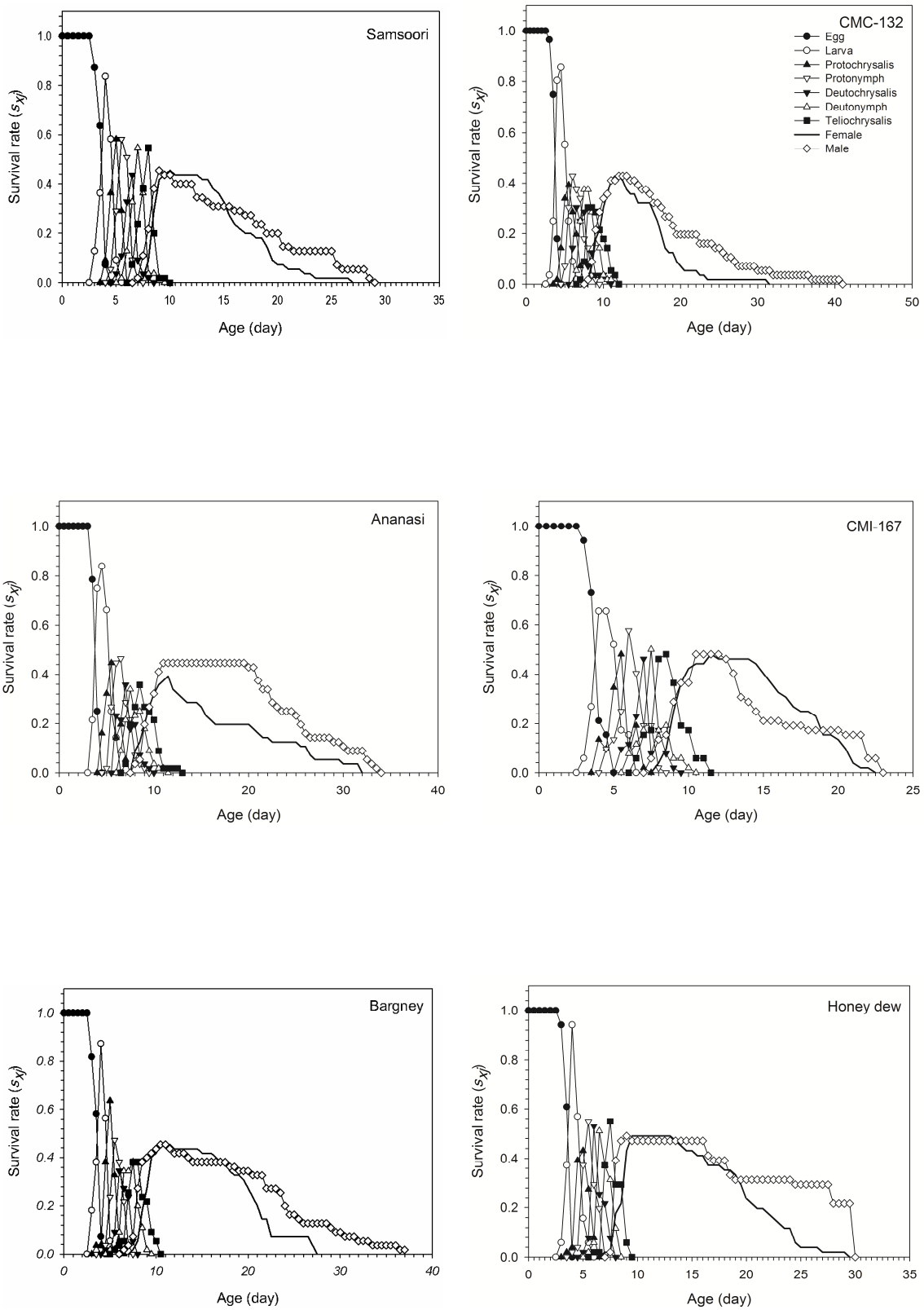

Figure 2. Age–stage specific survival rate (s_{xj}) of *Tetranychus turkestani* on the different melon genotypes.

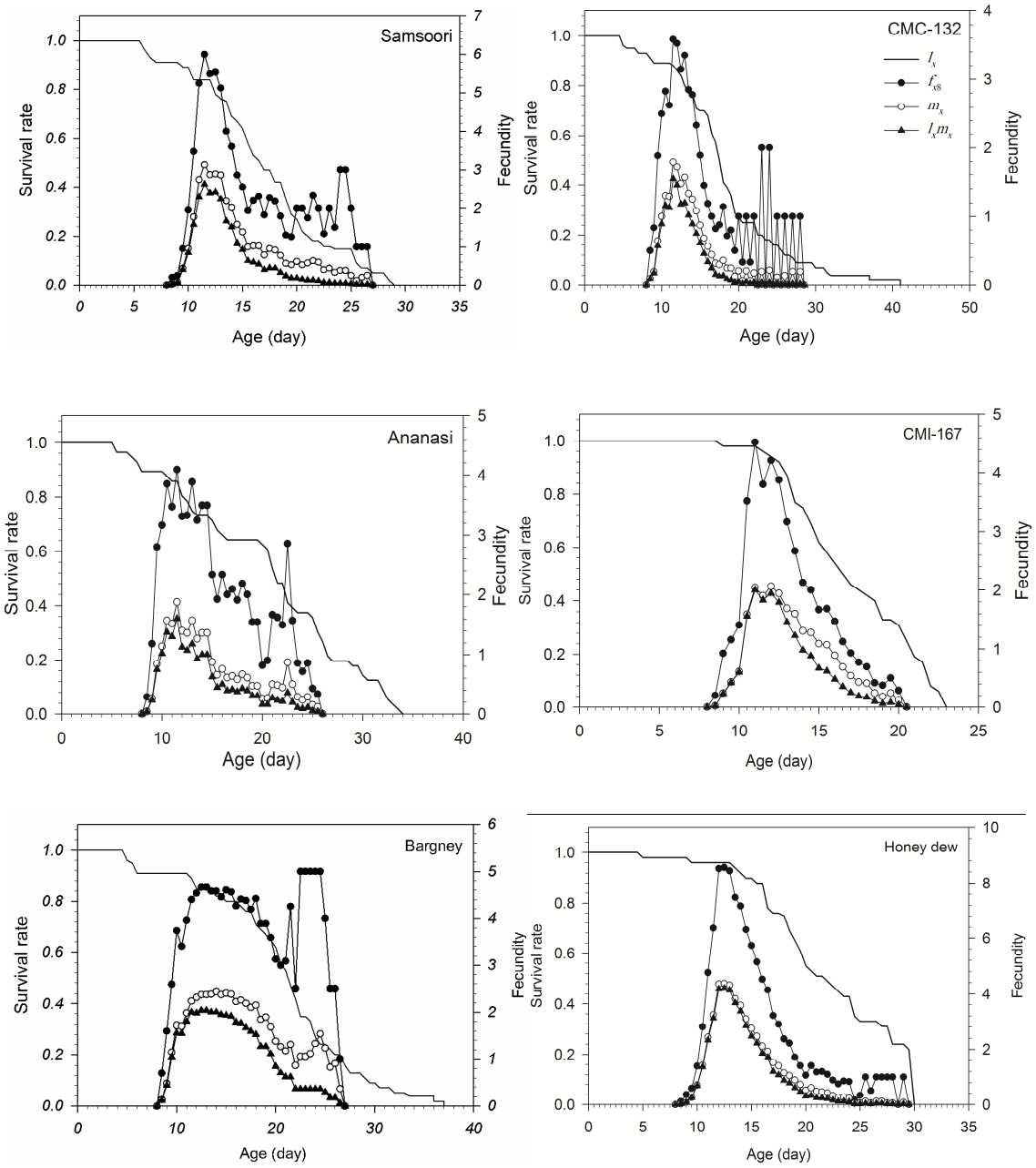

Figure 3. Age–specific survival rate (l_x), female age–specific fecundity (f_{x8}), age–specific fecundity (m_x), and age–specific maternity ($l_x m_x$) of *Tetranychus turkestani* on the different melon genotypes.

Discussion

This study indicated different performance of *T. turkestani* on melon genotypes in the limited free-choice assay. This was useful in demonstrating the difference in susceptibility of melon genotypes to *T. turkestani*. The CMI-167, Samsoori and Ananasi genotypes were less preferred by this mite, which could be due to morphological differences among the genotypes such as leaf structure, presence and density of leaf trichomes (Traw & Dawson 2002), epidermal properties (Herms & Mattson 1992), or allomones that inhibit the initiation of feeding or oviposition (Flores *et al.* 2008).

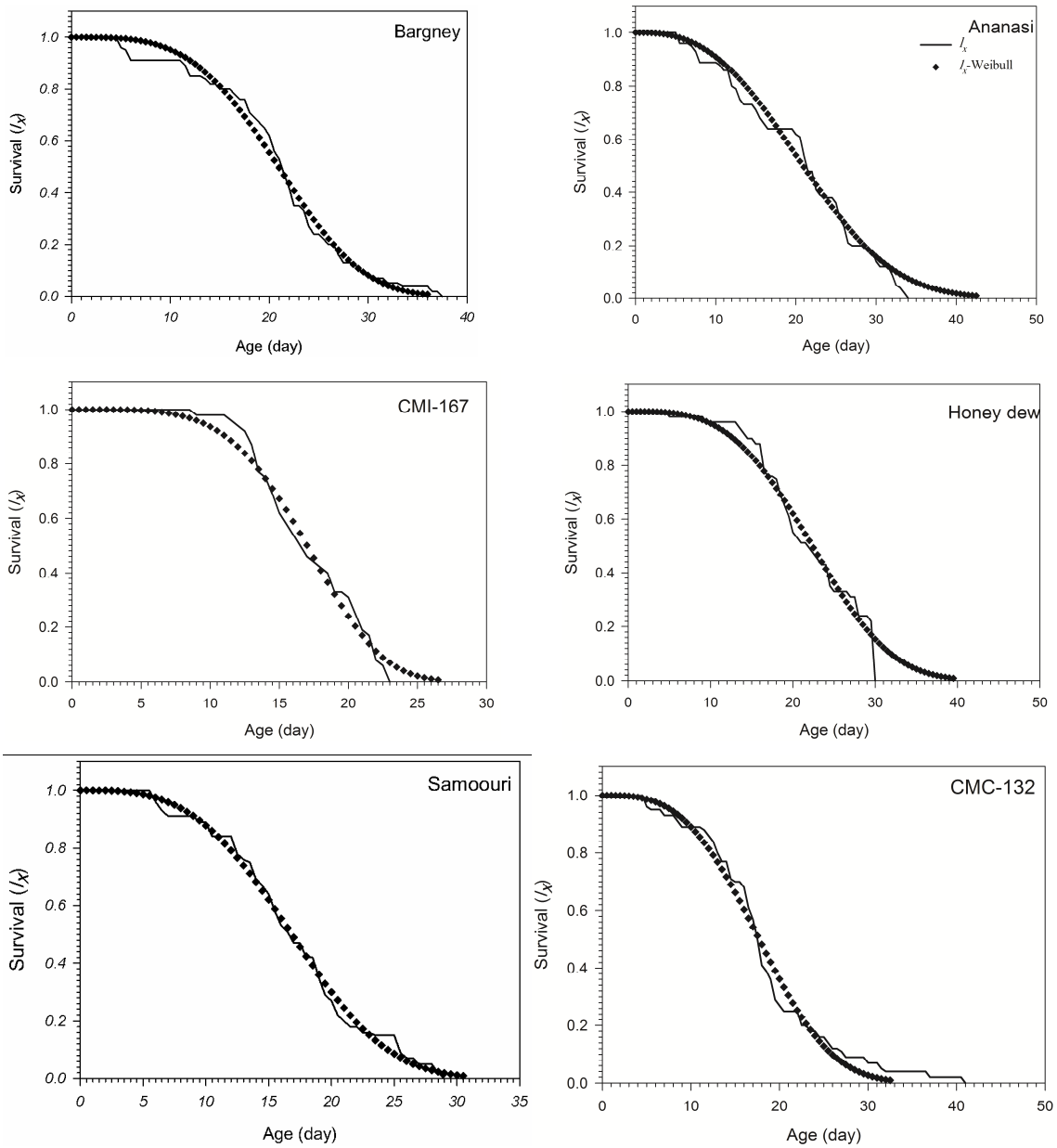

Figure 4. Observed age–specific survival rate (l_x) of *Tetranychus turkestani* on different melon genotypes using Weibull function.

In the antibiosis experiment, significant differences in *T. turkestani* fecundity emphasized the divergence between the feeding quality of the leaves of resistant and susceptible genotypes (Sabelis 1981). The greatest fecundity was recorded on the most preferred genotypes Honey Dew and Bargney. By contrast, the mite's fecundity was lowest on the least preferred genotypes SMC-167 and Samsoori. It can be concluded that these genotypes are examples of plant hosts in which antibiosis and antixenosis resistance mechanisms are linked. These results are largely in agreement with previous studies on melon (Mansour *et al*. 1987; Scully *et al*. 1991; Shoorooei *et al*. 2013).

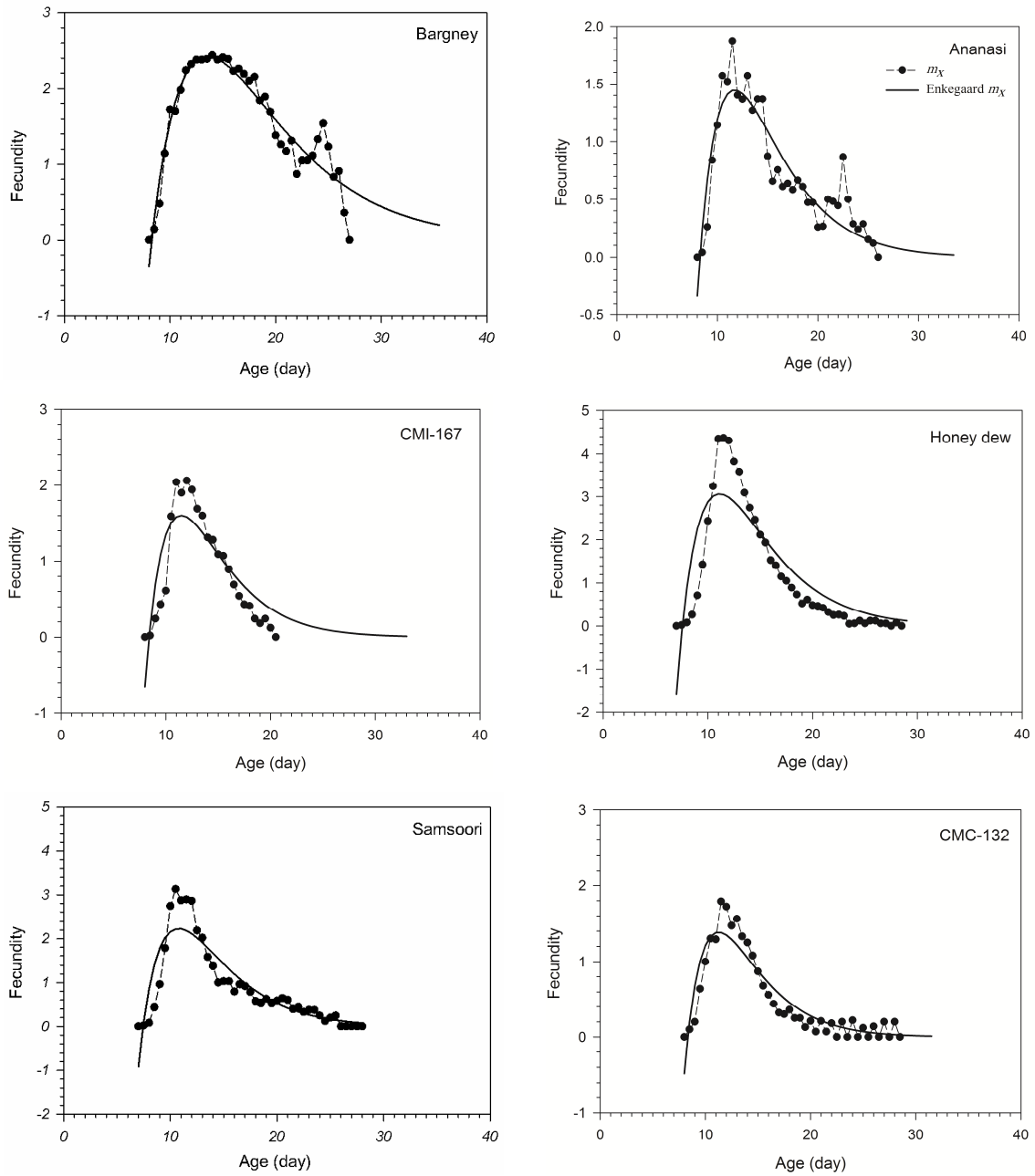

Figure 5. Observed age–specific fecundity (m_x) of *Tetranychus tuekestani* on the different melon genotypes and curves fitted using Enkegaard model.

There are many morphological and chemical characteristics of a leaf such as glandular and non-glandular trichomes that could affect preference or biology of an insect and mites. Certain phytochemicals, phytoalexins, secondary plant metabolites (ketones, alcohols, aldehydes, terpenes) or other anti-insect and anti-feedant factors present in plant leaves could affect the mite's behavior and biology (Herms & Mattson 1992). Trevisan *et al.* (2003) reported that after infestation by spider mites, peroxidases (POX) activity increased in the leaves of the host plant, and study on certain insects also indicated resistance to be closely related with an increase in peroxidases (POX) activity (Moran 2001; Shoorooei *et al*. 2013).

Table 3. Life table parameter (±SE) of *Tetranychus turkestani* on different melon genotypes.

Genotypes	Net reproductive Rate (R_0)	Intrinsic Rate of Increase (r_m)	Mean generation time (T)	Finite Rate of Increase (λ)
CMI-167	17.9±3.51b	0.2272±0.01bc	12.9±0.25b	1.2550±0.02bc
Bargney	42.05±7.32a	0.2636±0.01ab	14.2±0.27a	1.3015±0.01ab
CMC-132	14.6±3.12b	0.2034±0.01c	13.3±0.31ab	1.2254±0.02c
Honey Dew	45.6±7.99a	0.2880±0.01a	13.3±0.2ab	1.3337±0.01a
Samsoori	25±5.58b	0.2559±0.01ab	12.8±0.36b	1.2914±0.02ab
Ananasi	18.7±4.42b	0.2207±0.01bc	13.9±0.4ab	1.2468±0.02bc

Means in each column followed by the same letter are not significantly different ($P < 0.05$, Tukey)

Table 4. Goodness of fit and parameters of Weibull model fitted to the age specific survivorship (l_x) and Enkegaard models fitted to the age specific fecundity (m_x) of *Tetranychus turkestani*.

Model	GF & P	CMI-167	Barg ney Kashan	CMC-132	Honey Dew	Varamin Samsuri	Ananasi
Weibull	SSE	0.055	0.101	0.11	0.067	0.035	0.087
	AIC	−303.195	−491.635	−532.83	−402.02	−423.94	−446.75
	c	4.44	3.574	3.13	3.37	3.21	2.71
	b	18.46	23.199	19.89	24.91	18.88	23.94
Enkegaard	SSE	2.98	1.975	1.66	18.70	6.87	1.62
	AIC	−48.311	−108.333	−127.606	−29.63	−59.69	−107.66
	a	−13712.1	−2130.18	−8291.86	−6464.51	−13076.44	−1214.13
	b	1631.	257.69	938.69	801.12	1646.70	146.80
	c	4.31	3.76	3.57	3.55	4.43	2.45
	d	0.33	0.189	0.34	0.28	0.23	0.29

Survival schedule of *T. turkestani*, was correspond to type I survivorship curves, which is an important factor to be considered in IPM of this mite, because the highest mortality occurs in the last age time, that is, when the females, already laid their eggs. Some authors believe this kind of behavior is typical of tetranychid mites, which depends also on the kind of nutrient which they receive (Razmjou *et al*. 2009; Sedaratian *et al*. 2011).

Curve fitting is helpful in regard to processing the age-specific fecundity & age-specific survival rate (Carey 1993). The data obtained could not be fitted to the analytis model, but it was closer to the Weibull-fitted l_x, although there are problems, which need to be discussed. Firstly, because the Weibull l_x has extended too much older age than the experimental data, and secondly, the Weibull function is a descending function, it gives always $l_{x+1} < l_x$. But we should consider that the real survival curves are seldom a smooth descending curve and sometimes there are no mortalities during a specific period or stage. The Enkegaard-m_x shows similar problems. Moreover, some Enkegaard-m_x is negative.

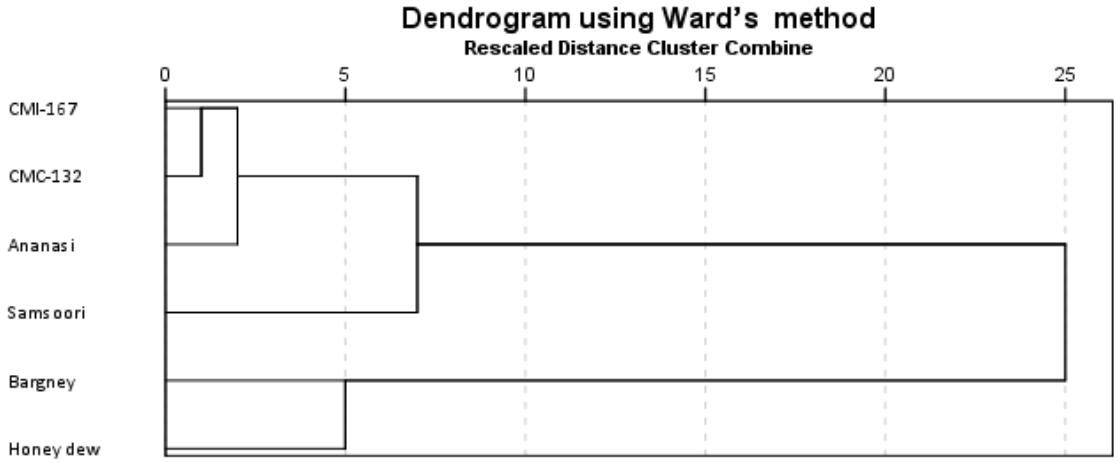

Figure 6. Genotypes Ward's dendrogram generated from the details assessed on *Tetranychus tuekestani* populations developed on the assayed genotypes.

All of these show that the use of Weibull function and Enkegaard model should be reconsidered. Although, in our study of *T. turkestani*, we used Weibull-l_x and Enkegaard-m_x indexed from age 0 (the egg stage), and not "adult" age, so we could express that our results of fittings are more real than those based on adult age. Our results showed that the net reproduction rate (R_0) to be 14.6, 45.6 offspring (Table 3) in CMC-132 and Honey Dew, respectively, we could propose that higher values of R_0 shows higher sensivity of plants to pests. Some other authors found a higher value of R_0 for *T. turkestani* infesting strawberries, so, they showed the Black Eye variety of strawberries, as to be a suitable host, highly sensitive for the pest (Sohrabi & Shishehbor 2008).

In our finding, the intrinsic rate of increase on the Honey Dew genotype is the highest. Higher values of r_m of phytophagous arthropods indicate the susceptibility of a host plant to their attacks; while lower values of this parameter show that the host plant has a degree of resistance to pests. According to the above mentioned results, Honey Dew genotype is one of the most sensitive genotype that population of the pest could easily increase on it.

The cluster analysis based on comparative life history and fecundity of *T. turkestani* on different melon genotypes indicated that Bargney and Honey Dew are suitable host plants for *T. turkestani* and severe mite outbreaks are likely to occur under favorable conditions in the field, while CMI-167, CMC-132 and Ananasi seem to be more resistant. However, field experiments need to be conducted to confirm these findings. The differential suitability of melons to the mite could be an important factor to consider while exploring IPM solutions for *T. turkestani* in melon production region in western Iran. In case the resistance of CMI-167, CMC-132 and Ananasi genotypes can be confirmed in the field, this genotypes should be preferred to the other when growing melons to minimize damage by *T. turkestani*. Although our findings could help to arrive to a better understanding of plant-pest interaction, but we propose to continue the similar studies on melon which photochemical could adversely affects the build-up of *T. turkestani* on melon cultivars to be identified and isolated for using in IPM programs of melons.

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پارامترهای جمعیتی کنه *Tetranychus turkestani* (Acari: Tetranychidae) روی چهارده ژنوتیپ خربزه

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چکیده

اثرهای آنتی‌زنوزی ژنوتیپ‌های گالیا، CMD-158، CMC-132، CMI-157،CMI-167، CMI-175، آناناسی، زرد قناری، سمسوری، هانی‌دیو، برگ‌نی، CM-170، خاقانی و گرمسار، و پارامترهای زیستی کنه تارتن دو لکه‌ای *T. turkestani* روی ژنوتیپ‌های CMC-132، CMI-167، آناناسی، سمسوری، هانی‌دیو و برگ‌نی در شرایط آزمایشگاهی ۱± ۲۸ درجهٔ سلسیوس، رطوبت نسبی ۵±۶۵ درصد و دور نوری ۱۶ ساعت روشنایی و ۸ ساعت تاریکی مورد بررسی قرار گرفت. در آزمون انتخاب آزاد، کنه‌های بالغ کمترین میزان ترجیح را نسبت به ژنوتیپ‌های CMI-167، سمسوری و آناناسی نشان دادند. برخلاف آن ژنوتیپ‌های هانی‌دیو و برگ‌نی بیشترین ترجیح را نسبت به کنه‌های تارتن دو لکه‌ای نشان دادند. طولانی‌ترین زمان رشد و نموی هر دو جنس بر روی ژنوتیپ‌های CMC-132 و آناناسی مشاهده شد در حالی که کوتاه‌ترین زمان رشد و نموی برای جنس ماده روی ژنوتیپ‌های هانی‌دیو و سمسوری به دست آمد. کمترین و بیشترین میزان زادآوری روی ژنوتیپ CMC-132 مشاهد شد در حالی که بیشترین میزان آن روی ژنوتیپ هانی‌دیو به ثبت رسید. افزون بر این، بیشترین نرخ ذاتی رشد (r_m)، نرخ خالص تولیدمثلی (R_0)، نرخ متناهی افزایش جمعیت (λ) کنه تارتن دو لکه‌ای روی ژنوتیپ هانی‌دیو مشاهده شد. مدل‌های ویبول و انکگارد به ترتیب برای برازش داده‌های بقای ویژه سنی (l_x) و باروری ویژه سنی (m_x) استفاده شدند. در پایان، مقایسه و تجزیه کلاستر پارامترهای زیستی کنه تارتن دو لکه‌ای روی ژنوتیپ‌های مختلف خربزه نشان داد که ارقام CMC-132، آناناسی و CMI-167 دارای بیشترین میزان مقاومت نسبت به این آفت هستند.

واژگان کلیدی: نرخ ذاتی رشد، دورهٔ زندگی، تولیدمثل، مقاومت گیاه، میزبان گیاهی.

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