

## Comparative life table parameters of five *Tetranychus urticae* Koch, 1836 (Acari: Tetranychidae) populations in Iran

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### Abstract

The two-spotted spider mite *Tetranychus urticae* Koch is one of the most important pests of agricultural crops worldwide, infesting a wide range of plants including some economically important crops. An investigation was carried out to study the life table parameters of five Iranian populations of *T. urticae* from Urima, Dashtnase, Faryman, Razkan and Tehran under laboratory conditions of 27 °C, 60% RH and 16 L: 8 D hours on *Malus domestica* Borkh leaves. There was a significant difference in the developmental time of *T. urticae* among tested populations. The total survival rate of *T. urticae* ranged from 76% to 81%. The adult longevities were significantly different. The adult longevities of the Faryman and Dashtnase populations were different from the Razkan population. Total fecundity of the Urima, Razkan and Tehran populations were higher than that observed for the other tested populations. The highest value of  $R_0$  was for the Urima and Dashtnase populations and the lowest was for the Faryman population. The  $r$  values of the Dashtnase (0.248 day<sup>-1</sup>) and Urima populations (0.200 day<sup>-1</sup>) were significantly higher in comparison to the Faryman population (0.124 day<sup>-1</sup>). The observed variation of the two-spotted spider mite collected from different localities showed that ecological factors such as geographical separation can influence the life table parameters of a phytophagous organism.

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### Introduction

The two-spotted spider mite *Tetranychus urticae* Koch, 1836 is one of the most important agricultural pests globally, infesting a wide range of plant families including economically important crops ranging from field and greenhouse vegetables and ornamentals to fruit trees and vines. It has been recorded on over 900 species, 478 genera and 124 families of plants (Bolland et al., 1998). Adult and immature stages of *T. urticae* feed primarily on leaves, producing tiny gray or silvery spots known as stippling damage. Severe infestation can result in premature leaf fall, shoot dieback and decrease in plant vigor (Zhang, 2003; Jafari, 2010).

This phytophagous mite is a serious pest of various agricultural plants. Owing to its rapid development

and high reproductive capacities, *T. urticae* has spread worldwide (Bolland et al., 1998). The population genetic structure of an organism is determined by various factors, such as geographical barriers, ecological difference and historical processes, as well as the dispersal ability of the species (Mitchell, 1973). *Tetranychus urticae* has multiple dispersal mechanisms. Spider mites are wingless and usually rely on crawling for their dispersal, but they can also be carried for long distances by the wind and by human activities. Due to the complex dispersal mechanisms of *T. urticae*, the population structure and diversity may be complex (Riahi et al., 2011). Because of its short development time and high fecundity, *T. urticae* can increase its population in a short time, by up to 40% per day (Shih et al., 1976; Jafari et al., 2012).

The genetic differentiation of *T. urticae* populations seems to be correlated with distance; for example, differentiation was observed between *T. urticae* samples collected on different host plants located within a 50 m<sup>2</sup> area. In contrast, samples from plants at 150 m or more from one another display significant genetic differentiation (Tsagkarakou et al., 1997). Fry (1988) reported that *T. urticae* populations varied widely in the fitness measures and degree of acceptance of host plants. Individual populations of *T. urticae* are broadly polyphagous, different populations may vary considerably in performance on a particular host species or variety. For evolutionary expansion of host range to occur in an herbivore population, genetic variation in ability to survive on and/or accept new hosts must be present to determine whether a population of the phytophagous mite *T. urticae* contained such variation. *Tetranychus urticae* populations should be able to respond to temporal and spatial variation in host availability by adapting to the most abundant hosts (Fry, 1989).

Climatic conditions, particularly temperature, are critical abiotic factors influencing the mite's population dynamics and its natural enemies (van den Boom et al., 2003). At the population level, some degree of specialization has been found in *T. urticae* as evidenced by the observation of genetically differentiated populations associated with particular host species (Magalhaes et al., 2007). The biological parameters of this pest can be used to manage *T. urticae* populations on economically important crops ranging from field and greenhouse vegetables and ornamentals to fruit trees and vines.

Therefore, the aim of this study was to compare the development, reproduction and life table parameters of five populations of *T. urticae*. The different populations were selected from apple orchards in some northern provinces of Iran. The age-specific life table of five populations (Urima, Dashtnase, Faryman, Razkan and Tehran strains) of *T. urticae* was investigated.

## Material and Methods

### Mite colony

The different populations of *T. urticae* were collected from apple trees in some northern provinces of Iran (West Azerbaijan, Tehran, Mazandaran and Khorasan Razavi). Table 1 shows the geographical location of these regions. The stock culture of *T. urticae* was separately maintained on detached apple leaves in a growth chamber (27±1 °C, 70±5 relative humidity (RH) and 16-hour light (L): 8-hour dark (D)).

### Experiments

The life table parameters of five populations of *T. urticae* at 27±1 °C, 70±5% RH and a 16 L: 8 D photoperiod in a growth chamber were determined. We used apple leaves for experiments. The apple

leaves were cut into a 15 × 15 mm square leaflet and then placed upside down on agar (3%) in a 6 cm diameter Petri dish with a ventilated lid for each of populations of *T. urticae* (Rezaie et al., 2017).

To obtain eggs of the same age for each test arena, two to five females of *T. urticae* were placed on leaf disc and allowed to lay eggs. After eight hours, the females and extra eggs were removed to get one egg per each disc. Developmental time and survival of all immature stages including egg, larva, protonymph and deutonymph were determined by daily observation until adulthood. The developmental stages of *T. urticae* (egg, larva, protonymph, deutonymph and adult) are shown in Figure 1 (The images were taken with a camera attached to a Nikon Stereo Microscope (2M2645)). The number of replicates was 62, 69, 51, 40 and 60 for the Urima, Dashtnase, Faryman, Razkan and Tehran populations, respectively. After the emergence of the adult, it was coupled with an individual of the opposite sex from the cohort. The females were differentiated by their round caudal end as compared to the pointed caudal end of males (Rezaie et al., 2013). Because more females than male emerged, additional young males from the mass rearing colony were used for mating when necessary.

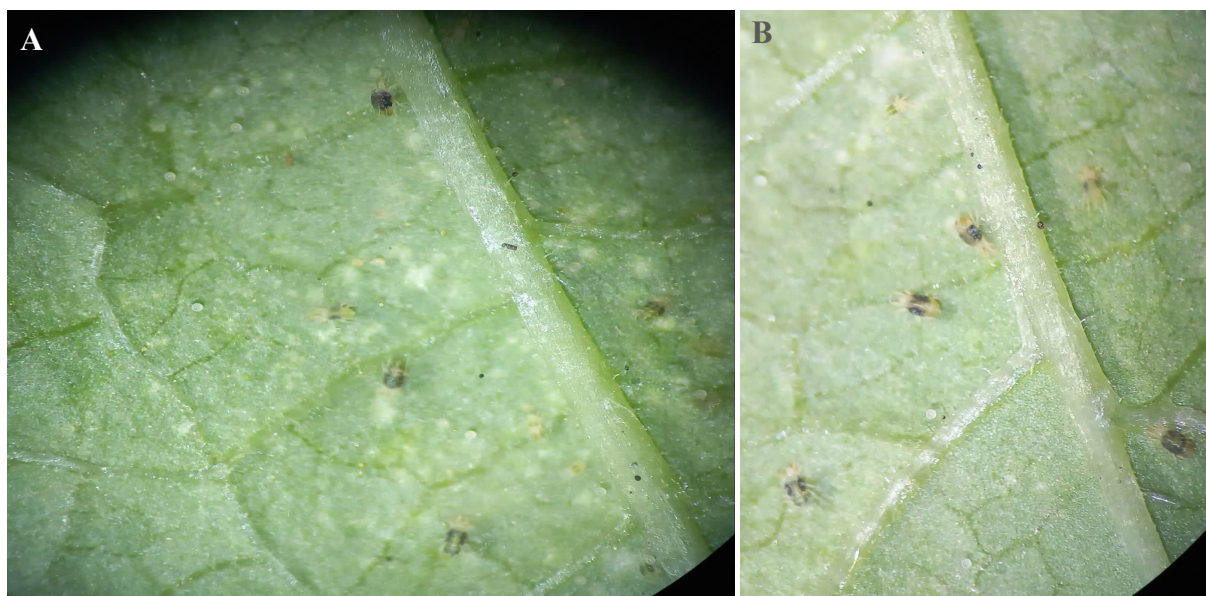
To reduce the effect of plant age on mite development and its fecundity, new leaflets were replaced every 4–5 days. Then fecundity of females was checked, and the eggs removed daily from each leaflet of the different populations. This experiment continued until all experimental females and males died.

### Statistical analysis

Life table data were analyzed using age-stage, two-sex life table theory (Chi and Liu, 1985). The population growth parameters including net reproductive rate ( $R_0$ ), intrinsic rate of increase ( $r$ ), finite rate of increase ( $\lambda$ ) and mean generation time ( $T$ ) were estimated using the TWOSEX-MSChart program (Chi, 2018). The bootstrap procedure was used to estimate the variances and standard errors of the developmental times, reproduction periods, fecundity, adult longevity and population growth parameters (Huang and Chi, 2013; Eini et al., 2022; 2023). We used 10,000 bootstrap samples to analyze the data. Bootstrap values of different populations of *T. urticae* were compared using paired bootstrap tests in the TWOSEX-MSChart program (Bahirai et al., 2019; Eini et al., 2023; Jafarian et al., 2023).

## Results

The different populations of *T. urticae* completed their development on apple leaves in the laboratory. The developmental times of different populations of *T. urticae* are given in Table 2. There were significant differences in developmental time among populations for the egg, larvae, protonymph and deutonymph (Table 2). The survival rates of the immature stages are given in Table 3.



**Figure 1:** The developmental stages of *Tetranychus urticae* (egg, larva, protonymph, deutonymph and adult). (A) Adult and eggs of *Tetranychus urticae*; (B) larva, protonymph and deutonymph of *Tetranychus urticae*.

**Table 1:** The geographical location of the regions of Iran that *Tetranychus urticae* populations were collected.

<i>Tetranychus urticae</i> strain	Province	Region	Geographical location	Height above the sea level (m)
Urima	West Azerbaijan	Miandoab	51.11° E, 41.81° N	1366
Razkan	Tehran	Razkan	51.15° E, 35.59° N	1115
Tehran	Tehran	Jaban	52.26° E, 35.64° N	2197
Faryman	Khorasan Razavi	Faryman	35.57° E, 59.70° N	1690
Dashtnase	Mazandaran	Dashtnase	53.20° E, 36.69° N	0

**Table 2:** Developmental time, adult longevity, life span and reproductive parameters (mean  $\pm$  SE) of different populations of *Tetranychus urticae*.

Developmental time	Populations				
	Urmia	Dashtnase	Faryman	Razkan	Tehran
Egg	3.56 $\pm$ 0.08 <sup>a</sup>	3.81 $\pm$ 0.48 <sup>a</sup>	3.08 $\pm$ 0.12 <sup>b</sup>	3.74 $\pm$ 0.09 <sup>a</sup>	3.52 $\pm$ 0.13 <sup>a</sup>
Larva	1.30 $\pm$ 0.07 <sup>a</sup>	1.12 $\pm$ 0.33 <sup>b</sup>	1.06 $\pm$ 0.04 <sup>b</sup>	1.04 $\pm$ 0.04 <sup>b</sup>	1.20 $\pm$ 0.07 <sup>ab</sup>
Protonymph	1.51 $\pm$ 0.08 <sup>b</sup>	1.18 $\pm$ 0.05 <sup>c</sup>	1.67 $\pm$ 0.09 <sup>ab</sup>	1.14 $\pm$ 0.07 <sup>c</sup>	1.78 $\pm$ 0.11 <sup>a</sup>
Deutonymph	2.11 $\pm$ 0.41 <sup>a</sup>	1.16 $\pm$ 0.06 <sup>b</sup>	1.48 $\pm$ 0.51 <sup>b</sup>	1.11 $\pm$ 0.07 <sup>b</sup>	1.35 $\pm$ 0.11 <sup>b</sup>
Adult longevity of female	7.23 $\pm$ 1.74 <sup>ab</sup>	6.87 $\pm$ 1.59 <sup>b</sup>	5.57 $\pm$ 1.99 <sup>c</sup>	5.25 $\pm$ 1.05 <sup>c</sup>	8.13 $\pm$ 1.89 <sup>a</sup>
Adult longevity of male	6.20 $\pm$ 4.32 <sup>ab</sup>	6.46 $\pm$ 2.22 <sup>a</sup>	3.89 $\pm$ 1.30 <sup>b</sup>	3.57 $\pm$ 0.97 <sup>b</sup>	6.40 $\pm$ 2.70 <sup>a</sup>
APOP†	1.20 $\pm$ 0.40 <sup>a</sup>	1.26 $\pm$ 0.50 <sup>a</sup>	1.08 $\pm$ 0.2 <sup>a</sup>	1.26 $\pm$ 0.21 <sup>a</sup>	1.17 $\pm$ 0.5 <sup>a</sup>
TPOP††	9.00 $\pm$ 0.5 <sup>a</sup>	8.36 $\pm$ 0.9 <sup>a</sup>	7.80 $\pm$ 1.3 <sup>a</sup>	8.00 $\pm$ 0.74 <sup>a</sup>	8.27 $\pm$ 1.3 <sup>a</sup>
Total fecundity	25.78 $\pm$ 8.72 <sup>a</sup>	18.70 $\pm$ 4.51 <sup>b</sup>	12.93 $\pm$ 6.92 <sup>c</sup>	24.41 $\pm$ 9.41 <sup>a</sup>	27.0 $\pm$ 7.08 <sup>a</sup>
Lifetime longevity	9.87 $\pm$ 0.75 <sup>ab</sup>	10.86 $\pm$ 0.55 <sup>a</sup>	7.96 $\pm$ 0.57 <sup>a</sup>	8.0 $\pm$ 0.60 <sup>b</sup>	7.70 $\pm$ 0.48 <sup>ab</sup>

Means within a row followed by the same letter are not significantly different (paired bootstrap test,  $p < 0.05$ ); †APOP (pre-oviposition period of female); ††TPOP (total pre-oviposition period of female counted from birth).

**Table 3:** The survival rate percentage of immature stages of different populations of *Tetranychus urticae*.

Developmental time	Populations				
	Urmia	Dashtnase	Faryman	Razkan	Tehran
Egg	92.90	94.75	93.88	94.79	94.99
Larva	92.48	94.99	93.94	94.38	94.99
Protonymph	95.72	93.92	94.95	94.92	95.98
Deutonymph	94.99	94.95	94.98	95.94	94.98
Total	76.09	78.61	77.75	80.03	80.94

APOP (adult pre-oviposition period) and TPOP (total pre-oviposition period) did not show any significant differences among tested populations. More than 93% of eggs of five populations of *T. urticae* (range

93%–97%) hatched. The total immature survival rate of *T. urticae* ranged from 76% to 81%. The male and female longevity (mean number of days from adult emergence to death) of *T. urticae* were significantly

different for females and males. In addition, the duration of the total lifespan of *T. urticae* indicated significant difference among the tested populations. The lifetime longevity of the Faryman and the Dashtnase populations was different to the Razkan population. Total fecundity of the Urmia population ( $25.78 \pm 8.72$ ), the Razkan population ( $24.41 \pm 9.41$ ) and the Tehran population ( $27.0 \pm 7.08$ ) was higher than that observed for the other populations.

The analysis of the life table parameters of *T. urticae* indicated significant difference among the tested populations (Table 4). The highest  $R_0$  of *T. urticae* were in the Urmia and the Dashtnase populations and the lowest in the Faryman population. The  $r$  values of the Urmia population ( $0.200 \text{ day}^{-1}$ ) and the Dashtnase population ( $0.248 \text{ day}^{-1}$ ) were significantly different from the values of the Faryman population ( $0.124 \text{ day}^{-1}$ ). The individuals of the Urmia population and the Dashtnase population had the highest intrinsic rate of increase. In addition, our research revealed that the generation time of the different populations of *T. urticae* did not show any significant differences.

## Discussion

The two-spotted spider mite is a ubiquitous polyphagous arthropod herbivore that feeds on a remarkably broad array of plant species, with more than 150 these being of economic value. It is a major pest of greenhouse crops, especially of Solanaceae and Cucurbitaceae, greenhouse ornamentals, annual field crops and in perennial culture, in addition to the extreme polyphagy that makes it an important agricultural pest (Cazaux et al., 2014). *Tetranychus urticae* populations, therefore, should be able to respond to temporal and spatial variation in host availability by adapting to the most abundant hosts (Fry, 1989). The life cycle of the two-spotted spider mite consists of five stages of development: the egg, larva, protonymph, deutonymph and adult. Different populations of *T. urticae* were able to develop and reproduce on apple leaves. The present study demonstrated that three of five populations were significantly different in performance.

The egg incubation periods of *T. urticae* in our study varied between 3.08–3.81 days. This developmental period differed in our study and those reported by other researchers. The incubation periods of this mite on cucumber leaves lasted 4 and 2.36 days at the constant

temperatures of 25 °C and 30 °C, respectively (Ali et al., 2017). It was reported on bean cultivars as 4.08–4.20 days (Uddin et al., 2015), on strawberry cultivars as 4.13–4.87 days (Fahim et al., 2002), on okra as 2.92 days (Krishna and Bhaskar, 2014) and on apple cultivars as 3.8–4.1 days (Kasap, 2004). The incubation period of these populations on several host plants and geographical locations were different.

The development time of *T. urticae* ranged from 7.39–9.32 days in this study and the lowest period was observed for the Dashtnase population and the Razkan population and the longest period was observed for the Urmia population. The developmental times of *T. urticae* were reported as 11.85 days (Ali et al., 2017), 7.6 to 8.8 days for females and from 7.1 to 8.4 days for males on soybeans of different genotypes (Sedaratian et al., 2009), which is close to the obtained results in the present study. A larval period of 0.83 and 1.19 days, protonymphal period of 0.36 and 0.58 days and deutonymphal period of 0.67 and 0.29 days were recorded, respectively in male and female *T. urticae* on okra (Krishna and Bhaskar, 2014).

The adult longevity of *T. urticae* was different among our treatments with ranges of 5.25–8.31 days for females and 3.57–6.46 days for males. The total developmental time of *T. urticae* in this study ranged between 7.96 days (the Faryman population) and 10.86 days (the Dashtnase population); however, Kasap (2004) reported that the total developmental time of *T. urticae* ranged between 9.3 and 9.7 days. Krishna and Bhaskar (2014) reported that the total developmental period from egg to adult emergence was shorter for males (6.73 days) compared to females (7.52 days). Rajakumar et al. (2005) revealed that female and male *T. urticae* lived for 18.7 and 12.1 days, respectively. Female longevity ranged from 14.48–20.31 days on strawberry cultivars (Fahim et al., 2002). Developmental periods of *T. urticae* females ranged from 10.67–12.87 days in this study. These results are comparable with the results on ten rose cultivars by Golizadeh et al. (2017). Host plants, experimental conditions, as well as mite strain, may provide an explanation for shorter or longer developmental times. The chemical content and morphology of the leaf surface of host plants affect the reproductive potential, mortality and development rate of the mite (van der Boom et al., 2003).

**Table 4:** Mean  $\pm$  SE of population growth parameters of different populations of *Tetranychus urticae*.

Population growth parameters	Population				
	Urmia	Dashtnase	Faryman	Razkan	Tehran
Net reproductive rate ( $R_0$ ) (offspring/individual)	9.32 $\pm$ 1.698 <sup>a</sup>	8.13 $\pm$ 1173 <sup>a</sup>	4.04 $\pm$ 1.090 <sup>b</sup>	7.28 $\pm$ 1.428 <sup>ab</sup>	6.75 $\pm$ 1.568 <sup>ab</sup>
Intrinsic rate of increase ( $r$ ) ( $\text{day}^{-1}$ )	0.200 $\pm$ 0.019 <sup>a</sup>	0.248 $\pm$ 0.014 <sup>a</sup>	0.124 $\pm$ 0.027 <sup>b</sup>	0.186 $\pm$ 0.020 <sup>ab</sup>	0.170 $\pm$ 0.023 <sup>ab</sup>
Finite rate of increase ( $\lambda$ ) ( $\text{day}^{-1}$ )	1.222 $\pm$ 0.023 <sup>a</sup>	1.282 $\pm$ 0.017 <sup>a</sup>	1.131 $\pm$ 0.030 <sup>b</sup>	1.204 $\pm$ 0.024 <sup>ab</sup>	1.185 $\pm$ 0.027 <sup>ab</sup>
Mean generation time ( $T$ ) (day)	11.15 $\pm$ 0.496 <sup>a</sup>	10.65 $\pm$ 0.190 <sup>a</sup>	11.27 $\pm$ 0.662 <sup>a</sup>	10.68 $\pm$ 0.292 <sup>a</sup>	12.89 $\pm$ 0.411 <sup>a</sup>

The means followed by different superscript letters in the same row are significantly different (paired bootstrap test,  $p < 0.05$ ).  $R_0$  = net reproductive rate;  $r$  = intrinsic rate of increase;  $\lambda$  = finite rate of increase;  $T$  = mean generation time.

The pre-oviposition period of these populations on apple leaves did not show any significant difference and varied from 1.08–1.26 days; however, for example, this period lasted 0.58 days on okra (Krishna and Bhaskar, 2014).

Fecundity of *T. urticae* depends on ecological conditions, such as temperature and host plants (James and Price, 2002; Kasap, 2002). Total fecundity varied from 12.93–27 eggs; the lowest was reported for the Faryman population. The oviposition rate of *T. urticae* on different strawberry cultivars ranged from 26.70–64.16 eggs/female (Rezaie et al., 2013). The total fecundity of *T. urticae* was significantly higher on apple leaves (Golden Delicious). Daily egg production per female ranged from 3.5–4.6 eggs (Kasap, 2004), 33.62–153.22 eggs/female on fourteen soybean genotypes (Sedaratian et al., 2009), 82.45–142.05 eggs/female on seven bean cultivars (Modarres Najafabadi, 2012), 5.25–29.23 eggs/female on seven eggplant cultivars (Khanamani et al., 2.13), 79.28 eggs on bean plants, 71.48 eggs on sweet pepper and 71.22 eggs on cucumber (Praslička and Huszár, 2004). Such different numbers can be attributed to variations in the quantity of nutrients and secondary substances. Spider mite fecundity was positively correlated with the nitrogen and carbohydrate content of the leaves and negatively with phenolic content (Wermelinger et al., 1991).

The intrinsic rate of population increase has been used as an indicator of *T. urticae* population performance (Sabelis, 1985). The intrinsic rate of natural increase is one measure used to evaluate the level of plant resistance to insects or mites (Yang and Chi, 2006; Razmjou et al., 2009; Modarres Najafabadi, 2012; Modarres Najafabadi and Zamani, 2013). However, comparisons of  $R_0$  and  $r$  commonly give great insight beyond the parameters of life history (Zhang et al., 2007). Kasap (2004) reported that the intrinsic rate of increase ( $r$ ) of *T. urticae* ranged from 0.231–0.243 day<sup>-1</sup> on five different apple varieties. The reported  $r$  values of *T. urticae* on bean leaves were 0.336 day<sup>-1</sup> and 0.265 day<sup>-1</sup> (Kasap, 2004), on cucumber 0.247 day<sup>-1</sup> (Kasap, 2002), on rose 0.200 day<sup>-1</sup> (Kasap, 2002), on strawberry 0.170–0.251 day<sup>-1</sup> (Rezaie et al., 2013), on the Delicious apple variety 0.372 day<sup>-1</sup> and 0.199 day<sup>-1</sup> (Bengston, 1970; Herbert, 1981), on Granny smith 0.170 day<sup>-1</sup>, on Gravenstein 0.130 day<sup>-1</sup> and on Jonathan 0.163 day<sup>-1</sup> (Bengston, 1970). In this study,  $r$  values ranged between 0.124–0.250 day<sup>-1</sup>. Fathipour et al. (2006) showed the most suitable spider mite host plant (bean cultivars) had  $r$  values between 0.221 and 0.340 day<sup>-1</sup>.

Navajas et al. (2000) studied the genetic variation of the two-spotted spider mite collected on rose from several localities. They reported that the relative role of ecological factors (host plant) and geographical distance in the ongoing differentiation process potentially lead to speciation. The spider mite has a broad range of host plants. However, the spider mite

does not accept all plants because of differences in nutritive and toxic constituents. The morphology of a leaf surface (hairs or glandular trichome) and the presence of natural enemies also play an important role in plant acceptance (van der Boom et al., 2003).

Fytrou and Tsagkarakou (2014) investigated reproductive incompatibility between genetically differentiated populations of *T. urticae* from different host plants. Their results suggested the existence of a citrus-associated *T. urticae* host race. Gotoh et al. (1993) studied genetic differentiation, host plant preference and mate choice in a tomato and a cucumber strain. They suggested that the two strains represent host races. Mozaffarian et al. (2007) reported that the wing size and shape differences of *Ectomylois ceratoniae* (Zeller) among tested populations may not have a genetic basis and could happen because of differences in the nutritional content of the host plant. Genetic differentiation of females of *T. urticae* was found to be correlated with distance, but not with the species, of colonized host plants (Tsagkarakou et al., 1997).

## Conclusions

We observed the biological variation of the two-spotted spider mite collected on several localities. The variation might be due to the chemical contents, food quality, secondary metabolites and leaf texture of the host plants and the geographical differences between collection sites. The present study revealed that there were significant differences in the performance of five two-spotted spider mite populations.

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## Author contributions

Two authors contributed to the design of this study. M.R. conceived and designed the analysis, contributed data and analysis tools, performed the analysis and wrote the paper. F.A. collected the data.

## Conflict of interest

The authors declare that there is no conflicting issue related to this research article.

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