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Genetic and morphological features of some Turkish populations of *Amblyseius swirskii* (Athias-Henriot) (Acari: Phytoseiidae)

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Original research

ABSTRACT

Amblyseius swirskii is one of the most important phytoseiid mites commercialized worldwide for controlling pest mites and small insect pests. The study aims to investigate morphological and genetic variation among seven populations collected from different locations and plant species (cotton, orange) in Türkiye. The DNA sequences (12S rRNA and Cytb mitochondrial DNA markers) were also compared with those of commercial populations. The average genetic distance among the Turkish populations was quite low (0.7% for 12S rRNA and 0.9% for Cytb mtDNA), ranging from 0 to 2.8% and 0 to 1.5%, respectively. The phylogenetic trees show two distinct groups, separated by genetic distances of 0.9% and 1.3% for the 12S rRNA and the Cytb mtDNA fragments, respectively. The genetic differences were not explained by location or host plant. However, specimens from some populations were exclusively or predominantly included in one of the two clades, and commercialized specimens of *A. swirskii* only included in one clade, along with specimens collected in orange orchards. Specimens from cotton fields and *Solanum nigrum*, were found in both clades, but in different proportions. Results show a globally low genetic diversity within *A. swirskii* for the two DNA fragments. The existence of two clades raises questions about the presence of a clade derived from commercial releases. However, this result may be related to other factors. Morphological analyses demonstrated substantial variability among the populations, except for the population sampled from orange in Adana Kozan. Despite this, the morphological and molecular results are relatively consistent.

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Introduction

Predatory mites from the family Phytoseiidae (Acari: Mesostigmata) play a crucial role in biological control (McMurtry *et al.* 2013; Tixier 2018). Various species are used to control pest mites and small insect in many crops (Kostiainen and Hoy 1996; McMurtry and Croft 1997). Phytoseiid mites are reported on every continent except Antarctica (Tixier *et al.* 2008a; McMurtry *et al.* 2013), with more than 2,500 valid species described to date (Chant and McMurtry 2007; Demite *et al.* 2024). Several studies have investigated intraspecific variations in some phytoseiid species for taxonomy and biological adaptation. Morphological and molecular analyses have revealed significant intraspecific variations, which are critical for accurate species identification (Okassa *et al.* 2011; Tixier *et al.* 2017; Lima *et al.* 2018;

Tixier *et al.* 2021). These variations are also associated to ecological factors such as host plants, climatic conditions, seasonal changes (i.e., overwintering females), and prey species. For instance, Tixier *et al.* (2010a), demonstrated genetic differentiation between populations of *Phytoseiulus longipes* Evans, based on their ability to feed or not on *Tetranychus evansi* Baker & Pritchard. Similarly, Queiroz *et al.* (2021) and Tixier *et al.* (2022a) suggested that genetic differentiation in populations of *Phytoseiulus macropilis* Banks, and several other phytoseiid species - such as *Amblyseius swirskii* Athias-Henriot, *Kampimodromus aberrans* (Oudemans), *Neoseiulus californicus* (McGregor), *Phytoseius finitimus* Ribaga, *Phytoseiulus persimilis* Athias-Henriot, *Typhlodromus (Typhlodromus) pyri* Scheuten, and *Typhlodromus (Anthoseius) recki* Wainstein - might be associated to climatic conditions. Tixier *et al.* (2003, 2020) also showed morphological differentiation in *T. (A.) recki* and *K. aberrans* based on their host plants. This study focuses on *A. swirskii*, one of the most widely used phytoseiid species alongside with *N. californicus* and *P. persimilis* (Knapp *et al.* 2018). This species preys on tetranychid and eriophyid mites, thrips, whiteflies, and pollen (Lee and Gillespie 2011; McMurtry *et al.* 2013; Buitenhuis *et al.* 2015). This predatory mite is used in various crops, including greenhouses, vineyards, fruit orchards, vegetable fields, and citrus groves (Castagnoli and Falchini 1993). It is commercially available in Türkiye since 2009, and is also known to occur naturally in this country (Döker and Kazak 2019; Demite *et al.* 2024). Notably, it was the the predominant phytoseiid species found in commercial citrus orchards in Adana province (Southern Türkiye) between 2009 and 2015 (Kazak *et al.* 2016). Tixier *et al.* (2022b) recently studied molecular variations in this species across Europe and Africa, including populations commercialized by several companies. They showed very low genetic variation among these populations, with the exception of the population from Cape Verde. They proposed two hypotheses: (i) low intrinsic genetic variation within the species, or (ii) an overdispersion of commercial populations replacing the natural ones. Turkish populations of *A. swirskii* were not included in their study, despite the species' naturally occurrence in this country on various crops. The present study aims to investigate the genetic variations in Turkish populations of *A. swirskii* and compare their DNA sequences with those of commercial populations to test these latter hypotheses. Furthermore, because morphological traits can also reflect ecological adaptations, this study includes morphological analyses to provide additional elements for taxonomical purposes and species identification.

Material and methods

Populations considered

Specimens of *A. swirskii* were collected from crops (cotton: *Gossypium hirsutum* L., Malvaceae and orange: *Citrus sinensis* (L.) Osbeck, Rutaceae) and a weed species (*Solanum nigrum* L.,

Table 1 Collection details of *Amblyseius swirskii* specimens used for molecular and morphological analyses and accession numbers of their sequences in GenBank.

Location	GPS coordinates	Plant	12S rRNA	Cytb mtDNA	Morphology (numbers of females measured)
Adana-Ceyhan	36°59'15.3"N 35°49'26.5"E	<i>Gossypium hirsutum</i>	PQ134490, PQ134491, PQ134492, PQ134493, PQ134495	0	3
Adana-Karatas 1	36°42'41.5"N 35°08'18.1"E	<i>Gossypium hirsutum</i>	PQ134494, PQ134496, PQ134497, PQ134498, PQ134499	PP997641, PP997642, PP997643	11
Adana-Karatas 2	36°43'13.4"N 35°11'18.0"E	<i>Gossypium hirsutum</i>	PQ134512, PQ134513, PQ134514	PP997655, PP997656, PP997657	5
Adana-Kozan	37°24'52.7"N 35°47'21.0"E	<i>Citrus sinensis</i>	PQ134515, PQ134516, PQ134517, PQ134518, PQ134519	PP997658, PP997659, PP997660, PP997661, PP997662	4
Adana-Merkez	36°55'30.0"N 35°19'17.2"E	<i>Solanum nigrum</i>	PQ134510, PQ134511	PP997653, PP997654	1
Mersin-Tarsus	36°50'51.4"N 34°59'20.1"E	<i>Gossypium hirsutum</i>	PQ134500, PQ134501, PQ134502, PQ134503, PQ134504, PQ134505	PP997644, PP997645, PP997646, PP997647, PP997648	10
Osmaniye-Kadirli	37°18'31.4"N 35°56'56.5"E	<i>Gossypium hirsutum</i>	PQ134506, PQ134507, PQ134508, PQ134509	PP997649, PP997650, PP997651, PP997652	7

Solanaceae) in different locations in 2022 and 2023. Collection sites include various locations in Adana (Ceyhan, Karataş 1, Karataş 2, Kozan, Merkez), as well as in Mersin (Tarsus) and Osmaniye (Kadirli) provinces (Supplementary file 1). Samples were obtained from commercial cotton and orange orchards, where *A. swirskii* had not been released. Additionally, specimens were collected on *S. nigrum* in one orchard. Table (1) shows details on the localities, the plants sampled, and the numbers of specimens considered per population for both molecular and morphological analyses. Although the specimens for morphological and molecular analyses were sourced from the same populations, they were not exactly the same specimens due to the measurement distortions during DNA extraction.

Morphological analyses

Forty-one *A. swirskii* females from seven populations were mounted on slides in Hoyer's medium and observed using a phase and differential interference contrast microscope (Leica DMLB, Leica Microsystems, Le Pecq, France) (40× magnification). In phytoseiid mite taxonomy, the length of dorsal setae is commonly considered important. Therefore, measurements of 25 dorsal idiosomal setae of females were obtained: *j1*, *j3*, *j4*, *j5*, *j6*, *J2*, *J5*, *z2*, *z4*, *z5*, *Z1*, *Z4*, *Z5*, *s4*, *S2*, *S4*, and *S5*. Additionally, macrosetae on the leg IV (SgeIV, StiIV, STIV) and the dimensions (length and width at level of *z4*) of the dorsal shield (DSL and DSW, respectively), as well as length and the width of the ventrianal shield (at level of *ZV2* and at level of anus), were measured. The idiosomal setal terminology used in this study follows that of Lindquist and Evans (1965), as adapted by Rowell *et al.* (1978) for the family Phytoseiidae. The terminology of macrosetae on the leg IV follows the terminology of Athias-Henriot (1957). All measurements are provided in micrometers. As for one population only one specimen was available, ANOVA analyses were not performed. Instead, a Principal Component Analysis (PCA) was conducted to determine if the combination of morphological characters could enable differentiate among the specimens considered. The statistical analyses were conducted using R Core Team (2021) software, with the "FactoMineR" (Lê *et al.* 2008) and "factoextra" packages (Kassambara and Mundt 2020).

Molecular analyses

Total DNA was extracted from each specimen using the DNeasy Blood and Tissue Kit (Qiagen, Hilden, Germany), following the 'Purification of Total DNA from Animal Blood or Cells' protocol (Spin-Column Protocol), modified for extracting total DNA from mites (Kanouh *et al.* 2010a, b; Tixier *et al.* 2010a). Following DNA extraction, the mite carcasses were collected and mounted on slides using the procedure described by Tixier *et al.* (2010b) to confirm species identity.

The primers used to amplify the DNA fragments were: 12S rRNA, 5'-3' TACTAT-GTTACGAC TTAT ve 3'-5' AAAC TAGGATTAGATACCC (Jeyaprakash and Hoy 2002), Cytb mtDNA, 5'-3' TAWRAARTATCAYTCDGGTTKRATATG, and 3'-5' CCWTGAGGA-CAAATAWSWTTYTGAGG (Tixier *et al.* 2012). Polymerase chain reactions (PCR) were performed in a 25 µL volume, containing 4 µL of mite DNA, 2.5 µL (1 mM) of buffer X, 1 µL (1.5 mM) of MgCl₂, 0.5 µL (0.05 mM for each) DNTps, 0.175 mL (0.7 mM) for each primer, 0.125 mL (0.625 U) of Taq Polymerase (Qiagen) and 16.525 µL of water (Tixier *et al.* 2012). Thermal cycling conditions were as follows, for the 12S rRNA marker: 95 °C for 1 min, followed by 35 cycles of 94 °C for 30 sec, 40 °C for 30 sec and 72 °C for 1 min, and 72 °C for 5 min. For the Cytb mtDNA marker: 94 °C for 3 min, followed by 35 cycles of 92 °C for 20 sec, 53 °C for 1 min, and 72 °C for 1 min and 72 °C for 5 min (Tixier *et al.* 2012). PCR products were sequenced along both strands using Dynamic ET Terminator Cycle Sequencing kit, and purified using ExoSAP-IT (Amersham). Sequencing was performed using the Megabase 1,000 apparatus. The sequences were analysed on both strands (forward and reverse), and the resulting consensus sequences were compared to those in the NCBI GenBank database to identify potential contaminations. Sequences alignment and analyses were performed

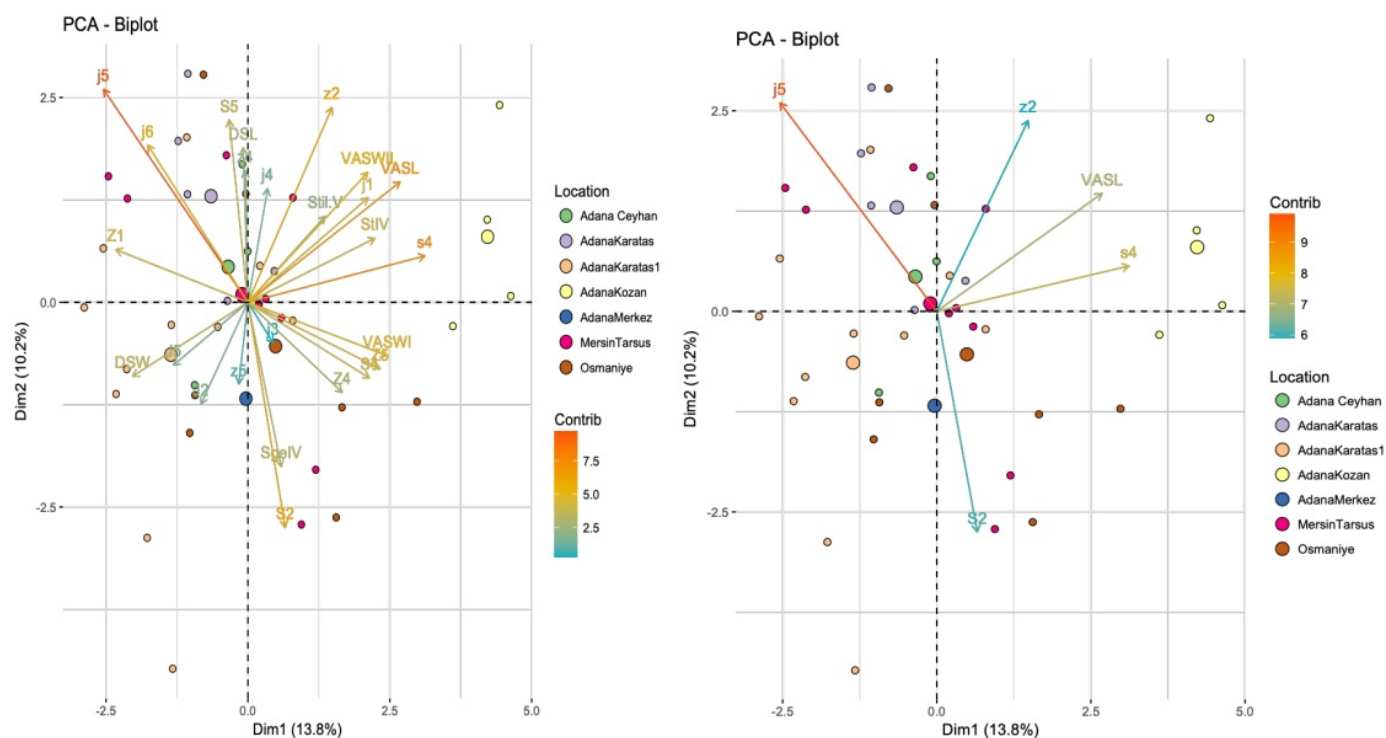


Figure 1 PCA biplot showing the contribution of the variables (measurements of setal length and body regions of females) and the seven populations of *Amblyseius swirskii* collected in different locations in Türkiye (on the left with all the variables, on the right with the variables whose contribution is > 5), DSL: Dorsal Shield Length, DSW: Dorsal Shield Width, VAS L: Length of the Ventrianal Shield, VAS W1: Width of the Ventrianal Shield at level of ZV2, VAS W2: Width of the Ventrianal Shield at level of anus.

using the MEGA X software (Kumar *et al.* 2018). Genetic distances were calculated using the Kimura-2-parameter model, and maximum likelihood trees were constructed using the substitution of evolution models TrN+I for the 12S rRNA sequences and GTR+I for the Cytb mtDNA sequences. Node support was determined using 1000 bootstrap replicates. *Amblyseius andersoni* (Chant) was selected as the outgroup species, as it belongs to the same sub-family (Amblyseinae) and is morphologically similar to *A. swirskii* (12S rRNA and Cytb mtDNA GenBank accession numbers: HQ404858, KU318207). The GenBank accessions numbers for the 12S rRNA sequences of specimens commercialized by Agrobio, Koppert, and Bioplanet are MW404026, MW404023 and MW404028, respectively. The GenBank accessions numbers for the Cytb mtDNA sequences of specimens commercialized by Koppert are MT828779, MT828780, and MT828781.

Results

Morphological analyses

The supplementary file (2) shows the means and min-max values of the 25 morphological traits of the seven populations studied. The PCA (Principal Component Analysis) explains 24% of the total variation of the system, with axis 1 explaining for 13.8% and axis 2 for 10.2% (Figure 1). The five most well represented morphological traits were the length of the setae *j5*, *z2*, *s4*, *S2*, and the ventrianal shield (VAS). Generally, specimens from the same population were not grouped together, except for those collected from orange trees in Adana Kozan and, to a lesser extent, the populations from Adana Karatas and Adana Karatas 2. Specifically: (i) the population collected on orange in Adana Kozan was characterized by shorter seta *j5*, and longer

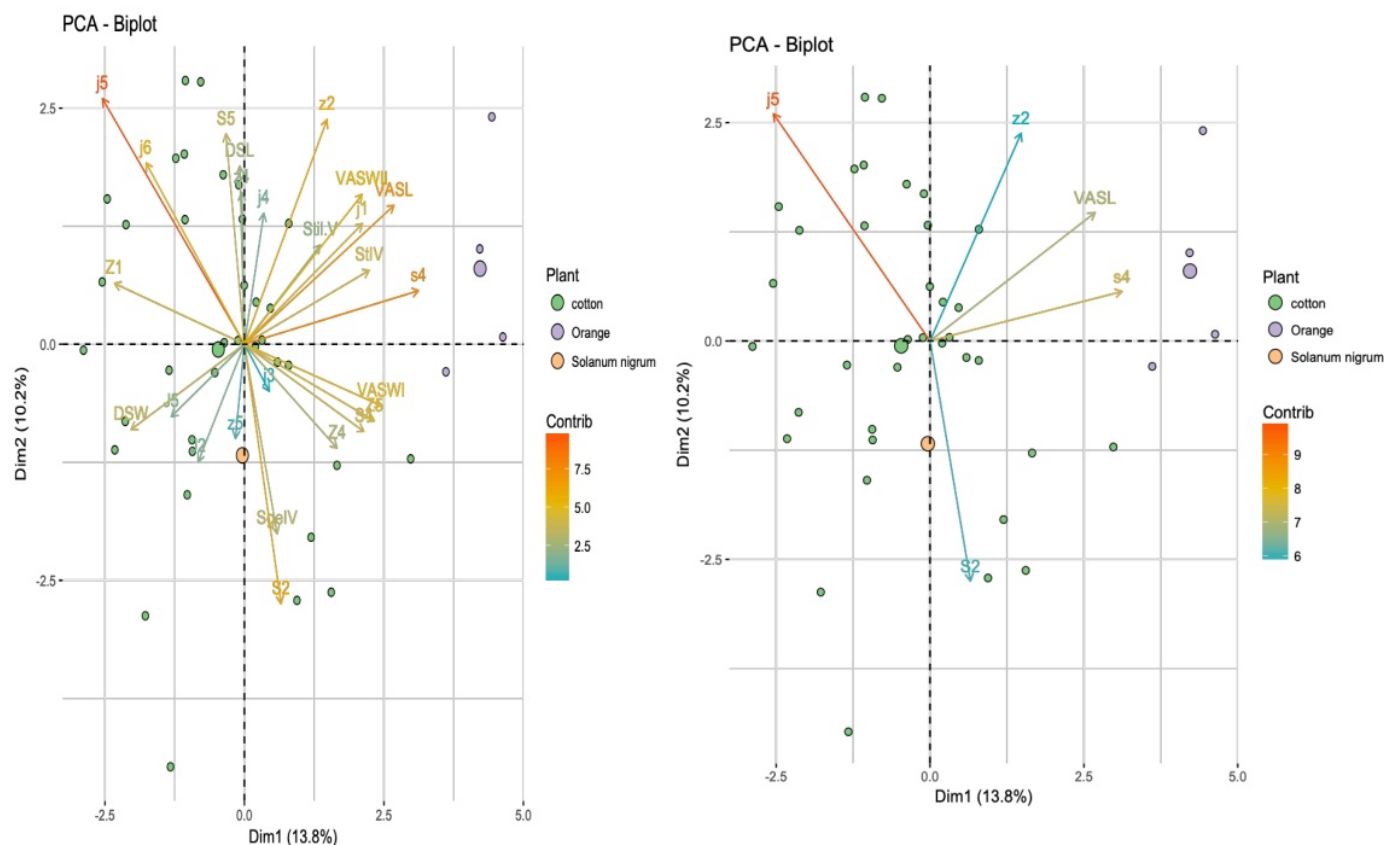


Figure 2 PCA biplot showing the contribution of the variables (measurements of setal length and body regions of females) and specimens of *Amblyseius swirskii* sorted according to the host plant where they were collected in Türkiye (on the left with all the variables, on the right with the variables whose contribution is > 5), DSL: Dorsal Shield Length, DSW: Dorsal Shield Width, VAS L: Length of the Ventrianal Shield, VAS W1: Width of the Ventrianal Shield at level of ZV2, VAS W2: Width of the Ventrianal Shield at level of anus.

seta *s4* and of VAS, (ii) the Adana Karatas population on cotton was characterized by longer setae *j5* and *z2*, with shorter seta *S2*, and (iii) the Adana Karatas 2 population differs from Adana Karatas 1, especially along axis 2, which is mainly explained by lengths of setae *j5* and *S2*. No clear morphological differentiation among populations based on geographic location was observed. When PCA was performed based on the plant species from which specimens were collected (Figure 2), specimens on orange trees were distinctly separated from those collected on cotton. A great variation was observed among specimens collected from cotton across various locations. The specimens collected on orange trees came from a single population, which may explain their homogeneity and distinct separation from the cotton specimens. The two specimens collected from *S. nigrum* were also distinct from those collected on orange trees and fell within the overall variation of the cotton specimens. Although a morphological differentiation based on plant species could be suggested, additional measurements from orange orchards in different locations and cotton populations from Adana Kozan would be required for conclusive results.

12S rRNA analyses

A total of 30 12S rRNA sequences from *A. swirskii* were obtained. The genetic distances between these 30 specimens were low (0.7% in mean) ranging from 0 to 2.8% (Table 2). The mean genetic distances within populations ranged from 0% (for the Osmaniye population on cotton) to 1.1% (for the Adana-Karatas 2 population on cotton). The genetic distances between

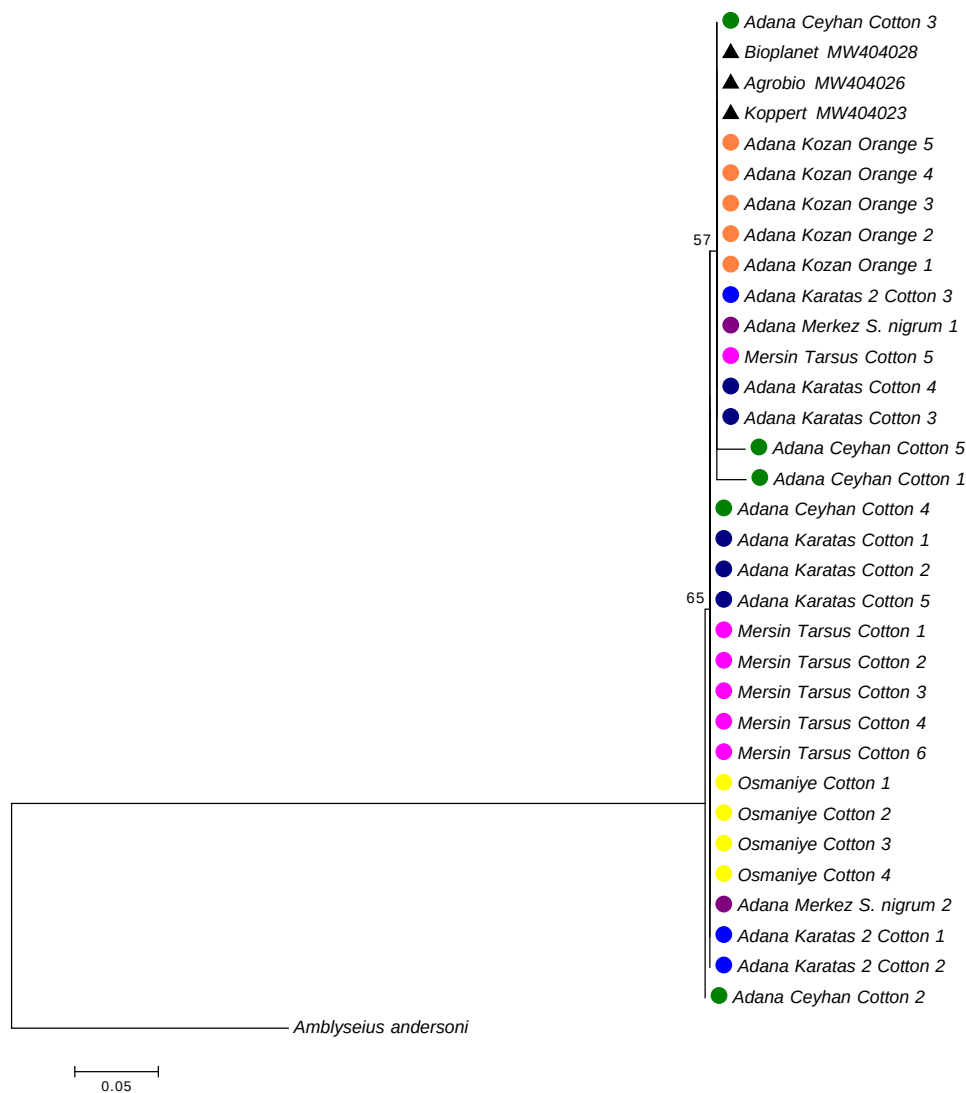


Figure 3 Maximum likelihood phylogenetic trees based on 12S rRNA sequences, including specimens of *Amblyseius swirskii* collected in Türkiye and three specimens from commercial populations, and *Amblyseius andersoni* (as an outgroup).

populations were quite similar to intra-populations distances, ranging from 0.2% to 1.2%. The lowest genetic distances were observed between the populations collected in Adana Merkez

Table 2 K2P genetic distances (%) within (in grey) and between populations of *Amblyseius swirski* based on the 12S rRNA fragment.

Location	Adana-Ceyhan	Adana-Karatas 1	Mersin-Tarsus	Osmaniye	Adana-Merkez	Adana-Karatas 2	Adana-Kozan
Adana-Ceyhan	0.9						
Adana-Karatas 1	0.7	0.7					
Mersin-Tarsus	0.7	0.6	0.6				
Osmaniye	1.2	1.1	0.7	0			
Adana-Merkez	0.5	0.4	0.4	0.8	0.3		
Adana-Karatas 2	1.0	0.8	0.7	0.8	0.6	1.1	
Adana-Kozan	0.5	0.4	0.5	1.0	0.2	0.7	0

on *S. nigrum* and in Adana Kozan on orange, while the highest distances were found between the populations from Adana-Ceyhan on cotton and those from Osmaniye and Adana Karatas 2 on cotton. The population from Osmaniye also differed from the populations of Karatas 1 on cotton and Adana Kozan on orange, with a mean genetic distance of 1%. When specimens were grouped according to the three plant species, the mean genetic distance within the “cotton group” was 0.8%, within the “*S. nigrum* population” was 0.3%, and within the “orange group” was 0%. The mean genetic distance was 0.6% between the “orange group” and “cotton group”, 0.2% between the “orange group” and “*S. nigrum* population”, and 0.5% between the “cotton group” and “*S. nigrum* population”. These results suggest that genetic variations were not related to host plants or their geographic locations. The phylogenetic tree revealed two clades, despite the low bootstrap values (Figure 3). The first clade included all specimens collected from orange trees in Adana Kozan, specimens from cotton in Adana Ceyhan (two specimens), Adana-Karatas 1 (three specimens), Mersin-Tarsus (one specimen), Adana Karatas 2 (one specimen), and one specimen from *S. nigrum* in Adana-Merkez. The second clade contained all specimens collected from cotton in Osmaniye, specimens from cotton in Adana Ceyhan (two specimens), Adana-Karatas 1 (three specimens), Mersin-Tarsus (five specimens), Adana Karatas 2 (two specimens), and one specimen from *S. nigrum* in Adana-Merkez. The mean genetic distance between these two clades was 0.9%, while the genetic distances within clade 1 and clade 2 were of 0.4% and 0.5%, respectively. Table (3) shows the proportion of specimens per population within these two clades, revealing the following trends: (i) populations with a majority of specimens in clade 1: Adana Kozan on orange, (ii) populations with a majority of specimens in clade 2: Mersin Tarsus on cotton, Osmaniye on cotton and Adana Karatas on cotton, and (iii) populations with specimens equally distributed in the two clades: Adana Ceyhan on cotton, Adana Karatas 1 on cotton, and Adana Merkez on *S. nigrum*. Specimens from commercial populations sold by Koppert, Agrobio, and Bioplanet were included in the clade 1.

Cytb mtDNA Analyses

A total of 22 Cytb mtDNA sequences from *A. swirskii* were obtained. The genetic distances among these specimens were low, with a mean of 0.9%, ranging from 0 to 1.5% (Table 4). The mean genetic distances within populations ranged from 0% (for the “Adana Kozan population on orange”) to 1% (for the “Adana-Merkez” population on *S. nigrum*). The mean genetic distances between the populations ranged from 0.6% to 1.5%. The genetic distances between the Adana Kozan population on orange and the other populations were higher than 1%, whereas the genetic distances among the other six populations were lower than 0.8%. When the specimens were grouped according to the three plant species, the mean genetic distance within the “cotton group” was 0.7%, within the “*S. nigrum* population” was 1.0%, and within the “orange group” was 0%. The genetic distances between these groups were 0.7% between

Table 3 Number (and proportion) of *Amblyseius swirski* specimens of each population included within the two clades obtained based on the 12S rRNA and Cytb phylogenetic trees.

Location	Plant	12S		CYTB	
		Clade 1 (proportion)	Clade 2 (proportion)	Clade 1 (proportion)	Clade 2 (proportion)
Adana-Ceyhan	<i>Gossypium hirsutum</i>	2 (50%)	2 (50%)	-	-
Adana-Karatas 1	<i>Gossypium hirsutum</i>	3 (50%)	3 (50%)	3 (75%)	1 (25%)
Adana-Karatas 2	<i>Gossypium hirsutum</i>	1 (33%)	2 (67%)	1 (33%)	2 (67%)
Adana-Kozan	<i>Citrus sinensis</i>	5 (100%)	0 (0%)	5 (100%)	0 (0%)
Osmaniye	<i>Gossypium hirsutum</i>	0 (0%)	4 (100%)	1 (25%)	3 (75%)
Adana-Merkez	<i>Solanum nigrum</i>	1 (50%)	1 (50%)	1 (50%)	1 (50%)
Mersin-Tarsus	<i>Gossypium hirsutum</i>	1 (17%)	5 (83%)	0 (0%)	4 (100%)
Osmaniye	<i>Gossypium hirsutum</i>	0 (0%)	4 (100%)	1 (25%)	3 (75%)
Total		13 (43%)	17(57%)	11 (50%)	11 (50%)

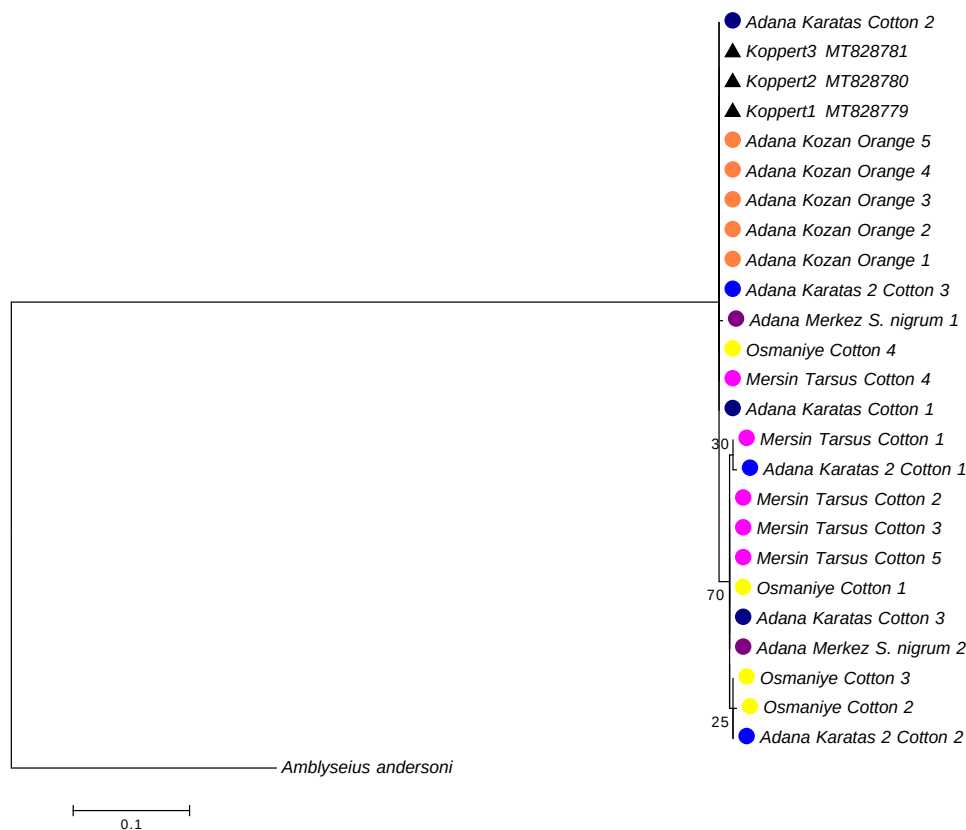


Figure 4 Maximum likelihood phylogenetic trees based on Cytb mtDNA sequences, including specimens of *Amblyseius swirskii* collected in Türkiye and three specimens from commercial populations, and *Amblyseius andersoni* (as an outgroup).

the “*S. nigrum* population” and “cotton group”, and 1.4% and 1.2% between the “orange group” and the “cotton group” and “*S. nigrum* population”, respectively. As observed with the 12S rRNA fragment, the phylogenetic tree revealed two clades, despite the low bootstrap values (Figure 4). The first clade included all specimens collected on orange trees in Adana Kozan, as well as specimens collected on cotton in Adana-Karatas 1 (three specimens), Osmaniye (one specimen), Adana Karatas 2 (one specimen), and one specimen collected from *S. nigrum* in Adana-Merkez. The second clade contained specimens collected on cotton in Osmaniye (four specimens), Adana-Karatas 1 (one specimen), Mersin-Tarsus (four specimens), Adana Karatas 2 (two specimens), and one specimen from *S. nigrum* in Adana-Merkez. The genetic distance between these two clades was 1.3%, while the genetic distances within the clade 1

Table 4 K2P genetic distances (%) within (in grey) and between populations of *Amblyseius swirski* based on the Cytb mtDNA fragment.

Location	Adana-Ceyhan	Adana-Karatas 1	Mersin-Tarsus	Osmaniye	Adana-Merkez	Adana-Karatas 2	Adana-Kozan
Adana-Ceyhan	-						
Adana-Karatas 1	-	0.7					
Mersin-Tarsus	-	0.7	0.5				
Osmaniye	-	0.6	0.7	0.6			
Adana-Merkez	-	0.6	0.8	0.6	1.0		
Adana-Karatas 2	-	0.7	0.7	0.6	0.8	0.9	
Adana-Kozan	-	1.0	1.5	1.4	1.2	1.4	0

and clade 2 were 0.8% and 0.4%, respectively. Table (3) shows the proportion of specimens per population within these two clades, revealing the following trends: (i) populations with a majority of specimens in clade 1: Adana Kozan on orange and Adana Karatas 1 on cotton, (ii) populations with a majority of specimens in clade 2: Mersin Tarsus on cotton, Osmaniye on cotton and Adana Karatas 2 on cotton, and (iii) populations with specimens equally distributed in the two clades: Adana Merkez on *S. nigrum*. These clades contain the same specimens as those included in the two clades obtained with the 12S rRNA fragment, showing concordant results with the two DNA fragments analyzed. Specimens from commercial populations sold by Koppert were included in clade 1, as observed in the phylogenetic tree based on the 12S rRNA fragment. Notably, all specimens collected in orange orchards at Adana Kozan, that were morphologically differentiated from the other populations, were included in the genetic clade 1, indicating a concordance between the morphological and molecular results.

Discussion

Measurements of the *A. swirskii* females examined are close to those reported by Zannou *et al.* (2007), Zannou and Hanna (2011), Abo-Shnaf and Moraes (2014), Kreiter *et al.* (2016), and Döker *et al.* (2020). Additionally, the min and max values of each character mostly overlapped between all populations. The multifactorial analysis revealed substantial variability within the populations, with the exception of the population from orange at Adana Kozan, which displayed comparatively less variation. It is interesting to note that this population was also genetically differentiated, with all its specimens included in the genetic clade 1, along with commercial specimens. It would be thus interesting in further studies to consider measurements of commercial specimens to assess their similarities with the Adana Kozan population from orange. We can also hypothesize that the morphological differentiation of the population collected on orange trees might be due to a plant effect, as already observed for other phytoseiid species (Schmidt 2014; Tixier 2018; Tixier *et al.* 2020). Additional studies, including the measurements of specimens from orange orchards and also from other cotton populations from Adana Kozan, would thus be required to draw more definitive conclusions.

The sequences of 12S rRNA and Cytb mtDNA from seven populations of *A. swirskii*, collected from various locations in southern Türkiye, are reported here for the first time. Despite the identification of approximately 140 phytoseiid species morphologically in Türkiye (Faraji *et al.* 2011; Döker *et al.* 2016, 2017a,b, 2018, 2019, 2020; Demite *et al.* 2024), molecular data are still limited. The genetic distances both for the 12S rRNA and Cytb mtDNA fragments were low for *A. swirskii* from Türkiye (0.7% for 12S rRNA and 0.9% for Cytb mtDNA). These findings are in line with findings from Tixier *et al.* (2022b), who reported mean genetic distances of 0% to 1% for 12S rRNA and 0.1% to 1% for Cytb mtDNA among *A. swirskii* populations from various countries including Egypt, Israel, Reunion Island, Benin and commercial populations. The low genetic distances suggest low genetic variation within *A. swirskii*, which might indicate high dispersal and gene flow among populations. However, despite these low genetic distances, two distinct clades were observed in the phylogenetic trees using both DNA fragments. There was no clear correlation between these clades and the seven populations of *A. swirskii*. However, some populations were found exclusively in one of the clades, such as the population from orange trees in Adana Kozan in clade 1 and the population from cotton in Osmaniye in clade 2. However, clades 1 and 2 contained a mixture of specimens from different populations, although varying in proportions. This structuration does not seem to be solely based on locations or the plant species from which the specimens were collected. Other ecological factors might explain this differentiation, such as feeding habits as observed for *P. longipes* (Tixier *et al.* 2010a) or climatic conditions, as observed for *P. macropilis* (Queiroz *et al.* 2021). Another hypothesis is that differentiation might be associated to differences between natural and commercial specimens. The present results show that the commercial specimens sold by various companies were similar and included in the clade 1, together with

the Adana Kozan orange population and some specimens from other populations. Predatory mites, because released in large quantities for biological control purposes, can become more prevalent than naturally occurring species. The observed low differentiation within *A. swirskii*, as noted by Tixier *et al.* (2022b), might be attributed to introductions and the “invasion” of the commercial specimens. Tixier *et al.* (2008b) also proposed such an hypothesis to explain the low genetic distances between commercialized specimens and populations of *N. californicus* collected all over the World. However, this hypothesis would imply a high dispersal ability of *A. swirskii* through great distances, as no commercial introduction was reported in this region (I. Döker, pers. comm.).

Conclusion

This study is the first to provide DNA sequences 12S rRNA and Cytb mtDNA from seven *A. swirskii* populations in southern Türkiye. The analysis revealed low genetic distances between populations, indicating limited genetic variation within this species in Türkiye. Phylogenetic analyses identified two clades with no clear association to geography or host plants. An other hypothesis is that this differentiation might be related to differences between “commercial specimens” and “natural ones”; however no introduction of commercialized population is reported in the regions where the samples were taken. To confirm this hypothesis, it would be interesting to carry out additional studies, taking into account specimens of *A. swirskii* collected from uncultivated areas and also from other regions of Türkiye where commercial introductions of *A. swirskii* are reported. The analysis of morphological traits seem to show a differentiation of populations according the host plant; again additional studies with more plants would be required to determine how plant can affect *A. swirskii* phenotype, taking into account also other characters as the measurements of macrosetae on legs other than leg IV and the ventral setae JV5.

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