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Integrated taxonomy supports the identification of some species of Phytoseiidae (Acari: Mesostigmata) from Georgia

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Original research

ABSTRACT

The present study reports results of a survey carried out mostly on Citrus sp. and Rubus sp. in Georgia. Morphological and molecular (12S rRNA, COI and CytB mtDNA markers) data were analysed in a framework of integrative taxonomy. Eleven species were identified and among them seven are new for the Georgian fauna. Euseius stipulatus and Phytoseius finitimus were the most abundant species during this survey. We assume that Amblyseius eharai, only reported from eastern Asia, was most probably introduced. Neoseiulus californicus, retrieved from uncultivated vegetation, was almost certainly originating from commercial strains. DNA sequences comparisons disclosed phylogenetic closeness between Amblyseius andersoni and Transeius wainsteini, despite these species (i) being morphologically well differentiated and (ii) classified in different genera, thereby questioning the reliability of the genus Transeius. General morphological characters, including measurements, are provided for species for which diagnoses were doubtful.

Keywords Phytoseiidae; CytB mtDNA; COI mtDNA; 12S rRNA; taxonomy; distribution

Introduction

Mites of the family Phytoseiidae are predators used for biological control of mite and small insect pests of various crops (McMurtry and Croft 1997; McMurtry et al. 2013; Knapp et al. 2018). The family Phytoseiidae, distributed worldwide, contains 2,521 valid species, with some biogeographic regions characterised by the highest number of species and associated reports, namely the Neotropic and Palearctic regions (Tixier et al. 2008b, 2012a; Demite et al. 2021). However, the species diversity and distribution of phytoseiids are only partially known and the fauna of some countries remains poorly investigated (Demite et al. 2021). Gaining in the knowledge on the distribution of Phytoseiidae is interesting for meta-analysis approaches aiming to characterise factors affecting diversity at local and global scales (i.e. Tixier et al. 2008b; Tixier and Kreiter 2009; Tixier 2018). Furthermore, this information is particularly relevant in biological control studies, by providing background data on the availability of...
natural enemy species / populations adapted to specific environmental conditions or pest availabilities.

The Phytoseiidae fauna in Georgia has been partially explored (Demite et al. 2021). As an additional contribution to the knowledge of this group of mites in the country, this paper presents results of surveys carried out in 2019. Among the 53 valid species of Phytoseiidae reported from Georgia, we were particularly interested in detecting *Amblyseius swirskii* Athias-Henriot, as this species is known for its interest in biocontrol (Knapp et al. 2018). It was introduced from the Middle-East in the 1960s to control *Panonychus citri* (McGregor) on citrus and according to Wainstein and Vartapetov (1973), it seemed to have successfully acclimated and was recovered three years later on citrus and *Rubus* spp. According to these objectives, surveys focused on regions where this species was previously reported in the country: Western coast of Adjara (Wainstein and Vartapetov 1973) and Eastern plains along Kura connected to Azerbaijan (Abbasova 1970). Eleven species were identified from our surveys, including seven that are new for the Georgian Fauna. While we did not find *A. swirskii*, a very closely related species, *Transeius wainsteini* (Gomelauri) was identified. Identifications were performed using an integrative taxonomy approach, including morphological analyses and molecular markers.

**Material and methods**

Field surveys were carried out in June 2019. Leaves and sprouts were carefully examined with a hand magnifier and when mites were detected, the plant parts were collected in paper or plastic bags for later examination in the laboratory. Mites were directly collected on leaves under a stereoscopic microscope, and transferred to vials: (i) filled with 70% ethanol for further morphological studies and (ii) filled with 100% ethanol for molecular analyses. Mites were mounted in Hoyer’s medium and identified with a phase and interferential contrast microscope (Leica DLMB, Leica Microsystems) (400x magnification).

The generic classification proposed by Chant and McMurtry (2007) was used. The terminologies used for chaetotaxy were those proposed by Lindquist and Evans (1965) as adapted by Rowell et al. (1978) for dorsal idiosomal setae of Phytoseiidae and by Chant and Yoshida-Shaul (1991) for ventral idiosomal setae. Adenotaxy and poroidotaxy terminologies are those proposed by Athias-Henriot (1975). All measurements are given in micrometers (µm), average value provided first followed by minimum and maximum values into brackets. Specimens are deposited at the SupAgro-CBGP Acari collection at Montpellier, France.

For specimens preserved in 100% ethanol, DNA sequences of CytB, COI mtDNA and 12S rRNA markers were obtained for assisting morphological diagnosis (Tixier et al. 2012b, Dos Santos and Tixier 2017). DNA extraction and amplification follow the protocols well detailed by Kanouh et al. (2010) and Tixier et al. (2012b), respectively. The primers used are those proposed by Tixier et al. (2012b) for Cytb and COI mtDNA fragments and by Jeyaprakash and Hoy (2002) for the 12S rRNA fragment. After DNA extraction, voucher specimens were retrieved as described in Tixier et al. (2010b) to confirm molecular assignment. For the COI and CytB fragments, a preliminary analysis was conducted to check for the absence of stop codons. The sequences were analysed both strands (forward and reverse). The consensus sequences obtained were compared to those included in the NCBI GenBank database to detect possible contaminations. DNA sequences were aligned (using ClustalW) and analysed using MEGA 6.0.6® (Tamura et al. 2013). Genetic distances (using the Kimura 2 parameter) were calculated for comparing DNA sequences to references (sequences published in Genbank). Neighbour-Joining phylogenetic trees were built to assess relationships (i) between *T. wainsteini*, *A. swirskii*, and *Amblyseius andersoni* (Chant) and (ii) between *Amblyseius eharai* Amitai & Swirski, *A. largoensis* (Muma) and *A. herbicolus* (Chant). For all these phylogenetic trees, *Euseius stipulatus* (Athias-Henriot) was used as out-group.
Results

The Phytoseiidae species identified during the survey are listed below. Measurements of morphological characters are provided when they were necessary for species identification and comparison with morphologically close species. Table 1 presents the localities where species were retrieved and Genbank accession numbers of the DNA sequences obtained. When available, biological information is provided, especially for traits relevant to biological control. Data on the known distribution of the species is retrieved from the online Phytoseiidae catalogue (Demite et al. 2021).

Amblyseius eharai Amitai & Swirski

Amblyseius eharai Amitai & Swirski 1981: 60.

Specimens examined. At Lanchkhuti, Grigoleti (42.0192° N, 41.7629° E): 10 ♀♀ and 2 ♂♂ on Rubus sp. (Rosaceae), one ♀ on Citrus trifoliata (L.) Rafinesque (Rutaceae).

Previous records. China, Hong Kong, Japan, Malaysia, South Korea, Taiwan, Thailand.

Measurements of females (5 specimens)

Dorsum. Dorsal shield 362 (340–400) long and 199 (188–212) wide, smooth, with seven pairs of solenostomes (gd1, gd2, gd4, gd5 not well visible, gd6, gd8 and gd9), 17 pairs of dorsal setae and two pairs of sub-lateral setae: j1 35 (32–37), j3 44 (42–45), j4 4 (2–5), j5 4 (2–5), j6 4 (2–5), J2 4 (2–5), J5 4 (2–5), z2 7, Z1 5, z4 4 (2–5), z5 4 (2–5), Z4 104 (100–110), Z5 255 (250–262), s4 98 (97–100), S2 5, S4 7, S5 5, r3 11 (10–12) and R1 7 in length. All setae smooth.

Peritreme. Extending forwards to the bases of the setae j1.

Venter. Sternal shield with three pairs of setae and two pairs of poroids; one pair of sternal setae (st4) on small metasternal platelets; posterior margin with a truncated median projection. Distances between st1–st3 67 (65–70), st2–st2 70 (67–72), st5–st5 72 (70–77). Two pairs of metapodal plates, the largest one 19 (17–22) long and 6 (5–7) wide, the smallest one 8 (7–10) long and 2 wide. Ventrianal shield with three pairs of pre-anal setae JV1, JV2, ZV2 and pre-anal crescent pores (gV3) present, just under the setae JV2. Integument surrounding ventri-anal shield with four pairs of setae ZV1, ZV3, JV4 and JV5; ventri-anal shield 109 (100–130) long, 57 (55–62) wide at level of anterior corners, and 72 (67–77) wide at level of anus. JV5 64 (60–67) long.

Legs. Legs IV with three macrosetae: on the genu 126 (120–130), tibia 90 (85–95) and basitarsus 62 (60–65). SgeI 46 (42–47), SgeII 39 (37–42), SgeIII 47 (45–50), StiII 36 (32–37). Genu II with seven setae (2–2/0, 2/0–1), Genu III with seven setae (2–2/0, 2/0–1). Genu III with seven setae (2–2/0, 2/0–1).

Chelicera. Fixed digit 47, movable digit 42. Dentition not visible because the chelicerae are closed, but the fixed digit is clearly multideterminate.

Spermatheca. Spermatheca with elongate cervix 21 (20–22) long, distal two-thirds gradually flaring, round atrium.

Remarks. Amblyseius eharai is morphologically close to A. herbicolus (Chant). Seta lengths are clearly overlapping and do not allow differentiating between these two species (Table 2). The only clear differences are the shape of the posterior border of the sternal shield (straight for A. herbicolus and with a truncated median projection for A. eharai) and the length and shape of the cervix of the spermatheca (long (23–29), distal two-thirds gradually flaring to 2–2.5 times basal diameter in A. herbicolus and short (18–24), flaring distally to 2–3 times narrowest diameter in A. eharai) (McMurtry and Moraes 1984). Because of these minor differences and because of the distribution of A. eharai only reported from Asia (whereas A. herbicolus is a cosmopolitan species), molecular markers were applied to assess further the identity of the Georgian specimens. Six DNA sequences (three sequences for CytB mtDNA, and three sequences for the COI mtDNA) were obtained from three specimens. The COI sequences were blasted in the Genbank database and were clearly assigned to A. eharai. Table 4a shows the COI genetic distances between the Georgian specimens and Amblyseius largoensis (Muma),
Table 1 Collection data of phytoseiid species studied, followed by GenBank accession numbers for 12S rRNA, COI and CytB mtDNA sequences, and the number of specimens studied morphologically.

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<tr>
<th>Phytoseiid species</th>
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<th>Geographic coordinates</th>
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<th>Morphological observations</th>
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Table 2. Measurements of morphological features of Neoseiulus umbraticus, *N. californicus*, *Amblyseius eharai*, *Transeius wainsteini* (specimens collected in Georgia and data retrieved from original description and re-descriptions) and *A. swirski* and *A. andersoni* (re-descriptions).

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<td><strong>r3</strong></td>
<td>mm</td>
<td>56-88</td>
<td>25-30</td>
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<td><strong>S5</strong></td>
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<td>76-86</td>
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<td><strong>J5</strong></td>
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<td><strong>j1</strong></td>
<td>mm</td>
<td>8 (7-10)</td>
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<td>4 (3-5)</td>
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<tr>
<td><strong>j2</strong></td>
<td>mm</td>
<td>26-28</td>
<td>32 (27-35)</td>
<td>25 (22-27)</td>
<td>21 (18-22)</td>
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<tr>
<td><strong>j3</strong></td>
<td>mm</td>
<td>21 (18-22)</td>
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<td>17</td>
<td>20 (17-22)</td>
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<td>14 (12-15)</td>
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<td><strong>j4</strong></td>
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<td><strong>j5</strong></td>
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<td><strong>j7</strong></td>
<td>mm</td>
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It is the first time that this species is reported from this country and outside eastern Asia. In this survey, it was reported on *Rubus* sp. and *Citrus trifoliata* (L.) Rafinesque both at Lanchkhuti (near the Black Sea coast). Its unexpected presence in Georgia could be due to introduction from eastern Asia, as *C. trifoliata* is a species originating from Korea and north of China. Because *A. eharai* was also found on *Rubus* sp., it is possible that this species has adapted to new plants after its introduction into the region. *Amblyseius eharai* is considered to be an efficient natural enemy of mite pests and thrips in various crops, included citrus orchards (i.e. Ji et al. 2013, Park & Lee 2020).

**Euseius stipulatus** (Athias-Henriot)


**Specimens examined.** At Chokhatauri (42.0247° N, 42.2512° E): 9 ♀♀, 3 ♂♂ and 2 immatures on *Citrus limon* (L.) (Rutaceae), at Chokhatauri (1 km from Chokhatauri) (42.0233° N, 42.2512° E).

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*A. herbicolus* and *A. eharai*. The COI mtDNA sequences of the three Georgian specimens are identical (0%). They differ from *A. laroensis* and *A. herbicolus* sequences in Genbank by high genetic distances (27.2 and 29.2%, respectively), and from the 15 DNA fragments of *A. eharai* retrieved from Genbank by very low distances (2.1–3.2%), corresponding to intraspecific variation. The phylogenetic tree also illustrates that the Georgian specimens belong to the clade including the 15 DNA sequences retrieved from Genbank and assigned to *A. eharai* (JX080331–JX080345) (figure 1). No CytB mtDNA sequence of *A. eharai* is available in Genbank, whereas they are for *A. laroensis* and *A. herbicolus* (Supplementary Table S1b).

The CytB genetic distances between the specimens herein considered and (i) *A. herbicolus* range between 39.1% and 40.3%, and (ii) *A. laroensis* range between 42.7% and 44.5%, clearly showing that Georgian specimens do not belong to these two latter species. Thus, based on morphological characteristics and molecular data, we conclude that the Georgian specimens belong to the species *A. eharai*.
Figure 1 Neighbour joining phylogenetic tree including *Amblyseius eharai* from Georgia, specimens of *Amblyseius eharai*, *Amblyseius largoensis* and *A. herbicolus* from Genbank and *Euseius stipulatus* (as an outgroup) obtained with COI mtDNA fragment.

N, 42.2598° E): 5 ♀♀ and 2 ♂♂ on *Citrus* sp. (Rutaceae), at Kobuleti (1 km East Khala) (41.7032° N, 41.8058° E); 8 ♀♀ and 3 ♂♂ on *Citrus* sp. (Rutaceae), at Kobuleti (2 kms from Esat Chakvi) (41.7135° N, 41.7556° E); 14 ♀♀ and 4 ♂♂ on *Citrus* sp. (Rutaceae), at Kobuleti (Daba Chakvi) (41.7180° N, 41.7384° E); 8 ♀♀ and 1 ♂♂ and 1 immature on *Citrus* sp. (Rutaceae), at Kobuleti (Daba Chakvi) (41.7184° N, 41.7384° E); 9 ♀♀ and 1 ♂ on *Citrus* sp. (Rutaceae), at Kobuleti (Kkhal) (41.7070° N, 41.7912° E); 8 ♀♀ and 2 ♂♂ on *Citrus* sp. (Rutaceae) and 1 ♀, 2 ♂♂ and 4 immatures on *Rubus* sp. (Rosaceae), Kobuleti (Leghva) (41.8517° N, 41.9003° E); 8 ♀♀ on *Citrus* sp. (Rutaceae), at Kobuleti (Mukhaestate) (41.8413° N, 41.8629° E); 10 ♀♀ and 2 ♂♂ on *Citrus* sp. (Rutaceae), at Kvareli (Eniseli) (41.9988° N, 45.6702° E); 4 ♀♀ and 1 ♂ on *Ulmus minor* Miller (Ulmaceae), at Ozurgeti (Nasakikali) (41.9869° N, 42.0697° E); 1 ♀ on *Carpinus betulus* L. (Betulaceae) and 1 ♀ on *Malus orientalis* Uglitzkich ex Iouzptchouk (Rosaceae), at Ozurgeti (2 kms from Nagomari) (42.0097° N, 42.1236° E); 4 ♀♀ and 1 ♂ on *Rubus* sp. (Rosaceae), at Senaki (Sakharbedio) (42.2858° N, 42.0381° E); 7 ♀♀ and 1 immature on *Corylus avellana* L. (Betulaceae)

**Previous records.** Algeria, Azores Island, Canary Island, France, Greece, Hungary, Italy, Iran, Madeira Islands, Montenegro, Morocco, Peru, Portugal, Slovenia, Spain, Syria, Tunisia, Turkey, USA.

**Remarks.** *Euseius stipulatus* was the second most frequent species found (36%), with most of the specimens retrieved from citrus (78% of *E. stipulatus* specimens). This species occurs in the south of the West Palearctic region especially around the Mediterranean basin.
especially on citrus orchards (Ferragut and Escudero 1997, Demite et al. 2021). Prior to this study only one species of *Euseius, E. finlandicus* (Oudemans) was known from Georgia. This is the first report of *E. stipulatus* for the Georgian mite fauna. Molecular sequences obtained (23 sequences for 12S rRNA, COI mtDNA markers and 22 sequences for CytB mtDNA fragment) were compared to those of the *Euseius* species reported from the West Palearctic region (*E. stipulatus, E. scutalis* (Athias-Henriot), *E. finlandicus* and *E. gallicus* Kreiter & Tixier). For all markers studied here, the sequences of the Georgian specimens are similar to the reference sequence of *E. stipulatus* (Supplementary Tables S2a, b, c). However, two specimens collected on *Citrus limon* at Chokhatauri are differentiated from the others and from the *E. stipulatus* references, by a distance of 11.1% – 12.3% for the CytB mtDNA, 2.8% for the 12S rRNA and 8.4% for the COI mtDNA (Supplementary Table S2a, b, c). Such high genetic distances in mitochondrial DNA have been already observed at the intraspecific level (up to 21.7% within *Typhlodromus (Anthoseius) rhenanoides* Athias-Henriot for the CytB mtDNA and up to 10.5% within *Neoseiulus californicus* (McGregor), for the COI mtDNA) (Okassa et al. 2011; Tixier et al. 2019). Furthermore, the genetic distances between these two specimens and *E. gallicus, E. finlandicus* and *E. scutalis* are high for all the DNA fragments considered, showing that these two specimens clearly do not belong to these three species (Supplementary Table S2a, b, c). We thus provisionally conclude that these two specimens belong to *E. stipulatus* and suggest that molecular difference might reflect some adaptations and different biological traits (i.e. Tixier et al. 2010a), but biological trials would be required to test this hypothesis.

**Euseius finlandicus** (Oudemans)

*Seiulus finlandicus* Oudemans 1915: 183.
*Typhlodromus finlandicus*, Oudemans 1930: 50.
*Amblyseius finlandicus*, Athias-Henriot 1958: 34.

**Specimens examined.** At Kvareli (Eniseli) (41.9988° N, 45.6702° E): 1 ♀ on *Ulmus minor* Miller (Ulmaceae).

**Previous records.** Albania, Algeria, Angola, Argentina, Armenia, Austria, Azerbaijan, Belarus, Belgium, Bosnia and Herzegovina, Bulgaria, Canada, Caucasus Region, China, Croatia, Cyprus, Czech Republic, Denmark, England, Finland, France, Georgia, Germany, Greece, Hungary, India, Indonesia, Iran, Italy, Japan, Kazakhstan, Latvia, Lithuania, Macedonia, Mexico, Moldova, Montenegro, Netherlands, Nicaragua, Norway, Poland, Portugal, Russia, Scandinavia, Serbia, Slovakia, Slovenia, South Korea, Spain, Sweden, Switzerland, Tunisia, Turkey, Ukraine, USA.

**Remarks.** This species was reported from Georgia by Samsoniya (1972, 1977) and Wainstein and Vartapetov (1973) on tea, citrus trees and *Prunus* spp., especially in mountainous regions. It is reported to feed on eriophyid mites by Wainstein & Vartapetov (1973). One 12S rRNA sequence (from a specimen collected on *Ulmus minor* Miller) was obtained; it differs to the two DNA reference sequences of this species by 2.2 – 3.3% (Supplementary Table S2b).

**Neoseiulus californicus** (McGregor)


**Specimens examined.** at Ozurgeti (Nasakirali) (41.9869° N, 42.0697° E): 8 ♀♀ on Rubus sp. (Rosaceae), at Ozurgeti (2 kms from Nagomari) (42.0097° N, 42.1236° E): 4 ♀♀ and 1 ♂ on Rubus sp. (Rosaceae).

**Previous records.** Argentina, Azores, Brazil, Canada, Canary Islands, Chile, Colombia, Cuba, Cyprus, France, Greece, Guadeloupe, Guatemala, Italy, Japan, Madeira Islands (Kreiter et al. 2021), Mexico, Peru, Portugal, Reunion Island, Senegal, Serbia, Slovenia, South Africa, South Korea, Spain, Syria, Taiwan, Tunisia, Turkey, USA, Venezuela, Vietnam.

**Measurements of females (4 specimens)**


**Peritreme.** Extending forwards to the bases of the setae j1.

**Venter.** Sternal shield with three pairs of setae and two pairs of poroids; one pair of sternal setae (st4) on small metasternal platelets; posterior margin straight. Distances between st1–st3 62 (60–62), st2–st2 57 (55–60), st5–st5 62 (60–65). Two pairs of metapodal plates, the largest one 22 (20–25) long and 4 (3–5) wide, the smallest one 8 (7–10) long and 2 wide. Ventrianal shield with three pairs of pre-anal setae JV1, JV2, ZV2 and pre-anal crescent pores (gv3) present, posterior-paraxial to setae JV2. Integument surrounding ventrianal shield with four pairs of setae JV1, ZV3, JV4 and JV5; ventrianal shield 102 (100–105) long, 107 (100–110) wide at level of anterior corners, and 80 (75–85) wide at level of anus. JV5 41 (40–42) long.

**Legs.** Legs IV with three macrosetae: on the genu 15, tibia 15 and basitarsus 47. Genu II with seven setae (2–2/0, 2/0–1) and Genu III with seven setae (1–2/1, 2/0–1).

**Chelicera.** Fixed digit 27, movable digit 22 (dentition not visible as the chelicerae are closed).

**Spermatheca.** Calyx cup-shaped 7–9 long and 7 in width, with a small atrium in base of the calyx.

**Remarks.** Neoseiulus californicus is commonly used in biological control. It is mass-released in crops, especially in vegetables for controlling *Tetranychus urticae* Koch, all over the World. This species can also naturally occur in vineyards and orchards (McMurtry and Croft 1997; Tixier et al. 2008a). The measurements of the Georgian specimens globally match with those reported in the re-description of Tixier et al. (2008a) (Table 2). Although the setae Z5 and JV5 are shorter on average in the Georgian specimens than in Tixier et al. (2008a, compiling 300 specimens from 10 populations), these differences are consistent with intraspecific variation range. Morphological identification was confirmed by DNA sequences obtained: one 12S rRNA, four cytB and one COI mtDNA. The CytB and the 12S RNA sequences were compared to those reported in Okassa et al. (2011). The CytB and the 12S rRNA mean genetic distances between the Georgian and the commercial specimens (from different companies and those retrieved world-wide after commercial releases) are 0.04% and 0.1 %, respectively (Okassa et al. 2011). For COI sequences, the Georgian specimens are separated by distances ranging from 0.6 to 0.11% from specimens of *N. californicus* collected in apple orchards in France (Tixier et al. 2008a).

This is the first report of *N. californicus* collected in the wild in Georgia. Because of molecular similarity with the commercial specimens, we assume that the presence of *N. californicus* results from commercial releases and specimens herein collected on *Rubus* sp. might have dispersed from where they were released.
**Neoseiulus umbraticus** (Chant, 1956)


**Specimens examined.** At Telavi (5 kms West from Telavi) (41.9283° N, 45.4241° E): 8 ♀♀ and 4 ♂♂ on *Salvia verticillata* L. (Lamiaceae), at Gurjaani (_velistsikhe_) (41.8545° N, 45.8035° E): 3 ♀♀ on *Populus alba* L. (Salicaceae).

**Previous records.** Armenia, Azerbaijan, Azores Island, Belarus, Caucasus Region, Denmark, England, France, Georgia, Germany, Hungary, Iran, Italy, Latvia, Lithuania, Madeira Islands (Kreiter et al. 2021), Morocco, Mexico, Moldova, Montenegro, Norway, Poland, Russia, Slovakia, Slovenia, Spain, Switzerland, Turkey, Ukraine, USA.

**Measurements of females (6 specimens)**


**Peritreme.** Extending forwards to the bases of the setae *j3*.

**Venter.** Sternal shield with three pairs of setae and two pairs of poroids; one pair of sternal setae (*st4*) on small metasternal platelet; posterior margin straight. Distances between *st1*–*st3* 62 (60–65), *st2*–*st2* 63 (60–65), *st5*–*st5* 65 (62–67). Two pairs of metapodal plates, the largest one 20 (15–25) long and 4 (2–5) wide, the smallest one 13 (10–15) long and 2 wide. Ventrianal shield with three pairs of pre-anal setae *JV1*, *JV2*, *ZV2* and pre-anal pores (*gv3*) present, posterior-paraxial to setae *JV2*. Integument surrounding ventrianal shield with four pairs of setae *ZV1*, *ZV3*, *JV4* and *JV5*; ventrianal shield 106 (100–115) long, 78 (75–80) wide at level of anterior corners, and 68 (62–72) wide at level of anus. *JV5* 35 (32–37) long.

**Legs.** Legs IV with three macrosetae: on the genu 33 (30–37), tibia 20 (20–22) and basitarsus 45 (42–47). Genu II with eight setae (2–2/0, 2/1–1), Genu III with eight setae (2–2/0, 2/1–1).

**Chelicera.** Fixed digit 29 (27–30), movable digit 26 (23–30). Dentition not visible because the chelicerae are closed.

**Spermatheca.** Calyx cup-shaped 11 long and 11 in width, with an atrium well differentiated at the basis of the calyx.

Measurements on a male specimen are provided in the Table 2.

**Remarks.** This species was first described in England on *Rubus fruticosus* L. (Rosaceae) and then recorded mainly in the West Palearctic zone. It was reported from Georgia by Wainstein and Vartapetov (1973) on *Rubus* sp., *Alnus* sp. (Betulaceae), *Ficus carica* L. (Moraceae) and herbs. The measurements of specimens from Georgia fit with those provided by Tixier et al. (2016) for specimens collected from Morocco and with those of the original description (Table 2). The molecular distances range from 0 to 0.3 % between the four CytB mtDNA sequences and are null between the three COI mtDNA sequences. Only one 12S rRNA sequence was obtained. The eight DNA sequences for the three molecular fragments are now included in the Genbank database and will serve as references for further molecular identification of this species. Very few studies refer to the biology of *N. umbraticus*. This species seems able to feed on *T. urticae* and *Thrips tabaci* (Lindeman) (Sengonca and Dresher 2001, Kazak et al. 2002). Wainstein and Vartapetov (1973) reported that this species feeds on *P. citri* and *T. urticae*, and that it tends to prefer humid areas.

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**Transleus wainsteini** (Gomelauri)

*Amblyseius wainsteini* Gomelauri 1968: 518.


*Transleus wainsteini*, Chant & McMurtry 2004: 185,

**Specimens examined.** At Gurjaani (Veliistikhe) (41.8545° N, 45.8035° E): 8 ♀♀ on *Populus alba* L. (Salicaceae), at Telavi (5kms West from Telavi) (41.9283° N, 45.4241° E): 1 ♀ on *Rubus* sp. (Rosaceae), at Telavi (Rd Tetri Tskelebi to Telavi) (41.8870° N, 45.3636° E): 7 ♀♀ and 2 ♂♂ on *Rubus* sp. (Rosaceae), at Telavi (41.9141° N, 45.4579° E): 5 ♀♀ and 3 immatures on *Quercus* sp. (Fagaceae).

**Previous records.** Denmark, Georgia, Germany, Iran, Slovakia, Turkey.

**Measurements of females (10 specimens)**

**Dorsum.** Dorsal shield 362 (340–382) long and 170 (155–177) wide, smooth with small striation in the lateral posterial part, with seven solenostomes (gd1, gd2, gd4, gd5, gd6, gd8 and gd9), 17 pairs of dorsal setae and two pairs of sub-lateral setae: j1 26 (22–30), j3 51 (50–55), j4 8 (7–10), j5 7, j6 8 (7–10), j2 9 (7–10), j5 6 (5–7), z2 22 (17–27), z4 32 (22–35), z5 7 (5–7), Z1 11 (7–12), Z4 63 (60–67), Z5 119 (110–127), s4 68 (65–72), S2 27 (25–32), S4 13 (12–15), S5 9 (7–10), r3 25 (22–27) and RI 17 (15–20) in length. All setae smooth.

**Peritreme.** Extending forwards to the bases of the setae j1.

**Venter.** Sternal shield with three pairs of setae and two pairs of poroids; one pair of sternal setae (st4) on small metasternal platelets; posterior margin straight. Distances between st1–st3 65 (62–70), st2–st2 69 (65–72), st5–st5 67 (65–70). Two pairs of metapodal plates, the largest one 24 (22–25) long and 5 (4–5) wide, the smallest one 10 (7–12) long and 2 wide. Ventrianal shield with three pairs of pre-anal setae JV1, JV2, ZV2 and a pair of crescent pre-anal pores (gv3) present, slightly posterior-paraxial to setae JV2. Integument surrounding ventrianal shield with four pairs of setae ZV1, ZV3, JV4 and JV5; ventrianal shield 116 (112–125) long, 84 (80–90) wide at level of anterior corners, and 82 (77–90) wide at level of anus. JV3 64 (60–70) long.

**Legs.** Legs IV with three macrosetae: on the genu 55 (52–57), tibia 41 (35–40) and basitarsus 63 (60–70). SgelI 31 (30–35), SgelII 32 (30–35), StilII 26 (25–27). Genu II with seven setae (2–2/0, 2/0–1), Genu III with seven setae (1–2/1, 2/0–1).

**Chelicera.** Fixed digit 37 long, movable digit 32 long. Dentition not visible because the chelicerae are closed.

**Spermatheca.** Spermatheca with a cup-shaped calyx 8–10 long and 5 wide, with a well differentiated round and small atrium at the base of calyx.

The table 2 provides measurements of three males.

**Remarks.** This species was described from Georgia (Manglisi) on *Corylus* sp. (Betulaceae) and according to Wainstein and Vartapetov (1973), it is quite common across the country. These authors also noted that *T. wainsteini* feeds on *P. citri* and *T. urticae*. The measurements of the Georgian specimens are close to those reported in the original description and in the re-description of Faraji *et al.* (2011) (from Turkey), except for the setae STIV that were shorter in our specimens (60–70) than in those measured by Faraji *et al.* (2011) (75–78) (Table 2). However, the difference is minor and it is the only difference with *T. wainsteini* studied by Faraji *et al.* (2011); we therefore conclude that the specimens from Georgia belong to *Transleus wainsteini* (Table 2).

Differences between *Amblyseius swirskii*, *Amblyseius andersoni* (Chant) and *T. wainsteini* are minor. *Amblyseius andersoni* differs from *A. swirskii* and *T. wainsteini* by longer setae Z5 (Table 2). The main differences between *A. swirskii* and *T. wainsteini* are the measurements of the setae z2, z4, the ratio s4/S2 and the dentition of the chelicerae.

CytB (8), 12S (5) and COI (8) DNA sequences of Georgian specimens of *T. wainsteini* were obtained, respectively. Phylogenetic trees are presented in the figure 2. The mean genetic distances between these specimens are 1.6% (0–3.1%) for the CytB mtDNA marker, 0% for the 12S rRNA fragment, and 1.2% (0–3%) for the COI mtDNA marker. The mean genetic
distances between *T. wainsteini* and *A. swirskii*, observed for the three molecular markers, support that these species are distinct taxa (CytB mtDNA marker: 44.2% (43.7% – 45.1%), 12S rRNA: 19.7%, COI mtDNA: 24.9% (23.8% – 25.9%)). *Transeius wainsteini* differs from *A. andersoni* by 26.3% (25.5% – 27.2%) for the CytB mtDNA, 9.1% (8.8% – 9.4%) for the 12S rRNA marker and 19.9% (18.6% – 21.1%) for the COI mtDNA fragment (Supplementary Table S3a,b,c). These distances are clearly smaller than those observed between *T. wainsteini* and *A. swirskii*, suggesting that *T. wainsteini* is phylogenetically closer to *A. andersoni* than to *A. swirskii*. Interestingly, these genetic relationships do not reflect morphological similarities as (i) *A. swirskii* and *A. andersoni* are more similar to each other than to *T. wainsteini* and (ii) *T. wainsteini* is morphologically more similar to *A. swirskii* than to *A. andersoni*. The morphological similarities between *T. wainsteini* and *A. swirskii* differ from *T. wainsteini* and *A. andersoni* by 26.3% (25.5% – 27.2%) for the CytB mtDNA, 9.1% (8.8% – 9.4%) for the 12S rRNA marker and 19.9% (18.6% – 21.1%) for the COI mtDNA fragment (Supplementary Table S3a,b,c). These distances are clearly smaller than those observed between *T. wainsteini* and *A. swirskii*, suggesting that *T. wainsteini* is phylogenetically closer to *A. andersoni* than to *A. swirskii*. Interestingly, these genetic relationships do not reflect morphological similarities as (i) *A. swirskii* and *A. andersoni* are more similar to each other than to *T. wainsteini* and (ii) *T. wainsteini* is morphologically more similar to *A. swirskii* than to *A. andersoni*. The morphological similarities between *T. wainsteini* and *A. swirskii* suggest evolutionary convergence especially for the length of setae Z5. Further analyses would be interesting to carry out based, in particular, on the observation of spermatheca structures (atrium, calyx).

A very close relationship between *A. andersoni* and *T. wainsteini* is clearly supported by the 12S sequences (9.1%) (Supplementary Table S3b). In the absence of additional parameters (morphology and other molecular markers), this small distance could have wrongly lead to conclusion that they belong to the same species. The maximal intraspecific distance using the 12S rRNA marker for Phytoseiidae, was observed for the species *Amblyseius largoensis* (7.8% in Barbosa-Lima et al. 2018) and the minimal interspecific distances observed range between 9.5% and 12.5% (between *Neoseiulus californicus* and *N. fallacis* and *N. californicus* and *N. idaeus*, respectively) (Jeyaprakash and Hoy 2002; Okassa et al. 2011).

The phylogenetic closeness of *A. andersoni* and *T. wainsteini* questions the monophyly of the genus *Amblyseius* and the validity of the genus *Transeius*, as already stated by Tsolakis et al. (2012) who showed the proximity between *A. andersoni*, *A. swirskii* and *Transeius montdorensis* (Schicha). Further phylogenetic analyses would be required including additional *Amblyseius* and *Transeius* species, to conclude that *Transeius* is not a valid genus and that *Amblyseius* is paraphyletic.

**Galendromus (Galendromus) longipilus (Nesbitt)**

*Typhlodromus (Typhlodromus) longipilis* [sic], Chant 1959: 59.
*Galendromus longipilis* [sic], Muma 1961: 26.
*Metaseiulus (Galendromus) longipilis*, Wainstein 1973: 176.
*Typhlodromus longipilis* [sic], Ozman & Çobanoğlu 2001: 482.
*Typhlodromus longipilis* [sic], Çobanoğlu & Özman 2002: 92.
*Metaseiulus longipilis* [sic], Kulikova 2011: 59.

**Specimens examined.** At Kobuleti (Khala) (41.7070° N, 41.7912° E): 2 ♀♀ and 1 ♂ on *Rubus* sp. (Rosaceae).

**Previous records.** Austria, Bulgaria, Canada, Costa Rica, Cuba, Czech Republic, France, Galapagos, Germany, Hungary, Italy, Mexico, Moldova, Poland, Slovakia, Spain, Switzerland, Turkey, Ukraine, USA.

**Measurements of females (2 specimens)**

**Dorsum.** Dorsal shield 340 long and 155 wide, reticulated throughout, with two visible solenostomes (gd6 and gd9), 16 pairs of dorsal setae and one pair of sub-lateral setae inserted in the dorsal shield: j1 25, j3 65–67, j4 52–55, j5 60–62, j6 65–70, J2 75, J3 8, z2 67, z4 67–70, z5 62, Z4 70–75, Z5 60–65, s4 65–70, s6 80–82, S2 75–77, S5 62–70 and r3 55–57 in length. All setae smooth.

**Peritreme.** Extending slightly anteriorly to the bases of the setae z4.
Figure 2 Neighbour joining phylogenetic trees including *Transeius wainsteini* from Georgia, *Amblyseius swirskii*, *Amblyseius andersoni* and *Euseius stipulatus* (as an outgroup) obtained with a – COI mtDNA, b – CytB mtDNA and c – 12S rRNA markers.

**Venter.** Sternal shield with three pairs of setae and two pairs of poroid; one pair of sternal setae (st4) on small metasternal platelets; posterior margin straight. Distances between st1–st3 65–72, st2–st2 47–52, st5–st5 47. Two pairs of metapodal plates, the largest one 25 long and 4 wide, the smallest one 10 long and 2 wide. Ventrianal shield with four pairs of pre-anal setae JV1, JV2, JV3, ZV2 and a pair of small circular pre-anal pores (gV3) present, immediately posterior-mediad to JV3. Integument surrounding ventrianal shield with 3 pairs of setae JV1, ZV3 and JV5; ventrianal shield 107 long, 50–55 wide at level of anterior corners, and 65 wide at level of anus. JV3 55–57 long.

**Legs.** Legs IV with one long setae on the basitarsus 35. Genu II with nine setae (2–2/1, 2/1–2), Genu III with seven setae (1–2/1, 2/0–1).

**Chelicera.** Fixed digit 22 long; and movable digit 20 long. Dentition not visible because chelicerae closed.

**Spermatheca.** Spermatheca with elongated and tubular cervix 37 long and 3 wide, with a small atrium inserted at the base of the cervix.

**Remarks.** The measurements of the Georgian specimens are close to those reported in the re-description of *G. longipilus* provided by Chant and Yoshida-Shaul (1984) (Table 3). Some differences are however observed in some seta lengths, which are slightly shorter in the specimens examined in this study.

*Galendromus longipilus* is morphologically very close to *Galendromus occidentalis* (Nesbitt). However, because of the peritreme length and because j6 is longer than the distance between j6 and J2, we conclude that the specimens herein examined belong to *G. longipilus*. No material preserved in 100% ethanol was available for DNA analysis; therefore, we could not strengthen the identification with molecular markers at this time.

This is the first report of *G. longipilus* from Georgia. This occurrence is however consistent with the reported distribution of this species from Turkey and Europe.

**Typhlodromus (Anthoselus) recki (Wainstein)**


**Specimens examined.** At Telavi (5 kms West from Telavi) (41.9283° N, 45.4241° E): 3 ♀♀ and 1 ♂ on *Salvia verticillata* L. (Lamiaceae).

**Previous records.** Algeria, Armenia, Austria, Azerbaijan, Caucasus Region, Cyprus, France, Georgia, Greece, Hungary, Iran, Israel, Italy, Kazakhstan, Lebanon, Moldova, Morocco, Portugal, Russia, Slovenia, Spain (Ferrugat 2018), Syria, Tunisia, Turkey, Ukraine.

**Remarks.** This species was known from Georgia, reported by Wainstein (1958) on *Salvia nemorosa* L. (Lamiaceae), and is commonly found in the West Palearctic region, especially on plants of the family Lamiaceae (Tixier *et al.* 2020a).

Two DNA sequences (one of the CytB and of the COI fragment) were obtained. CytB genetic distance between the Georgian specimen and the 54 specimens collected in South of France and Italy was 5.7% (4.7% – 14%) (Tixier *et al.* 2020b). Genetic distances among the COI sequences, ranged from 2 to 2.2% between the Georgian specimen and the four reported in Genbank (MT828361–364, from France and Italy). This differentiation can be due to population isolation or result from adaptation to climatic conditions (Tixier *et al.* 2020b; Queiroz *et al.* 2021).

**Typhlodromus (Anthoseelus) halinae (Wainstein & Kolodochka)**

**Amblydromella halinae**, Moraes et al. (1986): 163.


**Specimens examined.** At Terjola (Chognari) (42.2305° N, 42.7781° E): 3 ♀♀ on *Rubus* sp. (Rosaceae).

**Previous records.** Iran, Italy, Moldova, Norway, Russia, Slovakia, Ukraine.

**Measurements of female.** One specimen: voucher molecular specimen in the “best” state, the two other specimens are also voucher specimens and not all the characters can be measured.

**Dorsum.** Dorsal shield 310 long and 140 wide, reticulated throughout, five solenostomes not well visible (gd2, gd4, gd6, gd8 and gd9), 18 pairs of dorsal setae and two pairs of sub-lateral setae: j1 23, j3 20, j4 15, j5 13, j6 18, J2 20, J5 5, z2 20, z3 25, z4 20, z5 13, Z4 25, Z5 43, s4 25, s6 25, S2 30, S4 25, S5 20, r3 23 and R1 23 in length. All setae smooth.

**Peritreme.** Extending forwards between the bases of the setae j3 and j1.

**Venter.** Sternal shield with three pairs of setae and two poroids; one pair of sternal setae (st4) on small metastral platelets; posterior margin straight. Distances between st1–st3 50, st2–st5 50, st5–st5 53. Two pairs of metapodal plates, the largest one 25 long and 3 wide, the smallest one 13 long and 2 wide. Ventrianal shield with four pairs of pre-anal setae JV1, JV2, JV3, JV2 and a pair of small circular pre-anal pores (gv3) present (horizontally aligned with JV3 and vertically aligned with JV2). Integument surrounding ventrianal shield with three

### Table 3 Measurements of morphological features of *Galendromus longipilus*, *Typhlodromus (Anthoseius) kerkirae*, T. (A.) halinae (specimens collected in Georgia and data retrieved from original description and re-descriptions) and T. (A.) salviae and T. (A.) rhenanus (original description and re-descriptions).

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pairs of setae ZV1, ZV3 and JV5; ventrianal shield 88 long, 88 wide at level of anterior corners, and 75 wide at level of anus. JV5 33 long.

Legs. Legs IV with one macroseta on the basitarsus (23), and setae (not macrosetae) on the genu (18), tarsus (20). Genu II with seven setae (2–2/0, 2/0–1), Genu III with seven setae (1–2/0, 2/1–1).

Chelicera. Fixed digit 25 long; and movable digit 23 long. Dentition not visible because chelicerae closed.

Spermatheca. Spermatheca with cervix 15–18 long (on the two sides) and 10 wide, with an atrium inserted in the cervix.

Remarks. The specimen studied is morphologically close to Typhlodromus (Anthoseius) rhenanus (Oudemans), even if some differences are observed in spermatheca shape (Table 3). Molecular comparisons with specimens from our own database show high CytB distances between the sequences herein obtained and those referring to T. (A.) rhenanus (19.6% – 20.3%). Similar high distances have been previously observed at the intraspecific level (i.e. Tixier et al. 2017, 2019). However, for the COI fragment, 22% divergence was observed between T. (A.) rhenanus and our specimens. Such large divergences indicate that these specimens do not belong to T. (A.) rhenanus, but to a morphologically similar species.

They are also close to T. (A.) georgicus Wainstein, but difference in spermatheca shape and S5 length (30 for T. (A.) georgicus and 20 for the presently examined specimen) (Hajizadeh and Mortazavi 2015) seem to show that the specimen observed do not belong to this latter species. It is difficult to assign a single specimen to a species. Tixier (2013) tried to provide some decision rules and proposed based on statistical analysis, that a difference of 11 microns between two specimens would be sufficient to conclude that these specimens might belong to different species. We see that in the present case the difference between the specimen examined and T. (A.) georgicus (10 microns) would be just included in this interspecific variation. However, because of this slight difference, we can have some doubts. Considering other species, especially Typhlodromus (Anthoseius) halinae, it seems that the specimen observed is much closer to the latter species than to T. (A.) georgicus. However, the specimens were also morphologically very close to Typhlodromus (Anthoseius) salviae (Kolodochka) but unfortunately we did not find in the description of this latter species, information on the differentiation with T. (A.) halinae (Table 3).

Even if some doubts exist between an identification assigned to T. (A.) halinae or to T. (A.) georgicus, because of closer morphological traits with the former species, we considered that the specimen herein collected belong to T. (A.) halinae. Molecular sequences would help in assisting the diagnosis of these morphological close species in the future, as well as in clarifying the fact that some authors stated that differentiation between some Typhlodromus (Anthoseius) species is only possible based on male observation (Kolodochka 1978). This would be the first report of T. (A.) halinae from Georgia. Because of its current distribution in Eastern Europe and Middle East, the report of the species in Georgia is not surprising.

Typhlodromus (Anthoseius) kerkrare Swirski & Ragusa

Anthoseius kerkrare, Rivnay & Swirski 1980: 177.
Typhlodromus kerkyrae [sic], Papaioannou-Souliotis 1981: 41.
Amblydromella kerkrare, Moraes et al. 1986: 165.
Amblydromella (Aphanoseia) kerkrare, Denmark & Welbourn 2002: 308.

Specimens examined. At Telavi (5 kms from West Telavi) (41.9283° N, 45.4241° E): 1 ♀ on Salvia verticillata L. (Lamiaceae) and 2 ♀♀ on Rubus sp. (Rosaceae), at Tbilisi (240 David Aghmashenebeli Alley) (41.8068° N, 44.7668° E): 1 ♀ on Eryngium caeruleum L. (Apiaceae).

Previous records. Croatia, France, Greece, Iran, Italy, Spain, Turkey.

Measurements of female (1 specimen: voucher molecular specimen in “best” state)
Dorsum. Dorsal shield 315 long and 135 wide, reticulated throughout, with six solenostomes (gd2, gd4, gd6, gd8 and gd9), 18 pairs of dorsal setae and two pairs of sub-lateral setae: j1 20, j3 22, j4 15, j5 15, j6 18, j2 23, j5 8, z2 20, z3 25, z4 20, z5 18, Z4 32, Z3 52, s4 25, s6 30, s2 30, s4 30, s5 27, r3 18 and R1 18 in length. All setae smooth except Z5 lightly barbed.

Peritreme. Extending nearly reaching the bases of the setae j1.

Venter. Sternal shield with three pairs of setae and two pairs of poroids; one pair of sternal setae (st 4) on small metaternal platelets; posterior margin straight. Distances between st1–st3 not visible, st2–st2 not visible, st5–st5 63. Metapodal shields not visible due to mountings (DNA voucher specimen). Ventrianal shield with four pairs of pre-anal setae JV1, JV2, JV3, ZV and a pair of small circular pre-anal pores (gv) present, at level of setae JV3, posterior or slightly postero-paraxial to setae JV2. Integument surrounding ventrianal shield with four pairs of setae ZV1, ZV3, JV4 and JV5; ventrianal shield 98 long, 75 wide at level of anterior corners, and 63 wide at level of anus. JV5 33 long.

Legs. Legs IV with one macrosetae on the basitarsus 27. Genu II with seven setae (2–2/0, 2/0–1), chaetotaxy of the Genu III not clearly visible (leg folded).

Chelicera. Fixed digit 28 long; and movable digit 23 long. Dentition not visible because chelicerae closed.

Spermatheca. Spermatheca with campanulate calyx 13 long and 8 wide, with an atrium incorporated at the basis of the cervix.

Remarks. The morphological features reported above are in line with those reported by Tixier et al. (2019) for T. (A.) kerkraine (Table 3). Four DNA sequences were obtained for CytB, one for 12S and two for the COI fragments. The Genbank database only includes CytB sequences for T. (A.) kerkraine (accession number: MK014094), which have 15.4% – 16.1% divergence with sequences from our specimens from Georgia. In contrast, the mean distance between the four Georgian specimens is 0.25%. Although the genetic distance between the French and Georgian specimens is high, it is lower than the intraspecific variation already observed for species of the sub-family Typhlodrominae and the genus Typhlodromus (Anthoseius) (i.e. 21.7% for T. (A.) rhenanoides in Tixier et al. 2019). The COI and 12S rRNA sequences newly included in the Genbank database will serve as references for further molecular identification of this species.

Phytoseius finitimus Ribaga

Phytoseius finitimus Ribaga 1904: 178.
Phytoseius (Duhlinellus) finitimus, Wainstein 1959: 1365.
Phytoseius (Phytoseius) finitimus, Denmark 1966: 16.

Specimens examined. At Bolnisi (Kveshi) (41.4401° N, 44.4463° E): 9 ♀♀ and 5 ♂♂ on Rubus sp. (Rosaceae), at Bolnisi (Parizi) (41.4709° N, 44.7361° E): 9 ♀♀ and 5 ♂♂ on Rubus sp. (Rosaceae), at Gardabani (Vaziani) (41.7004° N, 45.0543° E): 9 ♀♀ and 4 ♂♂ on Rubus sp. (Rosaceae), at Gurjaani (Chalaubani) (41.6291° N, 45.7946° E): 11 ♀♀ and 3 ♂♂ on Rubus sp. (Rosaceae), at Kharagauli (Rd S1 2.5km East of Tsakva) (42.0965° N, 43.4532° E): 13 ♀♀, 2 ♂♂ and 1 immature on Rubus sp. (Rosaceae), at Kobuleti (Daba Chakvi) (41.7180° N, 41.7384° E): 1 ♀ on Citrus sp. (Rutaceae), at Kvareli (Eniseli) (41.9988° N, 45.6702° E): 2 ♀♀ on Ulmus minor (Ulmaceae), at Lanchkhuti (Grigoliet) (42.0192° N, 41.7629° E): 8 ♀♀ and 3 ♂♂ on Rubus sp. (Rosaceae), at Lanchkhuti (Maltakva Univ. Research Center) (42.0258° N, 41.7273° E): 9 ♀♀ and 1 ♂♂ on Rubus sp. (Rosaceae), at Sagarejo (Tokhliauri) (41.7299° N, 45.4236° E): 11 ♀♀ and 3 ♂♂ on Rubus sp. (Rosaceae), at Senaki (Sakharbedio) (42.2858° N, 42.0381° E): 9 ♀♀, 1 ♂♂ and 1 immature on Rubus sp. (Rosaceae) and 1 ♀ on Corylus avellana (Betulaceae), at Telavi (5 kms West from Telavi) (41.9283° N, 45.4241° E): 3 ♀♀ on Rubus sp.
(Rosaceae), at Terjola (Chognari) (42.2305° N, 42.7781° E): 1 ♀ on *Rubus* sp. (Rosaceae), at Tetri Tskaro (Koda) (41.5953° N, 44.7767° E): 12 ♀♀, and 3 ♂♂ on *Rubus* sp. (Rosaceae).

**Previous records.** Algeria, Azores, Egypt, France, Greece, Iran, Israel, Italy, Montenegro, Morocco, Portugal, Slovenia, Spain, Syria, Tunisia, Turkey, USA.

**Remarks.** According to the world database of Demite et al. (2021), *P. finitimus* is not reported from Georgia. However, *Phytoseius plumifer* (Canestrini and Fanzago) has been reported several times from this country. Because of its long history of misidentification with *P. finitimus* (Duso and Fontana 2002), we can wonder about the specimens reported under the name of *P. plumifer* from Georgia.

*Phytoseius finitimus* was the most frequent species retrieved herein (41% of the specimens collected).

CytB (29), COI (28) and 12S (18) sequences were obtained and compared to those of Tixier et al. (2017) for specimens collected on *Viburnum tinus* (Adoxaceae), *Vitis vinifera* (Vitaceae) from Italy and *Actinidia deliciosa* (Actinidiaceae) from France. The supplementary table S4 shows the genetic distances obtained. Low intraspecific variation was observed for the Georgian specimens. The Georgian specimens are molecularly closer to those from *A. deliciosa* and *V. vinifera* than to those from *V. tinus*, whatever the samples considered (locations and plants). It is worth to note that for the three molecular fragments, a high genetic distance is observed between a specimen collected from *Rubus* sp. at Bolnisi-Kveshi and all the others (Supplementary Table S4).

**Conclusion**

Eleven species of Phytoseiidae were identified during this survey, and among them seven are new for the Georgia Fauna. Results show that despite the reduced number of host plant species sampled, new occurrences were revealed, emphasizing knowledge gaps on Phytoseiidae distribution. Main features resulting from the survey include (i) the occurrence of common East European species, already retrieved from this country and neighbouring countries, and (ii) the unexpected occurrence of some species, which could be explained by exotic introductions (accidental or for biological control purposes). The fact that *E. stipulatus* and *P. finitimus* were observed for the first time in Georgia, while they were the two most abundant species retrieved, is quite unexpected. Fauna modification due to climate change (especially for *E. stipulatus* as this species is mainly reported from the Mediterranean coast climate) and/or misidentifications (especially for *P. finitimus* because of repeated misidentification with *P. plumifer*) are hypotheses that can be put forward to explain these results. The study also illustrates the utility of integrative taxonomy for diagnosis purposes. The observation of the lowest intraspecific distance never detected for the 12S rRNA marker and the validity of the genus *Transeius* are the main taxonomic issues pinpointed.

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**References**


