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The spider mite *Oligonychus yothersi* (Acari: Tetranychidae), a new alien pest in Europe: joint records from insular Portugal, Spain and Italy revealed by integrative taxonomy

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Original research

ABSTRACT

The spider mite *Oligonychus yothersi* (McGregor, 1914) is for the first time reported in Europe from four European insular regions with mild oceanic and Mediterranean climates- the Azores and Madeira archipelagos (Portugal), Canary Islands (Spain) and Sicily (Italy). Although populations were detected in the Canary and Azores islands since 2006 and 2015, respectively, their taxonomic identification remained unresolved due to the lack of male specimens and the unavailability of DNA reference sequences. An integrative taxonomic approach based on morphological traits of two males collected in September 2024 and on recently and previously obtained *COI* DNA sequences from multiple localities and host plants samples allowed its accurate identification and host plant records. Specimens have been collected from a range of 21 host plants, including native, cultivated and invasive species. New host plant records suggest host adaptation in the colonized areas. Six *COI* haplotypes have been identified in the studied areas. *COI* DNA sequences obtained from accurately identified specimens which can support further identifications are provided. Its pest status on other continents is detailed along with the warning on the risk that this spider mite poses for Europe.

Keywords *Mangifera indica*; *Vitis vinifera*; Tetranychidae; invasive phytophagous mites; host adaptation; plant protection

Introduction

Arthropod invasions represent a growing concern both worldwide (Venette and Hutchison, 2021) and at the regional level, particularly in insular ecosystems (Cardoso *et al.* 2009; Florencio *et al.* 2013; Borges *et al.* 2013). Spider mites (Tetranychidae) include some of the most important agricultural pests, raising increasing concern due to their *i*) broad distribution

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and host range (Migeon and Dorkeld, 2025); *ii*) ability to rapidly colonize new areas and adapt to new host plants (Boubou *et al.* 2011); *iii*) populations can be favored by host plants water stress (Migeon *et al.* 2023); and iv) economic impact on agricultural, ornamental and forest crops (Hoy 2011).

Along the last decades some alien spider mites became invasive pests in Europe causing impact on agricultural crops (Navajas *et al.* 2010; Auger *et al.* 2023; Ferragut *et al.* 2013). Remarquable examples are *Oligonychus perseae* Hirst on avocado, and *Eutetranychus orientalis* (Klein) and *E. banksi* (McGregor) on citrus, for which control remains challenging (Torres *et al.* 2023; López-Olmos and Ferragut 2023).

The most effective way to manage the risks posed by invasive pests is to prevent their establishment in new areas. Early detection has critical role in this process, enabling rapid response measures before pests can spread and cause impacts (EPPO 2021; Desneux *et al.* 2022). Carrying out an accurate identification is essential for surveillance, early warning systems, and the implementation of targeted management strategies. However, for certain groups of organisms—such as phytophagous mites—early detection is particularly challenging, due to their cryptic habitus and absence of symptoms at low population densities (Dhooria 2016; Vargas Madriz *et al.* 2025). Moreover, taxonomic identification can be particularly challenging due to the limited number of reliable morphological diagnostic traits (Ovalle *et al.* 2020; Razuvaeva *et al.* 2023), absence or low number of male specimens for some species, and the lack of available genetic data, even for groups of significant agricultural importance such as spider mites (Navia *et al.* 2011; Migeon and Dorkeld 2025).

Herein we report the first occurrence of *Oligonychus yothersi* (McGregor, 1914) in Europe, which was detected from four insular territories – the Macaronesian Azores, Madeira (Portugal) and Canary (Spain) archipelagos, and the largest Mediterranean island, Sicily (Italy). Host plants in the studied areas are presented, including three new host families – Apocynaceae, Myricaceae, Pittosporaceae. Haplotypes have been characterized.

Materials and methods

Mite collection

In the Azores, Portugal, surveys of plant inhabiting mites were carried out on exotic (both cultivated or invasive) and native plant species in July 2015 and in May and September 2024, in São Miguel, Faial, Flores and Pico islands by AM, DN, FF, LBS, LS, PA. In Madeira, surveys were carried out in 2022 by PA, AM, PN and DN. In Palermo and Messina provinces, Sicily, Italy, in April and July 2025 on mango trees by FA, TG, HT and Gabriela Lo Verde. We have also added an older sample collected by FF, AM and Maria Navajas in the Canary Islands in 2006. Collection localities and data are detailed in Table 1. Specimens were collected directly from symptomatic rusting or chlorotic leaves with a brush under a stereomicroscope. Specimens were preserved in 100% ethanol for molecular analysis, and in 70% ethanol, for morphological studies.

Morphological identification

Mites were cleared in lactic acid (50%) for a day and mounted in Hoyer's medium for phase contrast and differential interference contrast (DIC) microscope observation. Morphological identification was performed using the key of Mushtaq *et al.* (2021) for the genus *Oligonychus* as well as the descriptions of *O. yothersi* by McGregor (1914, 1950) and Pritchard and Baker (1995) and of closely related species. Voucher specimens are deposited at the Centre de Biologie pour la Gestion des Population, 2018, "CBGP - Continental Arthropod Collection", Montferrier-sur-Lez, France, https://doi.org/10.15454/D6XAKL, in Zoological Collection of Arthropods at CIBIO-Açores, Ponta Delgada, São Miguel, Portugal and in Acarological Collection at SAAF Department, Palermo University, Italy.

Table 1 *Oligonychus yothersi* collection data in Europe, including host plants/families, collection sites and dates. Samples marked with an asterisk (*) were used for morphological analyses. New host plant records are in bold.

Sample name	Country	Island	Elementary administrative unit	Locality	Date of collect	Latitude	Longitude	Plant family	Plant species
2006-095	Canary Is.	Tenerife	La Orotava	Plaza de la Constitución	2006-X-22	28.39346	-16.52189	Myrtaceae	***Myrtus communis***
2022-002	Madeira Is.	Madeira	Câmara de Lobos	Jesus Maria José	2022-V-17	32.66175	-16.98061	Anacardiaceae	*Mangifera indica*
2022-035	Madeira Is.	Madeira	Santana	E211 Faja Alta - São Jorge	2022-V-18	32.81748	-16.89864	Annonaceae	***Annona cherimola***
2022-043	Madeira Is.	Madeira	Santana	Arco de São Jorge, Museu do Vinho	2022-V-19	32.82431	-16.95375	Lauraceae	***Laurus novocanariensis***
2015-156	Azores Is.	Faial	Flamengos	Jardim botanico	2015-X-07	38.5508	-28.6392	Platanaceae	***Platanus hispanica***
2015-158	Azores Is.	Faial	Pedro Miguel	Praia da Almoxarife	2015-X-07	38.5677	-28.617	Theaceae	***Camellia japonica***
2015-162	Azores Is.	Faial	Castelo Branco		2015-X-08	38.5419	-28.7447	Rosaceae	*Malus domestica*
2015-173	Azores Is.	Pico	Terra do Pao	Lajes do Pico, Hotel Aldeia da Fonte	2015-X-06	38.4139	-28.2833	Solanaceae	***Lycium europaeum***
2024-214	Azores Is.	São Miguel	Sete Cidades	Freiras	2024-IX-17	37.85838	-25.78351	Pittosporaceae	***Pittosporum undulatum***
2024-217	Azores Is.	São Miguel	Sete Cidades	Freiras	2024-IX-17	37.85805	-25.78312	Fagaceae	***Quercus robur***
2024-229	Azores Is.	São Miguel	Sete Cidades	Freiras	2024-IX-17	37.86093	-25.78515	Myricaceae	***Myrica faya***
2024-240	Azores Is.	São Miguel	Sete Cidades	Lagoa Azul West	2024-IX-18	37.86892	-25.79477	Fabaceae	*Acacia melanoxylon*
2024-265	Azores Is.	São Miguel	Sete Cidades	Lagoa Azul West	2024-IX-18	37.86918	-25.79355	Polygonaceae	***Reynoutria japonica***
2024-267	Azores Is.	São Miguel	Sete Cidades	Freiras	2024-IX-17	37.86002	-25.78368	Fagaceae	***Quercus palustris***
2024-287	Azores Is.	São Miguel	Nordeste	C. de Praia do Lombo Gordo	2024-IX-20	37.7861	-25.145959	Platanaceae	*Platanus hispanica*
2024-290	Azores Is.	São Miguel	Nordeste	C. de Praia do Lombo Gordo	2024-IX-20	37.7861	-25.145959	Lauraceae	***Persea indica***
2024-299	Azores Is.	São Miguel	Maia	Cha Gorreana	2024-IX-20	37.81885	-25.40184	Theaceae	*Camellia japonica*
2024-302	Azores Is.	São Miguel	Nordeste	Miradouro da Ponta da Madrugada	2024-IX-20	37.78921	-25.14609	Rosaceae	*Rosa sp.*
2024-310	Azores Is.	São Miguel	Maia	Cha Gorreana	2024-IX-20	37.81885	-25.40184	Fagaceae	*Castanea sativa*
2024-318*	Azores Is.	São Miguel	Nordeste	C. de Praia do Lombo Gordo	2024-IX-20	37.78516	-25.14575	Vitaceae	*Vitis sp.*
2024-323	Azores Is.	São Miguel	Rosto Do Cão (Livramento)	Rua do Cacto	2024-IX-21	37.75047	-25.6108	Apocynaceae	***Plumeria alba***
2024-330	Azores Is.	Pico	São Caetano	Ponta des Formigas	2024-IX-22	38.42194	-28.42837	Pittosporaceae	*Pittosporum undulatum*
2024-352	Azores Is.	Pico	São Caetano	Ponta des Formigas	2024-IX-22	38.42194	-28.42837	Vitaceae	*Vitis vinifera*
2024-358*	Azores Is.	Pico	São João	Parque Florestal e Recreio de São João Pequenino	2024-IX-23	38.41794	-28.36073	Fabaceae	*Acacia melanoxylon*
2024-366	Azores Is.	Pico	São João	Parque Florestal e Recreio de São João Pequenino	2024-IX-23	38.41794	-28.36073	Myricaceae	*Myrica faya*
2024-369	Azores Is.	Pico	São João	Parque Florestal e Recreio de São João Pequenino	2024-IX-23	38.41794	-28.36073	Platanaceae	*Platanus hispanica*
2024-381	Azores Is.	Pico	Madalena	EN3 Dog shelter	2024-IX-24	38.51964	-28.50095	Lauraceae	*Persea indica*
2024-397	Azores Is.	Pico	São Caetano	Ponta des Formigas	2024-IX-22	38.42194	-28.42837	Fabaceae	*Acacia melanoxylon*
2024-405	Azores Is.	Flores	Santa Cruz das Flores	Ribeira dos Barqueiros	2024-IX-27	39.44961	-31.1398	Fagaceae	*Castanea sativa*
2024-407	Azores Is.	Flores	Fajã Grande	Ponta	2024-IX-27	39.46965	-31.25458	Ericaceae	***Rhododendron indicum***
2024-427	Azores Is.	Flores	Fajã Grande	Ponta	2024-IX-27	39.46965	-31.25458	Platanaceae	*Platanus hispanica*
2025-250	Italy	Sicilia	Palermo	Via Luparello	2025-IV-07	38.1143	13.3005	Anacardiaceae	*Mangifera indica*
	Italy	Sicilia	Messina	Milazzo	2025-VII-20	38.1134	15.1422	Anacardiaceae	*Mangifera indica*
	Italy	Sicilia	Messina	Milazzo	2025-VII-20	38.114	15.1353	Anacardiaceae	*Mangifera indica*

Molecular analysis

Total DNA from 64 isolated specimens, obtained from 34 samples (Table 1), was extracted using the DNeasy Blood & Tissue kit (Qiagen, Hilden, Germany), according to the DNA extraction protocol "Purification of Total DNA from Animal Blood or Cells" (Spin-Column Protocol) adapted for extracting total DNA from mites (Mendonça *et al.* 2011). The isolated DNA was directly used as a template for PCR amplification of two fragments of the mitochondrial cytochrome c oxidase subunit I (*COI*) gene using two primer sets: LCO1490 (5′-GGTCAACAAATCATAAAGATATTGG-3′) and HCO2198 (5′-TAAACTTCAGGGTGACCAAAAAATCA-3′) (Folmer *et al.* 1994); C1J1718 (5′-GGAGGATTTGGAAATTGATTAGTTCC-3′) and COIrevA (5′-CCWGTYARMCCHCCWAY-AGTAAA-3′) (Auger *et al.* 2023). For a final volume of 25 µL, the PCR mixture consisted of 12.5 µL of Qiagen Multiplex PCR Master Mix (2X), 1.25 µL of each primer (10 µM), 6 µL of nuclease-free water, and 4 µL of template DNA. The PCR conditions for LCO1490 / HCO2198 were conducted under the following thermal cycling conditions: an initial denaturation at 95 °C for 15 min; followed by 40 cycles of denaturation at 95 °C for 45 s, hybridation at 45 °C for 30 s, and elongation at 72 °C for 70 s; with a final elongation at 72 °C for 10 min. Amplification with C1J1718 / COIrevA was performed with an initial denaturation at 94 °C for 15 min, followed by 5 cycles of denaturation at 94 °C for 60 s, hybridation at 40 °C for 90 s, and elongation at 62 °C for 90 s; then 30 additional cycles of denaturation at 94 °C for 60 s, hybridation at 45 °C for 90 s, and elongation at 62 °C for 90 s; and a final elongation at 62 °C for 10 min. The amplified PCR products were sequenced by Eurofins Genomics Europe Pharma and Diagnostics (Sanger/PCR GmbH, Cologne Branch, Germany), using the same primers as in the PCR amplification.

Sequences were edited using Codon Aligner v.4.1.1 (CodonCode Corporation) and aligned using the default parameters. All the sequences were verified for stop codons and for insertions/deletions.

When it was possible, the two overlapping sequences were concatenated for phylogenetic analysis. New sequences were combined with all *Oligonychus* s. str. *COI* sequences longer than 400 pb retrieved from GenBank (one sequence per species, see Supplementary file S2). Six *Panonychus* species, were used as outgroup as proposed by Matsuda *et al.* (2018). The dataset obtained contained 28 sequences of 1268 pb (when aligned). A maximum likelihood (ML) analysis was conducted using Mega 12 (v12.0.15) (Kumar *et al.* 2024) with G+I model and fast adaptive bootstrap (Supplementary file S3).

Results and discussion

The red mite *O. yothersi* (Figure 1) was identified from four European insular regions: in the Macaronesia (Atlantic), the Azores and Madeira archipelagos (Portugal), the Canary Islands (Spain); and the Sicily Island (Italy) in the central Mediterranean sea.

Identification was based on an integrative taxonomic approach. Since male specimens are required for species-level identification in the *Oligonychus* genus, morphological identification was only possible for two of the 26 samples collected in the Azores in September 2024, which were the only ones containing each one male specimen. Perfect laterally mountings of these males enabled the reliable morphological taxonomic identification at species level. No *O. yothersi* DNA reference sequences being available in public databases, *COI* DNA sequences obtained from females of the morphologically identified two populations were then used as reference and enabled identification of all other populations. The delayed identification of this invasive mite in Europe — nearly twenty years after the first symptom observations — is mainly due to the species thelytokus parthenogenetic reproduction which can result in the absence of males (Ferla *et al.* 2024) and the lack of barcoding DNA sequences, highlighting the importance of availability of reference sequences in databases to support early detection and monitoring of invasive pests.

Figure 1 *Oligonychus yothersi* living specimens on *Vitis vinifera*: A – Two adult females; B – Nymphs and eggs.

Family Tetranychidae Donnadieu, 1875

Tribe Tetranychini Reck, 1950

Genus *Oligonychus* Berlese, 1886

Type species *Heteronychus brevipodus* Targioni -Tozzetti, 1878: 255

Oligonychus (*Oligonychus*) *yothersi* (McGregor, 1914)

Morphological identification

Distinctive characters (Figure 2): females of this species bear 7 tactile setae on the tibia of the leg I and have the first pair of dorsocentral setae (c_1) longer than the interval between the setae c_1 and d_1 (Figure 2 A-C), belonging to the *coffeae* species subgroup (Mushtaq *et al.* 2021). In this subgroup of 44 species, the male aedeagus of *O. yothersi* is unique, with the shaft deflexed sharply more than 90° from the axis and forming a hooked portion that is longer than the shaft, tapering to a thin (unbarbed) truncate tip (McGregor, 1950). According to McGregor's (1950) drawing of the aedeagus of *O. yothersi*, there is an indentation on the proximal part of the dorsal margin, which was also observed in both males collected (Figure 2 D, E). In addition, in several female specimens, we observed additional solenidia on the tarsus (from one to four) and tibia (from one to three) of the leg I as reported by Pritchard and Baker (1955).

Molecular analysis

Among the 34 samples collected, 31 gathering 1 to 4 individuals per sample, were successfully sequenced for the COI-C1J1718 fragment, yielding to 63 sequences of 876 bp, and 23, each gathering 1 to 4 individuals per sample, were successfully sequenced for the COI-LCO-HCO fragment, yielding to 48 sequences of 672 bp. The two fragments overlap by 462 pb and the variable nucleotide sites were present only on the COI-C1J1718 fragment. These sites and the Genbank sequence identifiers are reported in Table 2.

Interestingly, all the sequences showed high similarity, with 49 individuals sharing same haplotype, only 11 individuals sharing one mutation and four individuals with other mutations on the COI-C1J1718 (Table 2, Supplementary table 1). No genetic structuration was observed in regard of the geographic origin nor the host plants. Notably, the most common haplotype was shared by the majority of Azoreans and Madeiran specimens and all the four Sicilian specimens. The phylogenetic tree obtained is shown in Figure 3.

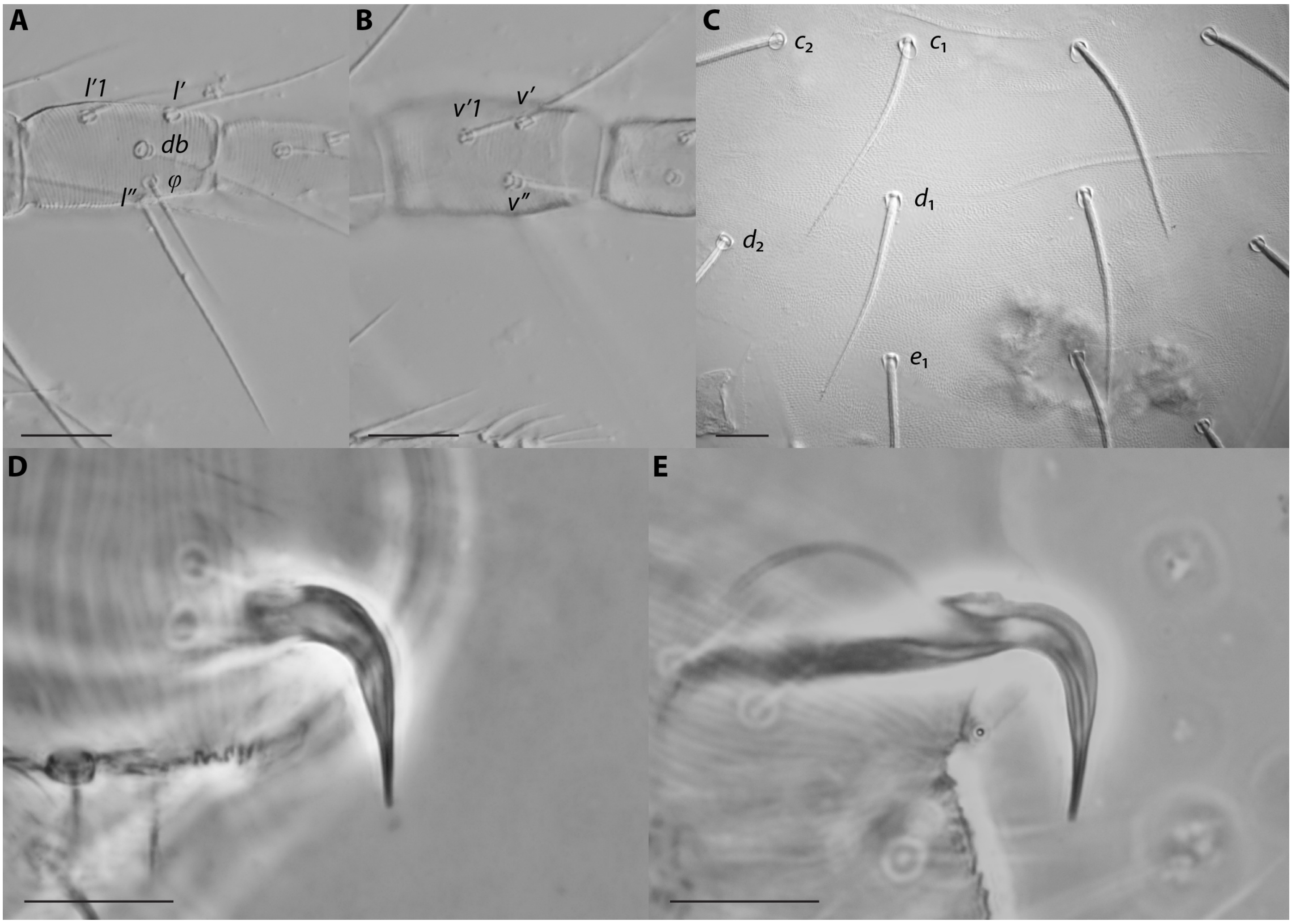

Figure 2 *Oligonychus yothersi* female: A–B – 7 tactiles setae and one solenidion on tibia I (A – dorsal view, B – ventral view); C – dorsohysterosomal setae c_1 longer than the distance c_1–d_1; male: D – aedeagus of the male collected on *Vitis* sp., E – aedeagus of the male collected on *Acacia melanoxylon*. Scale bars A–C = 20µm, D–E = 10µm.

Distribution

Oligonychus yothersi was described from the United States in 1914 (McGregor), being currently widespread (Figure 4) in the Americas (from the United States to Argentina and

Table 2 Variable nucleotide sites in mitochondrial *COI* sequences resulting in six *COI* haplotypes (H1–H6) and Genbank accession identifiers.

Haplotypes		Variables sites					Count	Genbank accession Ids	
	C1J1718 position	312	361	409	579	801		C1J1718	LCO
	LCO position	516	565	613					
H1		C	G	G	A	G	49	PX353980	PX353976
H2		.	.	.	G	.	10	PX353981	
H3		A	.	.	.	.	1	PX353982	PX353977
H4		.	.	A	.	.	1	PX353983	PX353978
H5		.	.	.	.	A	1	PX353984	
H6		.	T	.	G	.	1	PX353985	PX353979

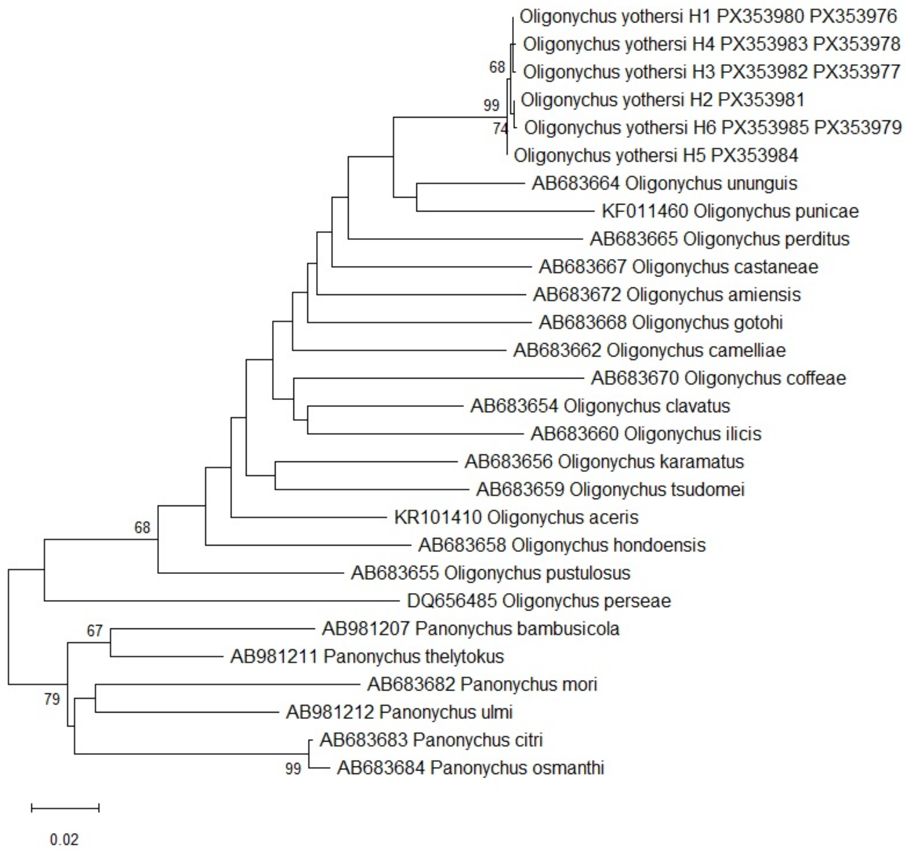

Figure 3 Maximum likelihood (ML) phylogenetic tree based on the mitochondrial *COI* gene using the G+T Gamma model. Bootstrap values (>50%) based on adaptive bootstrap (Mega 12) are indicated at nodes. Genbank accession numbers are indicated.

Chile), and has also been recorded in Asia (China) (Ma and Yuan, 1981) and the Middle East (Iran) (Sheikholeslam-Zadeh and Sadeghi-Nameghi, 2010). No prior records were known from Europe (Migeon and Dorkeld 2025). The record from Hawaii has never been confirmed, suggesting that the species may not be present in the Hawaiian Islands (Goff, 1986).

In this study, *O. yothersi* was collected from four of the nine Azorean islands: Faial, Flores, Pico, and São Miguel, including eastern, central and western island-groups. These results show that the mite is widespread in the Azorean archipelago, and can possibly occur on other Azorean islands where similar symptoms have been observed. In the Macaronesia, besides Azores, the mite was identified from three samples from Madeira and from one sample from Tenerife (Canary Islands). In addition, the species was identified from Sicily in the central Mediterranean Sea. Up to date the mite was not recorded from continental Europe, but further surveys should be conducted to assess its eventual distribution on the continent and to define measures to prevent its dissemination. Considering the new insular detections in Europe, the updated distribution map of *O. yothersi* is presented in Figure 4.

Introduction history and pathways

The wide distribution of *O. yothersi* in the Macaronesia area, as well as the high number of new host plants (Table 1), including native ones, suggest that its introduction in the region is not a recent event. Furthermore, its detection in samples collected in 2006 suggests an introduction

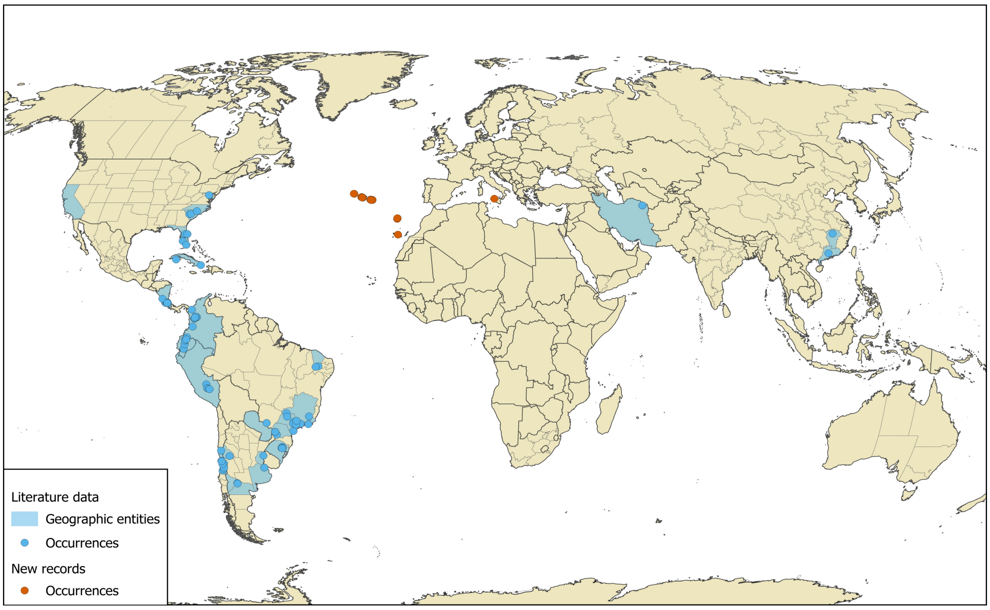

Figure 4 World distribution map of *Oligonychus yothersi*. TDWG 4 (TDWG, 2025) level and known occurrences derived from GBIF (2025) and Migeon and Dorkeld, (2025). New records from this study.

several years distant. The absence of highly conspicuous symptoms on plants of economic importance can explain how the species remained undetected for decades in Macaronesia, while in Sicily a high level of infestation with damages on cultivated plants was obvious. In the absence of significant genetic variability among populations, it would be interesting to determine the ecological and environmental conditions that explain why this mite is causing damage only on Sicily, and not in the Macaronesian Archipelagos.

The homogeneity of all the sequences suggests a single introduction. The high level of symptoms in Sicily suggests that the introduction, or at least the pest emergence, is recent and could not fail to be noticed. This homogeneity and the lack of reference sequences from the native area does not allow drawing more hypothesis on invasion pathways and history. However, based on evidence from other invasive spider mites, such as *Tetranychus evansi* Baker & Pritchard, 1960, *Eotetranychus lewisi* (McGregor, 1943) and *O. perseae* , which share comparable bioecological traits, plant trade is considered the most probable pathway of introduction (Navajas *et al.* 2013; EFSA 2021; Torres *et al.* 2024).

Host plant symptoms, pest status and potential risks for Europe

The spider mite *O. yothersi* is a highly polyphagous species recorded on more than 80 host plant species belonging to over 40 botanical families. Plant families most commonly reported as *O. yothersi* hosts are Rosaceae, Myrtaceae and Fabaceae (Migeon and Dorkeld, 2025).

In this study, *O. yothersi* was collected on 21 plant species belonging to 16 angiosperm families (Table 1). Among them, there are native and Macaronesia endemic species such as *Laurus novocanariensis* Rivas Mart., Lousã, Fern.Prieto, E.Días, J.C.Costa & C.Aguiar, and *Myrica faya* Dryand., invasive species such as *Acacia melanoxylon* R. Br. and *Pittosporum undulatum* Vent.; and agricultural, forestry or ornamental species such as *Annona cherimola* Mill., *Fagus sylvatica* L., *Malus domestica* Borkh., *Mangifera indica* L., *Myrtus communis* L., *Persea indica* (L.) Spreng., *Platanus hispanica* Mill. ex Münchh., *Plumeria alba* L., *Quercus palustris* Münchh., *Quercus robur* L., *Castanea sativa* Mill., *Rosa* sp., *Reynoutria japonica* Houtt. and *Vitis vinifera* L. The high number of host plants in the Macaronesia, including several new reports (families and species) and endemic plants, suggests that the red mite has

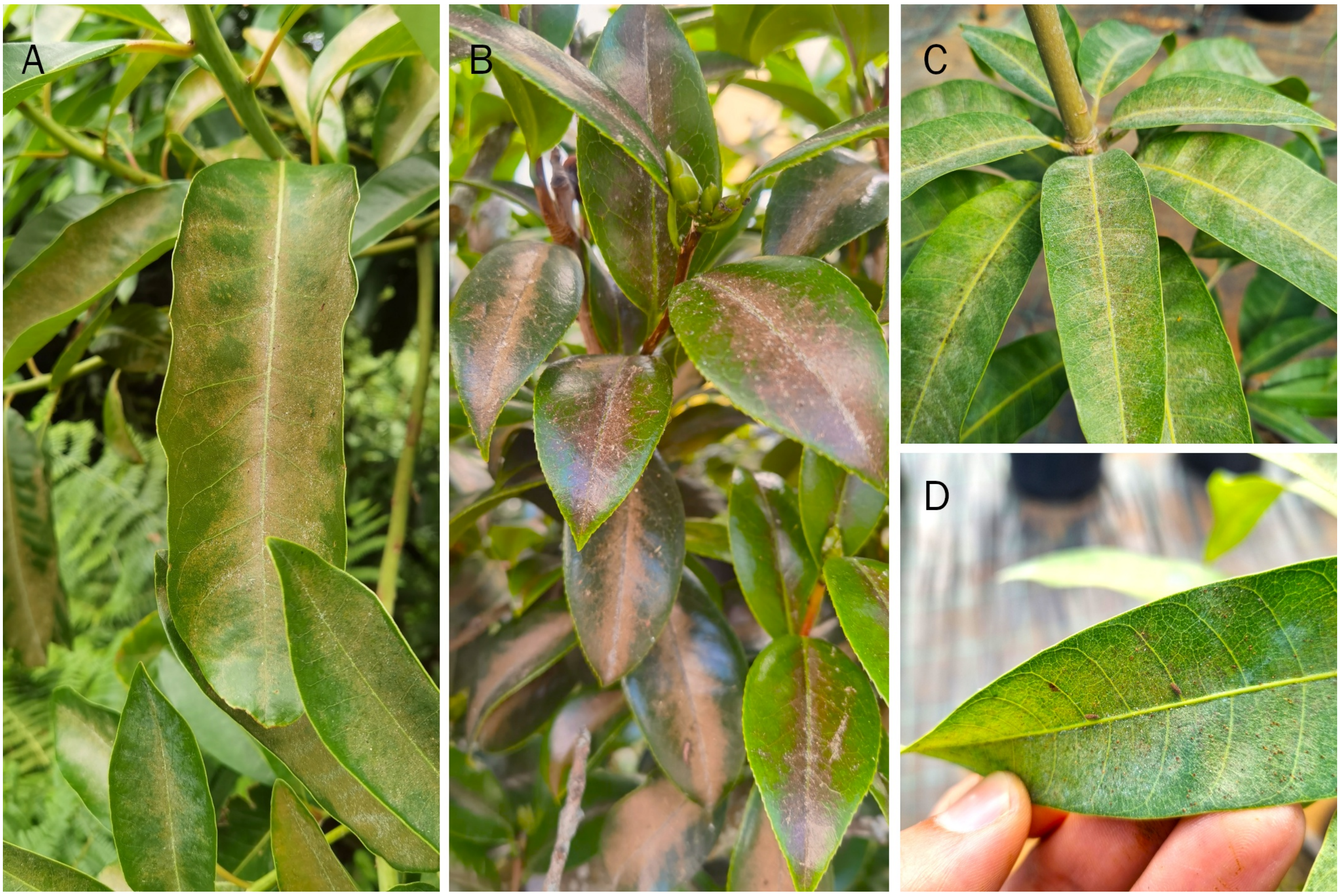

Figure 5 Feeding damage caused by *Oligonychus yothersi* in the Azores Archipelago and Sicily (Italy). A – Yellowing and necrosis on *Persea indica* (Azores). B – Central leaf bronzing on *Camellia japonica* (Azores). C – Typical feeding symptoms on *Mangifera indica* (Sicily). D – Colony of *O. yothersi* with two *Stethorus* sp. larvae (predators) on *Mangifera indica* (Sicily).

adapted to new hosts along the establishment process, and confirm its polyphagy as reported from other continents. It is worth noting that *O. yothersi* was found infesting *P. undulatum*, one of the most aggressive and widespread invasive plants in the Azorean archipelago (Borges Silva *et al.* 2018, 2022). In Sicily and Madeira, *O. yothersi* was collected from mango orchards, as it also has been reported from several countries in Central and South America (see Ochoa *et al.* 1990, and for the last update Migeon and Dorkeld, 2025). Mites were observed primarily on the upper surface of the leaves, but colonies were also found on the undersides, sometimes in association with *Stethorus* sp. larvae(Coleoptera: Coccinellidae), which are known predators of tetranychid mites (Figure 5).

Oligonychus yothersi has been reported as a major foliar pest of avocado (*Persea americana* Mill.) under the name of 'avocado red mite' in Central and South America (Rioja *et al.* 2019), and it has also been reported causing damages in 'erva-mate', *Ilex paraguariensis* A.ST.-Hil. (Aquifoliaceae) in South Brazil, (Dameda *et al.* 2021; Rode *et al.* 2023) and recently on vine (*Vitis vinifera* L.) in Brazil (Ferla *et al.*, 2024).

Considering the current host plant range of *O. yothersi* around the world (Migeon and Dorkeld, 2025) the main concerns in Europe would be for the mango, avocado and vine plantations in Mediterranean areas such as Italy, France, Portugal and Spain. Other important crops, such as *Prunus* and *Malus* fruit trees, are also widely cultivated in continental Europe and could potentially be affected. Additionally, this mite could also cause some impact to the recent development of tea plantations in continental Europe (Tea Grown in Europe Association, 2023) Its association with ornamental plants can contribute to its dissemination across the European continent, and facilitate its establishment in new areas a process that would also be reinforced by its association with other plant species, such as native oaks (*Quercus* spp.) and others. As a precautionary measure, phytosanitary measures should be implemented at a regional level to avoid its spread to continental areas and minimize potential impacts.

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