



SHORT NOTE

First Record of the Introduced Ant *Myrmica specioides* in the Eastern United States

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Abstract

The ant *Myrmica specioides* Bondroit, 1918 (Hymenoptera: Formicidae) is reported for the first time from the Eastern United States. This species is native to the West Palearctic region and has previously been known as an introduced species in Northwestern North America. It was found in 2013 in the Boston metropolitan area. The species was identified by morphometric comparison to type specimens and DNA-barcoding. The distribution and invasive potential of *M. specioides* are discussed.

Introduction

Invasive alien species are considered one of the main causes of the current biodiversity crisis (Pyšek et al., 2020). At least 200 ant species (Hymenoptera: Formicidae) have been introduced outside their natural range by humans, and some of them have become invasive (Wong et al., 2021). *Myrmica* Latreille, 1804, is a diverse ant genus distributed throughout the Holarctic. A total of three species of *Myrmica* are so far known to have established major populations outside their native range: *M. rubra* (Wheeler, 1908), *M. scabrinodis* (Ellison et al., 2012; Seifert, 2018) and *M. specioides* (Jansen & Radchenko, 2008), all of which are of Palearctic origin and have been introduced to the Nearctic region. However, only *M. rubra* seems to have become widespread yet (Janicki et al., 2016). This is the only one of the three species known to establish supercolonies (van der Hammen et al., 2002) and is now considered invasive in North America (Naumann & Higgins, 2015). Most *Myrmica* species inhabit rather moist

and cool habitats, and their colonies are typically medium-sized compared to other ants. They possess a powerful sting and prey on small arthropods. To a lesser extent, they also engage in symbioses with plant sap-feeding insects such as aphids (Hemiptera).

Ants of the genus *Myrmica* are notably difficult to determine, and some groups are still taxonomically unresolved, especially in the Nearctic region (Jansen et al., 2009). The morphological traits used for species delimitation in this genus are predominantly measures of body shape, although cuticular sculpture may also differ between taxa. The shape and relative size of the antennal scapes and of ridges (carinae) and processes thereof are of particular taxonomical importance. In addition, the distance between the frontal carinae, the shape of the petiole, and the length of the propodeal spines are also diagnostic characters. Not rarely, there is gradual variation in such traits within populations of the same taxon or between closely related taxa, complicating morphological species delimitation. For example, the taxonomically relevant



antennal scapes of *M. specioides* Bondroit are reported to have small posterior lobes (Fig 1a, b) in the West of the distribution range, with the size of this lobe increasing notably in Eastern European and Western Siberian populations (Seifert, 2018). It is also not well studied if these phenotypic traits may be under selection by the environment or the result of phenotypic plasticity. In previous studies, the concordance between morphology and mitochondrial DNA trees was found to be rather low in *Myrmica* ants (Blatrix et al., 2020; Seifert et al., 2018). Therefore, future work is required to clarify this genus's taxonomy and systematics. For now, morphology aided by DNA-barcoding appears to be the best strategy to identify *Myrmica* specimens. The aim of this work is to identify an ant species from the Palearctic *Myrmica scabrinodis*-group found in the Boston metropolitan area and to clarify if it is an alien or invasive species.

Materials and Methods

A nest of *Myrmica* ants was found along the sidewalk of Beacon Street, Somerville, MA, USA (42.38283° N, -71.11181°E, 16 m) (Fig 1) on July 15, 2013 (Fig 2). A total of 11 specimens were collected in 95% ethanol and preserved at -20°C. A total of three workers were pinned for morphological studies. The specimens were visually inspected and measured using a Leica EZ4 binocular with graticule at 16-70 × magnification. Multiple specimen images were created by using an Apple iPhone 12 mini through a Leica EZ4 binocular with changing focus. The images were aligned using align_image_stack v. 2019.0.0 and stacked using GIMP v. 2.10. A total of 12 measurements which can be obtained from photographs taken in standard view (full face, lateral and dorsal view) were taken from a photographed specimen of interest, as well as AntWeb (2022)-images of 15 type and 3 non-type specimens representing 18 species of the *M. scabrinodis*-group for comparison: CW, Cwb, CL, SL, SW, PEW, ML, MW, EL (Seifert, 2018), FW, FLW and ESL (Radchenko & Elmes, 2010). Allometric effects were removed from all these raw measurements using the method

of Leonart et al. (2000) as implemented in the R package “allomr” (Schär, 2022), by scaling all specimens to the mean head size ($CS=(CW+CL)/2$) of 1.09 mm. A 13th morphometric variable (pcSLd) was defined de novo: the proportion of the antennal scape (SL) being reached by a basal dorsal carina. Measured in dorsal view along SL, from the proximal anterior corner of the antennal scape to the distal end of the dorsal carina at the scape base, divided by SL (Fig 1b, $pcSLd=a/SL$). Equal to 0 if a dorsal carina is lacking. Dendrogram clustering of the 13 obtained morphometric variables was performed using the R package “cluster” (Maechler et al., 2021) in R v. 4.1.1.

DNA-barcoding of a specimen from Somerville was performed by the Centre for Biodiversity Genomics, University of Guelph, Canada, using the primers LepF1 and LepR1 (deWaard et al., 2008). The resulting sequence was compared to a set of 154 previously published reference sequences from the *M. scabrinodis*-group (Blatrix et al., 2020; Jansen et al., 2010). Only unique sequences (mitotypes) were subsequently used (n=89). DNA sequences were aligned using the R package “msa” (Bodenhofer et al., 2015), and a maximum likelihood tree with 1000 ultrafast bootstrap replications was created in IQTREE (Minh et al., 2020). The nucleotide substitution model (TIM2+F+I+G4) was chosen using ModelFinder (Kalyaanamoorthy et al., 2017). The resulting dendrogram was visualized using the R-package “ggtree” (Yu et al., 2017).

Results

The specimens are stored at the research collection of R. Vila (voucher MM21B014a1) and the private collection of S. Schär (collection code SS13B020). The habitat of the ants reported here was a small urban hedgerow with some tree stumps surrounded by asphalt and concrete. These *Myrmica* ants have an antennal scape that is sharply bent near its insertion and with a well expressed caudal carina (Fig 1). This antennal morphology is not found among native *Myrmica* ants of New England (Ellison et al., 2012). However, it is present in the Palearctic *M. scabrinodis*-group. Morphometric

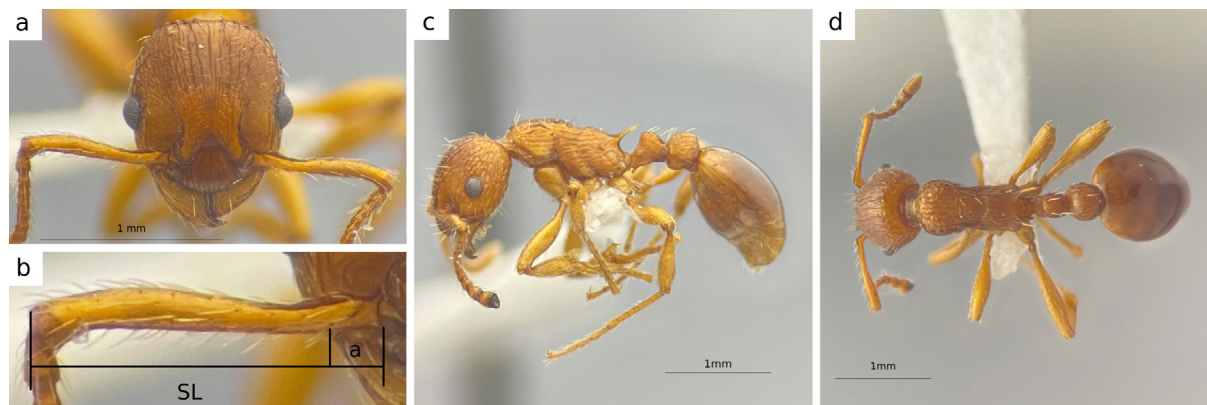


Fig 1. Full face view (a), definition of the morphometrical index $pcSLd=a/SL$ (b), lateral (c) and dorsal view (d) of a worker of *Myrmica specioides* collected in Somerville, MA, USA. Scalebar: 1 mm.

data is given in Table S1. Morphometric comparison to type and non-type worker specimens of the *Myrmica scabrinodis*-group suggests that these specimens from Sommerville are morphometrically most similar to the type of *M. speciooides* (Fig 3). There are a few morphological traits that further support this hypothesis: The antennal scape has a very short dorsal carina, but a well visible caudal carina (Fig 1a, b). However, the latter is not extended into a large posterior lobe (Fig 1a). The frontal lobes are rather distant in their middle section (mean FI (Radchenko & Elmes, 2010): 0.39, n=3) and not strongly diverging anteriorly (mean FLI (Radchenko & Elmes, 2010): 1.28, n=3) (Fig 1a). Typically for *M. speciooides*, the propodeal spines of are relatively short (Fig 1c, d). In lateral view, the petiole lacks a dorsal plane. Instead, it is more or less gradually sloping downwards posteriorly (Fig 1c). The petiole is rather narrow, as seen in dorsal view, but not as narrow as in *M. constricta* or *M. rugulosa* (mean PW/CS: 0.27, n=3). Finally, the antennal scape is sharply bent near its insertion, as seen in the caudal view (Fig 1d).

The complete DNA-barcode (658 bp of the mitochondrial gene COI) could be obtained for a specimen from the colony of Sommerville (BOLD Process ID: ANTEU038-21, GenBank accession number OY397299). The phylogenetic tree based on a set of 89 COI mitotypes belonging to 12 taxa of the *M. scabrinodis*-group (Fig 4), recovers the sequenced specimen from Sommerville as most closely related (0.5%-0.7% divergence) to two *M. speciooides* (Fig 4), both of which collected from Canada. A comparison with COI sequences on BOLD (December 2022) revealed 70 closely related sequences (<0.5% divergence), 67 from Europe and 3 from North America. Of those, 64 (91%) were identified as *M. speciooides* too. The remaining sequences were either not identified to species level (n=1), identified as *M. scabrinodis* (n=3), *M. constricta* (n=1), or *M. hellenica* (n=1). The latter sample is interesting, as it was also found in the Eastern United States (New York state). A 100% match was found with two specimens, one *M. speciooides* from Switzerland and an unidentified *Myrmica* from Germany.



Fig 2. Distribution of *M. speciooides* in both native (yellow) and introduced (red) range (a) (data from AntMaps 2022, Guénard et al., 2017; Kass et al., 2022). The precise locality of the new record (b) is represented by a red star.

Discussion

This article reports the first record of the introduced ant *Myrmica speciooides* in the Eastern United States. However, it cannot be ruled out that it has been recorded under other names in this region before (e.g., *M. hellenica* or *M. scabrinodis*).

For example, Clark et al. (2011) reported a morphologically similar *M. scabrinodis* from the Boston Harbor Islands. Ellison et al. (2012) mentioned the same species from Porter Square, Cambridge, which is located <1 mile away from our finding of *M. speciooides* (Fig 2b). We encourage future DNA-barcoding of these and other specimens of the *M. scabrinodis*-group from

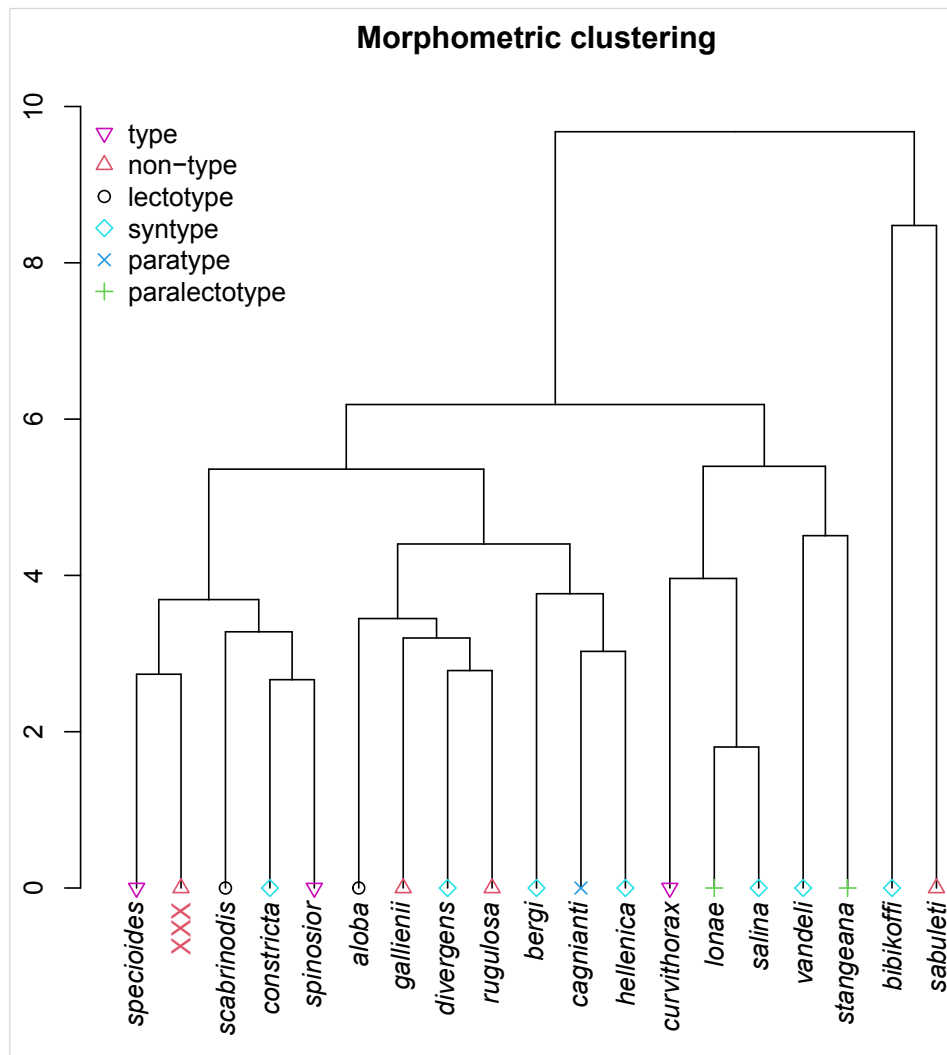


Fig 3. Dendrogram clustering of 13 morphometric measurements and indices (see main text) of 13 reference (type) specimens of the *Myrmica scabrinodis* group, and a specimen of the sample to be identified collected in Somerville (labeled “XXX”, photographed in Fig 1). The type status of the reference specimens is indicated by colored symbols.

Eastern North America in order to rule out earlier confusion of *M. specioides* with other taxa and to better understand the introduced range of this species. *Myrmica specioides* has been known as an introduced species in Northwestern North America for some time, namely in the state of Washington (Jansen & Radchenko, 2008) and Southwestern British Columbia (Naumann & Higgins, 2015) (Fig 2). Given the results here published, this species is now also recognized as present in New England and the area of Boston in particular. Not much is known about the ecology and behavior of *M. specioides* in the introduced range. It is known to be an aggressive, polygynous, and locally abundant species, traits that suggest it could potentially become invasive (Jansen & Radchenko, 2008). In both the native and introduced range, it is a species found in urban areas. *Myrmica specioides* is also known to prey on other species of ants (Seifert, 2018). However, evidence that it behaves as an invasive species in North America has not been published so far. The population in Somerville in 2013 appeared to be rather inconspicuous.

Nevertheless, we suggest that the ecological impact and spread of *M. specioides* in North America should be monitored.

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Authors’ Contributions

SS: Conceptualization, Methodology, Software, Formal analysis, Investigation, Data Curation, Writing-original Draft, Writing-review & Editing, Visualization.

RV: Conceptualization, Investigation, Data Curation, Writing-original Draft, Writing-review & Editing, Project administration, Funding acquisition, Supervision.

MM: Conceptualization, Investigation, Data Curation, Writing-original Draft, Writing-review & Editing, Visualization, Project administration.

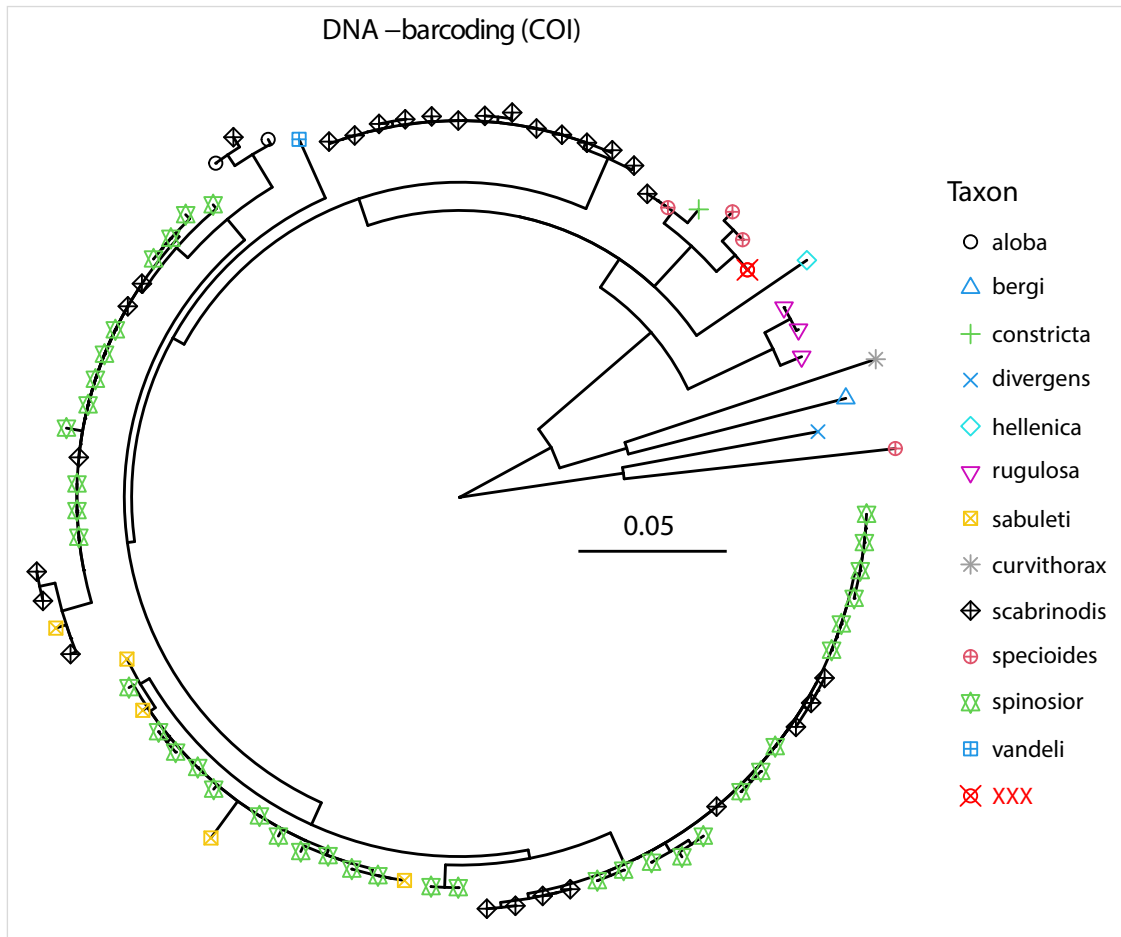


Fig 4. Midpoint-rooted maximum likelihood tree of 89 COI sequences representing 12 species of the *Myrmica scabrinodis* group. The sample to be identified collected in Sommerville is labeled “XXX”. Species’ identity is indicated by colored symbols. Scale bar: nucleotide substitutions/site.

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