Wasps going north? Triteleia peyerimhoffi (Hymenoptera: Platygastroidea: Scelionidae) in Germany

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SHORT COMMUNICATION

Wasps going north? *Triteleia peyerimhoffi* (Hymenoptera: Platygastroidea: Scelionidae) in Germany

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Abstract

The scelionid wasp *Triteleia peyerimhoffi* (Kieffer, 1906) is recorded from Germany for the first time, outside its circum-Mediterranean distribution range. Specimens from different parts of Germany were examined for morphological and molecular diversity as part of the "German Barcode of Life III: Dark Taxa" project.

Keywords: barcoding, dark taxa, new record, parasitoid.

Zusammenfassung

Die Wespe *Triteleia peyerimhoffi* (Kiefer, 1906) aus der Familie Scelionidae kommt erstmals in Deutschland und somit weit außerhalb ihres zirkum-mediterranen Verbreitungsgebietes vor. Im Rahmen des Projektes „German Barcode of Life III: Dark Taxa" werden Exemplare aus verschiedenen Regionen Deutschlands auf morphologische und molekulare Diversität hin untersucht.

Triteleia peyerimhoffi (Kieffer, 1906) is the only species of its genus that is known from Europe, and it has proven to be a remarkably variable scelionid. Popovici et al. (2011) conducted a comprehensive study on the taxonomy, nomenclature and morphology of this species, their results showing an unusually high intraspecific variation correlated with a circum-Mediterranean geographic distribution. These authors expressed their concern that morphological variants of *T. peyerimhoffi* could be erroneously interpreted as separate species, which would lead to taxonomic confusion and shift the focus from important and interesting unexplored topics.

An easy and straightforward solution is *COI* barcode referencing, but so far, no sequences of *T. peyerimhoffi* had been published and only one genome assembly is available in GenBank for the genus (ASM2281694v1; Sayers et al. 2022). The incompleteness of the Barcode of Life Database (BOLD) and, on occasion, inaccurately identified records do not make this task easier. At the time of writing (November 2022), BOLD held 69,074 public records of Scelionidae, with only 4,580 of them associated with species names (Ratnasingham & Hebert 2013), representing 426 of the over 3,500 described species (Awad 2023). At the same time, GenBank stored 14,711 barcodes for Scelionidae, of which more than 10,000 belong to only two genera: *Telenomus* Haliday and *Trissolcus* Ashmead (Sayers et al. 2022).

The databases are slowly accumulating valuable information, but there is still a long way to go until any species of parasitoid wasp from a moderately diverse fauna such as that of central and southern Europe can be reliably and rapidly identified by querying BOLD or GenBank. Contributing to the completion of these publicly available databases is a goal of the German Barcode of Life (GBOL) initiative. The "GBOL III: Dark Taxa" project (2020–2024) has targeted understudied, hyperdiverse groups of parasitoid Hymenoptera and Diptera, including the hymenopteran superfamily Platygastroidea (Hausmann et al. 2020). Within GBOL III, we are attempting to close the gap on the non-barcoded platygastroid taxa and address the shortcomings of German checklists and distribution records (Awad et al. 2021), which are very often outdated and severely incomplete (Dathe et al. 2001). This paper contributes one of the findings of the GBOL III project on Platygastroidea and illustrates the value of these data.

Material and methods

A total of 27 specimens identified as *Triteleia peyerimhoffi* using the diagnosis provided by Popovici et al. (2011) were collected with Malaise traps in Germany as part of Baden-Württemberg's "LUBW flying insect monitoring project" and other biomonitoring intiatives. Non-destructive extraction was performed on the specimens and DNA barcodes were obtained with the standard LCO1490/HCO2198 primers (Folmer et al. 1994) through Sanger sequencing. Bidirectional sequencing was performed on all samples; sequences were assembled and proofread using Geneious Prime. Sequences are deposited in GenBank under accession numbers OP628187–OP628211 (Supplemen-

tary File 1); voucher specimens were point-mounted on triangular black points (Fig. 1A–C) and are deposited in the collection of the Stuttgart State Museum of Natural History (SMNS).

Barcodes were compared with data publicly available in GenBank and BOLD through a direct BLAST. Barcode sequences were aligned in MEGA X with the CLUSTAL W algorithm (Thompson et al. 1994). 'Within group mean distance' and 'Mean diversity in entire population' were assessed. Analyses were conducted using the Maximum Composite Likelihood model (Tamura et al. 2004). The rate variation among sites was modelled with a gamma distribution (shape parameter = 1). This analysis involved 25 nucleotide sequences. The included codon positions were 1st+2nd+3rd+Noncoding. All positions with less than 95% site coverage were eliminated, i.e., fewer than 5% alignment gaps, missing data and ambiguous bases were allowed at any position (partial deletion option). There were a total of 349 positions in the final dataset. Evolutionary analyses were conducted in MEGA X (Kumar et al. 2018).

The distribution map (Fig. 2) was created using QGIS Project (2021).

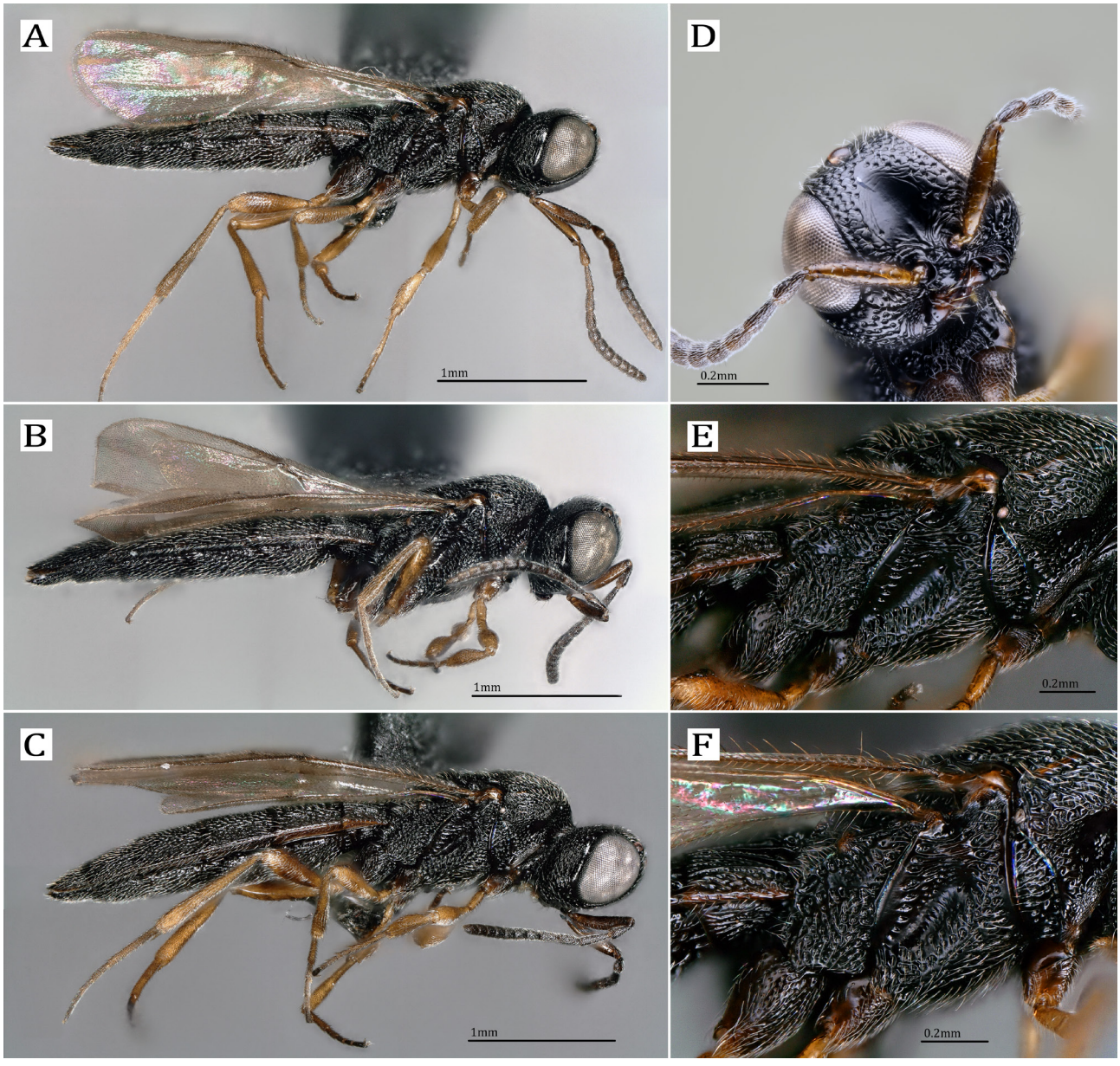

Fig. 1. Voucher specimens of *Triteleia peyerimhoffi* (Kieffer, 1906), sculpture variation. **A**. SMNS_Hym_Sce_001114, ♀; lateral habitus. **B**. SMNS_Hym_Sce_001085, ♀; lateral habitus. **C**. SMNS_Hym_Sce_000619, ♀; lateral habitus. **D**. SMNS_Hym_Sce_000612, ♀; frons. **E**. SMNS_Hym_Sce_001114, ♀; mesopleuron. **F**. SMNS_Hym_Sce_000619, ♀; mesopleuron.

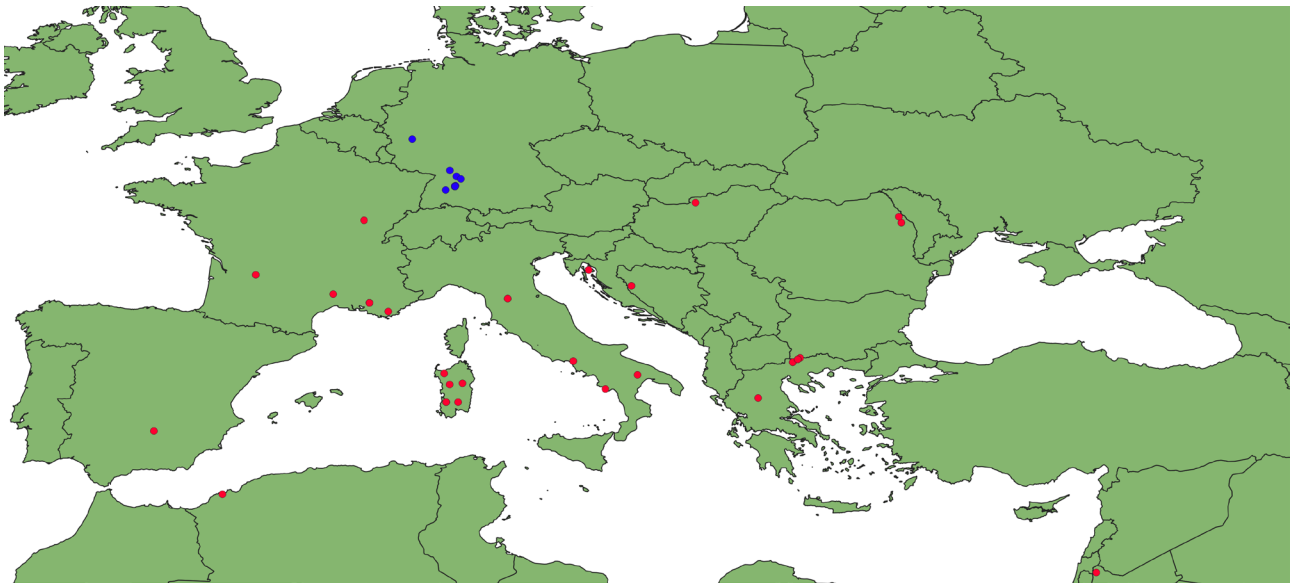

Fig. 2. Geographical distribution of *Triteleia peyerimhoffi* (Kieffer, 1906). Red dots represent data provided by Popovici et al. (2011). Blue dots represent data contributed by this project.

Results

Triteleia peyerimhoffi was found for the first time in Germany as far north as northern Rheinland-Pfalz. The new localities are well outside its previously known range from around the Mediterranean Sea, in southern Europe and North Africa (Popovici et al. 2011), suggesting that it prefers a warmer climate (Fig. 2). Our recent findings suggest the possibility that this species is expanding its distribution area due to climate change, as habitats further north become suitable.

The biology of this scelionid wasp is well established. It has been reared several times from eggs of orthopterans, and the species was originally described from specimens obtained from eggs of *Uromenus brevicollis* (Fischer, 1853) (Orthoptera: Tettigoniidae) (Kieffer 1906). In Romania, where there are no records of *U. brevicollis*, *T. peyerimhoffi* uses *Platycleis albopunctata* (Goeze, 1778) (Orthoptera: Tettigoniidae) as a host (Popovici et al. 2011). *Platycleis albopunctata* is present in Germany but considered endangered (Gottschalk et al. 2003); therefore, it is possible that in this area *T. peyerimhoffi* parasitizes some other, more common orthopteran(s). The use of several host species by *T. peyerimhoffi* may be responsible for the degree of morphological variation within this species.

The examined specimens exhibit some variation in external morphology, but this does not approach the extremes shown in Popovici et al. (2011). This is not a surprise, as there are no significant geographical barriers between the sampling localities. The most noticeable variation is in the size of the specimens, ranging from 3.39 mm to 4.32 mm (n=27). The shapes of tergites 1 and 2 (T1 and T2) are slightly different (Fig. 3A–F), with no correlation to the size of the specimens. The longitudinal sculpture on T1 and T2 can be straight (Fig. 3A), irregular (Fig. 3B, D), or a combination of the two (Fig. 3C, E, F). We recorded only minor variation in pleural sculpture: the femoral depression can be without sculpture and shiny (Fig. 1E) or finely reticulate (Fig. 1F), but no striae descending from the mesopleural epicoxal sulcus towards the anterior margin of the mesopleura could be detected. All our specimens have longitudinal striae on the sides of the frontal depression (Fig. 1D). Lastly, the coloration of the specimens varies from brown through brown with dark inflections to fully black (Figs. 1A–C, 3A–F). With the use of barcode sequences we were able to demonstrate, at least to some extent, that Popovici et al. (2011) were correct in treating the different morphs of *T. peyerimhoffi* as one species. In our dataset, the within-group genetic distance of the mitochondrial marker is 0.503%. The mean diversity index is also 0.5%; therefore, regardless of morphological differences, from a genetic point of view, these specimens clearly belong to the same species.

The BLAST query on GenBank did not retrieve any species- or genus-level identification, and the closest match was a sequence of unidentified "Hymenoptera sp." with a Pairwise Identity score of 82.31%. An identification request in BOLD returned mostly unidentified Scelionidae and one BIN identified as *Triteleia* sp.

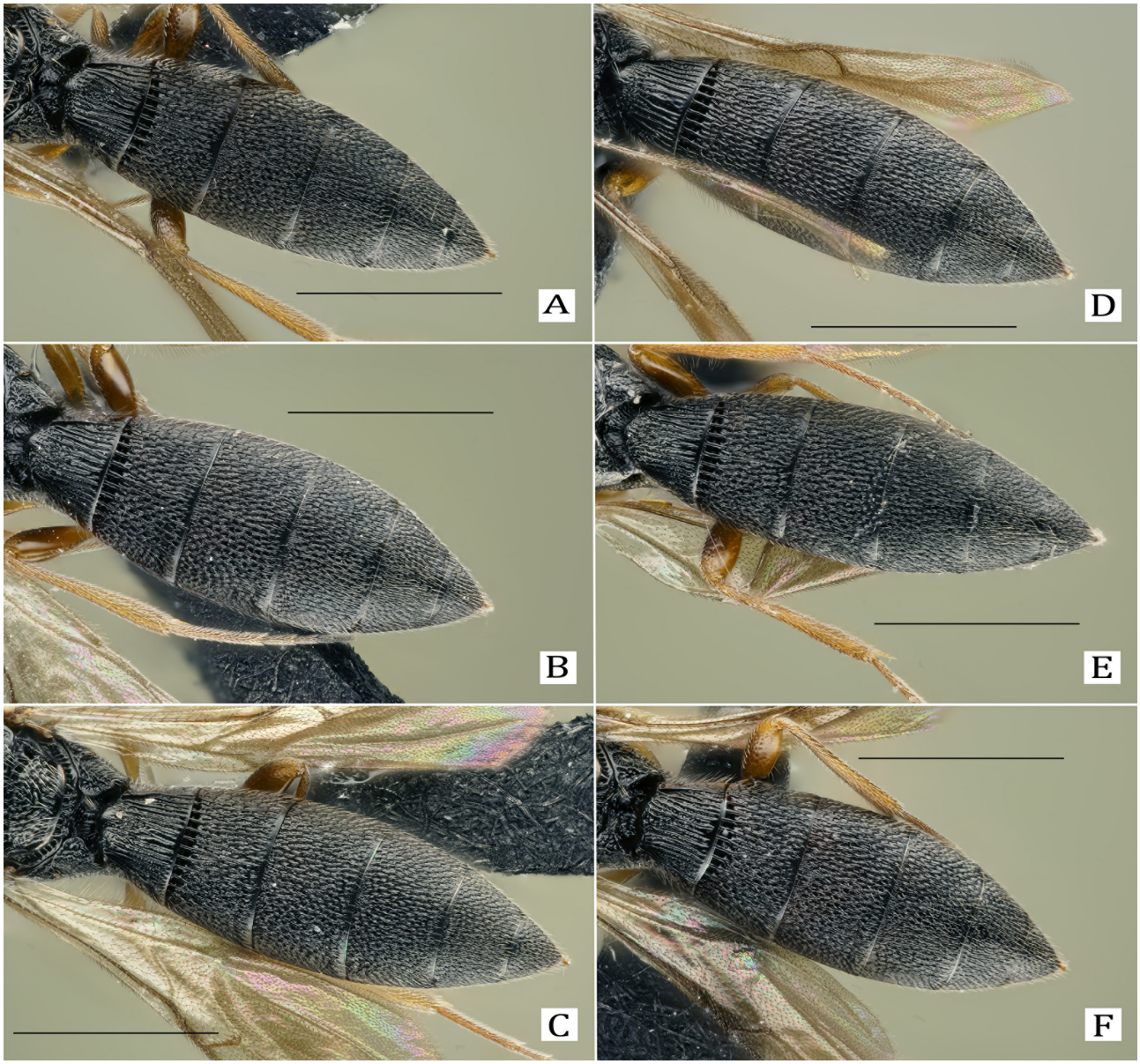

Fig. 3. Sculpture and shape variation of metasomal tergites in *Triteleia peyerimhoffi* (Kieffer, 1906). **A**. SMNS_Hym_Sce_000612, ♀. **B**. SMNS_Hym_Sce_000807, ♀. **C**. SMNS_Hym_Sce_000811, ♀. **D**. SMNS_Hym_Sce_001085, ♀. **E**. SMNS_Hym_Sce_001954 ♀. **F**. SMNS_Hym_Sce_002345, ♀. Scale bars: 1 mm.

(M409 BOLD:ACT9816; Ratnasingham & Hebert 2013). The public BIN contains sequences from six individuals of *Triteleia*, as confirmed by the images associated with the records. All belong to the same species and have a Distance to the Nearest Neighbor in BOLD of 7.13% (p-dist). However, this material originated in Costa Rica and the genetic divergence (p-dist) between our data and BOLD:ACT9816 is ~15%. Thus, there were no other reliably identified records to bridge the gap and investigate genus-level genetic diversity for *Triteleia* Kieffer.

With this publication, we again highlight the importance of associating reliable and verifiable identifications to barcode data. Gathering records of unidentified Scelionidae is of limited use, and misidentified vouchers are significantly counterproductive. Taxonomists, ecologists and other scientists that work with biodiversity data need to remember that one of the purposes of barcoding in taxonomy is to make the identification of the already described diversity easier and faster, so that more resources and focus can be oriented towards the unknown and the undiscovered.

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[Available from: https://doi.org/10.6084/m9.figshare.24802668.v1]

Supplementary File 1: Voucher accession numbers, GenBank IDs and collection data of specimens sequenced for this study.