

ABOL meeting 2020 – preface

Under the title *Days of Biodiversity 2020*, the 7th ABOL meeting took place together with the 3rd Austrian Forum on Biodiversity & Ecosystem Services (December, 4th–5th) as an online event for the first time, which was due to the Covid-19 pandemic. In a pre-phase, various biodiversity topics were discussed in workshops for a week. The results of which were presented together with other interesting lectures at the Biodiversity Forum.

The second day of the event was dedicated to the ABOL meeting, which offered an impressive overview of the various activities within the framework of ABOL in very diverse contributions, both methodologically and in terms of the great variety of organisms. The online format also gave the conference a more international visibility. Dr. Katrin VOHLAND, Director General of the Natural History Museum Vienna (NHM), opened the conference and emphasized the important role of the NHM in national and international biodiversity agendas. Two exciting keynote lectures – about the GBOL *Dark Taxa project* (Dr. RDUCH et al.) and the European Partnerships in Horizon Europe (Dr. BEGUSCH-PFEFFERKORN, BMBWF) – filled the morning. The afternoon sessions with a total of 13 flash-talks were dedicated to a wide variety of DNA barcoding projects and applications. Covering a broad range of topics and geography they were met with great interest.

The almost 190 registrations for the online meeting exceeded all previous ABOL meetings and the sessions were equally well attended!



Unter dem Titel *Tage der Biodiversität 2020* fand die 7. ABOL-Tagung gemeinsam mit dem 3. Österreichischen Forum für Biodiversität & Ökosystemleistungen (4.–5. Dezember) erstmals als Online-Veranstaltung statt, was der Covid-19-Pandemie geschuldet war. In einer Pre-Phase im Vorfeld der Veranstaltung wurden eine Woche lang in Workshops unterschiedliche Biodiversitäts-Themen erörtert, deren Ergebnisse zusammen mit weiteren interessanten Vorträgen im Biodiversitätsforum präsentiert wurden.

Der zweite Tag der Veranstaltung war der ABOL-Tagung gewidmet, die in organismisch und methodisch sehr diversen Beiträgen einen eindrucksvollen Überblick über die verschiedenen Aktivitäten im Rahmen der ABOL-Initiative bot. Das Online-Format ermöglichte auch eine stärkere internationale Beteiligung an der Tagung. Frau Dr. Katrin VOHLAND, Generaldirektorin des Naturhistorischen Museums Wien (NHM), eröffnete die Tagung und betonte die wichtige Rolle des NHM bei nationalen und internationalen Biodiversitätsagenden. Zwei spannende Keynote-Vorträge – über das GBOL *Dark Taxa-Projekt* (Dr. RDUCH et al.) und die European Partnerships in Horizon Europe (Dr. BEGUSCH-PFEFFERKORN, BMBWF) – füllten den Vormittag. Die Nachmittagssessions waren mit insgesamt 13 Flashtalks zu verschiedensten DNA-Barcoding-Projekten und -Anwendungen inhaltlich und geographisch breit aufgestellt und stießen auf großes Interesse.

Die fast 190 Anmeldungen für das Online-Meeting übertrafen alle bisher dagewesenen ABOL-Tagungen und die Sessions waren gleichmäßig gut besucht!

Extended abstract

Phylogeny of the freshwater Canthocamptidae (Crustacea, Copepoda, Harpacticoida) of the Palearctic including Lake Baikal: advances on molecular taxonomy of selected Austrian species

Santiago GAVIRIA MELO, Elena FEFILOVA & Elena KOCHANOVA

This study was designed to reveal phylogenetic relationships of the freshwater genera and species of the highly diverse family Canthocamptidae (Copepoda, Harpacticoida) in the Palearctic region. The purpose is to investigate the evolution of the family, starting with the brackish genera (*Itunella* BRADY, 1896, *Cletocamptus* SCHMANKEVITSCH, 1875), followed by the euryhaline (*Mesochra* BOECK, 1865) and the freshwater taxa (all other genera). With this analysis, we expect to find insights of the colonisation of freshwaters within the family. Twenty-two colonisation events of inland waters by the subclass Copepoda have been identified (BOXSHALL & JAUME 2000). Nevertheless, the pattern of colonisation history of the family Canthocamptidae has not been well explained, due to the lack of a coherent phylogenetic analysis. A particular focus will be the study of the genera *Moraria* T. & A. SCOTT, 1893, *Bryocamptus* CHAPPUIS, 1928 and *Canthocamptus* WESTWOOD, 1836, which are highly diversified at the Palearctic Region, and are considered the most species-rich canthocamptid genera of Lake Baikal (BORUTZKY 1964). 31 taxa of *Moraria*, 29 of *Bryocamptus* and 10 of *Canthocamptus* have been reported from the lake so far (EVSTIGNEEVA & OKUNEVA 2001, OKUNEVA 1983, 1989).

We expect to collect representatives of the 16 genera present in inland waterbodies of the region (BORUTZKY 1964, DEFAYE & DUSSART 2011, WALTER & BOXSHALL 2021), as far as possible the type species of each genus. Semi-terrestrial, epigeic (benthos) and hypogean (interstitial, phreatic groundwater, caves) species will be considered. Part of the taxa has been already sampled at selected localities from Central and Southern Europe, Fennoscandia and Russia. In some cases we will use specimens from already existing collections.

In Central Europe and particularly in Austria, species inhabiting mountain lakes, ponds and groundwater, as well as those from lowlands are included. 12 waterbodies of the 5 zoogeographical regions present in Austria (Hungarian Lowland Region, Carpathian Region, Lower Mountain Range, Alpine Region – colline zone, and Alpine Region – mountain zone) defined by ILLIES (1978), are considered in the project. From the 8 genera known from Austria (LÖFFLER & NEUHUBER 1970, GAVIRIA 1998), we found to date 4 genera and 6 species in Tyrol (Fernsteintsee: *C. staphylinus* (JURINE, 1820)), Salzburg (Zell am See: *C. staphylinus*, *C. microstaphylinus* WOLF, 1905, *Attheyella trispinosa* (BRADY, 1880), *Moraria brevipes* SARS, 1862) and Upper Austria (Hallstätter See: *C. staphylinus*, *A. trispinosa*, *Attheyella crassa* (G.O. SARS, 1862), *Bryocamptus minutus* (CLAUS, 1863), *M. brevipes*).

Of all species mentioned, DNA barcodes using partial sequences of the mitochondrial cytochrome c oxidase subunit 1 gene (CO1) were established and submitted to GenBank (NCBI). Currently, accession numbers of two of the species studied *C. staphylinus* and *M. brevipes* are already available: *C. staphylinus* (Lake Hallstättersee MN737570, Lake Fernsteintsee MN737567, Lake Zell am See MN737565-MN737566), *M. brevipes* (Lake Zell am See MN266958).

Within a preliminary study of the family, we studied the phylogenetic structure of *A. crassa* (KOCHANOVA & GAVIRIA 1918b) and *C. staphylinus* (KOCHANOVA et al. 2018a, 2018c) in Europe and the European Russia. Genetic and morphological divergences of populations from distant localities suggested the existence of distinct mitochondrial lineages which might possibly represent cryptic species.

The study of the remaining genera like the epigeal *Pesceus* ÖZDIKIMEN, 2008, some stygobiont species of *Elaphoidella* CHAPPUIS, 1928 and of the semi-terrestrial genera *Maraenobiotus* MRÁZEK, 1893 and *Epactophanes* MRÁZEK, 1893, are in progress.

In summary, we expect to clarify the phylogenetic relationship of the 20 genera of the family Canthocamptidae of the Palearctic Region, to reveal the colonisation history of freshwater by the family and its diversification, to compare the relationship between west and east Palearctic species, to study the main evolutionary lineages of the canthocamptid fauna of Lake Baikal and their role on the phylogeny of the family.

GAVIRIA MELO S., FEFILOVA E. & KOCHANOVA E., 2022: Phylogenie der Süßwasser-Canthocamptidae (Crustacea, Copepoda, Harpacticoida) der Paläarktis einschließlich des Baikalsees: Fortschritte in der molekularen Taxonomie ausgewählter österreichischer Arten.

Diese Studie soll die phylogenetischen Beziehungen der vor allem im Süßwasser vorkommenden Familie Canthocamptidae (Copepoda, Harpacticoida) in der Paläarktis untersuchen. Um die Evolution der Familie zu verstehen, werden die Brackwasser-Gattungen (*Itunella* BRADY, 1896, *Cletocamptus* SCHMANKEVITSCH, 1875), über euryhaline (*Mesochra*, BOECK, 1865) bis zu Süßwasser-Taxa (alle übrigen Gattungen) studiert. Damit erwarten wir Einblicke in die Kolonisierung des Süßwassers durch die Familie. 22 Besiedlungsereignisse von Binnengewässern durch die Unterklasse Copepoda wurden bereits bestimmt (BOXSHALL & JAUME 2000). Dennoch ist das Muster der Besiedlungsgeschichte der Familie Canthocamptidae durch das Fehlen einer zusammenhängenden phylogenetischen Analyse nicht vollständig geklärt. Ein besonderer Fokus liegt auf der Untersuchung der Genera *Moraria* T. & A. SCOTT, 1893, *Bryocamptus* CHAPPUIS, 1928 und *Canthocamptus* WESTWOOD, 1836, die äußerst vielfältig in der Paläarktischen Region vorkommen und die artenreichsten Gattungen der Canthocamptiden im Baikalsee darstellen (BORUTZKY, 1964). 31 Taxa von *Moraria*, 29 von *Bryocamptus* und 120 von *Canthocamptus* sind aus dem Baikalsee (EVSTIGNEVA & OKUNEVA 2001, OKUNEVA 1983, 1989) bekannt.

Wir erwarten, Vertreter aller 16 Gattungen, die in kontinentalen Wasserkörpern der Paläarktis vorkommen (DEFAYE & DUSSART 2011, WALTER & BOXSHALL 2021) zu finden, wenn möglich, die „type-species“ jeder Gattung. Semiterrestrische, epigäische (Benthos) und hypogäische (Interstitial, Grundwasser, Höhlen) Arten sollen dabei berücksichtigt werden. Ein Teil der Taxa wurde bereits an ausgewählten Stellen in Mittel- und Südeuropa, Fennoskandien und Russland gesammelt. In einigen Fällen werden wir auf Exemplare aus bereits existierenden Sammlungen zurückgreifen. In Mitteleuropa und speziell in Österreich sind Arten aus Bergseen, Teichen und Grundwasser sowie aus dem Tiefland eingeschlossen. Gewässer aus den 5 von ILLIES (1978) in Österreich definierten zoogeografischen Regionen (Ungarische Tiefebene, Karpaten, Zentrales Mittelgebirge, Alpen, Dinarischer Westbalkan) sind im Projekt berücksichtigt.

Von den 8 aus Österreich bekannten Gattungen (LÖFFLER & NEUHUBER 1970, GAVIRIA 1998) haben wir bis jetzt 4 Gattungen und 6 Arten in Tirol (Fernsteinsee: *C. staphylinus* (JURINE, 1820)), Salzburg (Zell am See: *C. staphylinus*, *C. microstaphylinus* WOLF, 1905, *Attheyellatrispinosa* (BRADY, 1880), *Morariabrevipes* SARS, 1862) und Oberösterreich (Hallstätter See: *C. staphylinus*, *A. trispinosa*, *Attheyella crassa* (G.O. SARS, 1862), *Bryocamptus minutus* (CLAUS, 1863), *M. brevipes*) gefunden.

Bei allen erwähnten Arten, wurden DNA-Barcodes analysiert (mittels Teilsequenzen des mitochondrialen Cytochroms c Oxidase subunit 1 Gen CO1) und der GenBank (NCBI) übermittelt. Die Zugangsnummern von 2 der untersuchten Arten, *C. staphylinus* (Hallstättersee MN737570, Fernsteinsee MN737567, Zell am See MN737565-MN737566), *M. brevipes* (Zell am See MN266958) sind bereits abrufbar.

Im Rahmen der vorläufigen Studie der Familie, untersuchten wir die phylogenetische Struktur von *A. crassa* (KOCHANOVA & GAVIRIA 1918b) und *C. staphylinus* (KOCHANOVA et al. 2018a, 2018c) in Europa und im europäischen Russland. Genetische und morphologische Divergenzen der Populationen aus unterschiedlichen Lebensräumen deuten die Existenz von unterschiedlichen mitochondrialen Evolutionslinien an, die möglicherweise kryptische Arten darstellen.

Die Untersuchung der übrigen Gattungen wie des epigäischen *Pesceus* ÖZDIKIMEN, 2008, einiger stygobionter Arten von *Elaphoidella* CHAPPUIS, 1928 und der semi-terres-

trischen Gattungen *Maraenobiotus* MRÁZEK, 1893 und *Epactophanes* MRÁZEK, 1893, sind in Arbeit.

Zusammenfassend erwarten wir die phylogenetische Beziehung der 20 Gattungen der Familie Canthocamptidae in der Paläarktis, die Besiedlungsgeschichte des Süßwassers durch diese Familie und ihre Diversifizierung zu klären, sowie die Beziehung zwischen Arten der westlichen und östlichen Paläarktis zu vergleichen, die evolutionären Hauptlinien der Canthocamptiden-Fauna des Baikalsees und ihre Rolle in der Phylogenie der Familie zu erforschen.

Keywords: systematics, cladistics, molecular & morphological taxonomy, evolution, aquatic zoogeography, diversity.

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Extended Abstract

The unexpected biodiversity of the genus *Phoxinus* (Leuciscidae) in Austria – a perfect example of pros and cons of the DNA barcoding region COI for taxonomical use

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Minnows of the genus *Phoxinus* (Leuciscidae) are small fishes, which inhabit various kinds of water bodies, such as mountain streams, lowland rivers and different types of lakes (Figure 1, 2). While initially several species were described (for example *Phoxinus morella* (LESKE, 1774) from central Germany, *P. marsilii* HECKEL, 1836 from Vienna, Austria, and *P. csikii* HANKO, 1922 from Montenegro), in the beginning of the 20th century, they were unified under one, widely distributed species, *Phoxinus phoxinus* (LINNAEUS, 1758) or European minnow. The taxonomy remained unmodified for over a century, until a morphological study by BOGUTSKAYA & NASEKA (2004) re-established *P. colchicus* BERG, 1910, while KOTTELAT (2007) described two new species (*P. septimaniae* and *P. bigerri*) and resurrected one (*P. stardnjae* DRENSKY, 1926). Afterwards, several molecular studies followed (PALANDAČIĆ et al. 2015, KNEBELSBERGER et al. 2015, PALANDAČIĆ et al. 2017) and exposed an unexpected biodiversity within the genus. *Phoxinus phoxinus* is a complex of species, which up to now includes 23 genetic lineages, thirteen of which are considered valid species (PALANDAČIĆ et al. 2020, DENYS et al. 2020). Nevertheless, most of the lineages were determined based on two mitochondrial (mt) genes – cytochrome b (cytb) and cytochrome oxidase I (COI), while analysis of nuclear markers proved to be ambiguous, contrasting the mtDNA results or were simply missing (PALANDAČIĆ et al. 2020). In addition, due to phenotypic diversity, morphological identification of species is difficult (RAMLER et al. 2016). The lineages also do not follow usual distribution patterns observed in the family Leuciscidae – according to the river drainages and water basins – but rather transverse those boundaries. Finally, natural and human-induced hybridisation was discovered in most of the lineages, and introductions were reported from all around Europe (MIRO and VENTURA 2015, MUSETH et al. 2007, GARCIA-RAVENTOS et al. 2020, DE SANTIS et al. 2021), making species delimitation in *Phoxinus* extremely difficult.

As in Europe, it was assumed that Austria is populated with *P. phoxinus*. However, genetic studies based on COI and cytb identified four species inhabiting Austrian waters, namely *P. csikii*, *P. lumaireul*, *P. marsilii* and *P. phoxinus*. Further, three distinct mtDNA sublineages of *P. lumaireul* (SCHINZ, 1840) (denoted as 1a, 1c and 1d according to PALANDAČIĆ et al. 2015, and partly corroborated with nuclear markers) are present. Of the two possible sublineages of the species *P. csikii*, the sublineage characteristic for Central Europe – 5b (PALANDAČIĆ et al. 2020) was detected. Due to above mentioned human introductions and ambiguities in distribution patterns, it was not clear if the different lineages/species occur naturally or were introduced. Thus, a comparison of the museum material and freshly collected samples was applied to assess the distribution of genetic lineages (PALANDAČIĆ et al. 2020) in Austria. The results suggested that the three species *P. csikii*, *P. marsilii* and *P. lumaireul* – sublineage 1d and possibly 1c occur naturally, while *P. phoxinus* and *P. lumaireul* 1a have been introduced. The amazing biodiversity of the genus *Phoxinus* came to light also due to various DNA barcoding projects, which provided data for comparison throughout Europe. However, most of the taxonomy is currently based on mitochondrial genes, which offers only one version of evolutionary history, and needs to be critically evaluated with nuclear markers and morphological analysis. In addition, in Austria, a reduced sampling, which is typically performed for the setup of a DNA barcoding reference databank (usually only 4 individuals) would not suffice to detect the complete biodiversity of *Phoxinus*. First,

a wider reference set is needed to observe the formation of two different clades when comparing closely related *P. lumaireul* and *P. csikii*. Second, *P. marsilii* has a very restricted distribution in Austria, as the Vienna area represents the westernmost area of its range. Thus, the presence of *P. marsilii* in Austria would have been easily overseen. Finally, due to frequently detected human introductions, it would be difficult to evaluate the species' natural distribution. In conclusion, DNA barcoding can surely be used as a first step in biodiversity assessment, but cannot substitute in-depth taxonomic studies.

PALANDAČIĆ A., KRUCKENHAUSER L., AHNELT H. & MIKSCHI E., 2022: Die unerwartete Artenvielfalt der Gattung *Phoxinus* (Leuciscidae) in Österreich – ein Beispiel für die Vor- und Nachteile des DNA-Barcodings für taxonomische Zuordnungen. Elritzen (*Phoxinus* sp.) bewohnen verschiedene Lebensräume wie Gebirgsbäche, Tieflandflüsse und verschiedene Arten von Seen. Über ein Jahrhundert lang wurde angenommen, dass in Europa nur eine einzige weit verbreitete Art, *Phoxinus phoxinus* – die Europäische Elritze – vorkommt. Ausgehend von mehreren morphologischen und molekularen Studien wurde jedoch deutlich, dass *P. phoxinus* ein Artenkomplex ist, der derzeit 23 genetische Linien umfasst, von denen 13 als gültige Arten sind. In den meisten Abstammungslinien wurde jedoch auch natürliche, oder vom Menschen, durch Aussetzungen aus Spanien, Portugal, Frankreich und Deutschland, induzierte Hybridisierung entdeckt. Dies erschwert die Abgrenzung der Arten in *Phoxinus* zusätzlich. Es wurde ursprünglich angenommen, dass in Österreich, wie in Europa, nur *P. phoxinus* vorkommt. Genetische Studien haben jedoch gezeigt, dass stattdessen vier Arten in den österreichischen Gewässern leben, nämlich *P. csikii*, *P. lumaireul*, *P. marsilii* und *P. phoxinus*. Durch die Analyse des Museumsmaterials in der ichthyologischen Sammlung des Naturhistorischen Museums Wien wurde gezeigt, dass drei Arten (*P. csikii*, *P. lumaireul*, *P. marsilii*) wahrscheinlich natürlich vorkommen, während *P. phoxinus* vermutlich eingesetzt wurde.

Die erstaunliche Artenvielfalt der Gattung *Phoxinus* wurde auch durch verschiedene DNA-Barcoding-Projekte, durch die europaweites Vergleichsmaterial zur Verfügung steht, deutlich. Die Taxonomie basiert derzeit jedoch fast ausschließlich auf mitochondrialen Genen, die nur eine Version der Evolutionsgeschichte darstellen und durch Untersuchungen von nukleären Markern und morphologischen Merkmalen kritisch bewertet werden müssen. Darüber hinaus würde in Österreich die im Rahmen der Erstellung einer DNA-Barcoding-Referenzdatenbank durchgeführte reduzierte Probenahme (meist nur 4 Individuen) nicht ausreichen, um die vollständige Artenvielfalt von *Phoxinus* nachzuweisen. Aufgrund der Einschleppungen ist es schwierig, die natürliche Verbreitung der Arten zu bewerten. Zusammenfassend kann DNA-Barcoding sicherlich als erster Schritt bei der Bewertung der biologischen Vielfalt verwendet werden, jedoch eingehende taxonomische Studien nicht ersetzen.

Keywords: *Phoxinus*, Austria, biodiversity, cytochrome oxidase I.

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Extended abstract

GBOL III: Dark Taxa – Background, Aims & Selected Taxa

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Since 2011, the ‘German Barcode of Life’ initiative (GBOL) has been running successfully. During the first (2011–2015) and the second phase (2016–2019), a network of professional and non-professional taxonomists was established to set up a DNA barcode reference library for the fauna, flora, and fungi of Germany. About half of the animal species occurring in Germany are covered within the database. Even species-rich groups like Coleoptera (beetles) and Lepidoptera (moths and butterflies) are well represented. However, looking at Hymenoptera (bees, ants, and wasps) and Diptera (mosquitos, midges, and flies), the situation is different. Considering the estimated number of species in Germany, only about 25% of Hymenoptera and about 33% of Diptera species are covered in the GBOL barcode library. On the one hand, these two organism groups are megadiverse and represent almost 10,000 species each in Germany, which is almost half of the animal species occurring in Germany. On the other hand, these two groups of insects comprise so called “Dark Taxa” which constitute a large fraction of the respective total species numbers: Most of the specimens cannot be assigned to species level or belong to groups that are not or not well documented. So far, these taxa are largely understudied: there are no reliable lists of species, no clear characterization of species, no identification keys, no reference collection, no DNA barcode information, and no taxonomic specialists (or only very few worldwide) for the respective groups. Accordingly, these taxa have been (widely) excluded from GBOL or other biodiversity research. In samples from Malaise traps these Dark Taxa can represent 50% or more of the specimens and for them, a species-specific determination via metabarcoding is not possible so far. Filling the gaps in the DNA barcode reference library in Diptera and Hymenoptera and thus increasing the size and quality of the database is one of the aims of the new phase *GBOL III: Dark Taxa*. Funded by the German Ministry of Education and Science (BMBF) the new phase started on 1st July 2020 with a duration of 42 months. The overall aim of completing the DNA barcode reference database can only be reached if we investigate the Dark Taxa within the Diptera and parasitoid Hymenoptera with a targeted integrative taxonomic approach. Traditional morphological characters might not be enough to reliably delimit and discriminate species. They are complemented by state-of-the-art and innovative methods (e.g., genital morphology, wing interference patterns, host records, DNA barcodes, taxonomic data). We need to characterize species and provide reliable taxon names in order to fill up the database. In the course of the project, we will train a new generation of taxonomists with expertise on diverse Dark Taxa and the latest methods and approaches in taxonomic science. Thus, *GBOL III: Dark Taxa* is not only a barcode initiative, but also a taxonomy initiative. The consortium consists of the Zoological Research Museum Alexander Koenig in Bonn (now part of the Leibniz Institute for the Analysis of Biodiversity Change) that further serves as leader and central coordination, the State Museum of Natural History in Stuttgart, the Zoological State Collection in Munich, the University of Würzburg (Lehrstuhl für Tierökologie und Tropenbiologie) and the Entomological Society of Krefeld. In total 11 PhD candidates will investigate one dark taxon each: Figitidae, Eurytomidae, Platygastridae, Ceraphronidae, Ichneumonidae, Diapriidae (all parasitoid Hymenoptera), Psychodidae, Limoniidae, Phoridae, Sciaridae and Chironomidae (all Diptera). Besides the PIs within the consortium, external taxonomic specialists are closely involved in the training of the PhD candidates. Further taxa selected to be focused on during the funding period are Ormyridae, Eupelmidae, Chalcididae, Mymaridae, Perilampidae, Torymidae, Trichogrammatidae, Encyrtidae, Eulophidae (all parasitoid Hymenoptera), Keroplatidae, Pediciidae, Tachinidae, Sarcophagidae, Cecidomyiidae and Empidoidea (all Diptera). One additional PhD project will investigate

the parasitoids of pest species as an application study. Two more subprojects complete the tasks of *GBOL III: Dark Taxa*. 1) Our web portal (www.bolgermany.de) provides access to the data and can already be used for reverse identification approaches. We will implement more tools, for example, one important aspect is the development of a platform for the use of ASVs (amplicon sequence variants). ASVs are DNA-barcodes without an assigned species name that emerge from metabarcoding studies. We will be able to database these ASVs so that they are available with the attached data for future analyses. 2) For some species of Dark Taxa, only a few, small and possibly degraded samples will be at hand. Further, some taxonomic and species delimitation issues will need more than morphology and DNA barcodes. Here the subproject steps in and addresses new and optimized approaches to poor-quality samples and taxonomies. Another important aspect of *GBOL III: Dark Taxa* is the communication and public outreach. For this, we updated our homepage (www.bolgermany.de) and we are present on Twitter (@GBOLIIIDarkTaxa), on Facebook (@germanbarcodeofflife) and on Instagram (@gbol_germanbarcodeofflife). We share general and specific information via these channels and inform the public and stakeholders about the progress of the GBOL project, DNA barcoding & integrative taxonomy, biodiversity loss and Dark Taxa. We would like to share knowledge and awake enthusiasm for these topics and for the Dark Taxa to highlight their importance within the Central European fauna.

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Die ‘German Barcode of Life-Initiative (GBOL) arbeitet seit 2011 sehr erfolgreich an der DNA-Barcode-Referenzbibliothek für die in Deutschland vorkommenden Tiere, Pflanzen und Pilze. Nach zwei Förderphasen ist etwa die Hälfte der heimischen Tierarten in der Datenbank vorhanden. Auch artenreiche Gruppen (Coleoptera oder Lepidoptera) sind gut abgebildet. Allerdings, in Bezug auf die geschätzten Artenzahlen in Deutschland, sind nur etwa 25 % der Hymenoptera (Bienen, Ameisen und Wespen) und 33 % der Diptera (Mücken und Fliegen) in der GBOL-Barcode-Referenzbibliothek vertreten. Diese Lücken in der Datenbank zu schließen ist das wesentliche Ziel der neuen Förderphase *GBOL III: Dark Taxa*, die, erneut gefördert vom Bundesministerium für Bildung und Forschung (BMBF), am 1. Juli 2020 für 42 Monate gestartet ist. Das gesteckte Ziel kann nur erreicht werden, wenn diese ‘Dark Taxa’ der Diptera und parasitoiden Hymenoptera mit einem gezielten integrativen taxonomischen Ansatz erforscht werden, um Arten zu charakterisieren und mit verlässlichen Artnamen zu versehen. Im Laufe des Projektes werden wir eine neue Generation von Taxonomen ausbilden, das Web-Portal (www.bolgermany.de) um weitere Werkzeuge erweitern (die Speicherung und Auswertung von ASV-Daten) und die Ansätze optimieren, um auch ein Arbeiten mit (oder ein Bearbeiten von) Proben von geringer DNA-Qualität oder Quantität zu ermöglichen. Ein weiterer Aspekt ist die Kommunikation der Ergebnisse sowie die Sensibilisierung der Gesellschaft für Dark Taxa.

Keywords: Barcoding Initiative, Integrative Taxonomy, Dark Taxa, Hymenoptera, Diptera, Parasitoid Wasps, Nematocera.

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ZOBODAT - www.zobodat.at

Zoologisch-Botanische Datenbank/Zoological-Botanical Database

Digitale Literatur/Digital Literature

Zeitschrift/Journal: [Verhandlungen der Zoologisch-Botanischen Gesellschaft in Wien. Frueher: Verh.des Zoologisch-Botanischen Vereins in Wien. seit 2014 "Acta ZooBot Austria"](#)

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