

DESCRIBING A NEW AMBER FOSSIL SPECIES

— RESEARCH PROPOSAL

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1. ABSTRACT

The family of *Ichneumonidae* (Darwin Wasps) have encountered a rapid radiation (Klopfstein, et al., 2019) which explains their high diversity and specimens that remain undescribed to date. Our goal in this research is to determine whether the provided fossil from the middle Eocene era embedded in Baltic amber (approx. 37-54 mya (Weitschat & Wichard, 2010)) can be described as a new species.

To reach our goal, we plan to establish a taxonomic placement of the specimen by describing the fossil in detail and using its characteristics for interpretation. We aim to use geometric morphometrics on the forewings in order to get a more precise classification and place the specimen in a specific tribe.

Even though Darwin Wasps are the most species-rich family among the parasitoid wasps, they are poorly described and lack information (Klopfstein, et al., 2019). Therefore, it is important to continuously classify new taxa.

2. INTRODUCTION

Darwin Wasps are a family of parasitoid wasps, which use Lepidoptera, Hymenoptera, Diptera, Coleoptera and rarely spiders or other arthropods as their host (Li, Shih, Kopylov, Li, & Ren, 2019). Already more than 24'000 species are described (Broad, Shaw, & Fitton, 2018). However, the fossil in our case originates from an era (Paleogene) where there is little information about the diversity of Darwin Wasps (Klopfstein, et al., 2019). Moreover, it is difficult to find synapomorphies in a subfamily or genus that are homologous, since their morphology is extensively related to the host they predate on (Spasojevic et al., 2018).

Original keys are often not conclusive enough to determine the genera of a specimen, which is why new and regional keys, as well as modern methods are needed for more detailed taxonomic placement (Klopfstein, et al., 2019). The way how the specimen has been entombed in its preservation medium including post-burial processes (eg. diagenesis) can affect the quality of the fossil (Martínez-Delclòs, Briggs, & Peñalver, 2004). The forewings are usually better preserved than the rest of the carcass, because it can rip off during its fossilization or may not be as informative for taxonomic placement (Spasojevic et al., 2018). Revision of priorly described specimens with geometric morphometrics could therefore be a useful approach to eliminate misplacements and to build a framework that facilitates higher-level classification of new specimens by their venation (Spasojevic et al., 2018). In Addition, forewing venation patterns are mostly specific for different subfamilies despite homoplasies (Klopfstein, et al., 2019). Geometric morphometrics has been increasingly used to describe phenetic relationships, but it is a relatively new method and its importance for constructing phenetic connections is not completely evaluated. In light of this we want to prove the following:

1. Our specimen belongs to a taxon that has not been described before.
2. With the help of geometric morphometrics the fossil can be classified into a subfamily and furthermore into a genus.

3. RESEARCH PLAN

3.1 MATERIAL AND METHODS

The fossil specimen which will be newly described is deposited in the *Hymenoptera* collection at the natural historical museum of Basel. It belongs to the family of the Darwin Wasps and has been preserved between 37 and 54 (arguably even less (Perkovsky et al., 2007)) million years in Baltic amber.

Morphological Approach: First we make a description of certain body parts from our specimen by using the morphological terminology of Broad et al. (2018) by looking at photographs of the fossil, that were previously taken by Alexandra Viertler under a [Keyence VHX 6000](#) with a magnification of 200, as well as carefully study the morphology with a binocular microscope. Afterwards, we determine the taxonomic placement in the higher groupings with a simplified determination key from Alexandra Viertler and also attempt to make a higher-level classification. If this is not possible, we then progress using geometric morphometrics on the forewings.

Morphometrical Approach: We use the dataset given by Alexandra Viertler, where 22 subfamilies are already described with 21 distinct type 1 landmarks of Bookstein's terminology and semilandmarks on the 2m-cu vein ((Bookstein, 1991); see Figure 3.1.1), to find out, whether it leads to the same conclusion as our classical approach with the description of body features.

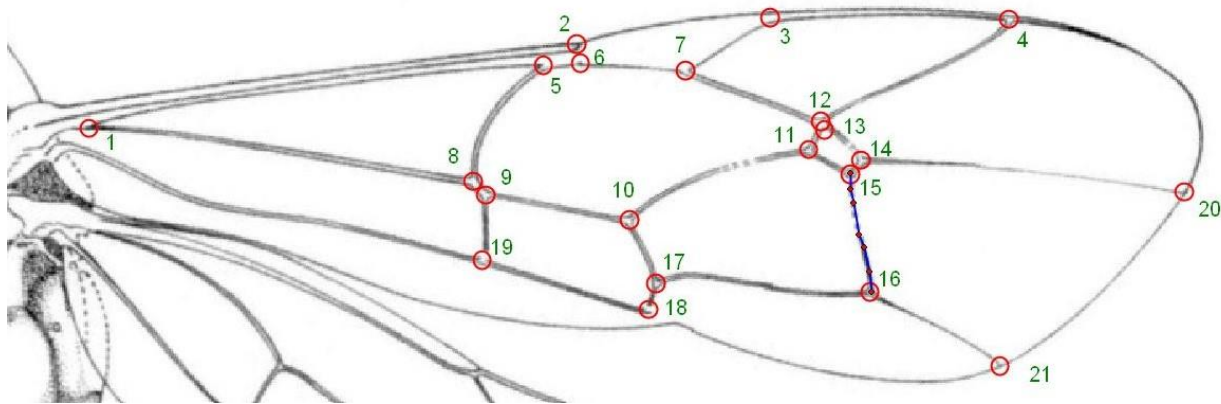


Figure 3.1.1: Illustration of *Deleboea* sp. (Townes, 1969) with landmarks (red circles), numeration (green letters) and curves (blue line) with semilandmarks (small red dots).

In order to make a more detailed placement in between the tribes of our defined subfamily, we construct another dataset by placing landmarks on the intercept between veins of 30-100 holotypes from illustrations of Townes 1969. We also plan to use these data in combination with semilandmarks to work out how informative they are for subsequent interpretation.

We compare the obtained landmarks with the program MorphoJ (version 1.06d) in order to obtain Procrustes distances that can be used for phylogenetic analyses. Since the format which is used in MorphoJ doesn't allow interpretation of semilandmarks, we also conduct manual interpretation in R (version 4.0.4) of different veins that we consider important. We then attempt to further classify our specimen on a genus-level by analyzing our data from geometric morphometrics in Cluster Analyses (CA) or Principal Component Analysis (PCA) as used by Li et al. 2019. For the analyses of landmarks, we will use MorphoJ and for the semilandmarks (also in combination with landmarks), we plan to use PAST 4 (version 4.05) instead of R since it is more convenient to conduct CA.

Species Description: Based on our data from morphological characteristics as well as from morphometric analyses we then describe the new specimen, ultimately place it in the right taxonomic order and name it reasonably. If a non-ambiguous placement after our investigation is not possible, we will follow an open-taxonomy approach, leaving out higher-level classification. By doing this, we prevent biased divergence time estimations as explained by Spasojevic et al. 2018.

3.2 RESEARCH SCHEDULE

	Monday	Tuesday	Wednesday	Thursday	Friday
Week 1 08.03.2020 - 14.03.2020	Research Proposal				
Week 2 15.03.2020 - 21.03.2020	Determine Subfamily + planing which body part we want to describe from the fossil	Description of Specimen and morphometrics	Obtaining morphometric data from holotypes in our subfamily	Creating morphometric data of our fossil and combine it with our dataset from other subfamilies	Analysis in MorphoJ and R with CA of combined data and record results
Week 3 22.03.2020 - 28.03.2020	Interpreting results and conclude	creating a new dataset with information from landmarks in MorphoJ and semilandmarks in R within our subfamily	CA with MorphoJ and R of the obtained data	Adjust data accordingly to results in order to obtain more concise result	Interpreting results and conclude
Week 4 29.03.2020 - 04.04.2020	Writing final report	Writing final report	Excursion	Easter	
Week 5 05.04.2020 - 11.04.2020		Preparing additional matter for presentation (Illustration, Fotos and evt. 3D-Model)	Preparing for presentation	Finish Final Report and presentation	Presentation + Final report

3.3 OUTLOOK

Since there are still various collections of fossils scattered over different localities and there are considerable concerns that we may not be able to establish the vast diversity of Darwin Wasps, we highly rely on inventive procedures to speed up this process (Klopfstein, et al., 2019). Geometric morphometrics is a relatively new method for describing phenetic relationships, but has shown success in various studies (eg. Spasojevic et al., 2018; Schwarzfeld & Sperling, 2014). With our research project, we want to show the importance of geometric morphometrics for determining yet undescribed fossils. This could extend the possibilities to handle such large data in a short and simple way. In combination with classic determination, we hope that, although it handles

specimens in a relatively simplified way, the outcome of these analyses remains conclusive and may be able to fill the gaps between phenetic relationships in the future.

4. REFERENCES

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