Poster Abstract

A year of barcoding Vienna's wild bees

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DNA barcoding has evolved as a standardized tool to differentiate morphologically similar groups like Apiformes, detect cryptic species and observe the biodiversity within a region. In cooperation with the Natural History Museum Vienna, the Austrian Barcode of Life (ABOL) and the MA22 Vienna, the Institute for Integrative Nature Conservation Research is investigating the biodiversity of Vienna's wild bees. In addition to creating a reference database, we intended to compare sequences from traditional Sanger sequencing with those from NGS methods, in this case Illumina MiSeq. To do so, we analyzed 250 bee samples collected in multiple gardens across Vienna using standardized primer pairs for Apiformes in both methods. Applying Sanger sequencing, we generated 67 barcodes, while with the Illumina MiSeq we produced 55 sequences with a length of 460 base pairs and 195 sequences with a length of 418 base pairs. The generated Illumina DNA barcodes differ in length, but not in quality or in information content. We conclude that the Illumina DNA barcodes of wild bees have proven themselves as specific and effective. Around 70 species of Vienna's wild bees were sequenced with both sequencing methods and will be submitted to public databases i.e. NCBI and BOLD. Additionally, we will be able to add a not yet registered DNA barcode of Anthidium septemspinosum Lepeletier, 1841 to the databases. Our results show that NGS approaches like Illumina can be an alternative method to Sanger sequencing. NGS methods are less time consuming, produce large amounts of data with less expense and according to our results, are a reliable species determination tool.

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ZOBODAT - www.zobodat.at

Zoologisch-Botanische Datenbank/Zoological-Botanical Database

Digitale Literatur/Digital Literature

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