

**DNA barcodes generated with Illumina:
Applicability of species assignment of wild bees and their endosymbiont
*Wolbachia***

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The accurate identification of wild bees demands taxonomic expertise, due to morphological similarities and the high abundancy of cryptic species. For certain taxonomic groups, e.g., wild bees, DNA barcoding is particularly important as an additional determining tool also with respect to assessing their biodiversity. For over two decades, the Sanger method has been the standard technique and later has been used in projects dedicated to DNA barcoding. With the development of Next Generation Sequencing (NGS) methods a new era of sequencing has taken hold. The applicability of Illumina was tested in the present study on DNA barcodes of wild bees. Specimens were collected in communal gardens in Vienna. DNA isolation and amplification strategies were optimized to obtain high-quality DNA libraries. Identification analyses focusing on the Illumina sequences were computed. Although DNA barcodes derived from Illumina were comparatively short (418 base pairs), the sequences were specific. Moreover, the Illumina technique allows to deal better with some general problems of DNA barcoding.

Due to the additional information content gleaned from the Illumina DNA barcodes, first insights into the relationship between wild bees and their endosymbionts *Wolbachia sp.* were possible. Phylogenetic analyses were calculated for both groups to test a putative co-evolution pattern. In general, *Wolbachia* sequences seemed to be quite closely related and there was no evidence for co-evolution. Interestingly, kleptoparasitic and their (putative) host species share the same *Wolbachia* sequences. This leads to the assumption that frequent horizontal transfer between cuckoo bees and their hosts appeared quite recently. Further investigations have to be performed to evaluate this aspect