

DNA barcoding halictine bee species from Europe and Africa

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Abstract

Background: The Halictinae constitute a large subfamily of bees with more than 150 species in Europe and some hundreds of species in Africa. Recently, DNA sequences were published for halictine bees mainly from the New World, but also from Central Europe (62 species) and Africa (89 species). For many groups of African and Mediterranean species, however, identification and classification remain exclusively based on morphological traits. Here we aim at collecting DNA barcode data for these halictine species, for which a large collection is available at the Royal Belgian Institute of Natural Sciences and the Royal Museum for Central Africa. Our goal is to improve the resolution of the species identification of African and European halictine species, to compare their DNA barcodes with those already collected, and, in combination with the sequencing of four nuclear genes of some key species, to classify the species in their respective subgenera. Results: Genetic sequences are currently analyzed for a set of 172 specimens representing 150 species. Few or no species from the groups to which these species belong were previously sequenced in published phylogenetic or barcoding studies. Significance: Our research is a renew effort to compile DNA barcodes from a large number of specimens representing all the subgenera of halictine bees across a broad geographic area of the Old World (Europe and Africa). It should allow us to propose an updated classification of the species of the Old World Halictinae in concordance with the subgenera proposed for the New World.

Introduction

- Halictinae is a subfamily of wild bees comprising many described species (> 2000 worldwide).
- Although many Halictinae species of North America have been DNA barcoded^{1,2,3}, many species from the remaining part of the world are only known from morphological descriptions.
- Classifications available for the species of the Palearctic and for those from the Nearctic have been constructed partly independently and are not in complete concordance.

Material and methods

- 172 bee specimens identified to the species level and belonging to species groups (genera and subgenera) occurring in Africa and Europe.
- Sequencing the DNA barcode fragment (5' end of COI).
- Focus on species that have not been DNA barcoded yet.

Results and discussion

- Overall, we obtained 172 COI sequences representing 150 species and produced the first barcodes for 148 of these species (Fig. 1).
- Barcodes obtained for the African taxa *Afrodialictus*, *Paradialictus*, *Zonalictus* and *Sellalictus* (Fig. 2A-C) show clear interspecific divergences (median=3.7%).
- European representatives of the taxa *Hemihalictus*, *Evylaeus*, *Dialictus* and *Sphecodogastra* show distinct barcodes (median interspecific distance=5.1%) and a few of them cluster with publicly available sequences (see one example in Fig. 2D).
- Intraspecific variation could not be assessed due to the small number of specimens analyzed per species.
- Additional nuclear markers are being sequenced in order to study interspecific relationships within Halictinae. Classification of these taxa into genera and subgenera will be revised accordingly.

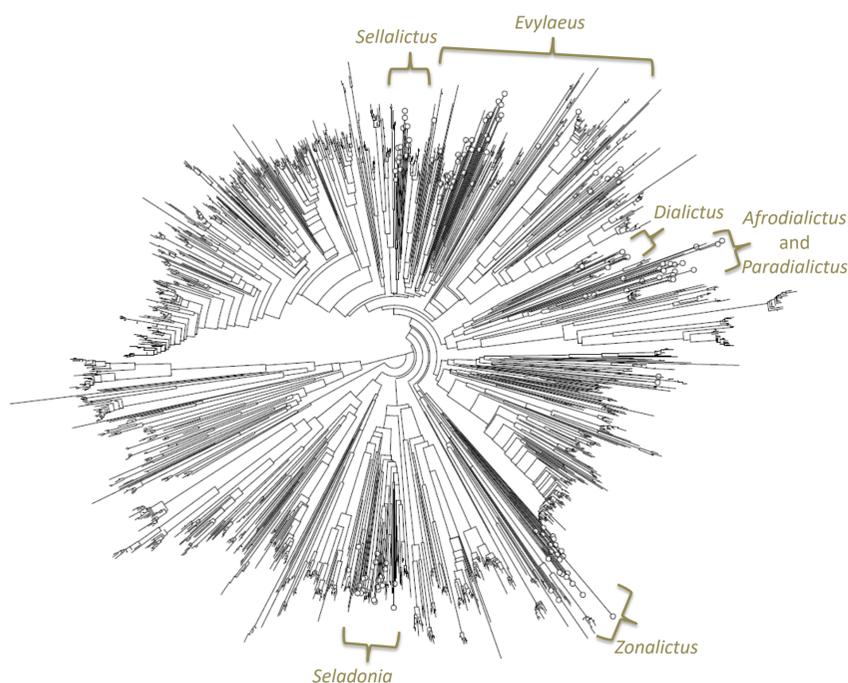


Fig. 1 Neighbour-joining (NJ) tree constructed with uncorrected p-distances among COI sequences of all Halictinae available in BOLD (simple tips) and obtained here (tips ending with a circle). Subgenera indicated on the tree are occurring in Africa and in Europe and are targeted in this study.

References

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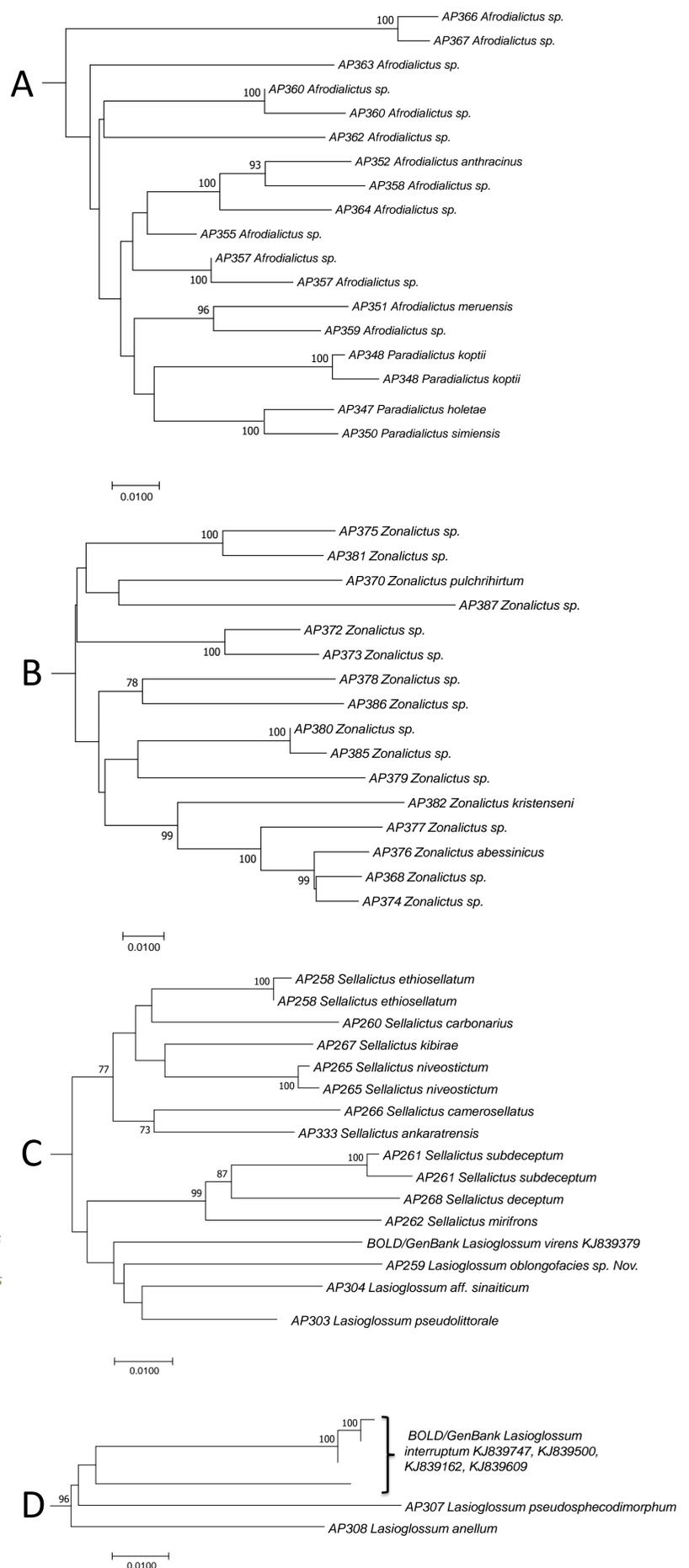


Fig. 2 Sub-trees extracted from the NJ tree of Fig. 1 and including representatives of the African taxa *Afrodialictus* and *Paradialictus* (A), *Zonalictus* (B) and *Sellalictus* (C). The last sub-tree (D) is one example of cluster grouping European representatives of *Lasioglossum* sequenced here and earlier. Bootstrap values >70 are shown at nodes. Sequences downloaded from public repositories are labelled as “BOLD/GenBank”.