



Conference Abstract

Heaven and hell: Spotlights on some DNA barcodes for species identification and delimitation in ground beetles

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Abstract

In the face of the decline of many insects, there is an increasing demand for contemporary, fast and cost-effective approaches to monitor the development of populations and species. Numerous scientists favor molecular methods, especially those involving barcoding of the CO1 gene, as an alternative to classical, morphology-based species identification. Moreover, DNA barcoding is also discussed as a suitable method to support species delimitations in complexes of closely related taxa. We used the available sequences of ground beetles from North and Central Europe with additional ones we generated from Southern Europe and the Middle East to draw conclusion about the practicability of such approach for ground beetles.

In general, while strong intraspecific differentiations within the CO1 fragment seem to characterize some wingless species (e.g. *Graphipterus serrator*, *Siagona longula*, *Carabus problematicus*, some *Platycarabus* species), others do not display much intraspecific variability (e.g. *Graphipterus multiguttatus* and *G. sharonae* within the “*G. serrator* clade”). These results certainly complicate the application of a metabarcoding approach without a larger database to delimitate these ground beetles. Furthermore, these results limit the applicability of the well-known barcoding gap, in ecological studies.

With regards to taxonomic problems, mitochondrial and nuclear DNA sequences can provide support for taxonomic decisions. For example, the two taxa *Carabus variolosus* and *nodulosus* are characterized predominantly by K2P values lower than the barcoding gap. In view of the otherwise strong intraspecific differentiation within the genus *Carabus*, these two taxa should be regarded as subspecies. In contrast, DNA barcoding can also help to identify “good” species. Mitochondrial and nuclear data suggest, for example, that an *Oreonebria* taxon and a *Platycarabus* taxon from the South-western Alps represent “good species”, although they were usually considered as synonyms or subspecies. In another case, two tiger beetle taxa, which until a few months ago were considered to belong to the same species, show such strong differentiation that only two species can be postulated (*Calomera aulicoides* and *C. littoralis winkleri*).

In summary, we can state that DNA sequences and the barcoding gap can help to define species delimitations in ground beetles. However, several species, including widespread sister species, cannot be identified by DNA barcoding for various reasons (e.g. young species or horizontal gene flow). Consequently, until an automated, fast, and reliable method to identify species from samples emerges, ecological investigations have to rely on classical, morphology-based identifications.

Keywords

DNA barcoding, metabarcoding, species identification, species delineation, species delimitation, taxa, automated species identification, barcoding gap, molecular taxonomy, Carabidae, *Graphipterus*, *Calomera*, *Carabus*, *Platycarabus*, *Oreonebria*, *Cicindela*

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