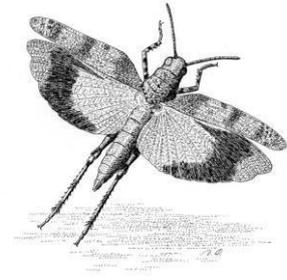


# Forschungsförderung der DGfO



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## Gefördertes Projekt:

Barcoding of Mediterranean grasshoppers

## Abstract

The Mediterranean is a global biodiversity hotspot with more than 400,000 known species and an endemism rate of 60%. The area served as the most important Western European refuge for warm adapted species during the Pleistocene, promoting speciation processes through isolation at various peninsulas. The high species richness was further promoted and is maintained by the heterogeneous landscape structure of the Mediterranean.

The Mediterranean is a particularly important area for European Orthoptera, as almost all families of the order show high numbers of species and endemics in the region. Even though Mediterranean Orthoptera have been well studied in the past, new species are still discovered. Modern methods, like genetic and genomic analyses, enable the differentiation of cryptic species. Tools like DNA barcoding allow the investigation of taxa without any previous taxonomic knowledge. For this a 600 bp long fragment of the COI gene is sequenced and curated in large public databases. Even though it's a criticized method in some taxa, it remains a useful and frequently used method in others and therefore has to be tested in grasshoppers.

Up to now, more than 1.3 million records are listed in BOLD (Barcode of Life Database), more than 46,000 of which represent Orthoptera. Only 23,519 of those are identified, belonging to 3,239 species from 112 countries. A total of 29,260 valid species of grasshoppers are listed in the public database OSF (Orthoptera Species File), more than 2,400 of which are known from the Mediterranean. Even though the number of already sequenced species of grasshoppers is relatively high, using DNA barcoding within the order remains controversial. Some studies on Central European grasshoppers show high rates of differentiation in most families. However, the family Acrididae remains poorly resolved. A similar outcome was shown for Acridids from Algeria. Studies of further geographic areas are mostly lacking. Potential reasons are the large genome size with potentially high rates of pseudo-genes (numts) and further, incomplete lineage sorting in some

younger lineages. Yet, also the completeness and accuracy of the databases remains a problem as relatively few species, especially from diverse regions such as the Mediterranean, have been sequenced and some entries rely on false identifications.

Hence, in this project we want to investigate the resolution of the barcoding fragment for more than 300 Mediterranean grasshopper species. We plan to barcode 5 to 10 specimens of each species from a broad geographic distribution to quantify the resolution of the COI fragment at different geographic and taxonomic levels and build a database of all sequences as a project within BOLD.

This project will help to gain more visibility and knowledge of the usage of COI data for species identification/differentiation in grasshoppers and will contribute to building a public database serving the scientific community to work on grasshoppers.