

## Barkodiranje faune komaraca Hrvatske Croatian mosquito fauna barcoding

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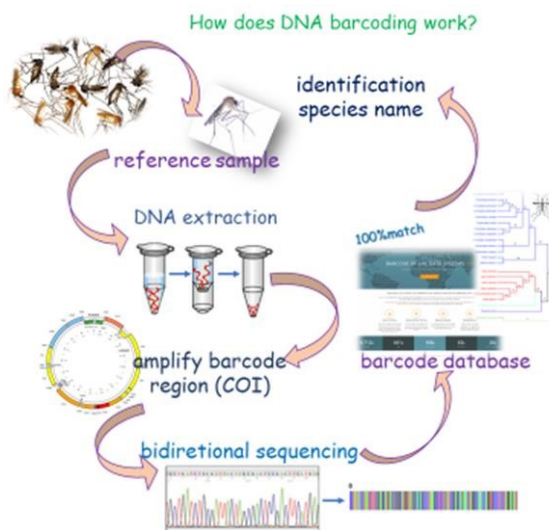
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The mosquitoes (*Culicidae*) represent a frequently investigated group of insects within the order (*Diptera*) precisely because they are human and animal disease vectors. Mosquito identification is therefore a key step in developing vector control strategies. To achieve more precise identification, morphological methods should be complemented with molecular methods of identification. DNA barcoding is a worldwide method of biodiversity recognition and the world's base is continually being supplemented. Currently, the most commonly used barcode region is a 50-segment of the mitochondrial gene Cytochrome Oxidase I (COI). DNA based identification makes it possible to use sequence data in order to determine the species and their sub-species. Fifty-three species of mosquitoes have been recorded in Croatia so far. Determining the genetic status of this

insect group will be of great taxonomic, phylogenetic and phylogeographic importance since Croatia stands out for its diversity of habitats that affect genetic diversity. During the project "DNA Barcoding of the Croatian Fauna" mosquitoes were sampled from the continental, alpine and Mediterranean regions of Croatia in the mosquito seasons of 2017. and 2018. Within the sampled mosquitoes twenty-four species have been determined and molecularly identified. We expect that by the end of this project we will have conducted DNA barcoding of as many species in Croatia. We intend to find cryptic and sibling species in the field (such as *Anopheles maculipennis* complex and *Culex pipiens* complex) to resolve genetic similarity. The results of this project will provide more knowledge about genetic diversity in relation to geographical distribution. Also, these results will contribute to complementing the world's DNA base (BOLD and NCBI).

*Keywords: species, mosquito identification, DNA barcoding, genetic diversity, species complexes*