



**INTERNATIONAL CONGRESS ON THE ZOOGEOGRAPHY AND  
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**ABSTRACTS**



## To meet modern taxonomical approach: developing molecular tools using short mitochondrial fragments from archival specimens

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Biodiversity protection, preservation and inventorization are leading concepts in modern biology. However, species identification and precise recognition of taxa still remain the key problems in basic and applied studies. It is indisputable that during the last 250 years, traditional taxonomy accumulated knowledge that was incorporated into every aspect of current research of biodiversity. Thus, current taxonomy is based exclusively on the typological species concept, following the International Codes of Nomenclature (Zoological, Botanical, Bacteria, etc.). Barcoding initiative lent insight into potentials of molecular methods to provide better taxonomic resolution in species recognition efforts. This is especially true after declining number of traditional taxonomic practitioners in past 30 years, which launched the molecular tools application in species characterization as a certain approach in future studies.

If we consider determination of any organism at the species level to be primarily based on traditional taxonomic methods, applying molecular methods to define genetic content of barcoding region (mtCOI gene) of archived type specimens should be treated as a method of choice for precise identification. Heaving in mind that DNA in archived specimens is usually more or less defragmented at a certain degree, employing methods of PCR amplification and sequencing of short mitochondrial fragments may lead to clarification of nomenclatural doubts accumulated in the past. In addition, the use of prior genetic information to identify short phylogenetically informative amplicons offers a useful approach for molecular phylogenetic analyses especially when *de novo* collected material is not available or feasible.

**Keywords:** barcoding region, short mitochondrial fragments, archived type specimens, molecular phylogeny