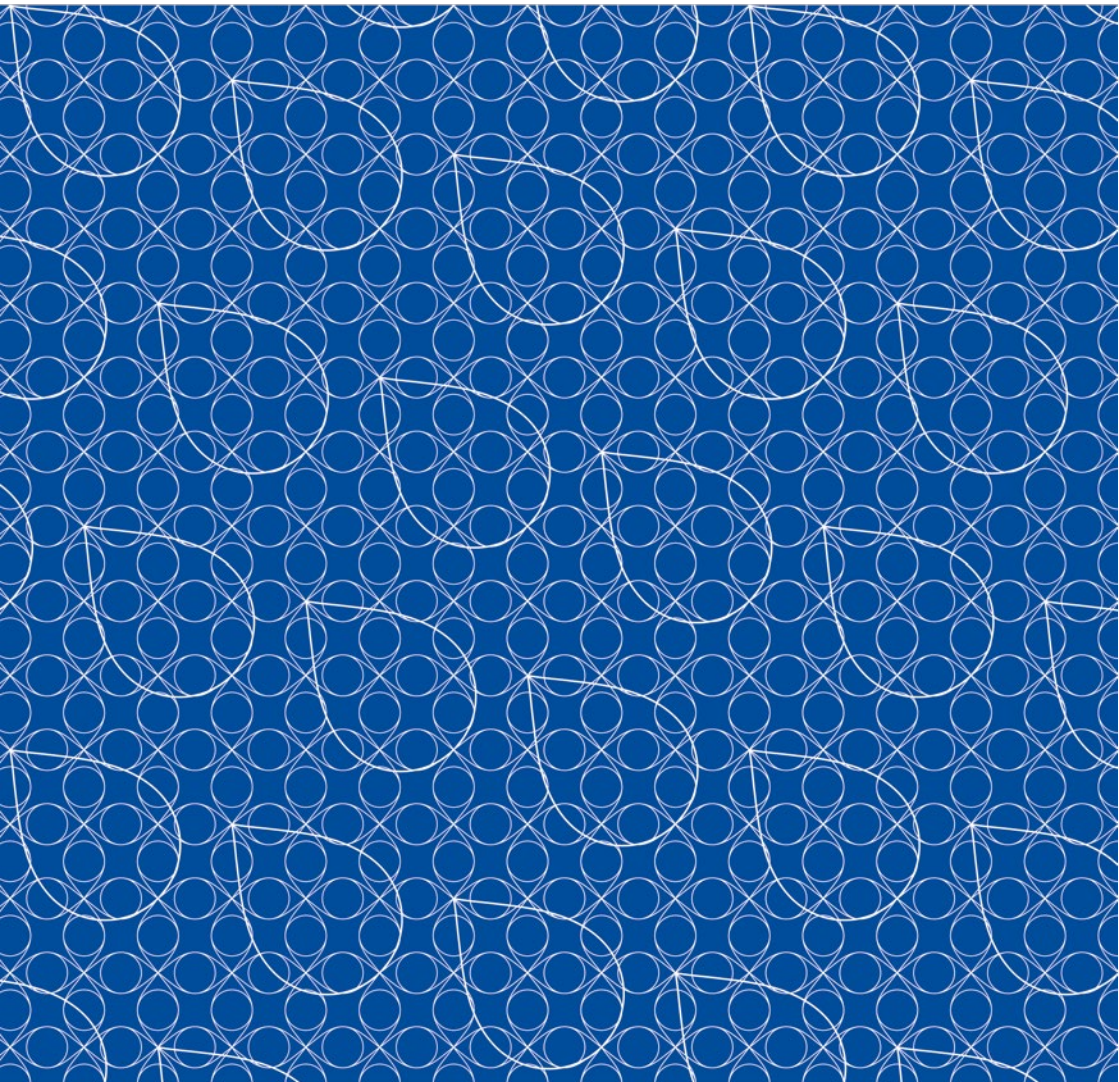


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ABSTRACT BOOK

HOW MUCH CAN ENVIRONMENTAL DNA (EDNA) REFLECT A LOCAL MACROINVERTEBRATE COMMUNITY IN A LOTIC SYSTEM?

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Recent developments in the use of molecular techniques for bio-assessment has led to a revolution in the way we can monitor aquatic systems. Current methods of monitoring macroinvertebrates in freshwater rely heavily on the capture or sighting of the target species, followed by correct taxonomic identification, which is not always possible. This is particularly true when referring to invasive alien species (IAS) which can be cryptic, in low density or in juvenile stages. This makes eDNA a particularly interesting complimentary tool when assessing macroinvertebrate communities and as an early warning system for new IAS. However, little is known about how molecular methods compare to established methods in lotic systems. Here we demonstrate the findings of a series of field experiments comparing established sampling techniques (kick samples) with molecular samples, namely - DNA “smoothies”, eDNA water and eDNA sediment samples.

DIVERSITY OF SOUTH AMERICAN RIFFLE BEETLES (COLEOPTERA: ELMIDAE) EXPLORED USING DNA BARCODES

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South America, and mostly its tropical Amazonia, is with no doubt an area with extraordinary high level of biodiversity. Beside the fact that its biota is the object of interest for biologists from around the World already for a long time, new species are still being discovered every day. The same situation is in the family Elmidae, a group of small beetles inhabiting various lotic habitats. Since the elmids are strictly aquatic and long-lived, spending (with few exceptions) whole life submerged, they form an important component of benthic macroinvertebrate communities, and can serve as good indicators of long-term ecological changes. Unfortunately, if compared with e.g. mayflies or caddisflies, little attention is paid to this group of aquatic insects. At present, slightly more than 1.500 species are known in the family, from which around one third inhabits streams and rivers in South America. Until recently, all descriptions of the new taxa (species, genera) were based exclusively on morphological characters. During our biodiversity research project (2011-2014), we have sampled small areas (in respect to the whole Amazonia) in Venezuela and Ecuador, and collected fresh and ample material, which is now being processed. But, it is for the first time for South American elmid fauna, that except morphology, also DNA barcodes are employed. Even our research is at the beginning, the first data gained reveal distinct advancement in describing the real diversity of the studied family.

In this work we analysed samples from several selected genera from both subfamilies, Larinae and Elminae, and here we present examples of how molecular data improved our knowledge on the taxonomy of Elmidae of South America. In the genus *Onychelmis* Hinton, 1941, which included 3 morphologically extremely similar known species we identified 5 new species; in the genus *Notelmis* Hinton, 1941, which had 2 known species, we identified 4 new species; in *Neblinagena* Spangler, 1985 we identified 2 new species. Beside discovery of the new species, the DNA barcodes allowed us to suggest paraphyly of several genera (*Neoelmis* Musgrave, 1935, *Gyrelmis* Hinton, 1940, *Neblinagena* Spangler, 1985, *Xenelmis* Hinton, 1936).

LANDSCAPE FEATURES AND SPECIES' INTRINSIC TRAITS SHAPE THE CONTEMPORARY PATTERNS OF GENETIC DIVERSITY OF PORTUGUESE ENDEMIC CYPRINIDS

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Over 68% of the native Iberian cyprinid species are currently highly endangered. Management and conservation actions should ideally be planned taking into account the genetic diversity shown by different populations of a given threatened species, reliable taxonomical identifications (including the detection of cryptic hybrids) and contemporary drivers of gene pool depletion. In this context, a broad genetic survey was conducted in the Portuguese hydrographical network (all the 34 river basins and 47 sub-basins), covering a total of 188 populations belonging to 16 cyprinid species of *Squalius*, *Luciobarbus*, *Achondrostoma*, *Iberochondrostoma*, *Anaocypris* and *Pseudochondrostoma*. The analysis of over 3,600 cytochrome b gene sequences revealed differences among populations from the same species and between species with identical distribution areas. Factors shaping the contemporary patterns of genetic diversity were explored and the results revealed the role of latitude, inter-basin connectivity, migratory behaviour, species maximum size, species range and other species intrinsic traits in determining the genetic diversity of sampled populations. Species intrinsic traits, maximum size attained, inter-basin connectivity and latitude explained over 30% of the haplotype diversity variance and, generally, the levels of diversity were significantly higher for smaller sized species, from connected and southerly river basins. Thus, contemporary determinants of genetic diversity (species' intrinsic traits and landscape features) are likely more important than historical factors, with strong implications for species conservation, in a context of climate change and highly disturbed fluvial habitats.

DNA BARCODING OF AQUATIC MACROINVERTEBRATE FAUNA OF SLOVAKIA – FIRST INSIGHT

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Water quality monitoring and biodiversity assessment of the European fresh waters is currently realized in terms of the EU-Water Framework Directive (WFD, 2000/60/EC) and it is based on morphological identification of freshwater taxa. Novel approaches and initiatives (e.g. DNAqua-Net) lead to future implementation of the modern genomic tools in bioassessment of European water bodies. Essential for achieving this milestone is existence of comprehensive databases of DNA data for freshwater taxa present in European waters. Reference barcode libraries of all main freshwater groups of organisms are built within several national DNA-barcoding campaigns. But, there are still countries where such activities are only starting or are not at all. In terms of accession to the EU and implementation of WFD, first detailed check-list of all macroinvertebrate taxa recorded from Slovak Republic was elaborated in 2003. The check-list comprises 1700 macroinvertebrate species present in Slovakia, and after several years of monitoring surface waters, following the WFD methodology, cca 50 additional species were included. Presently, together with sporadic new records and unknown cryptic species, there could be more than 2000 macroinvertebrate taxa present in the Slovak fresh waters.

However, the coverage of the Slovak aquatic fauna by DNA barcodes is very poor. Within the BOLD (The Barcode of Life Datasystem) database, there are only 165 public records of aquatic invertebrate taxa collected in Slovakia covering up to 60 OTUs (end of 2016), and bulk of them (95 %) represents older records mined from the GeneBank (NCBI). Considering these gaps and following the goals of the WG1 (“DNA Barcode Reference Databases”) of the “DNAqua-Net” COST Action, since 2016 our laboratory started to built reference barcode library of Slovak Aquatic Fauna. Presently we focus on the Slovak fauna of aquatic beetles and caddisflies. Primarily we started with collecting data from the alpine lakes and from the carstic springs, and here we present the preliminary data.

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