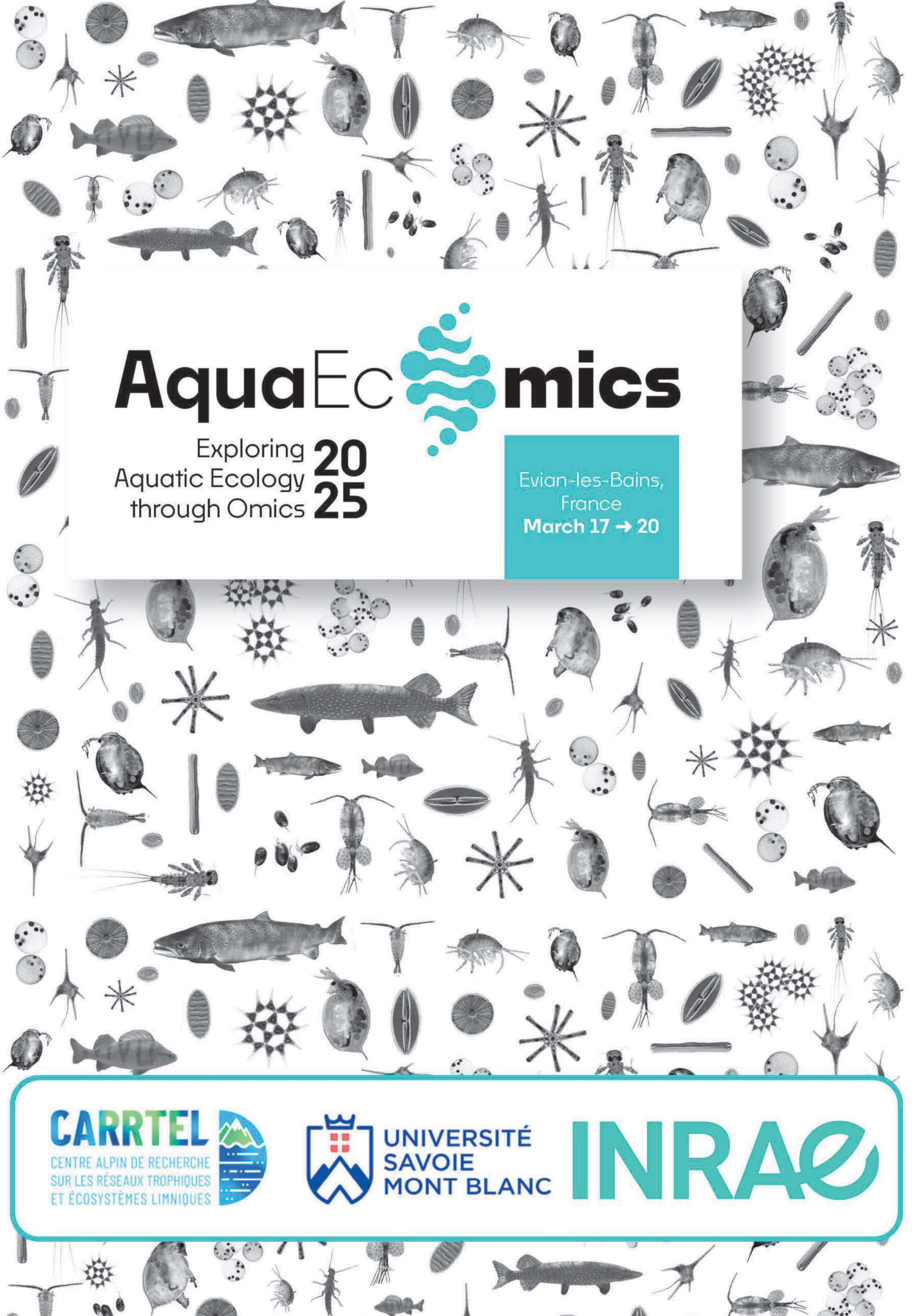

AquaEcomics

Exploring
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2025

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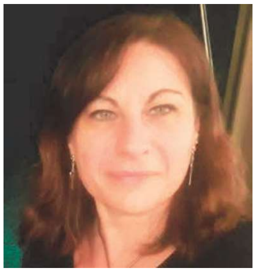
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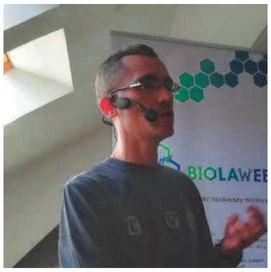
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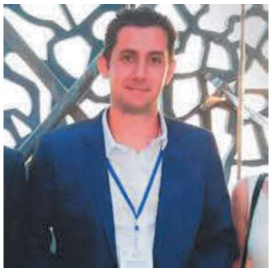
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SCIMABIO Interface

Environment Agency, Germany), Florian Leese (University of Duisburg-Essen, Germany), Astrid Schmidt-Kloiber (University of Natural Resources and Life Sciences, Vienna , Austria), **Arne J. Beermann** (University of Duisburg-Essen, Germany)

Identifying specimens to species or higher taxonomic level is a key component of biological monitoring. In recent times, species identification has been facilitated through high-throughput genetic methods, in particular DNA metabarcoding. One key aspect, that limits direct comparability of data and in particular hampers the defensibility of the results as part of regulatory monitoring tasks are uncertain taxonomic assignments via reference sequence databases. While these should ideally be complete, open, well-maintained, curated and updated continuously, they often lack quality assurance of taxonomic annotations. Existing solutions to this problem are researchers, industry and agencies creating their own, often closed reference databases. This is highly problematic as in closed databases the direct comparability of data sets is limited, and by this the key advantage of (meta)barcoding as a simple comparable, open tool gets lost. In view of the problematic situation and the need to also formally implement metabarcoding into regulatory monitoring programs, authoritative reference databases that are compiled according to community standards, have a version number, quality control and are maintained over time are needed. The ultimate goal of the dbDNA project was developing a system that aids in achieving robust taxonomic annotations when using DNA (meta)barcoding. The strategy reaching that goal is twofold, creating a pipeline that allows for grading individual sequences deposited in reference libraries as well as using graded references sequences to generate curated lists of reference sequences. The backbone of the developed pipeline are criteria for robust taxonomic annotations worked out by experts in two workshops. We will introduce the developed pipeline and criteria in detail and demonstrate the effectiveness of the approach on an existing taxa list for monitoring freshwater invertebrates in Germany.

O107. Challenges in the investigation of the diatom community of saline habitats: A case study of Plava Banja (Serbia)

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Plava Banja is an artificial saline lake in Vojvodina province (Serbia). It was formed during clay excavation by a local company, later abandoned and covered with gravel. In 2023, 12 diatom samples were collected during three seasons of sampling (spring, summer, and autumn) from reeds and artificial bricks. Two approaches were used to analyze the samples: traditional microscopic analysis and high-throughput sequencing (HTS) of the rbcL gene. This study aimed to see a difference in diatom diversity between these two approaches. In parallel with the analysis of the diatom community, physicochemical analyses of the water were also carried out. Plava Banja is characterized by elevated concentrations of sulfates, chlorides, alkaline pH, and high conductivity values. Around 55 taxa are recorded by microscope, and 82 taxa with molecular analysis. According to both analyses, *Nitzschia* was one of the most represented genera across the samples, but with mostly unassigned sequences. Traditional microscopic analysis showed higher diversity within the genus *Craticula* than molecular analysis. Out of 7 *Craticula* taxa identified by a microscope, two were recorded as dominant through seasons: *Craticula aff. simplex* (relative abundance 2.66 – 90.68%) and *Craticula aff. halophila* (relative abundance 0.24 – 36.65%). According to molecular data, only one Craticula ASV is noticed. The second significant discrepancy in diversity was observed among the genus *Navicymbula*. Three *Navicymbula* taxa (*N. pusilla*, *N pusilla* var. *lata*, and *Navicymbula sp*.) were recorded in Plava Banja by microscope. However, none of the obtained sequences were assigned to the genus *Navicymbula* because this genus is not included in any rbcL reference database. All three *Navicymbula* identified under the microscope were noticed in the same samples with different relative abundance (*N. pusilla* 1.24–24.34%, *N pusilla* var. *lata* 0.49–10.87% and *Navicymbula sp.* 0.25–14.80%).

O108. eDNA-based assessment of phytoplankton community structure and dynamics in a saline lake in Serbia: comparison with microscopy-based method

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Continental saline lakes are among the most endangered aquatic ecosystems, as a result of intensifying human pressures. However, these ecosystems are home to remarkable biodiversity that performs important ecological functions. Our understanding of the structure and development of their biological communities, such as phytoplankton, remains limited, hindering efforts to preserve the biodiversity of these fragile habitats. A significant challenge in studying these communities is the dominance of small-cell size plankton (e.g. picoplankton) that is underrepresented when assessment relies solely on microscopy. However, coupling a high-throughput sequencing method with a DNA metabarcoding approach provides access to this hidden phytoplankton diversity. The aim of our study was to use DNA metabarcoding (targeting 23S rRNA gene) and microscopy methods to study phytoplankton in a saline lake in Serbia. The samples were collected from four different sites within lake Pečena Slatina during spring, summer, and autumn 2023 to study the spatiotemporal dynamics of the community. A large difference between the two inventory lists (microscopy and metabarcoding) was