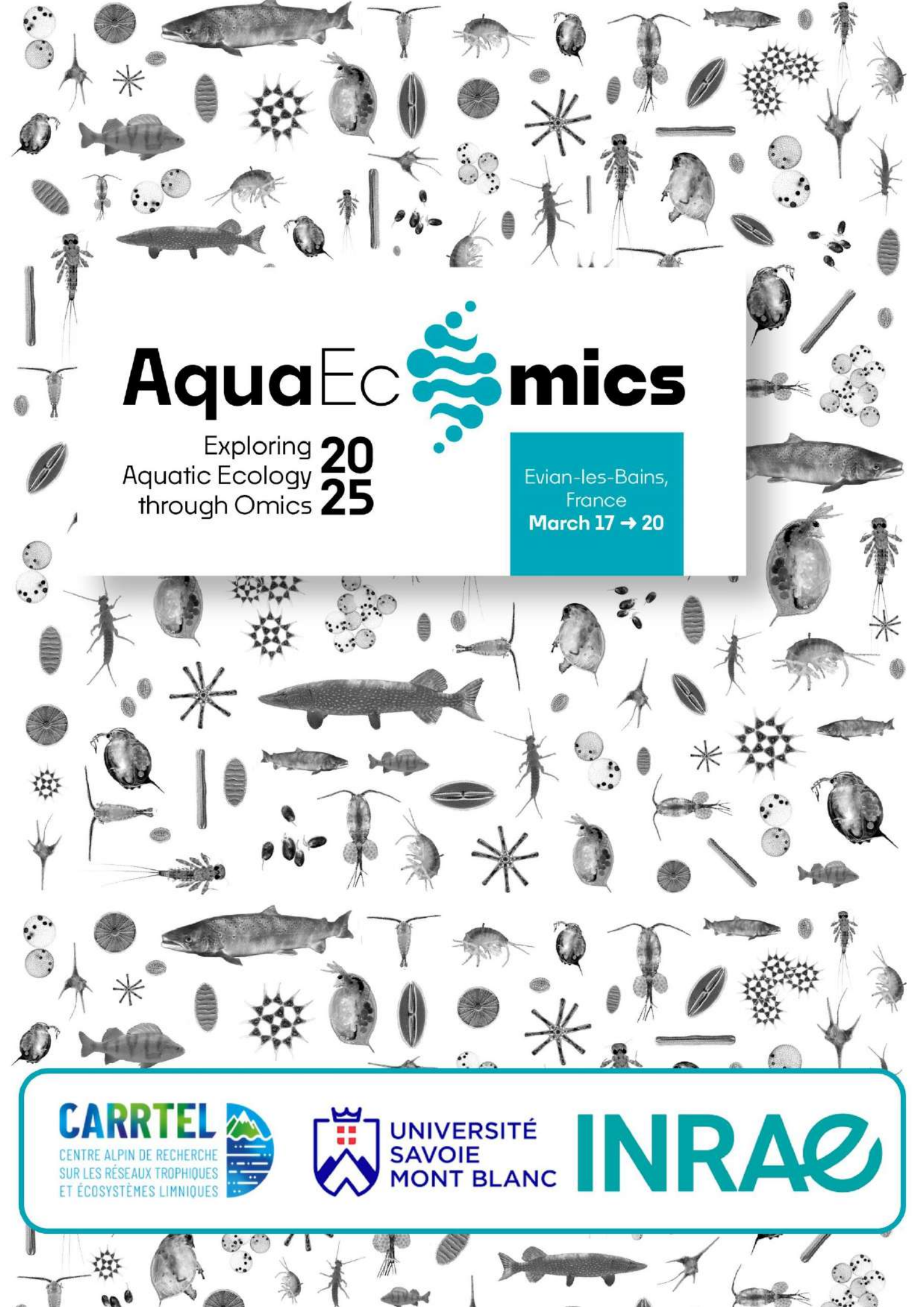

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CARRTEL
CENTRE ALPIN DE RECHERCHE SUR LES RÉSEAUX TROPHIQUES ET ÉCOSYSTÈMES LIMNIQUES

UNIVERSITÉ SAVOIE MONT BLANC

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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

Kristina Petrović (University of Belgrade, Institute of Chemistry, Technology and Metallurgy - National Institute of the Republic of Serbia, Department of Chemistry, Belgrade, Serbia), Clarisse Lemonnier (UMR CARRTEL, INRAE, Savoie-Mont Blanc University, Thonon-les-Bains, France), Benjamin Alric (UMR CARRTEL, INRAE, Savoie-Mont Blanc University, Thonon-les-Bains, France; Pôle R&D ECLA Ecosystèmes Lacustres, France), Andreas Ballot (Norwegian Institute for Water Research – NIVA, Oslo, Norway), Frédéric Rimet (UMR CARRTEL, INRAE, Savoie-Mont Blanc University, Thonon-les-Bains, France; Pôle R&D ECLA Ecosystèmes Lacustres, France), Jelena Avdalović (University of Belgrade, Institute of Chemistry, Technology and Metallurgy - National Institute of the Republic of Serbia, Department of Chemistry, Belgrade, Serbia), Srđan Miletić (University of Belgrade, Institute of Chemistry, Technology and Metallurgy - National Institute of the Republic of Serbia, Department of Chemistry, Belgrade, Serbia), Željka Milovanović (University of Belgrade, Institute of Chemistry, Technology and Metallurgy - National Institute of the Republic of Serbia, Department of Ecology and Technoeconomics, Belgrade, Serbia), Vladimir Petrović (University of Belgrade, Institute of Chemistry, Technology and Metallurgy - National Institute of the Republic of Serbia, Department of Ecology and Technoeconomics, Belgrade, Serbia), Miloš Ćirić (University of Belgrade, Institute of Chemistry, Technology and Metallurgy - National Institute of the Republic of Serbia, Department of Chemistry, Belgrade, Serbia)

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

observed. The metabarcoding approach yielded 344 ASVs, of which 156 were assigned to the genus level, and overall, 70 taxa were detected in eight phyla. On the other hand, 26 taxa belonging to four phyla were detected by microscopy. Both methods captured spatial and temporal variation in the phytoplankton community, but a better resolution was obtained by metabarcoding. During summer, coccal small-sized cyanobacteria dominated, while in autumn samples, filamentous Cyanobacteria such as Arthrospira and Anabaenopsis prevailed, both in terms of biomass and the number of reads. Spring samples showed a large discrepancy between the two methods: diatoms were the most frequently counted organisms, while the metabarcoding showed the codominance of euglenoids and cyanobacteria, but with a great percentage of unassigned reads in this season. The findings suggest that while metabarcoding can assess biodiversity in greater detail than microscopy, its effectiveness is currently constrained by gaps in reference barcoding library. Despite these limitations, it still provides a more comprehensive method for evaluating diversity compared to microscopy alone.

O109. MSFD and impact monitoring with eDNA: Insights from case studies in the Belgian Part of the North Sea and Avlékété Beach, Benin

Dukan Nergiz (ILVO, Belgium), Geldhof Ruben (Jan De Nul Group, Belgium), Van Acker Jonas (Jan De Nul Group, Belgium), Cornelis Isolde (ILVO, Belgium), De Backer Annelies (ILVO, Belgium), Van Hoey Gert (ILVO, Belgium), Sohou Zacharie (IRHOB, Benin), Yaovi Zounon (IRHOB, Benin), Midinoudewa Houangninan Emmanuel (IRHOB, Benin), Sofie Derycke (ILVO, Belgium)

With increasing anthropogenic impacts and changing climate conditions, monitoring biodiversity in marine ecosystems has become critically important. eDNA is a cost-effective and non-invasive monitoring method, but a standardized framework for reporting and storing eDNA results is currently lacking and the resulting species list highly depends on the available reference database. We demonstrate this with eDNA data from two use cases. The Belgian part of the North Sea (BPNS) is a highly exploited area, and monitoring for the Marine Strategy Framework Directive (MSFD) currently involves morphological datasets. Fish species in the area are well studied and an extensive barcode reference database exists. We reconstructed the spatial patterns of fish communities with eDNA, demonstrating a strong alignment with the long-term trawl monitoring data. This opens up the debate on how to use eDNA for MSFD reporting. The second case study – in collaboration with the dredging company Jan De Nul- uses eDNA to study the impact of a submerged breakwater parallel to the shore - constructed to prevent beach erosion and to create a safe swimming area - on fish communities near Avlékété, Benin. Fish diversity data were collected through examining fishing nets of local fishermen. We developed a custom 12S reference database using local fish fin clips and available reference sequences from NCBI. Among the 50 species detected morphologically, 28 were not detected with eDNA. Of these, only nine had available 12S reference sequences. Taxonomic identification revealed many Pacific species assignments, likely indicating that species in the area have highly similar sequences with their non-native relatives. Despite a reasonably good fish inventory in the Gulf of Guinea, the barcode database remains insufficient for fully representing marine fish diversity of the area with eDNA. These comparative studies underscore the importance of consistent barcoding efforts for developing cost-effective monitoring programs.