

Abstract Book





Organization



Committee



Regular Sessions (RS)

RS01 - Biogeochemistry	10
RS02 - Pollution and contamination of inland water ecosystems	20
RS03 - Planktonic communities	47
RS04 - Benthic communities	74
RS05 - Fish and fisheries	89
RS06 - Food Webs	105
RS07 - Multiple stressors on ecosystems	112
RS08 - Biodiversity conservation	132
RS09 - Restoration ecology	139
RS10 - Ecosystem services	145

Special Sessions (SS)

SS01 - State and Trends Of Latino-America Freshwaters	149
SS02 - Tropical floodplain lakes: ecological and hydrological processes	154
SS06 - From local to global water quality assessment with remote sensing	156
SS07 - Coupling remote sensing, modelling and in situ monitoring to support lentic ecosystems management: targeting lakes and reservoirs from Global South countries	163
SS08 - Mathematical Modeling in Limnology: Present and Future	168
SS09 - Deciphering Human- and Climate-Driven Impacts on Lakes using Paleolimnological Studies	177
SS10 - Landscape limnology	184
SS11 - Land-Use Changes on Neotropical Streams: Impacts and Scientific Advances	187
SS12 - Greenhouse gases emission and carbon sequestration in aquatic ecosystems: Unraveling drivers, magnitude and uncertainties	192
SS13 - Cyanobacteria; Nutrients; Control: from Science to Management	198
SS14 - Lake restoration - controlling eutrophication	209
SS15 - Ecosystem structure and function along the saline continuum: from freshwaters to hypersaline inland waters	218
SS16 - Challenges of Aquatic Biodiversity and Conservation Strategies in Mined Environments: Exploring Impacts and Pathways to Recovery	221
SS17 - Contributions from the Brazil-LTER /PELD and REC-Rio Doce projects to the restoration of the Rio Doce basin, Southeast Brazil: A Legacy	223
SS18 - Aquatic metacommunities: diversity patterns, assembly processes, spatial scales, and network connectivity	225
SS19 - The relevance of ponds ecosystems for the biodiversity and society in the context of global changes.	231
SS20 - The phytohelminths as aquatic ecosystems	240
SS21 - Ecology and conservation of temporary aquatic ecosystems	243
SS22 - Challenges and opportunities for implementation of the global freshwater biomonitoring agenda	250
SS23 - Homogenocene and Anthropocene in inland waters	252
SS24 - Plankton diversity in face of anthropogenic changes	253
SS25 - South American Spatially Extensive Biological Assessments: Gaps & Opportunities	261
SS27 - Advancing and implementing environmental DNA and RNA methods for assessing, monitoring and managing freshwater ecosystems	265
SS29 - Non-native taxa in freshwater ecosystems	268
SS31 - Scientific and societal challenges of macrophyte decline and recovery in inland waters	275
SS32 - Environmental education and outreach	279
SS33 - Resilience Capacity (Adaptation and Transformation) of Water Management and Governance Systems	283
SS36 - Eutrophic Waters Restoration by Biomanipulation of Aquatic Animals	286

Authors Index



Welcome to SIL 2024



After almost 30 years, Brazil is once again hosting a **SIL International Congress on Limnology**. As a historical indigenous land, Latin America and the Caribbean are blessed with incredible water resources and breathtaking landscapes! However, the fragmentation of the indigenous people and water bodies across the continent has led to scientific and economic inequalities with serious consequences for biodiversity conservation.

The diversity of water bodies in Latin America and the Caribbean is as great as their indigenous people and their culture, which are fully connected to the water. For these people and their descendants, freshwaters are considered a holy ground, a gift supporting the dignity of their people and ancestors. These characteristics make Brazil a relevant site to host this global Limnology event.

Therefore, in 2022, limnologists from 18 countries came together to reduce such distances and borders, in an effort to restore part of the connections between people and waters over these incredible territories!

The theme for the 37th SIL Congress is **“Building bridges between science and society to reduce the effects of fragmentation and degradation of inland waters”**. By bringing together researchers, policymakers, and stakeholders, it aims to reconcile the multiple uses of the water with the challenges for conservation in the face of climate change and human pressures. In this regard, the main issue we want to address is the legacy that we will need to leave in a fragmented world, where indigenous and non-indigenous people need to work together for a sustainable land.

In Brazil, indigenous people say “Never again a Brazil without us”. After the 37th SIL we expect to address this claim, indicating that the world needs to break the barriers between science and society to reduce impacts under the water resources over the world. This is the greatest challenge and certainly will be a legacy for the next generations.

To maintain and restore our water resources, we will need to work together on a common path! This conciliation embraces the challenges that the global south scientists and societies have been facing to sustain water bodies conservation. This challenge permeates the history of limnology in Latin America and the Caribbean and represents an excellent opportunity to meet developed and developing countries in bilateral and mutual support.

Join us for SIL 2024, May 5-9! Brazil, Latin America and the Caribbean are waiting for you! Let's make the world an indigenous land again!

Luciana Barbosa

President of Brazilian Limnology Association and Leader of Latin American and Caribbean Limnology Network and Chair SIL 2024

ORGANIZING COMMITTEE

General coordination:

Elaine C. R. Bartozek
ABLimno - Foz do Iguaçu/Brazil
coordination@sil2024.org

Cleto K. Peres
Unila - Foz do Iguaçu/Brazil

Anderson Coldebella
IFPR - Foz do Iguaçu/Brazil

Vanessa Neres
Indigenous people/Brazil

Andre Luis Caetano
Indigenous people - State school Fág Kavá/Brazil

Patrícia Iatskiu
Unioeste - Cascavel/Brazil

Margaret S. Nardelli
Unioeste - Cascavel/Brazil

André A. Padiál
UFPR - Curitiba/Brazil

Richard W. Lambrecht
Universität Konstanz - Germany/Brazil

Gisele C. Marquardt
UFPR - Curitiba/Brazil

Ênio Wocylí Dantas
UEPB - João Pessoa/Brazil

INTERNATIONAL

Esteban Balseiro (*Argentina*)

Eduardo Vicente (*Spain*)

Jesus Delegido (*Spain*)

Jose Galizia Tundisi (*Brazil*)

Franco Teixeira (*Uruguay*)

CHAIRS

Luciana Gomes Barbosa
General Chair

Elaine Bartozek
Chair of Organizing Committee

José Luiz Attayde, Nestor Mazzeo
and Susie Wood
Chairs of Scientific Committee

Franco Teixeira and Esteban Balseiro
Chairs of Latin American and Caribbean Committee

Jeymmy Walteros
Chair of Women Committee

Carlos Lopez
Chair of Scientific Communication

José Galizia Tundisi
Chair of National Articulation

LATIN AMERICAN AND CARIBBEAN COMMITTEE

General coordination:
Franco Teixeira de Mello (*Uruguay*)

Eugenia López-López (*Mexico*)

Esteban Balseiro (*Argentina*)

Gerardo Umaña Villalobos (*Costa Rica*)

Gregorio A. López Moreira Mazacotte (*Paraguay*)

Jorge Jose Garcia Polo (*Guatemala*)

Nelson Aranguren Riaño (*Colombia*)

Marcela Matamoros (*Honduras*)

Margaret Dix (*Guatemala*)

Carla Fernandez Espinoza (*Bolivia*)

Ernesto Gonzalez (*Venezuela*)

Miriam Stenitz-Kannan (*Ecuador*)

Patricio R. De los Rios-Escalante (*Chile*)

Ruth H. Bastardo (*Dominican Republic*)

Iris Samanez (*Peru*)

Belgis Chial Zambrano (*Panama*)

Orlando Rolando Laiz Averhoff (*Cuba*)

Eugenia López-López (*Brazil*)

SCIENTIFIC COMMITTEE

Coordinators:
José Luiz Attayde
Federal University of Rio Grande do Norte/Brazil

Nestor Mazzeo
University of República de Uruguay/Uruguay

Suzie Wood
Cawthron Institute, University of Canterbury/New Zealand

North America
Joshua Thienpont
York University/Canada

Elizabeth Walsh
University of Texas/USA

Latin America
José Luiz Attayde
Federal University of Rio Grande do Norte/Brazil

Carla Olmo
Girona University/Chile

Irina Izaguirre
Buenos Aires University/Argentina

María de los Ángeles González Sagrario
CONICET/Argentina

Nestor Mazzeo
University of República de Uruguay/Uruguay

Asian
Egor Zaderev
Central European University/Russia

Oceania
Alisha Steward
Griffith University/Australia

David Hamilton
Griffith University/Australia

Suzie Wood
Cawthron Institute, University of Canterbury/New Zealand

Europe
Erik Jeppesen
Aarhus University/Denmark

Antonio Camacho
València University/Spain

Zsófia Horváth
Institute of Aquatic Ecology/Hungary

Manuela Morais
University of Évora/Portugal

Verónica Ferreira
University of Coimbra/Portugal

SS27 - Advancing and implementing environmental DNA and RNA methods for assessing, monitoring and managing freshwater ecosystems

1498

Having IMPACT on monitoring aquatic parasite diversity – presenting a new pipeline evaluating eDNA as an integrative tool for studying parasites

KAMIL HUPALO¹; Daniel Grabner¹; Florian Leese¹; Rachel Paterson²; Bernd Sures¹;

Parasites are usually presented as biological villains due to threats posed to human health and wildlife conservation. However, most metazoan parasites have no zoonotic potential and are instead known to be crucial organisms that contribute to the health and functioning of ecosystems and make up an overwhelming proportion of current biodiversity. Nonetheless, parasites remain the most neglected components of biodiversity monitoring and management strategies, and have only recently begun to be considered in conservation discussions. Monitoring of parasite biodiversity is hampered by inefficient tools for detecting parasites, with current methods involving the sacrifice of many hosts to quantify parasite biodiversity, and still, parasites occurring in low prevalence may be difficult to detect. Thus, for ethical reasons and amid a potential 6th mass species extinction, it is necessary to develop less invasive and non-lethal monitoring methods. Environmental DNA (eDNA) offers a potential solution, particularly for studying aquatic parasites by allowing them to be monitored in environmental matrices without the need to sacrifice hosts. Recent literature reviews show that eDNA has proven useful in the detection of single parasite species. However, very few studies targeted multiple parasite species within and across defined parasite groups at once. Given that eDNA is increasingly used in aquatic biodiversity monitoring worldwide, it offers a great opportunity for obtaining parasite diversity data in existing monitoring programs. Here, we present a methodological pipeline for the simultaneous detection of multiple fish parasite groups using eDNA that will be tested within the framework of the newly acquired project IMPACT.

1645

Application of eDNA metabarcoding to phytoplankton research in freshwater and saline lakes

MILOS CIRIC¹; Claisse Lemonnier²; Benjamin Alric³; Srđan Miletic¹; Jelena Avdalović¹; Biljana Dojčinović¹; Željka Milovanović⁴; Vladimir Petrović⁴; Andreas Ballot⁵; Frédéric Rimet³;

Freshwater lakes have been heavily altered by multiple stressors for decades, including a wide range of harmful human activities. Similarly, it is estimated that most of continental saline lakes will have undergone changes in their functioning by 2025. In the European Water Framework Directive (WFD), the ecological status assessment of lakes is based on the survey of key communities (i.e., Biological Quality Elements, BQEs). Due to its ecological features, phytoplankton is one of the key BQEs required by the WFD. In current assessments, phytoplankton is studied using a standardised microscopy approach. The advent of methods based on molecular techniques (e.g., eDNA metabarcoding) provides an alternative to overcome issues associated with microscopy-based assessment. The aim of our study was to compare phytoplankton data obtained by microscopy approach with eDNA metabarcoding based on the 23S RNA marker gene. Water was sampled in eight sites: four sites in Savsko lake (urban freshwater lake) and four sites in Plava Banja (saline clay pit pond) during spring, summer, and autumn 2023. The water quality analyses showed that nutrient concentrations (especially total nitrogen), chlorophyll a and conductivity were several times lower in the freshwater lake than in the saline lake. The very high total dissolved mineral content in Plava Banja had a substantial impact on the phytoplankton composition. The results of lake species inventories obtained using both approaches will be presented. Particular attention will be paid to the level of congruence between the floristic lists. This study is a part of the EU funded BIOLAWEB project.

SS27 - Advancing and implementing environmental DNA and RNA methods for assessing, monitoring and managing freshwater ecosystems

1663

Evaluation on the use of eDNA metabarcoding in microbial communities as potential bioindicators of ecosystem integrity in a tropical river with anthropogenic pollution gradient.

RICARDO IVAN CRUZ CANO¹; Melanie Kolb¹; Luz Bretón-Deval¹; Martha Martinez¹; Pindaro Diaz-Jaimes¹;

Aquatic bioindicators are a valuable tool that provide insights into various aspects of water quality beyond what physicochemical analysis can reveal, like the ecological status of rivers, and are cost-effective. Microorganisms, including bacteria and protozoa, play crucial roles in nutrient cycling and productivity but have not been used widely as bioindicators because their use requires taxonomic expertise and specialized equipment for organism collection. Environmental DNA (eDNA) can be used to characterize aquatic communities and identify a wide range of microorganisms that are difficult to detect through other methods. This study used eDNA metabarcoding to assess the potential of microbial communities in a tropical river in Mexico City as bioindicators of the ecosystem integrity along a gradient of human influence. Community diversity and abundance of identified groups decreased with increased human influence. In forests and rural sites, bacterial communities are dominated by Cyanobacteria, Planctomycetota, and Verrucomicrobiota, while eukaryotic microbial communities by Diatomea, Cercozoa, and Arthropoda. Urban sites with high human influence show a dominance of Campilobacterota, Fusobacterota, and Firmicutes (bacteria) and Chlorophyta, Ciliophora, and Oligohymnophorea (eukaryotes). This approach can help connect ecological integrity studies with public health implications. The study demonstrated that microbial communities are influenced by human impact and seasonality, making them suitable for biomonitoring.

1861

Diversity of planktonic microeukaryotes by metabarcoding in the Araguaia River floodplain, Brazil

JOCILAINE SANTOS DE JESUS¹; DIEGO ORTIZ DA SILVA¹; CÍNTIA PELEGRINETI TARGUETA²; WALTER ROSA DA CONCEIÇÃO FILHO¹; JOÃO CARLOS NABOUT³; THANNYA SOARES NASCIMENTO¹;

Phototrophic planktonic microeukaryotes are organisms that play a fundamental role in sustaining life on Earth. The diversity and composition of their communities are primarily influenced by the environment, and can be analyzed from three main aspects: alpha diversity, beta diversity, and gamma diversity. The use of NGS tools, such as the molecular technique of metabarcoding, has become common for obtaining diversity and community composition data, due to the precision and effectiveness of the method. Here, we investigate the diversity of planktonic microeukaryotes (phytoplankton) across 121 lakes in the floodplain of the Araguaia River, one of the most important rivers in the Central-West region of Brazil. For this, we sequenced the 18S-V4 gene from water samples collected and filtered with a 0.45µm membrane. The PIMBA pipeline was used for bioinformatic analyses. We calculated alpha, beta (turnover and nestedness) diversity indices, gamma diversity, and the relative abundance of identified Operational Taxonomic Units (OTUs). In total, we obtained 6122 OTUs, of which 4443 could be taxonomically assigned. The total OTU richness was 3293, varying between 1 and 120 OTUs per lake. Shannon diversity ranged from 2.46 to 5.93 across locations, presenting a total richness of 6.04. Simpson diversity varied from 0.71 to 0.99, with a total richness of 0.99. Beta diversity obtained through the Sorensen index (β SOR) was 0.97, and in terms of partitioning, 0.95 was attributed to turnover and 0.01 to species nestedness. The results indicate that the lakes exhibit high turnover, meaning the environments have distinct OTUs.