

Book of Abstracts



LIMNOLOGIA2018

XIX Conference of the Iberian Association of Limnology
Inland waters and XXI century challenges: from scientific knowledge to environmental management
24 – 29 June 2018, Coimbra, Portugal

Welcome to LIMNOLOGIA 2018

Inland freshwaters represent only a minor fraction of total waters of our planet; however they comprise a large variety of systems, including lakes, lagoons, ground waters, streams and rivers that greatly differ in size, and water chemistry. Inland waters also support a strikingly and disproportionately high level of the world's biodiversity.

Historically, inland waters are linked to the rise of ancient civilizations. Many ancient civilizations grew and flourished along large rivers or other large sources of freshwaters as centers of intensive anthropogenic activities. Some civilizations collapsed due to environmental changes resulting in water scarcity. Some of the worst recent environmental disasters are related to bad water management (e.g. the collapse of the Aral sea). The misuse of water resources is an ongoing process, with large rivers that run dry (e.g. Colorado, Indus, Yellow) and dubious hydrological plans threatening biodiversity and marginalized human societies (e.g. inner Niger Delta). Unsafe water kills more people than all wars; it is estimated that every year 1.7 million people die in the world because of water related problems.

Inland waters provide ecosystem services to humans, including clean water for consumption, irrigation and hydropower, food, cultural and spiritual values. However, humanity's growing water needs, global climatic change, nutrients and pollutants run-off are exacerbating challenges of water scarcity and quality, which will in turn, increase the pressure we place on our inland waters.

These pressures challenge human societies to better understand rivers to properly manage freshwater resources. The Iberian Limnological Association meeting, to be held in Coimbra in June 2018, will be an interactive platform for scientists, policy makers, environmental managers, industry and all those interested in inland waters to discuss and share their ideas and expertise. We welcome all to the 2018 AIL meeting.



Venue

University of Coimbra, Polo II
Rua Silvio Lima
3030-790 COIMBRA

40°11'10.98"N 8°24'41.57"W

Organizing Committee

Manuel Graça (President)
Maria João Feio (Secretary)
Verónica Ferreira (Treasurer)
Ana Marta Gonçalves
Ana Pereira
Ana Raquel Calapez
João M. Neto
Julio Arce-Funck
Melissa Bergamann
Olímpia Sobral
Sandra Ramos
Seená Sahadevan
Sónia Serra

Scientific committee

Rui Cortes, Universidade de Trás os Montes e Alto Douro, Portugal (President)
Amadeu Soares, Universidade de Aveiro, Portugal
Ana Marta Gonçalves, Universidade de Coimbra, Portugal
Antonio Camacho, Universitat de València, Espanha
Arturo Elosegi, Universidad del País Vasco, Espanha
Beatriz Modenutti, Universidad del Comahue, Argentina
Catherine Pringle, University of Georgia, USA.
Cláudia Pascoal, Universidade do Minho, Portugal
Cedo Maksimovic, Imperial College, U.K.
Fernanda Cássio, Universidade do Minho, Portugal
Isabel Muñoz, Universitat de Barcelona, Espanha
Jesús Pozo, Universidad del País Vasco, Espanha
João M. Neto, Universidade de Coimbra, Portugal
José Lino Costa, Universidade de Lisboa, Portugal
Lúcia Guilhermino, Universidade de Porto, Portugal
Marcos Callisto, Universidade Federal MG, Brasil
Margaret Palmer, University of Maryland, USA
Michael Danger, Université de Lorraine-METZ, France
Miguel Cañedo, Universitat de Barcelona, Espanha
Núria Bonada, Universitat de Barcelona, Espanha
Pedro R. Almeida, Universidade de Évora, Portugal
Pedro Anastácio, Universidade de Évora, Portugal
Pepe Barquín, Universidad de Cantabria, Espanha
Sergi Sabater, Universitat de Girona, Espanha
Vítor Gonçalves, Universidade dos Açores, Portugal

Improving freshwater biodiversity assessment: application of molecular tools on preservative ethanol from macroinvertebrate bulks

Martins FMS^{1,2}, Galhardo M², Teixeira A³, Pinheiro P⁴, Filipe AF^{2,5}, Alves PC^{1,2}, Beja P^{2,5}

¹ Departamento de Biologia, Faculdade de Ciências da Universidade do Porto, Portugal

² CIBIO/InBio, Centro de Investigação em Biodiversidade e Recursos Genéticos, Campus Agrário de Vairão, Portugal

³ CIMO-ESA-IPB, Centro de Investigação de Montanha, Instituto Politécnico de Bragança, Portugal

⁴ AQUALOGUS - Engenharia e Ambiente, Lda., Lisboa, Portugal

⁵ CEABN/InBio, Centro de Ecologia Aplicada "Professor Baeta Neves", Instituto Superior de Agronomia, Universidade de Lisboa, Portugal
filipamsmartins@gmail.com

Traditional biodiversity assessment methods rely on morphological identification of bioindicator species such as benthic macroinvertebrates. This is the case of the Water Framework Directive (WFD), the key legislation for the protection and sustainable use of European freshwater resources (2000/60/EC). The possibility of identifying all life stages is particularly relevant, but it requires high levels of specialization and expertise and entail procedures that are expensive and time consuming. Also, the majority of these bioindicator taxa are in their larval stage, which imposes constraints on their morphological identification at lower taxonomic levels (e.g. genus or species). Advanced molecular tools, such as metabarcoding, allow the processing of complex multi-species assemblages at greater resolution (up to species level), by combining DNA taxonomy with high-throughput DNA sequencing. Here, we demonstrate the potential use of preservative ethanol from macroinvertebrate bulk and metabarcoding tools to assess macroinvertebrate communities and biological quality of surface water bodies. We examined ethanol samples collected from five macroinvertebrate bulks of Tua sub-basin (Douro) and morphologically identified organisms down to the lowest practical taxonomic level. Our results showed that 60% of the taxa found in ethanol were macroinvertebrate taxa targeted by WFD, while the remaining percentage was identified as e.g. Bacteria, Stramenopiles, terrestrial invertebrates, amphibians and fishes. In comparison with morphological identification, molecular methods detected in average 70% of the WFD families and 86% of the EPTO (Ephemeroptera, Plecoptera, Trichoptera and Odonata) families. Yet, the percentage of families matching between ethanol metabarcoding and morphological identification increased when rare families (<5 individuals) were excluded (80 and 92.2% respectively) and was maximum on groups well represented in DNA reference databases, such as the order Trichoptera. Also, 113 species were successfully identified from ethanol samples but only half was detected morphologically. Ethanol metabarcoding can potentially be a faster, low-priced and more refined approach for assessing biological quality than traditional methods, by increasing taxonomic resolution and thus sensitivity of metrics to fine variations in stream ecosystem functioning. Nevertheless, further validation is needed as well as expanding the existing DNA reference databases.

Análisis por NGS de la estructura de la comunidad bacteriana en el sedimento de lagunas ibéricas con marcados gradientes tróficos, hídricos y salinos

Miralles-Lorenzo J, Picazo A, Rochera C, Santamans AC, Belenguer M, Morant D, Camacho A

Cavanilles Institute of Biodiversity and Evolutionary Biology, University of Valencia, 46980 Paterna, Spain

Javier.Miralles-Lorenzo@uv.es

En contraste con los estudios clásicos de análisis de la diversidad bacteriana en sedimentos, el uso de técnicas de NGS, aunque es relativamente reciente, ha supuesto una revolución por la mejora en la profundidad y el grado de conocimiento de la diversidad bacteriana no sólo en sedimentos, sino en una gran variedad de ambientes, además de ofrecer un nivel de detalle marcadamente superior. Estos tipos de estudios en el sedimento de los humedales españoles son relativamente escasos a pesar de que permiten una mayor comprensión no sólo de la diversidad microbiana sino de diferentes procesos biogeoquímicos que tienen lugar en el sedimento, como la sulfatoreducción, y de su interrelación con los diferentes microorganismos que los llevan a cabo. En este trabajo se muestra la diversidad bacteriana del sedimento de 17 lagunas localizadas en la Reserva de la Biosfera de la Mancha Húmeda junto con la de 2 marjales costeros valencianos. Las lagunas manchegas presentan entre si un marcado gradiente de salinidad, además de poseer un ciclo hidrológico con unos contrastes muy importantes. Además, muchas de ellas presentan una importante alteración en su estado trófico. Por otra parte, los marjales valencianos se encuentran en un tipo de clima diferente y presentan mayor estabilidad hídrica a lo largo del año, aunque también muestran diferentes grados de alteración antrópica. Para la determinación de la diversidad bacteriana en los sedimentos, se ha realizado una secuenciación por NGS con MySeq en base a librerías específicas del 16S rRNA. A partir de los resultados obtenidos en la secuenciación, se definieron exhaustivamente las comunidades de cada humedal y se realizaron diferentes análisis de ordenación para comparar los diferentes sedimentos entre sí y para relacionar la diversidad bacteriana con diferentes variables ambientales. Los análisis resultantes muestran que a niveles filogenéticos bajos hay una relación entre la tipología de laguna o las diferentes alteraciones antrópicas que presentan las lagunas con los microorganismos que se encuentran en su sedimento, por lo que se pueden establecer relaciones entre la diversidad bacteriana y los metabolismos predominantes en los sedimentos de las lagunas analizadas.