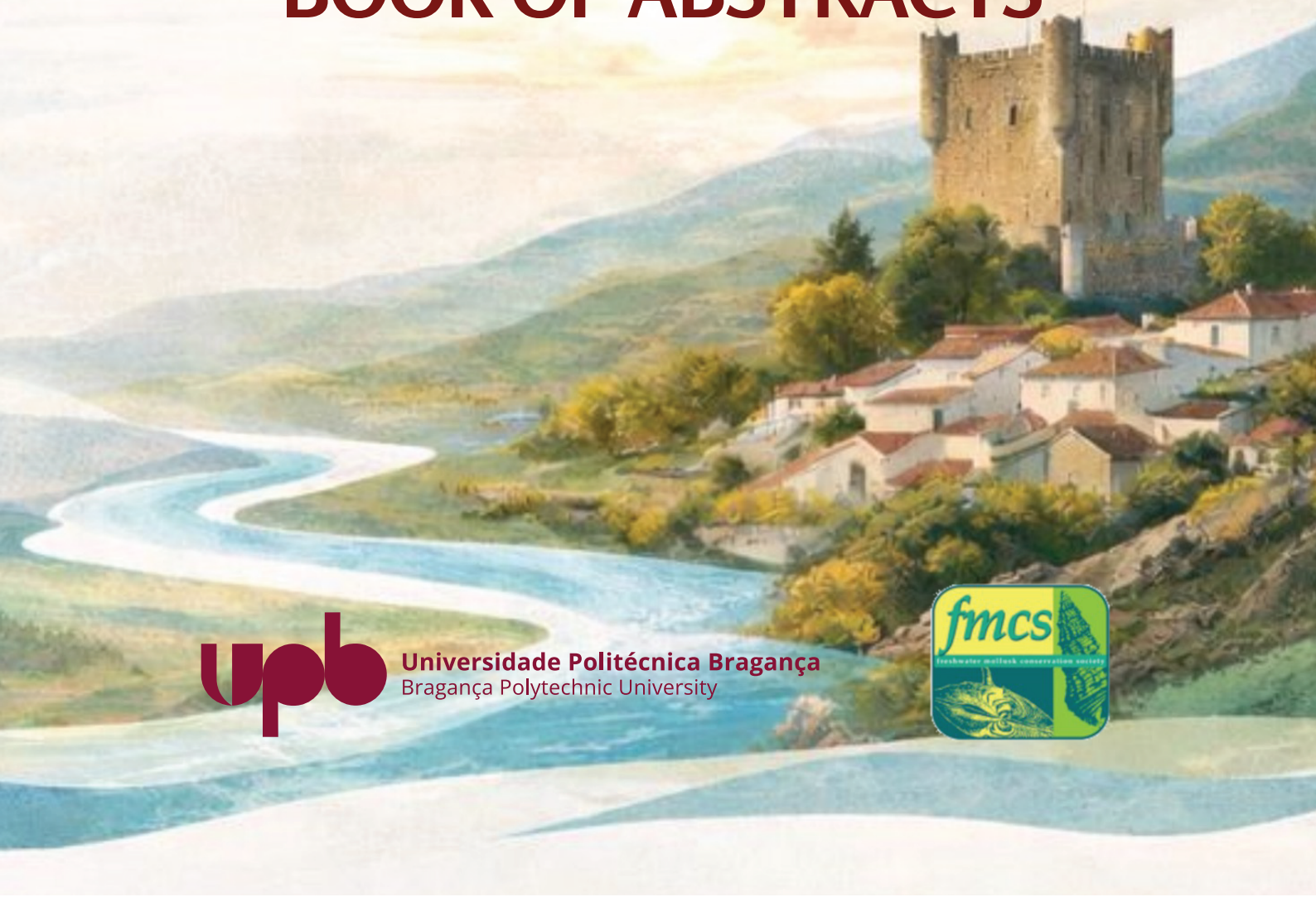
3rd EUROPEAN FMCS SYMPOSIUM

BRAGANÇA, PORTUGAL 7-10 SEPTEMBER 2026

Freshwater Mollusk Conservation in a Changing World

Learning from the Past, Protecting the Future

BOOK OF ABSTRACTS



Universidade Politécnica Bragança
Bragança Polytechnic University

3rd EUROPEAN FRESHWATER MOLLUSK CONSERVATION SOCIETY SYMPOSIUM: BOOK OF ABSTRACTS

7 – 10 September 2026

Bragança - Portugal

Edited by

Amílcar Teixeira

Manuel Lopes-Lima

Simone Varandas

Ronaldo Sousa

Elsa Froufe

André Gomes-dos-Santos

Joana Garrido Nogueira

Fernando Miranda

Fernando Teixeira

Universidade Politécnica Bragança
Bragança Polytechnic University

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Editors: Amílcar Teixeira, Manuel Lopes-Lima, Ronaldo Sousa, Simone Varandas, Elsa Froufe, André Gomes-dos-Santos, Joana Garrido Nogueira, Fernando Miranda, Fernando Teixeira

Amílcar Teixeira – CIMO, LA SusTEC, Bragança Polytechnic University, Portugal

Manuel Lopes-Lima – CIBIO-InBIO, Porto University, Portugal

Ronaldo Sousa – CBMA, Minho University, Portugal

Simone Varandas – CITAB, Trás-os-Montes e Alto Douro University, Portugal

Elsa Froufe – CIIMAR, Porto University, Portugal

André Gomes-dos-Santos – CIIMAR, Porto University, Portugal

Joana Garrido Nogueira - CIBIO-InBIO, Porto University, Portugal

Fernando Miranda - Bragança Polytechnic University, Portugal

Fernando Teixeira - Bragança Polytechnic University, Portugal

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September 2026

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FOREWORD

Fourteen years after the 1st European meeting dedicated to the conservation of freshwater bivalves, the 3rd European Freshwater Mollusk Conservation Society Symposium was held again in the historic city of Bragança (Portugal). This symposium was marked by a moment of reflection and strategic expansion: revisiting the challenges and opportunities identified in 2012, assessing which were successfully addressed, which remain unresolved, and redefining priorities for the next decade, now encompassing all freshwater mollusks. Following the successful establishment and consolidation of the Freshwater Mollusk Conservation Society (FMCS) in Europe, this symposium also represented a fundamental step towards internationalization, strengthening ties with the South American network BIVAAS, fostering transcontinental collaboration, and laying the groundwork for the expansion of FMCS activities in South America. This exchange enriched perspectives, highlighted common challenges among biogeographical regions, and promoted coordinated conservation strategies on a broader global scale. Through lectures, presentations, thematic discussions, debates, and informal social interactions, this meeting reinforced the network of shared knowledge to stimulate collaborative research, capacity building, and the development of common conservation guidelines for freshwater mollusks and their habitats.

We welcomed 120 participants, including organizers and collaborators, from 22 countries, spanning 5 continents, demonstrating the truly global and inclusive spirit in the study of freshwater mollusks. The presence of colleagues from many European countries, as well as Australia, Argentina, Morocco, United States, and other countries, highlighted our international reach and collaborative ambition. The scientific program was as diverse as our participants, featuring 60 oral communications and 21 poster presentations showcasing current research and new directions in the study of freshwater mollusks.

Organizing the 3rd European Freshwater Mollusk Conservation Society Symposium was both a challenge and a privilege. The Organizing Committee deeply appreciates all the support from the FMCS (USA), and research centers and universities: CIMO and LA SusTEC - Bragança Polytechnic University, CIIMAR and CIBIO-InBIO - University of Porto; CBMA - University of Minho, CITAB - University of Trás-os-Montes and Alto Douro. We also thank the scientific committee, and all collaborators, namely the Intermunicipal Association of Terras de Trás-os-Montes, the Municipal Councils of Bragança, Miranda do Douro and Vinhais, the Parish Council of Sé, Santa Maria and Meixedo, the Institute for Nature Conservation and Forests, the Portuguese Environment Agency, the Vale do Tua Regional Natural Park, Movhera, LR Wines & Experiences, NOG's, such as AEPGA and PALOMBAR, the numerous volunteers and, above all, each participant, whose enthusiasm and passion ensured the success of this meeting.

This Book of Abstracts records their contributions and energy and serves as a testament to the strength and talent of researchers in the protection of freshwater mollusks diversity.

The Organizing Committee
On behalf of the 3rd European FMCS Symposium

ORGANIZING COMMITTEE

- **Amílcar Teixeira** – CIMO, LA SusTEC, Bragança Polytechnic University, Portugal
- **Manuel Lopes-Lima** – CIBIO-InBIO, Porto University, Portugal
- **Ronaldo Sousa** – CBMA, Minho University, Portugal
- **Simone Varandas** – CITAB, Trás-os-Montes e Alto Douro University, Portugal
- **Elsa Froufe** – CIIMAR, Porto University, Portugal
- **André Gomes-dos-Santos** – CIIMAR, Porto University, Portugal
- **Joana Garrido Nogueira** - CIBIO-InBIO, Porto University, Portugal
- **Fernando Miranda** - Bragança Polytechnic University, Portugal
- **Fernando Teixeira** - Bragança Polytechnic University, Portugal

VOLUNTEERS

- **Liu Manchón del Peral** – CIBIO-InBIO, Porto University, Portugal
- **Maria Villa -** CIMO, LA SusTEC, Bragança Polytechnic University, Portugal
- **Nuno Paiva** – CIIMAR, Porto University, Portugal
- **Paulo Cortez -** CIMO, LA SusTEC, Bragança Polytechnic University, Portugal
- **Silvana Costa -** Universidad de La Coruña, Spain

SCIENTIFIC COMMITTEE

- **Manuel Lopes-Lima** – CIBIO-InBio of Porto University, Portugal
- **Ronaldo Sousa** – CBMA and Minho University, Portugal
- **Elsa Froufe** – CIIMAR and Porto University, Portugal
- **Amílcar Teixeira** – CIMO, Bragança Polytechnic University, Portugal
- **Simone Varandas** – CITAB and Trás-os-Montes e Alto Douro University, Portugal
- **Amy Maynard (President of the FMCS)** – Neosho National Fish Hatchery, USA
- **David Berg (President Elect of the FMCS)** – Miami University, Ohio, USA
- **Megan Bradley (Past President of the FMCS)** – U.S. Fish and Wildlife Service, USA
- **David Strayer** – Cary Institute of Ecosystem Studies, USA
- **David Aldridge** – Cambridge University, United Kingdom
- **Jürgen Geist** – Aquatic Systems Biology Unit, TU München, Germany
- **Arthur Bogan** – North Carolina Museum of Natural Sciences, USA
- **Agustín Bassó** – Universidad Nacional del Litoral, Santa Fe, Argentina
- **Mary Seddon** – IUCN, United Kingdom
- **Alexandra Zieritz** – University of Nottingham Malaysia Campus, Malaysia
- **Astrid Schwalb** – Texas State University, USA
- **Carla Atkinson** – University of Alabama, USA

- **Dan Hua** – Tennessee Wildlife Resources Agency, USA
- **Joaquim Reis** – Portuguese Institute of Malacology, Portugal
- **John Pfeiffer** – Smithsonian Institution, Natural Museum of natural History, USA
- **Jouni Taskinen** – University of Jyväskylä, Finland
- **Karel Douda** – Czech University of Life Sciences Prague, Czech Republic
- **Maria Urbańska** – Poznan University of Life Sciences, Poznan, Poland
- **Martin Österling** – Karlstad University, Sweden
- **Nicoletta Riccardi** – CNR – ISE, Italy
- **Paz Ondina** – University of Santiago de Compostela, Spain
- **Tadeusz Zając** – Inst. Nature Conservation, Polish Academy of Sciences, Poland
- **Teresa Newton** – U.S. Geological Survey in Wisconsin, USA
- **Vincent Prié** – Institute of Systematics, Evolution, Biodiversity (ISYEB), France

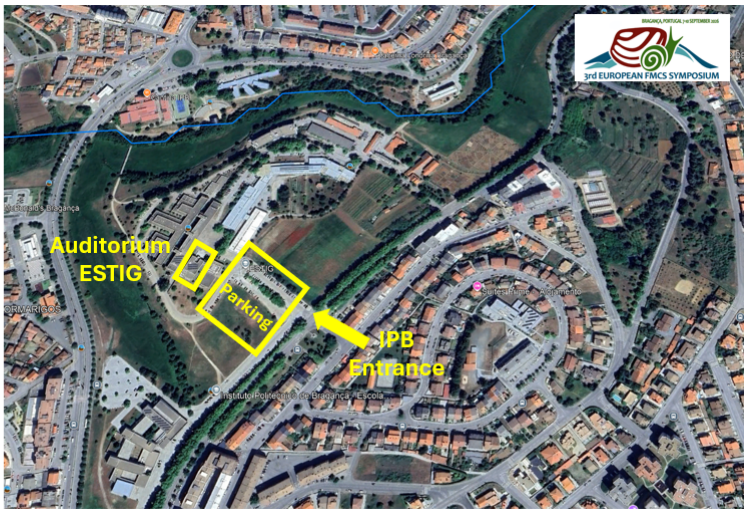
BRAGANÇA POLYTECHNIC UNIVERSITY: CAMPUS

Auditorium Alcínio Miguel & Auditorium Dionísio Gonçalves



School of Technology and Management - Bragança
Auditorium Alcínio Miguel (ESTIG-UPB)









SCIENTIFIC PROGRAM

KEYNOTE SPEAKERS



Dr. ARTHUR BOGAN

North Carolina Museum of Natural Sciences, Raleigh, North Carolina, United States of America

Dr. Bogan's research is focused on developing a phylogeny of the freshwater bivalves of the world. Other research interests lie in developing a handbook on freshwater gastropods of North Carolina. He is also part of a collaboration team that's been formed to produce a photographic catalog of the nearly 1,000 named taxa in the North American freshwater gastropod family Pleuroceridae.



Dr. DAVID ALDRIDGE

Department of Zoology, University of Cambridge, Cambridge, United Kingdom

Dr. Aldridge's research focuses on the ecology of aquatic ecosystems, and in particular invasive species and the role of bivalve molluscs. Much of his work centres on using biology and ecology to answer questions which have wider practical applications. He is also the founder and Managing Director of BioBullets, a company that produces bivalve antifouling particles, since its inception in 2003.



Dr. DAVID L. STRAYER

Cary Institute of Ecosystem Studies, Millbrook, New York, United States of America

Dr. Strayer's research is focused on the distribution and roles of freshwater invertebrates. He worked for many decades on the ecology of the Hudson River and on understanding the controls on distribution and abundance of pearly mussels.



Dr. JÜRGEN GEIST

Aquatic Systems Biology Unit, Technische Universität München, Freising, Germany

Dr. Geist's research is directed to the development of systems biology models for chronological and spatial distribution of biodiversity in water ecosystems which integrate molecular biology and ecology approaches. Focus is placed on the quality of the aquatic habitat, genetic and demographic structures of fish and mussel populations, aquatic food webs and the development of stress biomarkers to indicate pollution in water bodies.



Dr. MARY SEDDON

Emeritus of the SSC's Mollusc Specialist Group.

Dr. Mary Seddon is Emeritus of the IUCN Species Survival Commission's Mollusc Specialist Group and an internationally recognized expert in freshwater mollusk conservation. Her work focuses on the assessment, conservation, and sustainable management of threatened mollusk species worldwide, with particular emphasis on freshwater systems. Dr. Seddon has played a leading role in advancing global Red List assessments, shaping conservation policy, and strengthening international networks dedicated to mollusk biodiversity. Through her long-standing engagement with the IUCN and collaborative research initiatives, she has been instrumental in elevating the profile of freshwater mollusks in global conservation agendas.



Dr. AGUSTÍN BASSÓ

Universidad Nacional del Litoral. Santa Fe, Argentina / BIVAAS network South America

Dr. Agustín Basso is a biologist and researcher at the Universidad Nacional del Litoral (Argentina) with extensive experience in freshwater aquatic organism conservation and ecotoxicology. He is also a member of BIVAAS (Bivalves da Água Doce da América do Sul) and a key promoter of BIVALCONS, the South American network of sites dedicated to the conservation of freshwater bivalves. In addition, he contributes to scientific communication as an editor of the Bulletin of the Argentine Malacological Association.

3rd EUROPEAN FMCS SYMPOSIUM

SCHEDULE OVERVIEW

Time	Aud. Alcínio Miguel (ESTIG)	Aud. Dionísio Gonçalves (ESA)	Aud. Dionísio Gonçalves (ESA)	Field Trip
	Monday 07 Sept.	Tuesday 08 Sept.	Wednesday 09 Sept.	Thursday 10 Sept.
09:00		S3: Taxonomy, Systematics, Biogeog.	S7: Conservation Challenges	Douro International Natural Park Miranda do Douro
09:30		PT: Arthur Bogan	PT: Mary Seddon	
10:00		Oral Communications	Oral Communications	
10:30		Coffee-Break	Coffee-Break	
11:00		S4: Gastropod Diversity	S8: Population Ecology, Reproduction	
11:30		Oral Communications	Oral Communications	
12:00				
12:30				
		Lunch Break	Lunch Break	Lunch Break
14:00	REGISTRATION	S5: Monitoring & Conservation Plan	S9: Conservation Priorities, Genomics	River Rabaçal (Tua Basin) Unionid Sampling Survey
14:30	Opening Session	PT: Jürgen Geist	PT: Agustín Bassó	
15:00	Plenary Talk (PT): M. Lopes-Lima, R. Sousa	Oral Communications	Oral Communications	
15:30	S1: Biological Invasions & Impacts			
16:00	PT: David Aldridge O. Communications	Coffee-Break	Coffee-Break	
16:30	Coffee-Break	S6: Recovery, Rearing, Restoration	S10: Environmental stressors, Mass mort.	
17:00	S2: Ecosystem Functions, Services	Oral Communications	Oral Communications	
17:30	PT: David Strayer			
18:00	Oral Communications			
18:30		Poster Presentations	Closing Session	
19:00				
19:30				
20:00	Social Event Welcome "Ice Breaker" Cocktail: Bragança Castle	Social Event Gala Dinner FMCS Auction		
22:00				

OVERVIEW AND ORAL PRESENTATIONS

Day 1: September 07

14:00 - 15:30

Opening Session: Plenary Talk	
Author(s)	**Title**
Manuel Lopes-Lima, Ronaldo Sousa (Portugal)	**The dramatic decline of freshwater mussels in Europe**

15:30 – 16:30

Session 1 | Biological Invasions and Their Impacts Moderation: David Aldridge & Ronaldo Sousa	
Author(s)	**Title**
Plenary Talk **David Aldridge (UK)**	**Invasive bivalves in freshwater ecosystems: recent advances and future perspectives**
Lyubov Burlakova (USA)	Non-native mollusks in the Great Lakes: Invasion dynamics, density, and impact
Alexander Karatayev (USA)	Multiple invasions decimate the most imperiled freshwater invertebrates

17:00 – 19:00

Session 2 | Ecosystem Functions, Services and Nature-Based Restoration Moderation: David Strayer & Ronaldo Sousa	
Author(s)	**Title**
Plenary Talk **David Strayer (USA)**	**Progress and challenges for understanding relationships between freshwater mussels (Unionida) and nutrients**
Jonathan Lopez (USA)	Mussel-generated ecosystem function varies with long-term changes in secondary production
Jake Daviot (Australia)	Quantifying ecosystem services to promote freshwater mussel conservation in southwestern Australia
Ville Julkunen (Finland)	Freshwater mussel *Anodonta cygnea* reduces concentration, germination rate, and infectivity of pathogenic oomycete *Saprolegnia* spp. spores
Jouni Taskinen (Finland)	Water quality effects of freshwater mussels – Results of laboratory experiments
Matti Mako (Finland)	Agricultural and urban drainage water filtration by using MuFil (Mussel Filtration) - concept
Nicoletta Riccardi (Italy)	From Endangered to Essential: Freshwater Mussels as the Missing Link in Aquatic Restoration?

Day 2: September 08

09:00 – 10:30

Session 3 | Taxonomy, Systematics and Evolutionary Biogeography Moderation: Arthur Bogan & Manuel Lopes-Lima	
Author(s)	**Title**
Plenary Talk **Arthur Bogan (USA)**	**Unionida: an evolving concept**
Yulia Bespalaya (Russia)	Phylogeny, taxonomy, and biogeography of the subfamily Sphaeriinae (Bivalves: Sphaeriidae)
Camila F. Chacón (Argentina)	Revealing hidden diversity of neotropical freshwater bivalves
Ilya Vikhrev (Russia)	Taxonomic revision of endemic cementing river oysters from Madagascar and evolutionary biogeography of the genus in Africa
Vincent Prié (France)	Beyond eDNA surveys: taxonomic insights from a bushy batch of ASVs

11:00 – 12:15

Session 4 | Gastropod Diversity, Bivalve Distribution and Molecular Monitoring Moderation: Vincent Prié & André Gomes-dos-Santos	
Author(s)	**Title**
Diana Delicado (Spain)	Global drivers and patterns of extinction risk in the hyperdiverse family Hydrobiidae
Fatima Aroumy (Morocco)	Groundwater Hydrobiidae (Mollusca: Gastropoda) in the Bouhlou region (Morocco): distribution, groundwater quality and conservation importance
Michele Melchior (New Zealand)	Tracking an invasion in real time: habitat drivers and co-occurrence patterns between invasive *Corbicula fluminea* and native freshwater mussels in New Zealand
María García Álvarez (Spain)	Beyond Climate: Modelling Freshwater Mussel Distributions in River Networks
Gorazd Urbanič (Slovenia)	eDNA Uncovers Bivalve Diversity in Non-Wadable and Impounded Rivers in Slovenia

Day 2: September 08

14:00 – 16:00

Session 5 | Monitoring, Assessment and Conservation Planning Moderation: Jürgen Geist & Simone Varandas	
Author(s)	**Title**
Plenary Talk **Jürgen Geist (Germany)**	**Progress and challenges in freshwater mussel research and conservation**
Joana Nogueira (Portugal)	Can eDNA change the game in conservation?
Erin McCombs (USA)	Application of the Mussel Assemblage Health Index (MAHI) to address the decline of freshwater mussels
Rebecca Höß (Germany)	Status assessment and recovery potential of Denmark's only freshwater pearl mussel (*Margaritifera margaritifera*) population in the Varde River system
Joaquim Reis (Portugal)	Conservation Status of Freshwater Mussels in the South-Western Iberian Peninsula
Hugh Jones (Australia)	On the hunt for the rare and endangered Smooth Almond-shell mussel (*Hyridella narracanensis*) in Tasmania, Australia
Michael Klunzinger (Australia)	Conservation of freshwater bivalves in Australia: Challenges and solutions

16:30 – 18:15

Session 6 | Recovery, Captive Rearing and Restoration Practice Moderation: Nicoletta Riccardi & Joana Nogueira	
Author(s)	**Title**
Stefan Abreu Fernandes (Luxembourg)	Effects of pathogens on rearing success and reintroduction outcomes in the endangered thick-shelled river mussel: *Unio crassus*
Paulina Jakubiak (Poland)	The impact of chemical lake restoration on freshwater mussels
Keiko Nakamura (Spain)	Juvenile growth in *Pseudunio auricularius*: A multi-site semicaptivity study across the Ebro River basin
Michaela Tille (Germany)	When survival is not enough: a multi-endpoint approach to evaluate mussel translocation success
Fatima M'Hamdi (Morocco)	First attempt to develop a long-term individual marking protocol for *Pseudunio marocanus* (Pallary, 1918) (Mollusca: Margaritiferidae) in KBA Bouhlou, Morocco
Jon Magerøy (Norway)	Recovery of *Margaritifera margaritifera* in limed rivers in Norway
Emilia Nordfeldt (Sweden)	Improving aquatic ecosystems from source to sea: integrated conservation actions for threatened freshwater mussels in southern Sweden

Day 3: September 09

09:00 – 10:30

Session 7 | Conservation Challenges and Case Studies Moderation: Mary Seddon & Elsa Froufe	
Author(s)	**Title**
Plenary Talk **Mary Seddon (UK)**	**EU PULSE 2025: Revising the Red List of European Freshwater Molluscs**
Khadija Elbouhali (Morocco)	First ecological assessment of invasive *Corbicula fluminea* populations in Moroccan freshwater ecosystems
John Hyde (USA)	Resource Equivalency Analysis of Freshwater Mussel Populations Injured by the Certus, Inc. and Lone Mountain Processing, Inc. Toxic Spills in the Upper Tennessee River Basin, USA
Astrid N. Schwalb (USA)	Facing an uncertain future - What can we learn from 10 years of research in a drought-prone river system?
Grita Skujienė (Lithuania)	Freshwater Unionidae population dynamics in relation to the 2015 pollution incident in the Šešupė River

11:00 – 12:30

Session 8 | Population Ecology, Reproduction and Species Interactions Moderation: Tadeusz Zając & Elsa Froufe	
Author(s)	**Title**
Mafalda Gama (Portugal)	Spatial and temporal dynamics of native freshwater mussels in an intermittent Mediterranean stream
Sabrina Nykänen (Finland)	Using simulation models as tools for studying the food web and population ecology of freshwater pearl mussel
Juha Syväranta (Finland)	Do size and depth matter – some world records among freshwater pearl mussels?
Marie von Wesendonk (Germany)	Ecological functions of freshwater mussel shells for the macroinvertebrate community
Anna Łabęcka (Poland)	Do unionid freshwater mussels incur reproductive costs during the incubation of the bitterling fish?
Sandra Kaźmierczak (Poland)	Hidden Manipulators: The Influence of Parasites on the Behavior of Freshwater Mussels

Day 3: September 09

14:00 – 16:00

Session 9 | Conservation Priorities, Genomics and Restoration Moderation: Agustín Bassó & Elsa Froufe	
Author(s)	**Title**
Plenary Talk **Agustín Bassó (Argentina)**	**A Diagnosis of Knowledge on South American Freshwater Bivalves**
Alexandra Weber (Germany)	Reproductive mode and hybridisation shape conservation genomic patterns in *Anodonta* freshwater mussels
David Berg (USA)	Evaluating the three Rs of conservation utilizing population genomics
Arianna Lord (Switzerland)	A population genomics approach to understanding the *Unio crassus* species complex in Poland and Croatia
Paul Russell Stanley (USA)	Range-wide analysis of the phylogeography and genetic variation of *Lampsilis cariosa*, a widespread but potentially at-risk freshwater mussel of North American Atlantic Slope drainages
André Gomes-dos-Santos (Portugal)	Population-specific phenotypic plasticity of endangered bivalves in response to extreme events
Sarah Raubenheimer (UK)	From Habitat Restoration to Optimised Reinforcement: Progressing Freshwater Pearl Mussel Recovery in the River Irt

16:30 – 18:15

Session 10 | Environmental Stressors, Mass Mortality and Physiological Responses Moderation: Jouni Taskinen & Manuel Lopes-Lima	
Author(s)	**Title**
Daniel Cossey (New Zealand)	Freshwater mussel mass mortality events: current knowledge and future priorities
Silvana Costa (Portugal)	Multi-Species Biomarker Assessment of Olive Mill Wastewater Toxicity on Freshwater Bivalves
Kristi Dobra (USA)	Using high-resolution chemical analysis to explore patterns of trace element distribution in *Actinonaias ligamentina* shells from the Allegheny River, USA
Dulmini Perera (Australia)	Sublethal responses of Carter's freshwater mussel-*Westralunio carteri* Iredale 1943- to multiple stressors
Sebastian Rock (Sweden)	Divergent behavioral, metabolic and physiological responses of two salmonids to glochidiosis
Maria Urbańska (Poland)	From Ecological Disaster to Scientific Opportunity: Structural Studies of Mussel Shells from Lake Orta
Tadeusz Zając (Poland)	Massive die-off in freshwater mussels: indicators and underlying processes in *Unio nanus* from the Northern Carpathians

OVERVIEW AND POSTER PRESENTATIONS

Day 2: September 08

Author(s)	Title
Nuno Alves (Portugal)	Beyond Species Detection: Using eDNA for Genetic Diversity Monitoring in Threatened Mediterranean Freshwater Taxa
Andreas Dobler (Germany)	From disturbance to opportunity: Beaver slides can promote *U. crassus* reproduction in modified streams
Daniel Cossey (New Zealand)	A tool for the rapid assessment of mussel condition in the field
Dulmini Perera (Australia)	Thermal tolerance of Carter's freshwater mussel - *Westralunio carteri* Iredale 1934
Joana Nogueira (Portugal)	Prioritising Space and Actions for Freshwater Mussel Conservation in Southern Portugal
Joaquim Reis (Portugal)	About the presence of *Unio tumidiformis* in the Guadalquivir basin
Jon Magerøy (Norway)	Unintentional establishment of *Margaritifera margaritifera* populations through stocking of *Salmo trutta*
Liu Manchón del Peral (Portugal)	Save the Southern Naiads: An Integrated Conservation Strategy for Endangered Freshwater Mussels in Southern Portugal
Keiko Nakamura (Spain)	Evaluation of oxidative stress and neurotoxicity in the Asian Clam as a bioindicator
Marie von Wesendonk (Germany)	Effects of degrading freshwater mussel shells on the water chemistry
Michael Klunzinger (Australia)	New descriptions of glochidia from the wet-dry tropics of Australia
Sebastian Rock (Sweden)	Artificial light at night impacts the behaviour and gene expression of an endangered unionid mussel
Sebastian Rock (Sweden)	Parasitism under the spotlight: artificial light at night disrupts circadian and redox balance in fish, enhancing fitness of parasitic glochidia
Silvana Costa (Portugal)	Behavioural monitoring of Native versus Non-native bivalves exposed to olive mill wastewaters: A Valvometric Comparative Study
Silvia Signorini (Italy)	The bivalve *Unio elongatulus* as sentinel of environmental quality: a case study in Lake Orta
Catarina Varela (Spain)	Practical guidance for improving captive rearing success in *Margaritifera margaritifera* conservation programmes
Laurynas Orla (Lithuania)	Freshwater gastropod diversity in Lithuania: a review of historical and recent records
Jouni Taskinen (Finland)	Relationship between number and size of glochidia of the freshwater pearl mussel *Margaritifera margaritifera*
Adam Cmiel (Poland)	Genes or environment? What determines size at maturity, growth rate and shell shape in the thick-shelled river mussel Unio crassus?
Clemens Reuter (Luxembourg)	Environmental DNA survey reveals overlooked freshwater mussel diversity and new records of the *Unio crassus* species complex in Luxembourg
Esther Rodríguez (Spain)	Twenty Years Advancing the Conservation of the Freshwater Pearl Mussel (*Margaritifera margaritifera*) in Castilla y León, Spain

ABSTRACTS

ORAL COMMUNICATIONS

The dramatic decline of freshwater mussels in Europe

Manuel Lopes-Lima [1,2*] **& Ronaldo Sousa** [3*]

[1] BIOPOLIS Program in Genomics, Biodiversity and Ecosystems, CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal

[2] SSC/IUCN – Mollusc Specialist Group, Species Survival Commission, International Union for Conservation of Nature, c/o The David Attenborough Building, Pembroke Street, CB2 3QZ Cambridge, UK

[3] CBMA – Centre for Molecular and Environmental Biology/ARNET-Aquatic Research Network/ IB-S, Institute of Science and Innovation for Bio-Sustainability, Department of Biology, University of Minho, Campus Gualtar, 4710-057 Braga, Portugal

* Corresponding author: mlopeslima@cibio.up.pt; ronaldo@bio.uminho.pt

Abstract

Freshwater mussels are long-lived filter feeders that provide key ecosystem services, including water purification and substrate stabilization, and are widely used as sentinel species for river health. Despite this, they are among the most rapidly declining faunal groups in European ecosystems, and the scale of their loss is rarely quantified across nested spatial levels. Here we report and discuss these declines at three scales: (1) Europe; (2) Portugal; and (3) three northern Portuguese rivers considered strongholds for the pearl mussel *Margaritifera margaritifera*, a species protected under the EU Habitats Directive. At the European scale, 92% of species (22 of 25) are currently threatened with extinction. In Portugal, using standardized timed-search surveys and catch-per-unit-effort at 132 sites conducted in 2002 and repeated in 2022, we found that mussels had disappeared entirely from 60% of sites, and among sites where populations persisted, abundance had declined by 67% over the 20-year period. All Portuguese species showed significant losses, with the rarer *M. margaritifera*, *Unio tumidiformis* and *Potomida littoralis* identified as most in need of urgent conservation attention. At the finest scale, in the Mente, Rabaçal and Tuela Rivers, home to Portugal's best remaining pearl mussel populations, abundance fell by 77% over just nine years (2017-2026), accompanied by signs of low recruitment and possible local extirpation in the Mente River. These nested results show that declines documented at the continental level are mirrored, and in places exceeded, at national and local scales, underscoring the urgency of coordinated conservation action. Although the threats driving these declines are likely context-dependent, we discuss in greater depth the potential roles of climate change, particularly extreme events such as prolonged droughts, and the introduction of invasive species, both of which appear to interact with existing pressures such as habitat degradation, damming and altered flow regimes, and declining host-fish populations needed for larval development. We conclude that future conservation strategies for freshwater mussels in Portugal and across Europe should prioritize continued long-term monitoring, legal site protection and habitat restoration, ex-situ propagation and captive breeding programs, and expanded public outreach and stakeholder engagement to build broad support for freshwater biodiversity conservation.

Invasive bivalves in freshwater ecosystems: recent advances and future perspectives

David C. Aldridge [1,*]

[1] Department of Zoology, University of Cambridge, Cambridge CB2 3EJ, UK

* Corresponding author: da113@cam.ac.uk

Abstract

At the 2012 meeting in Bragança, work on invasive non-native species was still at a relatively early stage. Within the bivalve community, our understanding centred on a small number of high-profile cases, and most notably the severe biofouling caused by zebra mussels in North American water infrastructure. Although these examples highlighted clear economic consequences, our knowledge of the broader ecological and societal impacts of invasive bivalves remained limited. Since then, the field has advanced considerably. We now have a far more detailed appreciation of the ways in which invasive bivalves affect native biota, not only through direct interactions but also through complex cascading ecological effects. Alongside this scientific progress, our approach to risk assessment and prioritisation has become more structured and evidence-based, enabling resources to be allocated in a more strategic and cost-effective manner. In this talk, I will trace how our understanding of invasive bivalves has evolved since 2012 and evaluate the effectiveness of the management approaches adopted over this period. I will conclude by outlining emerging research needs and future management priorities in what remains a rapidly developing and continually shifting field.

Keywords: Invasive non-native species; invasional meltdown; horizon scanning, *Dreissena*, *Corbicula*

Funding: This research was supported by St. Catharine's College and by Corpus Christi College, University of Cambridge.

Non-native mollusks in the Great Lakes: Invasion dynamics, density, and impact

Lyubov Burlakova[1,*], and Alexander Karatayev[1]

[1] Great Lakes Center, SUNY Buffalo State University, Buffalo, New York, USA

* Corresponding author: burlakle@buffalostate.edu

Abstract

Non-native species can exhibit different population dynamics and densities in invaded ecosystems, compete with and/or prey on native species, alter habitats, and transmit diseases. Currently, 16 non-native mollusk species are established in the North American Laurentian Great Lakes, including 14 exotics introduced from other continents and two North American transplants. These species represent 52% of the diversity of all free-living non-native benthic invertebrates in the lakes. Early introductions (*Bithynia tentaculata, Pisidium moitessierianum, P. amnicum,* and *Valvata piscinalis*) arrived in the 19th century via solid ballast, whereas recent introductions (*Dreissena polymorpha, D. rostriformis bugensis,* and *Potamopyrgus antipodarum*) were primarily transported in ballast water. Most exotics originated from Eurasia (64%) or Asia (21%), with single species introductions from Europe and New Zealand. Mollusk densities vary greatly from rare (e.g., *Corbicula fluminea* and *Radix auricularia*) to extremely high (*D. r. bugensis*). Non-native mollusk diversity is highest in shallow Lake Erie and lowest in Lake Huron. The ecological impact of exotic species is largely proportional to biomass, ranging from negligible (e.g., sphaeriids, *C. fluminea*, and *Radix auricularia*) to substantial impacts from *D. r. bugensis*, which has transformed entire ecosystems in the four lower Great Lakes. We also examine potential future invaders (e.g., *Limnoperna fortunei*) and project their likely distributions and impacts. Ongoing and projected temperature increases will likely enhance conditions for currently restricted species and increase the risk of new introductions from warmer regions, further accelerating ecosystem change.

Keywords: exotic mollusks, density, spread, ecosystem impact

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Multiple invasions decimate the most imperiled freshwater invertebrates

Alexander Karatayev [1], Lyubov Burlakova [1,*], Vadim Karatayev [2], John Cooper [3], and Lars Rudstam [4]

[1] Great Lakes Center, Buffalo State University, 1300 Elmwood Ave, Buffalo, New York, USA

[2] University of Maryland College Park, Department of Biology, Maryland, USA

[3] Cooper Environmental Research, Constantia, New York, USA

[4] Cornell University, Cornell Biological Field Station and Department of Natural Resources and the Environment, Ithaca, New York, USA.

* Corresponding author: burlakle@buffalostate.edu

Abstract

Invaders can have devastating impacts on freshwater ecosystems, but these impacts can subside over time as ecosystems "adapt" to the invasion of new species. We analyzed changes in species composition and density of mollusks in Oneida Lake (New York, USA), one of the best studied North American lakes, based on detailed surveys conducted in 1915-17, 1967-68, 1992-95, 2012, and 2022-23, and on annual benthic surveys from 2009 through 2023. Eutrophication and habitat alteration after 1920 resulted in a 25% decline in species richness and a 95% decline in native gastropod density by 1967, while unionid species richness did not change. The arrival of zebra mussels in 1991 and quagga mussels in 2005 was associated with increases in species richness and density of native gastropods and the extirpation of unionids by 1995. However, an invasion by the round goby in 2013 led to a significant decline across all gastropod families, disproportionately impacting soft-shelled and shallow-dwelling species, while other species, including invasive dreissenids, partially recovered 3 to 7 years after the goby invasion. This mollusk recovery was limited to deeper areas. Altogether, molluscan communities were sensitive to ecosystem change and invasive species, with some invaders offsetting the impacts of eutrophication and habitat alterations. Overall, the impacts of multiple stressors resulted in declines in species diversity and density of native gastropods and extirpation of unionids, *Sphaerium* spp., and *Musculium* spp. Dreissenid mussels currently comprise 89% of the density and 99% of the wet biomass of all mollusks in Oneida Lake. While individual stressors have taxon-specific and sometimes positive impacts, eutrophication and species invasions have collectively decimated the native mollusk community over the past century.

Keywords: invasive species, *Dreissena*, mollusk, round goby, ecological impact

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PLENARY TALK

Progress and challenges for understanding relationships between freshwater mussels (Unionida) and nutrients

David L. Strayer[1]

[1] Cary Institute of Ecosystem Studies, Millbrook, NY 12545, USA; Graham Sustainability Institute, University of Michigan, Ann Arbor, MI 48104, USA

* strayerd@caryinstitute.org

Abstract

At the International Meeting on Ecology and Conservation of Freshwater Bivalves in Bragança in 2012, I tried to review what was then known about the relationships between unionids and nutrients (chiefly nitrogen and phosphorus). Now, 14 years later, I return to this subject (and to Bragança!) to discuss recent progress and identify important challenges. I will concentrate on three topics: (i) what are the consequences of large, widespread changes in nutrient loading (both increases and decreases) for unionid populations?; (ii) what functions do unionids play in nutrient cycles?; and (iii) under what conditions do unionids make a difference to the structure or function of ecosystems? Progress since 2012 has been considerable: about twice as many papers on unionids and nutrients have been published since then than in all the years before the 2012 conference. This progress has been uneven: revolutionary for topic (ii), modest and incremental for topic (i), and small for topic (iii). Important challenges remain for all three topics. Some of these challenges are specific and manageable; others are very general and will require hard work and ingenuity to solve.

Keywords: demography; ecosystems; eutrophication

Funding: This research received no external funding.

Mussel-generated ecosystem function varies with long-term changes in secondary production

Jonathan W. Lopez [1,*], Carla L. Atkinson [2], Garrett W. Hopper[3] and Wendell R. Haag [4]

[1] University of Mississippi, Department of Biology, Oxford, Mississippi, USA

[2] University of Alabama, Department of Biological Sciences, Tuscaloosa, Alabama, USA

[3] Louisiana State University AgCenter, Baton Rouge, Louisiana, USA

[4] United States Forest Service, Southern Research Station, Frankfort, Kentucky, USA

* Corresponding author: jwlopez@olemiss.edu

Abstract

A complete consideration of energy dynamics in freshwater ecosystems requires an understanding of biomass production by heterotrophic organisms over time, termed secondary production. Secondary production research in streams has largely focused on aquatic insects and has overlooked other animals such as freshwater mussels (Bivalvia: Unionidae), even though mussels dominate benthic biomass in mussel beds across the southern US. We estimated annual secondary production in two well-studied mussel beds in the Sipsey River, Alabama, over 20 years. We asked (1) how mussel biomass and shell production varies over time and among mussel taxa, (2) how mussel production compares with published estimates of aquatic insect production, and (3) how does secondary production modulate the mussel-driven on ecosystem carbon and nutrient budgets relative to whole-ecosystem pools and fluxes. We used generalized additive models (GAMs) with autocorrelated residuals to model temporal variation in mussel production. GAMs indicated that one site experienced significant temporal variation, while the other did not. At the temporally variable site, it was unclear whether this variation was cyclical, which would indicate natural population fluctuations, or monotonic, which might indicate mussel declines. Alternatively, this dynamic might indicate non-cyclical, natural population fluctuations. Most production was generated by long-lived equilibrium strategists that are adapted to stable environments. Mussel biomass production was higher than most estimates of insect production—however, when shell production was included, mussels produced much more total mass than insects. Shell production has key implications for matter and energy flow, as it generates long-term carbon and nutrient storage, well beyond the typical turnover times of organic biomass. Mussels were also a key part of carbon and nutrient budgets, but this importance presumably fluctuates over time with biomass and production. These findings underscore the important role of mussels in freshwater ecosystem function and the need for mussel conservation.

Keywords: Carbon; Ecosystem services; Monitoring; Nutrients; Surveys

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Quantifying ecosystem services to promote freshwater mussel conservation in southwestern Australia

Jake Daviot[1]*, Stephen Beatty[1], Alan Cottingham[1] and Alan Lymbery[1]

[1] Centre for Sustainable Aquatic Ecosystems, Harry Butler Institute, Murdoch University. Perth, Western Australia.

* Corresponding author: jake.daviot@murdoch.edu.au

Abstract

Freshwater mussels (Bivalvia: Unionida) are critical to ecosystem functioning but face heightened extinction risk due to environmental sensitivity, obligate parasitic reproduction, and limited mobility. *Westralunio carteri*, the sole freshwater mussel species in west-coast catchments of southwestern Australia, has experienced substantial range declines over the past 50 years. While previous research has documented distribution patterns and population declines, the ecological importance of this species remains poorly understood. As pressures increase on remaining *W. carteri* populations, effective conservation with meaningful engagement is critical to the survival of these remaining populations. This work collaborated with a key government agency in Western Australia and aimed to quantify ecosystem function and services provided by *W. carteri* to highlight their importance and the need for ongoing conservation. Baseline biofiltration capacity under laboratory conditions were firstly determined at three water temperatures (15, 20, and 25 °C). *Westralunio carteri* exhibited a mean clearance rate of 177.5 mL g tissue^{-1} h^{-1}, with higher rates at elevated temperatures. These rates aligned with other Hyriidae and Unionida species, indicating that *W. carteri* provides significant biofiltration under low-flow, high water residence conditions characteristic of drought refuge pools. We also assessed the capacity of *W. carteri* to clear *Escherichia coli* from inoculated river water and examined bacterial persistence in mussel biodeposits post-exposure. Over 24 hours, *W. carteri* achieved a maximum *E. coli* reduction of 2.73 log (99.8%), demonstrating substantial water purification potential. Finally, we also assessed nitrogen and phosphorus cycling and storage rates under the context of intermittently flowing rivers, showing *W. carteri* contributes substantially to nutrient storage, remineralization and potentially slows the nutrient turnover of freshwater pools. Together, these findings establish *W. carteri* as an important ecosystem engineer in southwestern Australian freshwaters and provides baseline data for predicting how declining mussel populations may affect water quality under future climate scenarios.

Keywords: ecosystem services; Hyriidae; biofiltration, applied conservation

Funding: This research was funded by Water Corporation, grant number PA011, with relevant APCs funded by Murdoch University under the CAUL Consortium.

Freshwater mussel *Anodonta cygnea* reduces concentration, germination rate, and infectivity of pathogenic oomycete *Saprolegnia* spp. spores

Ville Julkunen[1*], Viivi Pakarinen[1], Tiina Korkea-aho[2], Satu Viljamaa-Dirks[2], Jouni Taskinen[1], Katja Pulkkinen[1]

[1] Department of Biological and Environmental Science, P.O. Box 35, FI-40014 University of Jyväskylä, Finland

[2] Finnish Food Authority, Res. Centre Neulanen, Neulaniementie 4, 70210 Kuopio, Finland

* Corresponding author: ville.i.julkunen@jyu.fi

Abstract

Saprolegniosis, also known as water mould, is a lethal disease caused by Saprolegnia oomycetes, that threatens freshwater animals including fish, amphibians, and crustaceans, as well as aquaculture. It causes biodiversity loss and population declines, including those of endangered fishes. Controlling saprolegniosis in aquaculture is based on chemicals, which are often expensive, ineffective, and hazardous to environment. Filter feeding bivalves (Mollusca) remove pathogens, along with other particles, from the water. Therefore, it is important to test the capacity of freshwater mussels (Unionida) to filter *Saprolegnia* spp. to find out if the mussels could provide an environmentally friendly and sustainable solution to mitigate the problems caused by *Saprolegnia*. We tested (1) the capacity of swan mussels (*Anodonta cygnea*) to filter particles (spores and hyphal fragments) of *Saprolegnia ferax* and *S. diclina*, and (2) the effect of mussel biofiltration on the concentration of infective spores and the germination rate of *S. diclina* spores, and (3) the effectiveness of mussel biofiltration to prevent saprolegniosis in fish eggs. Mussels effectively filtered *Saprolegnia* particles from the water: particle concentrations decreased in mussel aquaria compared to controls within 1 hour of start and the difference remained until the end of the 24 h experiment. The number of colonies of *S. diclina* on oomycete-optimized culture plates was lower in samples originating from the water and sediment of mussel aquaria than in samples from control aquaria. Furthermore, mussel biofiltration reduced the germination rate of *S. diclina* spores in both water and sediment compared to controls. Additionally, we found that the proportion of fish eggs infected with saprolegniosis was much lower when the eggs were exposed to mussel aquaria water compared to control aquaria water. Our results show that freshwater mussels can reduce the concentration of infective *Saprolegnia* particles and the infectivity of remaining particles, and protect fish eggs from contracting saprolegniosis, thus highlighting the effect of valuable ecosystem service 'pathogen removal' provided by the mussels. Our findings encourage deployment of freshwater mussel biofiltration as a nature-based solution to mitigate the problems caused by *Saprolegnia* in freshwater ecosystems, aquaculture, and fish conservation.

Keywords: Aquaculture; fish diseases; mussel biofiltration; nature-based solutions; saprolegniosis

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Water quality effects of freshwater mussels – Results of laboratory experiments

Jouni Taskinen[1*]

[1] University of Jyväskylä, Department of Biological and Environmental Science, 40014 Jyväskylä, Finland

* Corresponding author: jouni.k.taskinen@jyu.fi

Abstract

Freshwater mussels provide important ecosystem services. They filter particles and deposit uneaten material to the bottom, thereby 'cleaning' the water. I present results of six laboratory experiments that we performed to investigate the effect of the common European duck mussel, *Anodonta anatina*, on water quality measures, phytoplankton density, turbidity caused by fines, concentration of the pathogenic bacterium *Eschericia coli* , concentration of *Flavobacterium* infecting fishes, larval density of the *Diplostomum* fish parasite, as well as on the transmission of the parasite to fish. The experiments were mainly performed in 80 L tanks; 10 replicate tanks with 3-5 mussels in each and 10 control tanks without mussels, for 48 h. (1) *A. anatina* removed phytoplankton, especially small Cryptophycea flagellates, and decreased chlorophyll-a, but also decreased pH of water. (2) *A. anatina* decreased the total organic content of water, but also released ammonium, but also reduced oxygen. (3) *A. anatina* decreased turbidity caused by fine inorganic particles. (4) *A. anatina* decreased the density of *Diplostomum* eye fluke larvae in water which caused a reduction in infestation of fish by this parasite. (5) *A. anatina* reduced concentration of the fish pathogen *Flavobacterium columnare*. (6) *A. anatina* reduced concentration of *E. coli*. Although laboratory evidences for freshwater mussels' effects are quite abundant while field evidences remain scarce (Zieritz et al. 2025, Limnol. Oceanogr. https://doi.org/10.1002/lno.70190), current results illustrate the variety of (potentially important) functions that a single freshwater mussel species can carry out in aquatic systems.

Keywords: Duck mussel, filtration, biodeposition, water quality, ecosystem functions

Funding: This research was funded by many funding organisations and foundations

Agricultural and urban drainage water filtration by using MuFil (Mussel Filtration) - concept

Matti Mako[1], Miia Tarkkio[1], Mikko Nurmi[1], Jouni Taskinen[1], Katja Pulkkinen[1] and Siiri Perämäki[2,*]

[1] Kaivotohtori Ltd. & Jyväskylä University, Dep. Biol. & Env. Sci., Univ. Jyväskylä, Finland

[2] Dep. Chemistry, Univ. Jyväskylä, Finland

* Corresponding author: matti.mako@kaivotohtori.fi

Abstract

Mussels have been detected to remove e.g. microbes, heavy metals, and microplastics from water in the laboratory, but field studies have given more mixed results, indicating a need for testing mussels' effect on water quality in the field (Zieritz et al. 2025, Limnol. Oceanogr. https://doi.org/10.1002/lno.70190). Therefore, two field tests were performed using the Mussel Filtration -concept – a transportable, scalable and reusable water hygiene & biofiltration concept - innovated by Matti Mako; agricultural ditches and another in urban sewage waste water treatment plant. Mussels' (Anodonta & Unio) capability to affect water quality parameters (TP, DOC, DN & NH 4 -N, NO 2 -N and NO 3 -N, pH, TURB, DO, conductivity and bacteria) and concentration of 13 elements was studied. Mussels were collected from a lake close to the test sites and were returned back to their home lake after the tests. MuFil filters reduced nitrogen almost significantly in agricultural ditches. MuFil filters reduced bacteria almost significantly, and reduced sulphur and calcium but increased calcium and silicon statistically significantly in waste waters. Mortality of mussels was low. Thus, the freshwater mussels and the MuFil concept could be used in improving water quality. Testing of MuFil concept will continue, concentrating next on filtration of microplastics and oomycetes.

Keywords: mussel filtration; water quality; drainage water

Funding: Runar Backstrom Foundation; MVTT Foundation; Centre for Economic Development, Transport and the Environment

From Endangered to Essential: Freshwater Mussels as the Missing Link in Aquatic Restoration?

Nicoletta Riccardi[1]*, Irene Geneselli[1], Simone Savi[1], Maria Urbańska[2], Maria Chiara Fontanella[3] and Gian Maria Beone[3]

[1] CNR Water Research Institute, Verbania, Italy

[2] Poznan University of Life Sciences, Poznan, Poland

[3] Università Cattolica del Sacro Cuore, Department for Sustainable Food Process, Piacenza, Italy

* Corresponding author: nicoletta.riccardi@irsa.cnr.it

Abstract

Freshwater mussels are among the most threatened but functionally important organisms in aquatic ecosystems, and demonstrating their practical value may be key to improving their conservation. Within the framework of the SYMBIOREM project, we investigated the potential of freshwater mussels as nature-based solutions for biomonitoring and bioremediation, focusing on three major and widespread environmental challenges that are difficult to address in situ using conventional physico-chemical approaches: eutrophication, metal contamination, and plastic pollution. To assess their role in mitigating eutrophication, we conducted laboratory and field experiments quantifying filtration rates under varying environmental conditions, including temperature, algal concentration, and mussel health status (with particular attention to parasitic infections). Results show substantial filtration capacity, modulated by environmental and physiological factors, confirming the potential of mussels to influence nutrient dynamics. For metal contamination, we implemented an *in situ* translocation experiment, transferring mussels from a reference unpolluted site to a lake affected by legacy contamination, and compared them with resident populations. This approach allowed the evaluation of bioaccumulation under realistic exposure conditions, revealing significant uptake and highlighting differences between non-adapted and adapted populations. Finally, preliminary experiments on plastic pollution involved controlled exposure to labeled nanoplastics, demonstrating their uptake, retention, and potential for biodeposition. Overall, our findings provide converging evidence that freshwater mussels can serve both as sensitive bioindicators and as active agents in pollutant removal and transformation. These results support their integration into innovative, nature-based strategies for aquatic ecosystem restoration, while reinforcing the argument that their conservation should be prioritized not only for biodiversity reasons but also for the ecosystem services they provide.

Keywords: biomonitoring, bioremediation, eutrophication, metal contamination, nanoplastics

Funding: This research was funded by the European Union's Horizon Europe, Grant agreement ID: 101060361.

Unionida: an evolving concept

Arthur Bogan[1,2,3*]

[1] North Carolin Museum of Natural Sciences, Raleigh, NC 27601 USA

[2] Research Associate, Carnegie Museum of Natural Sciences, Pittsburgh, PA 15213 USA

[3] Adjunct Assistant Professor, Applied Ecology, North Carolina State University, Raleigh, NC 27695 USA

* Corresponding author: Arthur.bogan@naturalsciences.org

Abstract

The Unionida constitute the largest group of freshwater bivalves, currently distributed across five of the six continents. Unionida has long been recognized, revised, and updated as time, technologies, and practices have changed. These bivalves typically have a unique life cycle in which the larva (glochidia, haustoria, lasidia) is an obligate parasitic stage on host vertebrates. Classifications of this group were initially based on shell characters, then on anatomical characters, later larval characters and finally on a changing variety of anatomical, histological and molecular techniques and tools. Part of the challenge in the Unionida is the demonstrated convergence in shell morphology and sculpture, and clinal variation. Life history traits converge, e.g. cementation is an adaptation not a defining phylogenetic character. The relationships of the groups within the Unionida have changed with new technologies and characters used, moving from a single family to now six families split into two major clades. The two superfamilies were erected based on divergent larval structures, and more recently the same relationship was found using an anchored hybrid enrichment probe set of nuclear genes. This group of bivalves has double uniparental inheritance of the mitochondria, with distinct male and female lineages. With increased molecular data, widespread species are being split into locally endemic species. Evolving molecular technology is opening new horizons and raising new questions. The next step currently being developed is the extraction and analysis of the complete genomes of Unionida, which will provide deeper insight into their taxonomy and evolution.

Keywords: evolution; methodology; morphology, molecular data, phylogeny

Funding: This research received no external funding

Phylogeny, taxonomy, and biogeography of the subfamily Sphaeriinae (Bivalves: Sphaeriidae)

Bespalaya Yu.V.[1]*, Vinarski M.V.[2], Aksenova O.V.[1], Babushkin E.S.[3], Kondakov A.V.[1], Kropotin A.V.[1], Travina O.V.[1], Bolotov I.N.[1]

[1] N. Laverov Federal Center for Integrated Arctic Research of the Ural Branch of the Russian Academy of Sciences, Arkhangelsk, Russia

[2] Laboratory of Macroecology & Biogeography of Invertebrates, Saint Petersburg State University, Saint Petersburg, Russia

[3] Surgut State University, Surgut, Russian Federation

* Corresponding author: jbespalaja@yandex.ru

Abstract

The subfamily Sphaeriinae is a diverse and ecologically significant group of freshwater invertebrates, playing a keystone role in the energy flow and nutrient cycling in aquatic ecosystems. Despite a long history of its study, the taxonomic structure and species content of this group are a matter of ongoing disputes between malacologists. We clarify the taxonomy, distribution, and evolutionary biogeography of the Sphaeriinae from around the world. Our 16S rRNA and two-locus phylogenies reveal that the Sphaeriinae is a monophyletic group, containing at least seven genus-level clades: *Sphaerium* Scopoli, 1777, *Pisidium* C. Pfeifffer, 1821 (s.s.), *Euglesa* Jenyns, 1832, *Odhneripisidium* Kuiper, 1962, *Conventus* Pirogov & Starobogatov, 1974, '*Pisidium*' *sterkianum* group, and *Hindupisidium* Vinarski & Bespalaya 2025. Four species new to science were described based on our own research. We provide re-descriptions of eight species of sphaeriid clams, whose taxonomic status has not been confirmed or needs to be clarified. Our fossil-calibrated phylogeny and generalized biogeographic model indicate that the most recent common ancestor of the Sphaeriidae could have originated somewhere within a broad area covering China near the Lower Cretaceous boundary.

Keywords: bivalves, Sphaeriidae, taxonomy, distribution, phylogeny

Funding: This research was funded by the Russian Foundation for Basic Research (project no. 26-14-00267).

Revealing hidden diversity of neotropical freshwater bivalves

Camila F. Chacón [1,2], Agustín Bassó [3,4], Cristhian Clavijo [5], Sabina Wlodek [6], Manuel Lopes-Lima [7,8]

[1] Laboratorio de Péptidos Bioactivos (LPB) | Departamento de Química Orgánica- Facultad de Bioquímica y Ciencias Biológicas, Universidad Nacional del Litoral (FBCB-UNL).

[2] Facultad de Ciencias de la Salud-Universidad Católica de Santa Fe (FCS-UCSF).

[3]Laboratorio de Ecología Molecular Aplicada (LEMA), Instituto de Ciencias Veterinarias del Litoral (ICiVet-Litoral), Facultad de Ciencias Veterinarias (FCV), Universidad Nacional del Litoral (UNL) / Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET).

[4]Escuela Superior de Sanidad (ESS), Facultad de Bioquímica y Ciencias Biológicas, Universidad Nacional del Litoral.

[5] Vida Silvestre, Uruguay, Montevideo, Uruguay.

[6] Museo Nacional de Historia Natural (MNHN), Ministerio de Educación y Cultura, Montevideo, Uruguay.

[7] CIBIO/InBIO – Research Center in Biodiversity and Genetic Resources, University of Porto, Campus Agrário de Vairão, 4485-661, Vairão, Portugal.

[8] SSC/IUCN – Mollusc Specialist Group, Species Survival Commission, International Union for Conservation of Nature, Pembroke Street, CB2 3QZ, Cambridge, UK.

* Corresponding author: cami.chacon@outlook.com

Abstract

Neotropics harbor approximately 25% of the world's freshwater bivalve species; however, the region remains underrepresented in global conservation assessments, limiting effective conservation planning. This lack of research has generated important gaps in the understanding of species richness, distribution, population trends, and ecological roles. In addition, the presence of cryptic species, characterized by high morphological similarity, complicates taxonomic identification and conservation efforts. In this study, we characterized the regional genetic diversity of freshwater bivalves from Argentina, Uruguay, and Paraguay, focusing on the genera *Anodontites*, *Diplodon*, *Castalia*, and *Mycetopoda*. Genomic DNA was extracted from collected specimens, and the mitochondrial *cytochrome c oxidase subunit I* (*COI*) gene was sequenced for phylogenetic analyses and species delimitation. Molecular identification based on sequence similarity and phylogenetic affinity revealed multiple taxonomic lineages across the sampled taxa. Specimens morphologically assigned to *Anodontites trapesialis* were separated into at least two molecular lineages, suggesting potential cryptic diversity, while *A. trapezea* clustered consistently within a single lineage (*A.* cf. *trapezea*). Within *Diplodon*, most individuals identified morphologically as *D. guaranianus* grouped as *Diplodon* cf. *guaranianus*, although one juvenile specimen showed closer affinity to *D.* cf. *parallelopipedon*, highlighting the difficulty of morphological identification at early developmental stages. Specimens of *D. parallelopipedon*, *Castalia ambigua*, and *Mycetopoda siliquosa* formed consistent molecular clusters. Overall, COI-based analyses showed general agreement with morphological taxonomy but also revealed

cryptic diversity and taxonomic incongruences, particularly within *Anodontites* and *Diplodon*. These findings highlight the importance of molecular approaches for improving species delimitation and supporting freshwater bivalve conservation in the Neotropical region.

Keywords: Neotropics; Genomics; Unionida

Funding: This research received support granted by the Fundação para a Ciência e a Tecnologia (FCT) of Portugal and the Mohamed bin Zayed Species Conservation Fund.

Taxonomic revision of endemic cementing river oysters from Madagascar and evolutionary biogeography of the genus in Africa

Ilya V. Vikhrev[1,2]*, Ivan N. Bolotov[1,2], Alexander A. Kondakov[1], Minaco E. Benitsiafantoka[3], Abiba Misere[3], Manuel Lopes-Lima[2,4], Vincent Prié[4,5], Brigitte A. Bezandry[3]

[1] N. Laverov Federal Center for Integrated Arctic Research of the Ural Branch of the Russian Academy of Sciences, Arkhangelsk, Russia

[2] SSC/IUCN – Mollusc Specialist Group, Species Survival Commission, International Union for Conservation of Nature, Cambridge, United Kingdom

[3] Higher Institute of Science, Environment and Sustainable Development (ISSEDD), University of Toamasina, Toamasina, Madagascar

[4] CIBIO-InBIO, Biopolis, Vairao, Portugal

[5] SPYGEN, Le-Bourget-du-Lac, France

* Corresponding author: vikhrevilja@gmail.com

Abstract

Madagascar is renowned for exceptionally high levels of endemism, estimated at approximately 90% across major animal groups, yet freshwater invertebrates remain severely understudied. Cementing river oysters of the genus *Etheria* Lamarck, 1807 (Bivalvia: Unionida: Etheriidae) represent a remarkable adaptation to fast-flowing waters: individuals permanently cement one valve to submerged rock outcrops and boulders. The only accepted record of the genus from Madagascar was *E. elliptica* Lamarck, 1807, treated as a single, broadly distributed species across most of Africa.

We present an integrative taxonomic revision of Malagasy *Etheria* based on newly collected topotype material from three populations discovered during a 2024 field survey of 12 rivers in northern Madagascar. Combining mitochondrial (COI, 16S rRNA) and nuclear (28S rRNA) sequence data with comparative shell morphology, we demonstrate that Madagascar harbours two species: *E. elliptica* and *E. semilunata* Lamarck, 1807 **stat. rev.**. Both Malagasy species represent unique components of the island's freshwater fauna and are potentially vulnerable to ongoing habitat degradation. In a broader phylogenetic context, a time-calibrated Bayesian phylogeny reveals at least four deeply divergent lineages within *Etheria* on mainland Africa (maximum pairwise COI divergence 19.5%), with the separation of the Malagasy subclade placed in the Early Miocene. Biogeographic modelling using the DIVALIKE model supports a Congo Basin origin of the group, with subsequent independent radiations in West Africa. These results are preliminary given the current incomplete sampling of mainland African diversity.

The Etheriidae is a small but ecologically remarkable family within Unionida, with disjunct, Gondwanan distribution. The present revision of the African genus *Etheria* constitutes the first step toward a comprehensive family-level revision, which must ultimately encompass the South American genera *Bartlettia* and *Mulleria*.

Keywords: Etheria; integrative taxonomy; phylogeny; biogeography

Funding: Russian Ministry of Science and Higher Education (project No. FUUW-2025-0022).

Beyond eDNA surveys: taxonomic insights from a bushy batch of ASVs

Vincent Prié[1,2,*], Benjamin Adam[3] and Manuel Lopes-Lima[2]

[1] SPYGEN, Savoie Technolac, 17 rue du Lac Saint-André, 73375 Le-Bourget-du-Lac, France

[2] BIOPOLIS Program in Genomics, Biodiversity and Ecosystems, CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal

[3] Biotope, 22 bd Maréchal Foch, 34 140 Mèze, France

* Corresponding author: prie.vincent@gmail.com

Abstract

Freshwater biodiversity surveys in megadiverse tropical environments such as French Guiana face major challenges: remote access, high turbidity, and natural hazards make traditional sampling of inconspicuous organisms like freshwater bivalves extremely difficult. Environmental DNA (eDNA) offers a powerful way to circumvent these constraints, enabling non-invasive detection from water samples alone. However, in poorly known regions, lacunar reference databases hamper its full potential, as ASVs cannot be easily attributed to species.

Here we show how this limitation can be turned into an opportunity. Using optimised sampling methods (over 100 sampling points across French Guiana, 2 × 30 L water samples along longitudinal transects, 12 PCR replicates, and a sequencing depth of 300,000 reads), combined with primers initially developed for Western Palaearctic freshwater bivalves — which proved equally effective at discriminating South American species — we generated a comprehensive ASV dataset for the freshwater bivalve fauna of French Guiana.

Orphan ASVs lacking reference matches were not discarded but treated as candidates for undescribed diversity. Three out of six species detected solely from eDNA were subsequently collected as live individuals. Sanger sequencing of mitochondrial markers (16S and COI) provided fragments placed in a global phylogeny and subjected to statistical species delimitation, formally confirming their status as new species.

This proof of concept demonstrates that eDNA surveys, even without extensive reference databases, constitute a powerful heuristic tool for discovering and describing biodiversity in megadiverse environments. The approach is readily scalable and could be extended to freshwater bivalves across Latin America, and more broadly to other taxonomically challenging groups worldwide.

Keywords: Environmental DNA; South-America; Molecular taxonomy; freshwater bivalves

Funding: This research was funded by Office de l'Eau de la Guyane, grant number 2019-16 and SPYGEN. The APC was funded by CIBIO-Biopolis.

Global drivers and patterns of extinction risk in the hyperdiverse family Hydrobiidae

Diana Delicado[1,*] and Torsten Hauffe[2]

[1] Department of Biodiversity and Evolutionary Biology, National Museum of Natural Sciences (MNCN-CSIC), Madrid, Spain

[2] Department of Biology, University of Fribourg, Fribourg, Switzerland

* Corresponding author: diana.delicado@mncn.csic.es

Abstract

With the global decline in biodiversity, there is an urgent need to assess the extent and drivers of extinction risk across various taxa and regions. However, invertebrates, particularly freshwater mollusks, remain insufficiently assessed within global conservation frameworks, limiting, and potentially biasing, our capacity to quantify their extinction risk and distribution across regions, habitats, and evolutionary lineages. Approaches that integrate geographic, environmental, and biological data to predict extinction risk offer a powerful means to close this gap and reveal large-scale patterns of species vulnerability. Utilizing the IUCN Red List and data from approximately 900 species within the largest gastropod family, Hydrobiidae, our study examined how contemporary extinction risk (CER) varies across regions, habitats, and clades. By employing automated assessments to predict CER for unevaluated species, we expanded taxonomic coverage and identified broader patterns of extinction risk within Hydrobiidae.
The extinction risk in Hydrobiidae is significantly underestimated, with predicted assessments suggesting that the number of threatened species likely surpasses the current IUCN estimates. Within the family, CER is predominantly influenced by spatial factors, with range size and area of occupancy emerging as the most robust predictors, indicative of the high levels of microendemism and limited dispersal capacity characteristic of Hydrobiidae. Climatic variables also exerted a significant influence, whereas biological traits and human footprint exhibited comparatively low predictive power. CER is not uniformly distributed and demonstrates distinct geographic, ecological, and phylogenetic structures. Hotspots of threatened species are concentrated in regions that are underrepresented in broader freshwater assessments. Across habitats, isolated systems, such as lakes and springs, exhibit disproportionately high levels of threat, whereas subterranean environments present a comparatively lower risk. Furthermore, extinction risk varies among subfamilies, suggesting that shared ecological and life history traits contribute to clustered vulnerability within evolutionary lineages. These findings underscore the necessity of incorporating overlooked invertebrate groups into global assessments to attain a more comprehensive and realistic understanding of the loss of freshwater biodiversity.

Keywords: Microgastropods, IUCN Red List, automated conservation assessment, freshwater biodiversity

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Groundwater Hydrobiidae (Mollusca: Gastropoda) in the Bouhlou region (Morocco): distribution, groundwater quality and conservation importance

Fatima Ezzahra Aroumy[1,2,*], Fatima M'Hamdi[1,2], Fayçal Ait Boumallassa[2], Tarik Hachimi[1,2], Khadija Elbouhali[1,2], Abderrahim S'Khifa[1,2], Noureddine Haddou[3], Mohamed Ghamizi[1,2].

[1] Faculty of Sciences Semlalia, Cadi Ayyad University, Marrakech, Morocco

[2] The Natural History Museum of Marrakech, Cadi Ayyad University, Marrakech, Morocco

[3]Association des Enseignants des Sciences de la Vie et de la Terre (AESVT) section Taza, Morocco

* Corresponding author: fatimaezzahra.aroumy@gmail.com

Abstract

Subterranean freshwater ecosystems are unique and fragile habitats characterized by stable environmental conditions and highly specialized fauna. Among groundwater gastropods, the family Hydrobiidae is particularly notable for its high degree of endemism and sensitivity to environmental disturbance, making these mollusks valuable indicators of groundwater ecosystem quality. In recent decades, numerous species have been discovered in Morocco's groundwater.

This study presents the results of two exploratory sampling campaigns conducted for the first time ever in the Bouhlou region (Morocco) between October and December 2025 to investigate the occurrence and distribution of Hydrobiidae in groundwater wells and assess their relationship with environmental conditions. Eight wells with contrasting hydrological and morphometric characteristics were surveyed. Biological sampling was performed using a phreatobiological net, and specimens were preserved in ethanol and identified using morphological criteria, following standard approaches in stygobiological studies on malacology. Physico-chemical analyses included measurements of pH, electrical conductivity, dissolved oxygen, total dissolved solids, nitrates, nitrites, sulfates, orthophosphates, and chemical oxygen demand.

Hydrobiidae were recorded in five of the eight wells investigated, displaying a heterogeneous spatial distribution across the study area. Their presence was associated with wells characterized by relatively stable environmental conditions, greater water depth, and lower exposure to surface disturbances. In contrast, Hydrobiidae were absent from shallow or unprotected wells showing higher mineralization and elevated nitrate concentrations, suggesting a negative influence of anthropogenic pressures on groundwater habitat suitability.

The results highlight the ecological importance of groundwater Hydrobiidae as sensitive indicators of aquifer health and emphasize the conservation value of subterranean freshwater ecosystems in Morocco. The observed vulnerability of these taxa underlines the urgent need for groundwater monitoring, protection of wells from contamination, and further taxonomic and molecular studies to support the conservation of these highly specialized and potentially endemic mollusks.

Keywords: Hydrobiidae, Groundwater biodiversity conservation, Subterranean freshwater ecosystems, Groundwater quality.

Funding: WWF MEDITERRANEAN NORTH AFRICA Grant under Restore NAW project

Tracking an invasion in real time: habitat drivers and co-occurrence patterns between invasive *Corbicula fluminea* and native freshwater mussels in New Zealand

Michele Melchior[1]*, Deborah Hofstra[1], Brian Smith, Elizabeth Graham, Anjali Pande [2]

[1] Earth Sciences New Zealand

[2] Biosecurity New Zealand

* Corresponding author: michele.melchior@earthsciences.nz

Abstract

Corbicula fluminea was first detected in the Waikato River system, New Zealand, in 2023 and has since established rapidly across multiple hydro-lakes within the catchment. This study focuses on the rapid establishment of *C. fluminea*, its spatial overlap with native freshwater mussel (*Echyridella menziesii*) populations during the early stages of invasion, and the environmental and biotic factors structuring clam populations during establishment. We combined annual quantitative shoreline surveillance and depth-stratified dive surveys undertaken between 2023 and 2026 to examine early invasion dynamics, population development, and co-occurrence patterns between *C. fluminea* and native *E. menziesii* populations across Lakes Karāpiro and Maraetai. Surveys quantified density, biomass, size structure, substrate composition, and habitat characteristics across multiple sites and depth zones. At an initial shoreline incursion site, mean clam densities increased nearly 50-fold within two years following detection, accompanied by increasingly complex size-frequency distributions and evidence of multi-cohort population establishment. Across both lakes, clam and mussel populations broadly co-occurred across sites and habitats, although clam densities and biomass remained highly heterogeneous spatially. The highest clam densities frequently occurred where mussel biomass was relatively low, particularly in Lake Karāpiro, although broad coexistence was still observed across the full range of mussel biomass values. Mixed models identified water depth as the strongest predictor of clam occurrence and density, while substrate composition contributed modest additional explanatory support and mussel biomass provided relatively weak explanatory power. At many sites and depth zones, particularly deeper habitats, *C. fluminea* contributed the majority of benthic bivalve biomass, suggesting the species may already represent a dominant benthic functional component within parts of the river system only a few years following invasion.

Keywords: *Corbicula fluminea*; *Echyridella menziesii*; invasion dynamics; Coexistence

Funding: This research was funded by Ministry of Business and Innovation and Employment, grant number NIW2475.

Beyond Climate: Modelling Freshwater Mussel Distributions in River Networks

María G. Álvarez[1,*], Mafalda Gama[2], Pedro Anastácio[2], Francisco Godinho[3], Paulo Pinheiro[3], Joaquim Reis[1,4,5]

[1] MARE - Marine and Environmental Sciences Centre/ARNET-Aquatic Research Network, Faculdade de Ciências da Universidade de Lisboa, Lisbon, Portugal.

[2] MARE—Marine and Environmental Sciences Centre/ARNET–Aquatic Research Network, Universidade de Évora, Évora, Portugal.

[3] AQUALOGUS - Engenharia e Ambiente, Lda, Lisbon, Portugal.

[4] Instituto Português de Malacologia, Faculdade de Ciências da Universidade Lisboa, Portugal..

[5] Biota – Estudos e Divulgação em Ambiente, Lda., Ramada, Portugal.

* Corresponding author: mgalvarezfwm@gmail.com

Abstract

Species distribution models (SDMs) are widely used tools for predicting potential species distributions and identifying environmentally suitable areas under current and future scenarios. By integrating multiple predictor variables, SDMs help to explore the ecological factors shaping species distributions and improving predictive performance. However, most SDM frameworks have traditionally been developed for terrestrial organisms, whereas their application to freshwater species remains limited due to the complexity of riverine systems, strong spatial dependence, and the importance of hydrological connectivity and biotic interactions. Freshwater mussels are among the most threatened faunal groups in freshwater ecosystems. In the Iberian Peninsula, habitat alteration, hydrological regulation, biological invasions, climate change, and the decline of host fish species have contributed to severe population declines. Despite the increasing use of SDMs in freshwater ecology, many modelling approaches still rely primarily on climatic predictors and rarely incorporate biotic variables relevant to species with complex life cycles, such as unionid mussels. This study explores the application of SDMs for modelling the distribution of freshwater bivalves across the Iberian Peninsula. We aim to combine machine-learning algorithms, spatial processing tools, and reproducible workflows to facilitate the integration of environmental and biotic predictors within a unified SDM framework. Occurrence records of freshwater mussels were compiled from multiple databases and standardized to a 1 × 1 km spatial grid, which was also used as the common resolution for predictor variables. The modelling approach incorporates hydrological and topographic descriptors related to river dynamics and network structure, land-use variables characterizing anthropogenic pressures at the catchment scale, and biotic predictors such as the predicted distributions of host fishes and invasive freshwater species affecting native mussel assemblages. This approach aims to provide a more realistic representation of freshwater mussel habitat suitability by incorporating species-specific ecological requirements, hydrological connectivity, and biotic interactions driving their distribution patterns.

Keywords: Host fish; invasive species; Iberian Peninsula; habitat suitability; Spatial modelling

Funding: This research was funded by Portuguese Foundation for Science and Technology (FCT), grant number 022.13463.BDANA.

ORAL PRESENTATION

eDNA Uncovers Bivalve Diversity in Non-Wadable and Impounded Rivers in Slovenia

Gorazd Urbanič[1]*, Vincent Prié[2], Alice Valentini[2] and Maja Pavlin Urbanič[3]

[1] University of Ljubljana, Biotechnical Faculty, Department of Biology, Jamnikarjeva 101, 1000 Ljubljana, Slovenia

[2] SPYGEN, rue du Lac Saint-André - CS 20274, 73375 Le Bourget-du-Lac Cedex, France

[3] URBANZERO Institute for holistic environmental management Ltd., Selo pri Mirni 17, 8233 Mirna, Slovenia

* Corresponding author: gorazd.urbanic@bf.uni-lj.si

Abstract

This study assessed freshwater bivalve biodiversity in the lower Sava River basin (Slovenia) using an environmental DNA (eDNA) metabarcoding approach. The objective was to determine species presence, relative density, and spatial distribution within a river system characterized by impoundments and ecologically diverse tributaries. Water samples were collected during the summer–autumn periods of 2024 and 2025 at 23 and 10 sites, respectively, with replicates obtained at each location. Metabarcoding results were complemented by quantitative PCR (qPCR) to provide a semi-quantitative proxy for biomass. The analysis revealed high bivalve diversity, including nine Unionidae taxa, 19 Sphaeriidae taxa, and two additional species, with some recorded in Slovenia for the first time. Three invasive species—*Sinanodonta woodiana*, *Dreissena polymorpha*, and *Corbicula* sp.—were also detected. Spatial patterns indicated that invasive species dominated certain impounded sections of the Sava River, while tributaries supported greater overall species richness. In contrast, eDNA concentrations were generally higher in impoundments, suggesting increased abundance and/or biomass. Longitudinal variation in species distribution and density was also observed within these sections.However, no significant relationships were found between eDNA concentrations and selected hydrological or morphological parameters ($p > 0.05$). Overall, the lower Sava River basin supports high bivalve diversity, including three protected species from the *Unio crassus* complex. Their presence in impounded sections highlights the importance of sustainable river basin management. The eDNA metabarcoding approach proved to be a sensitive and effective monitoring tool—particularly in non-wadable or impounded rivers—although careful interpretation is necessary due to potential downstream transport, concentration effects, and taxonomic challenges.

Keywords: mussels; impounded rivers; eDNA metabarcoding; biodiversity; sustainability

Progress and challenges in freshwater mussel research and conservation

Jürgen Geist [1*]

[1]Aquatic Systems Biology Unit, TUM School of Life Sciences, Technical University Munich, Muehlenweg 22, D-85354 Freising, Germany

* Corresponding author: geist@tum.de

Abstract

Since the first international meetings on freshwater mollusk conservation held in Bragança, Portugal in 2012, great progress has been made in terms of increased knowledge about freshwater mussels and their conservation, but some key questions essential to turn the wheel and halt their continuing declines are still to be answered. This presentations provides a critical reflection on essential achievements in freshwater mussel research and conservation over the past 15 years. For instance, more information on the genetic diversity and differentiation as well as on captive breeding is available, largely facilitated by technological advances and increased international collaboration through European funding. This also includes more harmonized approaches to monitoring of mussels through the implementation of CEN standards. In addition, many successful restoration projects have been implemented, providing role models for other regions. On the other hand, several pressures on freshwater mussels including man-made alterations of catchment land use and climate change put additional pressure on small and fragmented populations, challenging adaptation of restoration attempts for the future. Whilst many of the ageing mussel researchers including myself are getting into a critical life stage with limited field applicability, there is an emerging number of young and enigmatic scientists and conservationists which makes me feel optimistic about the future of freshwater mussels, despite the many challenges ahead.

Keywords: freshwater mussels; evidence-informed conservation; research prioritization; restoration; captive breeding

Can eDNA change the game in conservation?

Joana Garrido Nogueira[1,2*], Arnaud Lyet[3], Virgilio Hermoso[4,5], Pedro Beja[1,2,6], Manuel Lopes-Lima[1,2], and Vincent Prié[1,2,7,8]

[1] CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661, Vairão, Portugal

[2] BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661, Vairão, Portugal

[3] World Wildlife Fund, Wildlife Conservation, 1250 24th St, NW Washington, DC, 20037-1193, USA

[4] Departamento de Biología de la Conservación y Cambio Global, Estación Biológica de Doñana (EBD-CSIC), Avda. Américo Vespucio, 26, 41192, Sevilla, Spain

[5] Australian Rivers Institute, Griffith University, Nathan, 4111, Queensland, Australia

[6] CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Institute of Agronomy, University of Lisbon, Lisbon, Portugal

[7] Institute of Systematics, Evolution, Biodiversity (ISYEB), National Museum of Natural History (MNHN), CNRS, SU, EPHE, UA, CP 51, 57 rue Cuvier, 75005, Paris, France

[8] SPYGEN, 17, rue du Lac Saint-André, Savoie Technolac, 73375, Le Bourget du Lac, Cedex, France

* Corresponding author: joanafgnogueira93@gmail.com

Abstract

Accurate information on species distributions is fundamental for identifying priority areas for conservation, yet conservation planning still relies largely on conventional occurrence records and field surveys. Meanwhile, the potential of emerging tools such as environmental DNA (eDNA) to inform spatial conservation decisions remains untapped. Here, we evaluate whether integrating eDNA data with conventional biodiversity data can improve the efficiency and effectiveness of conservation prioritisation. We compiled distribution records for 29 freshwater bivalve species across France using public occurrence databases and field-based eDNA surveys. Species distributions were modelled under multiple data scenarios: conventional-only, eDNA-only, mixed datasets with different proportions of each data source, and a full dataset combining all available information, used as a proxy for true species distributions. Conservation planning solutions generated under each scenario were compared in terms of conservation target achievement, spatial efficiency, omission and commission errors, and spatial congruence with the full-data solution. Integrating eDNA data substantially increased species detectability and enabled the modelling of more species than conventional data alone. However, prioritisation based solely on eDNA data resulted in less efficient solutions, requiring larger areas to meet conservation targets. Conventional-only solutions, in contrast, were associated with higher commission errors, whereas eDNA-only solutions showed higher omission errors. Overall, combining eDNA and conventional datasets outperformed single-source approaches, producing conservation solutions that were both more efficient and more representative of species distributions. Our results demonstrate that eDNA can significantly strengthen systematic

conservation planning when used alongside conventional biodiversity data, highlighting its potential to support more robust and cost-effective freshwater conservation strategies.

Keywords: Conventional surveys; eDNA; Marxan; Spatial prioritisation; freshwater

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Application of the Mussel Assemblage Health Index (MAHI) to address the decline of freshwater mussels

Erin Singer McCombs[1], Wendell R. Haag[2]*, Traci DuBose[3] , Angela K. Burrow[4], and Steve J. Price[5]

[1] American Rivers, Asheville, NC, U.S.A

[2] U.S. Forest Service, Frankfort, KY, U.S.A

[3] U.S. Geological Survey, Upper Midwest Science Center, La Crosse, WI, U.S.A

[4] Michigan State University, East Lansing, MI, U.S.A

[5] University of Kentucky, Lexington, U.S.A

* Corresponding author: wendell.haag@usda.gov

Abstract

The causes of widespread mussel declines remain poorly understood, and few assessment methods quantify the extent of decline and overall assemblage health. These combined limitations pose challenges to policy and resource management efforts to protect this highly imperiled group before it's too late. Most previous studies focused on specific streams, and none have critically evaluated potential causes of mussel declines across a large geographical area. Similarly, available assessment tools are specific to particular streams or regions and depend on untested assumptions or subjective assessments of species' tolerance to various factors. Therefore, we developed a broadly applicable, objective mussel assemblage health index (MAHI). MAHI includes 4 metrics representing fundamental aspects of assemblage or population health (species loss, recruitment, abundance, and population growth). Metrics are scaled from 0 to 10 (representing increasing health), and the composite score is the unweighted mean of the 4 metrics. MAHI effectively discriminated healthy (median score 8.3) and degraded (3.2) assemblages. The composite score is robust to missing values. Composite scores were similar to independent scores provided by experts, but MAHI eliminates variation due to differences in individual perception or experience. MAHI can be applied to streams across eastern North America using commonly collected mussel survey data, and it may be adapted to other regions. MAHI is free of untested assumptions or subjective assessments, and it accounts for expected differences in mussel assemblages due to stream size, biogeographic region, and other intrinsic factors. Importantly, MAHI does not correlate to other commonly used assessments like fish and aquatic insect Index of Biotic Integrity (IBI) scores which further highlights the need for this assessment adoption to ensure we are capturing stressors to freshwater mussels to enable early detection of mussel declines, better understand the causes of declines, and evaluate the effectiveness of conservation strategies and management actions.

Keywords: freshwater mussels, biomonitoring, management, policy, assessment

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Status assessment and recovery potential of Denmark's only freshwater pearl mussel (*Margaritifera margaritifera*) population in the Varde River system

Rebecca Höß[1]*, Andreas Dobler[1], Michael Deacon[2], Flemming Sørensen[3], Michaela Tille[1], Ralph Kuehn[4], Jes Jessen Rasmussen[5], and Juergen Geist[1]

[1] Aquatic Systems Biology Unit, TUM School of Life Sciences, Technical University of Munich, Germany

[2] Frihedsvej 1, Rødding 6630, Denmark

[3] Varde Kommune, Bytoften 2, Varde 6800, Denmark

[4] Molecular Zoology, TUM School of Life Sciences, Technical University of Munich, Germany

[5] Dept. of Ecoscience, Freshwater Ecology, Aarhus University, Denmark

* Corresponding author: rebecca.hoess@tum.de

Abstract

The freshwater pearl mussel (*Margaritifera margaritifera*) is strongly declining throughout its Central European range. In Denmark, its conservation status is unclear, given that the last living specimen was found in the Varde River in 1995. This study assessed the current status and the recovery potential of *M. margaritifera* in the Varde River system by: (i) dive monitoring searching for living mussels, (ii) assessing habitat quality in the Varde River and its tributaries, (iii) assessing the host fish population status and trends, and (iv) identifying potential donor populations based on genetic analyses of DNA from museum specimen. Dive monitoring detected only empty shells, confirming the historic presence of the species. Habitat assessment revealed that most sites were unsuitable for juvenile pearl mussels due to mobile sand, low interstitial oxygen levels, or a lack of medium grained substrates, but few suitable spots were identified within two tributaries after substrate restoration. Despite removal of migration barriers, host fish population sizes have declined in recent years. The historic populations of *M. margaritifera* in Varde River were closely related to their conspecifics from Estonia and Southern Sweden, and not to the nearest population from Northern Germany. Knowledge on potential donor populations, and ongoing and planned stream restoration activities provide recovery potential for *M. margaritifera* in the Varde River system, but existing habitat quality needs substantial improvement to sufficiently support the return of the species. Habitat restoration should include extensification of fish farming facilities and catchment land use, and erosion control measures to reduce sand transport. Addressing the issues within the catchment is a prerequisite for a sustainable substrate restoration, as shown in a Swedish pearl mussel stream. Restoration success could be confirmed by bioindication using juvenile individuals from a related donor population before reestablishing a freshwater pearl mussel population in the Varde system.

Keywords: stream restoration; habitat quality monitoring; population genetics

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Conservation Status of Freshwater Mussels in the South-Western Iberian Peninsula

J. Reis[1,2,3], M. Garcia-Alvarez[1], F. Picazo[4], J. Pereira[3], F. Banha[5], M. Gama[5], P. Anastácio[5]

[1] MARE - Marine and Environmental Sciences Centre/ARNET-Aquatic Research Network, Faculdade de Ciências da Universidade de Lisboa, Lisbon, Portugal.

[2] Instituto Português de Malacologia, Albufeira, Portugal.

[3] Biota – Estudos e Divulgação em Ambiente, Ramada, Portugal.

[4] Department of Ecology/Research Unit Modeling Nature (MNat), Facultad de Ciencias, Universidad de Granada, Granada, Spain.

[5] MARE—Marine and Environmental Sciences Centre/ARNET–Aquatic Research Network, Universidade de Évora, Portugal

* Corresponding author: joaquim.reis@fc.ul.pt

Abstract

Freshwater mussels in the Iberian Peninsula are experiencing severe decline, becoming one of the most endangered animal groups. Species from the family Margaritiferidae (*Margaritifera margaritifera* and *Pseudunio auricularius*) are well known and have been object of numerous conservations projects over the last decades. Much less attention has been given, however, to species from the Unionidae family, with doubts remaining even in the basic distribution data for most species. Information was particularly scarce in the south-western region, encompassing the Guadiana, Guadalquivir and smaller coastal basins in the Portuguese regions of the Alentejo and Algarve and Spanish regions of Andalucia, Extremadura and Castilla-la-Mancha. Here, we present the combined results from multiple projects that have been undertaken in Portugal and Spain during the last two decades in this region. Five species are known to be currently present in these basins: *Anodonta anatina*, *Potomida littoralis, Unio delphinus, U. gibbus* and *U. tumidiformis*. There is evidence of severe declines of all species across all regions, as much as 80% loss for *U. tumidiformis*. The most threatened species is *U. gibbus*, currently restricted to a small stretch of the Barbate River in Andalucia. Some of the best-preserved unionid populations were found within NATURA2000 sites (e.g. rivers Vascão and Oeiras in Portugal, Estera in Castilla-la-Mancha, Guadalén in Andalucia), but others are at least partially not protected (Odeleite in Portugal, Guadiana in Portugal and Spain, Guadalquivir in Andalucia, Siguenza in Castilla-la-Mancha). The most significant threats identified were climate change and intensive agriculture use of the land, which led to severe drought events and changes in physical habitat. Invasive species is an increasingly relevant impact, with Zebra-Mussel and Asian Clam, Louisiana Crayfish, and multiple invasive fish species being widespread in the region. Conservation of freshwater mussels depends mainly on designation of protected areas where relevant populations subsist, while captive breeding and reintroduction actions are necessary for the most threatened species (*U. gibbus* and *U. tumidiformis*).

Keywords: Unionidae; Endemic; Protected Areas; Climate Change; invasive species.

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On the hunt for the rare and endangered Smooth Almond-shell mussel (*Hyridella narracanensis*) in Tasmania, Australia.

Hugh Jones [1*] and Michael Klunzinger [2,3,4]

[1] Centre for Ecosystem Science, School of Biological, Earth and Environmental Sciences, UNSW Science, Australia

[2] Centre for Sustainable Aquatic Ecosystems, Murdoch University, Murdoch, WA, Australia

[3] Australian Rivers Institute, Griffith University, Nathan, QLD, Australia

[4] Department of Aquatic Zoology, Western Australian Museum Collections & Research Centre, Welshpool, WA, Australia

* Corresponding author: hughajones@bigpond.com

Abstract

Our objective was to resurvey historical localities and new sites across several streams in northeastern Tasmania for *Hyridella narracanensis* to determine its extant distribution and to identify past and ongoing threats to the population. The Smooth Almond-shell mussel is restricted to the coastal rivers and streams of southern, mainland Australia and Tasmanian rivers which drain into Bass Strait. Prior to this survey, the species had only been collected from a single Tasmanian river since 2000, and fewer than six locations since European settlement. We surveyed five historical localities and 30 new sites on 17 rivers and streams in northeastern Tasmania by snorkelling or by wading and brailing for shells. The species was detected only in the Boobyalla River where it is common in the middle to lower sections and mostly protected from disturbance by livestock. In 2024, a previously unknown population of *H. narracanensis* was discovered in a small stream, emerging from native forest. However, it is threatened by stream modification by a riparian landholder. Most surveyed sites in rural areas were degraded from overclearing of streamside vegetation leading to destabilisation of stream channels and from agricultural runoff. Past gold and tin mining and forestry activities severely degraded the upper South Esk River and other rivers and streams in the region where this species was once found. Whilst aquatic habitats in some of these rivers have largely recovered (e.g. Great Forester River), the freshwater mussel populations have not returned. The recent listing of this species as 'Endangered' under the Tasmanian *Threatened Species Protection Act 1995* may encourage recovery efforts, but additional actions such as establishing new populations in suitable rivers and improved enforcement of Tasmanian environmental regulations is needed.

Keywords: Hyriidae; threatening processes; legacy effects; stream management; environmental legislation;

Funding: This research was funded by fellowship maintenance funding of MK from the Australian Rivers Institute, Griffith University, Brisbane.

Conservation of freshwater bivalves in Australia: Challenges and solutions

Michael Klunzinger[1,2,3*], Jake Daviot[1], Mariah Dorocinski[4], Michelle Hobbs[3], Chris Humphrey[5], Hugh Jones[6], Lisa Kirkendale[2], Manuel Lopes-Lima[7], Nicole McCasker[8], Emily Poelina-Hunter[9], Tarmo Raadik[10], Tim Storer[11], Andrew Storey[12], Sarah Treby[13], Corey Whisson[2], Stephen Beatty[1] & Fran Sheldon[3]

[1] Centre for Sustainable Aquatic Ecosystems, Murdoch University, Murdoch, WA, Australia

[2] Department of Aquatic Zoology, Western Australian Museum Collections & Research Centre, Welshpool, WA, Australia

[3] Australian Rivers Institute, Griffith University, Nathan, QLD, Australia

[4] College of Science and Sustainability, School of Health, Medical & Applied Sciences, Central Queensland University, Rockhampton, QLD, Australia

[5] Environmental Research Institute of the Supervising Scientist (ERISS), Department of Climate Change, Energy, the Environment and Water, Darwin, NT, Australia

[6] School of Biological, Earth and Environmental Sciences, University of New South Wales, Kensington, NSW 2033, Australia

[7] BIOPOLIS Program in Genomics, Biodiversity and Ecosystems, CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, Vairão, Portugal

[8] Gulbali Institute, Charles Sturt University, Thurgoona, NSW, Australia

[9] Madjulla Inc, Broome, WA, Australia

[10] Arthur Rylah Institute for Environmental Research, Department of Energy, Environment, and Climate Action, Heidelberg, VIC, Australia

[11] Department of Water and Environmental Regulation, Government of Western Australia, Perth, WA, Australia

[12] Wetland Research & Management, SLR Consulting, Burswood, WA, Australia

[13] School of Agriculture, Food and Ecosystem Sciences, University of Melbourne, Melbourne, VIC, Australia

* Corresponding author: m.klunzinger@gmail.com

Abstract

Recent conservation assessments have noted a decline in population size of many Australian freshwater bivalves. Frequency and severity of droughts, floods and fires from climate change have increased in recent decades, and combined with consequential riparian habitat degradation and sedimentation, are key contributing stressors. Contemporary surveys from coastal rivers of eastern Australia have revealed such climate-change-related declines in former population strongholds for some species that were formerly considered relatively secure. Other agents of population decline include land clearing, river regulation, surface water extraction, secondary

salinisation, nutrient pollution, river sand mining and invasive species, and collectively the gamut of stressors threaten freshwater bivalves at various scales across Australia. Some conservation efforts are in place for species already listed as threatened under state and federal legislation, while others deserve more attention. For example, mitigation strategies for reducing impacts on the Vulnerable Carter's Freshwater Mussel (*Westralunio carteri*) include translocation of subpopulations during road and rail construction projects.

Additionally, monitoring and management of the Critically Endangered Glenelg Freshwater Mussel (*Hyridella glenelgensis*) now includes efforts to captive rear glochidia to the juvenile stage to bolster natural populations. In other regions, proposed extractive industry projects may pose risks to species not currently threatened (e.g., *Batissa violacea*). Despite conservation efforts focused on threatened species, the effectiveness of long-term conservation is hindered by data deficiencies relating to taxonomic uncertainty, incomplete knowledge of species life histories, distribution limits, population sizes and absence of long-term population monitoring data. This overview will hopefully encourage collaboration and investment in the conservation of Australian freshwater bivalves.

Keywords: Hyriidae; Cyrenidae; threatened; species; Australasia

Funding: This research was funded by Australian Biological Resources Study (NTRGII000023), Griffith University and conference attendance was funded by the Centre for Sustainable Aquatic Ecosystems, Murdoch University.

Effects of pathogens on rearing success and reintroduction outcomes in the endangered thick-shelled river mussel, *Unio crassus*.

Stefan A. Fernandes[1]*, Michel Frisch[1], Lena Brouwir[2], Hetty KleinJan[2], Eva Lewisch[3], Frankie Thielen[1]

[1] Fondation Hëllef fir d'Natur, Haaptstrooss 14, L-9764 Marnach, Luxembourg

[2] CEBEDEAU, Campus de l'Université de Liège - Sart Tilman, All. de la Découverte 11, 4000 Liège, Belgium

[3] Clinical Division of Fish Health, University of Veterinary Medicine, Vienna, Austria

* Corresponding author: s.fernandes@naturemwelt.lu

Abstract

Freshwater mussels are among the most threatened invertebrate groups worldwide. Rearing facilities play a critical role in their conservation through population reinforcement programs.
This presentation will highlight two pathological investigations conducted at the freshwater mussel rearing facility of the Mill of Kalborn (Luxembourg), focusing on the endangered thick-shelled river mussel *Unio crassus,* with the aim of identifying pathologies affecting adult reproductive success and juvenile survival, and improving the overall outcomes of reintroduction efforts. Two approaches were used: (1) molecular analysis of periphyton diversity in rearing aquaria and its relationship with juvenile *U. crassus* mortality; and (2) histopathological and molecular examination of parasitic trematodes (*Rhipidocotyle campanula*) in the gonadal fluid of adult *U. crassus* and their correlation with glochidia output.
Regarding juvenile rearing, two potentially pathogenic bacteria were identified and consistently found at higher abundances in aquaria exhibiting the greatest mortality rates. Elevated water temperatures in these aquaria appeared to promote the proliferation of these pathogenic bacteria.
Regarding adult reproductive health, trematode infection was confirmed through both histopathological and molecular methods in individuals from two out of four sub-populations. Preliminary evidence suggests a negative association between infection and glochidia spewing.
These findings highlight that pathologies occurring across multiple developmental stages can compromise the success of mussel rearing programs and, by extension, broader conservation initiatives.
Expanding research on freshwater mussel pathogens is therefore essential to strengthen population reinforcement measures and safeguard these species globally.

Keywords: *Unio crassus;* freshwater mussel pathology; conservation rearing; trematode parasitism

Funding: This research was funded by "Fonds pour la Protection de l'Environnement, Ministère de l'Environnement, du Climat et de la Biodiversité du Grand-Duché de Luxembourg."

The Impact of Chemical Lake Restoration on Freshwater Mussels

Paulina Jakubiak[1*], Michał Rybak[1], Kinga Drzewiecka[2], Przemysław Niedzielski[3], Piotr Klimaszyk[1]

[1] Department of Water Protection, Faculty of Biology, Adam Mickiewicz University, Uniwersytetu Poznańskiego 6, Poznań 61-614, Poland

[2] Department of Chemistry, Poznan University of Life Sciences, Wojska Polskiego 75, Poznań, 60-625, Poland

[3] Department of Analytical Chemistry, Faculty of Chemistry, Adam Mickiewicz University, Uniwersytetu Poznańskiego 8, Poznań 61-614, Poland

* Corresponding author: paulina.jakubiak@amu.edu.pl

Abstract

The aim of this study was to evaluate the ecological effects of polyaluminum chloride (PAC) on two freshwater mussel species, *Anodonta anatina* and *Unio tumidus*. PAC is widely used in chemical lake restoration because it effectively controls algal blooms at relatively low cost. Despite its common application, little is known about its effects on non-target aquatic organisms such as freshwater mussels. To address this gap, we exposed *A. anatina* and *U. tumidus* to environmentally relevant PAC doses (2–20 g Al m^{-2}) and evaluated behavioural and physiological responses. We assessed filtration activity through continuous monitoring of shell-opening behaviour using a Hall-effect sensor system during a 72-hour exposure to PAC. In parallel, biochemical responses were examined by analysing elemental composition in leg tissue and oxidative stress biomarkers in the gills.

Exposure to PAC caused a clear dose-dependent reduction in filtration activity in both species. At concentrations ≥10 g Al m^{-2}, mussels showed a strong reduction in shell activity that persisted for up to 72 hours. These behavioural changes were accompanied by significant alterations in tissue chemistry, including strong dose-dependent aluminum bioaccumulation. At the same time, no oxidative stress response was detected. Interestingly, *A. anatina* appeared more sensitive than *U. tumidus*, pointing to species-specific differences in vulnerability.

The observed sublethal effects indicate potential long-term ecological risks, particularly under repeated restoration treatments. Overall, the results show that exposure to Al-based coagulants, especially at higher doses, can negatively affect freshwater mussels despite the effectiveness of PAC in eutrophication control. These findings highlight the need for optimized dosing strategies and routine ecological risk assessment during lake management practices.

Keywords: freshwater mussels; water restoration; polyaluminum chloride; PAC

Funding: This research received no external funding

Session 6: Recovery, Captive Rearing and Restoration Practice

ORAL PRESENTATION

Juvenile growth in *Pseudunio auricularius*: A multi-site semicaptivity study across the Ebro River basin

Keiko Nakamura[1*], Miquel Campos[2, 3], Miquel Ángel López[4], Oriol Comas Angelet[5], Núria Valls Granero[5], Eva Elbaile[1], Carlos Salinas[1], Joaquim Boix[1], Joaquín Guerrero-Campo[6]

[1] Sociedad Aragonesa de Gestión Agroambiental (SARGA), Environmental Service Department, Biodiversity section, Zaragoza, Spain.

[2] Freshwater Mussel Breeding Laboratory of Lake Banyoles, Consorci de l'Estany, Banyoles, Spain.

[3] Wildlife Conservation Medicine Research Group (WildCoM), Department de Medicina i Cirurgia Animals, Universitat Autonoma de Barcelona, Spain

[4] Forestal Catalana. Generalitat de Catalunya, Barcelona, Spain.

[5] Associació de Defensa i Estudi de la Fauna i Flora Autòctona (ADEFFA), Santa Maria de Merlès, Spain.

[6] Government of Aragon, Department of Environment and Tourism. Biodiversity section. Zaragoza, Spain.

* Corresponding author: knakamura@sarga.es - keikonakamura@hotmail.com

Abstract

The captive breeding program for *Pseudunio auricularius* conducted in Aragon (Spain) has produced enough juveniles to expand semi-captive breeding to sites outside the region, aiming to restore the species historical range throughout the Ebro River basin. We compare the long-term growth (2020-2025) of juveniles (*n*=30 x 4 sites) from the same cohort 2019 across different facilities. The control site supplied with water from the Ebro River, was located near Tudela city. Three other sites were situated in Catalonia region, supplied with natural waters from 1) the Noguera-Pallaresa River, 2) the Merlès River, and 3) Banyoles lake. Juvenile' shell lengths were recorded twice per year. Chlorophyll-a (Chl-a), particulate organic matter (POM), and particulate inorganic matter (PIM) mean concentrations were analysed from seasonal water samples. A comparison between the locations revealed a gradient in growth performance. Following a uniform start in August 2020 (mean length 10 mm), trajectories diverged by late 2021. The control group exhibited superior growth, reaching a mean lengths 68.4 mm by November 2025 with 16.6% of mortality. In contrast, Catalonian groups showed growth attenuation: Merlès achieved intermediate performance: 48.3 mm and 32.5% mortality, while Noguera-Pallaresa and Banyoles reached 37.8 mm - 3.4% mortality and 31.2 mm - 60% mortality, respectively. All groups shared synchronized seasonal patterns, with winter plateaus followed by spring-summer growth pulses. The divergence in survival and growth could be partly explained by Chl-a dynamics. Merlès exhibited the highest trophic availability, with recurring seasonal peaks of up to 12 µg/L, but it did not surpass the growth of the control site. Instead, these organic peaks caused significant drops in oxygen levels, leading to high juvenile mortality. The superior growth of the Ebro control occurred despite lower Chl-a concentrations (< 2 µg/L), probably driven by alternative resources, such as bacteria and POM. Conversely, Noguera-Pallaresa and Banyoles (Chl-a < 1.5 µg/L)

showed growth limitations during the critical spring and autumn periods, leading to an early slowdown in growth, especially in Banyoles due to its oligotrophic nature. Despite low growth rates in Noguera-Pallaresa, survival rates were the highest, suggesting a trade-off between growth and long-term survival.

Keywords: Chlorophyll-a; critically endangered species; freshwater mussel; semicaptivity breeding; shell length.

Funding: In Aragon the research was funded by Government of Aragon and EU funds (FEADER). Forestal Catalana was funded by Generalitat de Catalunya. Freshwater Mussel Breeding Laboratory of Lake Banyoles was funded by Consorci de l'Estany in collaboration with Generalitat de Catalunya.

When survival is not enough: a multi-endpoint approach to evaluate mussel translocation success

Michaela Tille[1], Andreas Dobler[1], Sebastian Beggel[1], Paul Schwarzenbeck[1] and Juergen Geist[1,*]

[1] Aquatic Systems Biology Unit, TUM School of Life Sciences, Technical University of Munich, Muehlenweg 22, D-85354 Freising, Germany

* Corresponding author: geist@tum.de

Abstract

Freshwater mussels face multiple stressors that have led to a severe decline in populations worldwide in recent decades. In certain situations, such as construction works or maintenance measures, translocating mussels to substitute habitats represents an effective conservation strategy. However, despite its frequent application, the effects of this measure on mussels are still not fully understood.

To better understand the ecophysiological responses of mussels to translocation, we relocated almost 50,000 individuals prior to a reservoir maintenance into three different receiving habitats (a fishpond, the river Schwarzach, and the pre-dam). We monitored the mussels over a period of three years, and assessed their performance using multiple endpoints including survival, growth and energy storage compounds such as glycogen, glucose, protein and lipids.

Survival rates differed substantially among the three substitute habitats: no mussel survived in the river Schwarzach, whereas survival rates were 38% in the fishpond and 66% in the pre-dam. Mortality also varied among mussel species, with *Anodonta anatina* showing lower mortality rates than *A. cygnea* and *Unio pictorum*. Relative growth rates were lower in the pre-dam area compared to the fishpond, while macromolecule levels significantly differed both over time and between habitats.

When using translocation as a conservation measure, not only suitable local habitat conditions but also species-specific resilience should be taken into account. The integration of multiple endpoints enables a comprehensive assessment of the translocation success in freshwater mussels, extending beyond survival-based metrics. These findings also suggest that risk mitigation of translocation actions by using different substitute habitats is important.

Keywords: Unionidae; conservation implications; storage compounds; management approach; biomarker

Funding: This study was partly supported via the Bavarian Mussel Coordination Office, Technical University of Munich, Germany funded by the Bavarian State Ministry of the Environment and the Bavarian Environment Agency, and by the Water Authority Weiden.

First attempt to develop a long-term individual marking protocol for *Pseudunio marocanus* (Pallary, 1918) (Mollusca: Margaritiferidae) in KBA Bouhlou, Morocco

Fatima M'Hamdi[1,2]*, Fayçal Ait Boumallassa[2,3], Khadija Elbouhali[1,2], Fatima Ezzahra Aroumy[1,2], Tarik Hachimi[1,2], Abderrahim S'Khifa[1,2], Noureddine Haddou[5], Amílcar Teixeira[4], Mohamed Ghamizi[1,2].

[1] Department of Biology, AQUABIOTECH Laboratory, Faculty of Sciences Semlalia, Cadi Ayyad University, Marrakech, Morocco

[2] The Natural History Museum of Marrakech, Cadi Ayyad University, Morocco

[3] Polydisciplinary Faculty, Sultan Moulay Slimane University, Beni Mellal, Morocco

[4] CIMO, SusTEC, Universidade Politécnica de Bragança, Bragança, Portugal

[5] AESVT section Taza, Morocco

*Corresponding Author E-mail: fm.mhamdi1@gmail.com

Abstract

Bouhlou (Province of Taza, Morocco) is a Key Biodiversity Area (KBA) of exceptional conservation significance, harboring one of the richest freshwater biodiversity in North Africa. Among its flagship species, *Pseudunio marocanus* (Pallary, 1918), a Critically Endangered freshwater mussel endemic to Morocco, finds in Bouhlou river one of its last strongholds, making this KBA a true symbol of hope for the species' long-term survival. Despite its critical conservation status, few quantitative population monitoring programs had previously been established for freshwater bivalves in Morocco, highlighting an urgent methodological gap to perform a conservation plan for endemic and threatened species.

Within the Restore Bouhlou project, funded by WWF MED-NA under the Restore NAW program, two preliminary field missions were conducted at Bouhlou in October 2025 and December 2025 to explore and compare individual marking techniques as a basis for long-term demographic monitoring of *P. marocanus* at two stations (SB1 and SB2) with standardized effort (two divers, 30 min, 100 m river stretch). Two individual marking techniques were tested: resin tagging (Mission 1, SB1) and shell engraving (Mission 2, SB1 and SB2), both documented for Unionidae in European contexts. A 48-hour interval between consecutive sessions within each mission allowed marked individuals to redistribute, reducing sampling bias. Population size was estimated using the Chapman capture-mark-recapture (CMR) correction with 95% confidence intervals by the Ricker method. Catch-per-unit-effort (CPUE) provided a complementary relative density index.

CMR for SB1 converged between 35 and 49 individuals (95% CI: 16–115), and for SB2 showed a substantially larger population ($\hat{N}$ = 185; 95% CI: 113–339), approximately four times that of SB1. CPUE values corroborated this pattern (17.6 vs. 75.0 ind.·h-pers.$^{-1}$·100 m^{-1}; ratio ×4.3), providing mutual method validation. 6 resin-tagged individuals from Mission 1 were recaptured at SB1 during Mission 2, two months later, demonstrating preliminary mark retention and individual site fidelity a foundational requirement for long-term demographic monitoring of sessile bivalves.

Results are considered preliminary given limited recapture numbers and the exploratory nature of the protocol. A third mission is planned for June 2026 to assess mark retention following the severe flood events that affected Morocco in early 2026.

Keywords: *Pseudunio marocanus*; Freshwater conservation; CMR; CPUE; Morocco

Funding: This research was funded by WWF MEDITERRANEAN NORTH AFRICA (MED-NA) under the Restore NAW program

Recovery of *Margaritifera margaritifera* in limed rivers in Norway

Jon H. Magerøy[1]*, Bjørn Mejdell Larsen[2], Kjell Sandaas[3], Jørn Enerud[4] and Randi Saksgård[2]

[1] Norwegian Institute for Nature Research (NINA), Sognsveien 68, 0855 Oslo, Norway.

[2] Norwegian Institute for Nature Research (NINA), P.O. 5685 Torgarden, 7485 Trondheim, Norway.

[3] Naturfaglige konsulenttjenester, Øvre Solåsen 9, 1459 Nesodden, Norway.

[4] Fisk og miljøundersøkelse, Øvre Båstad vei 39, 1387 Asker, Norway.

* Corresponding author: jon.mageroy@nina.no

Abstract

Acid rain had significant negative impacts on freshwater systems throughout large parts of Europe. The impact reached its peak in 1980, but the aftereffects are still impacting ecosystems[1]. In Norway, acid rain continues to have a negative impact on freshwater systems, especially in the southwestern region[2,3]. This has resulted in strong negative impacts on the Freshwater Pearl Mussel (*Margaritifera margaritifera*), both by impacting the mussels directly and their host fish[4]. In Agder County on the southern coast of Norway, ca. 90 % of the populations were thought to have been lost[5], primarily due to acidification[4]. To counteract the effects of acidification, primarily on fish populations, many of the watercourses have been limed[2,3]. *M. margaritifera* has been rediscovered in six limed rivers, where it was thought to have gone extinct. In these rivers and other rivers with populations previously in decline, recruitment is now occurring and the populations are increasing in size and distribution area[6-14]. In the best studied river, the Ogna, the population has recovered from ca. 500 mussels in 1997 to at least 15,000 mussels in 2025. However, recruitment levels have varied greatly during the recovery period[8]. Although many *M. margaritifera* populations have been permanently lost due to acidification in Norway, these findings show that it is possible to counteract pollution effects and aid the recovery of mussel populations.

Keywords: acidification; liming; *Margaritifera margaritifera*; recovery; Norway

Funding: “This research was funded by the Norwegian Environment Agency and the County Governors of Agder and Rogaland”.

Improving aquatic ecosystems from source to sea: integrated conservation actions for threatened freshwater mussels in southern Sweden

Emilia Nordfeldt Oswaldson[1, 2, *], Niklas Wengström[1, *] and Daniel Wendesten[1]

[1] Swedish Anglers Association

[2] University of Gothenburg

*Corresponding authors: emilia.nordfeldt@sportfiskarna.se; niklas.wengstrom@sportfiskarna.se

Abstract

The Improve Aquatic LIFE project conducts large-scale restoration measures across southern Sweden to improve aquatic ecosystem connectivity and ecological function from source to sea. The project is led by the County Board of Skåne in partnership with the eight other county boards in Southern Sweden, two municipalities, the Swedish Agency for Marine and water management, the Swedish Environmental Protection Agency, three universities and the Swedish angler association. Particular focus is given to the conservation of the Freshwater pearl mussel (*Margaritifera margaritifera*) and Thick-shelled river mussel (*Unio crassus*) through integrated habitat restoration and host fish infestation efforts.

Implemented and ongoing conservation in the project includes barrier removal, floodplain reconnection, habitat restoration, and wetland restoration across 20 river catchments and three coastal areas. To strengthen recruitment in threatened mussel populations, host fish infestations with glochidia are currently being conducted in multiple rivers. During spring 2026, follow-up electrofishing surveys were performed in three previously infested rivers, where fish carrying glochidia were successfully recaptured in all systems. These observations provide early evidence supporting successful infestation efforts.

In parallel with ongoing restoration actions, population genomic studies are being initiated to support long-term conservation management. Preliminary 2bRAD and microsatellite analyses of Swedish freshwater pearl mussel populations indicate low genetic diversity, elevated inbreeding levels, high relatedness among individuals, and potentially extensive self-fertilization in some river systems. These findings highlight the importance of integrating genetic perspectives into conservation planning, particularly for translocations and reinforcement measures.

The Improve Aquatic LIFE project demonstrates how practical restoration actions, monitoring, and emerging genomic tools can be combined to support the recovery of threatened freshwater mussel populations at a catchment scale.

Keywords: freshwater pearl mussel; thick-shelled river mussel; host fish infestation; aquatic restoration; conservation genetics

Funding: This research was funded by EU LIFE Nature programme (LIFE23/NAT/SE/101148230), and all partners.

EU PULSE 2025: Revising the Red List of European Freshwater Molluscs

Mary Seddon[1]*, Manuel Lopes-Lima[2], Zoltan Feher[3], Jozef Grego[1], Vincent Prié[1], Nicoletta Riccardi[4] and David Allen[5]

[1] IUCN SSC Mollusc Specialist Group, [2]CIBIO University of Porto,[3]World Wildlife Fund Hungary, [4] ISRA, Italy [5] IUCN Cambridge

* Corresponding author: mary.molluscsg@gmail.com

Abstract

In 2011, IUCN led a project to assess the conservation status of all of the Freshwater Molluscs in Europe. The results of this assessment showed that 43% of all European Freshwater Molluscs were threatened with 1% already Extinct. A total of 830 species were assessed. The main threats identified were 1) Over-abstraction of water, 2) pollution, 3) dam construction and canalization and 4) increasing number of non-native species competing with native species.
Priority actions suggested were:
1) Better knowledge on presence of spring-snails and communication on how to improve water off-take from sites without impacting species.
2) Conservation breeding programmes to restock rivers with freshwater bivalves.
3) Control of invasive species to reduce impact on native species.
4) Use of Environmental Impact Assessment's for any dam/drainage projects to plan for mitigation of any impacts on endemic species.
Between 2022 and 2025, a second project, reassessing all the freshwater species to establish changes in the threat status in the last 15 years and what causes most species to be threatened now.
This paper will present the results of the revised assessment based on the latest update (IUCN RedList version 2026.1). These results show major changes in the threats to the European fauna, with increasing impacts from climate change now being apparent. There is also another c. 300 species assessed that have been described from the region between 2011 and 2025. The results also reveal genuine changes in Red List assessments as some species have declined in their range and population abundance. This taxon group remains the most threatened freshwater species in Europe.
Keywords: Conservation, CBD Targets, A2P Plan, Europe

Funding: These results have arisen from the assessments undertaken during European Commission project 'Providing technical and scientific support in measuring the pulse of European biodiversity using the Red List Index'. Contract No 07.027755/2020/840209/SER/ENV.D.2.

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First ecological assessment of invasive *Corbicula fluminea* populations in Moroccan freshwater ecosystems

Khadija Elbouhali[1,2*], Fayçal Ait Boumallassa[2,3], Fatima M'Hamdi[1,2], Fatima Ezzahra Aroumy[1,2], Tarik Hachimi[1,2], Mokhtar Benlasri[1,2], Ronaldo Sousa[4], Mohamed Ghamizi[1,2]

[1] Faculty of Science-Semlalia, Cadi Ayyad University, Marrakech, Morocco

[2] The Natural History Museum of Marrakech, Cadi Ayyad University, Morocco

[3] Polydisciplinary Faculty, Sultan Moulay Slimane University, Beni Mellal, Morocco

[4] CBMA – Centre for Molecular and Environmental Biology/ARNET-Aquatic Research Network & IB-S, Institute of Science and Innovation for Bio-Sustainability, Department of Biology, University of Minho, 8 Campus Gualtar, 4710-057 Braga, Portugal.

*Corresponding Author E-mail: K.elbouhali2@gmail.com

Abstract

Freshwater ecosystems are increasingly threatened by biological invasions, with invasive bivalves representing a major concern for native biodiversity and ecosystem functioning. In Morocco, the Asian clam *Corbicula fluminea* has rapidly spread across several freshwater ecosystems, including the Oum Er-Rbia basin, raising concerns about its potential ecological impacts on native freshwater communities. As part of an ongoing research project investigating invasive species impacts on Moroccan freshwater fauna, this preliminary study provides a first ecological assessment of *Corbicula fluminea* abundance and morphometry in the Oum Er-Rbia basin.

Field surveys conducted across 13 sites within the Oum Er-Rbia basin and revealed considerable spatial variability in population density, with some localities exhibiting high abundances reaching 6.25 individuals/min/person, indicating successful establishment and spread of the species. These observations emphasize the rapid adaptive potential of invasive populations under environmental conditions within Moroccan freshwater ecosystems. To explore morphological variability, both traditional and geometric morphometric approaches were applied to specimens collected from different freshwater habitats.

Traditional morphometric analyses revealed significant differences in shell proportions among populations (ANOVA, $p < 0.01$), highlighting the presence of distinct shell forms ranging from elongated to more globular morphotypes. Geometric morphometric analyses further confirmed this spatial structuring. Principal Component Analysis (PCA) identified major variations associated with shell elongation and ventral expansion, while Canonical Variate Analysis (CVA) discriminated several groups and suggested the occurrence of localized morphotypes.

Overall, these findings provide essential baseline data for future investigations addressing ecological impacts and cryptic diversity, which may be informative for the implementation of measures devoted to freshwater mollusk conservation in North Africa.

Keywords: *Corbicula fluminea*, Invasive freshwater bivalves, Morphometric analysis, Population density, Freshwater conservation

Session 7: Conservation Challenges and Case Studies

ORAL PRESENTATION

Resource Equivalency Analysis of Freshwater Mussel Populations Injured by the Certus, Inc. and Lone Mountain Processing, Inc. Toxic Spills in the Upper Tennessee River Basin, USA

J. Murray Hyde[1,*] and Jess W. Jones [2]

[1] Department of Fish and Wildlife Conservation, Virginia Tech

[2] United States Fish and Wildlife Service

* Corresponding author: jmhyde891@gmail.com

Abstract

The Certus, Inc. and Lone Mountain Processing, Inc. (LMPI) Natural Resource Damage Assessment and Restoration (NRDAR) cases represent two of the earliest and largest freshwater mussel injury assessments conducted in the United States. The Certus spill was an acute event that caused primarily lethal effects, resulting in the estimated mortality of ~18,000 mussels, including three federally endangered species. In contrast, the LMPI spill affected approximately 65 miles of stream habitat and was characterized primarily by sub-lethal effects. We developed a Resource Equivalency Analysis (REA) framework to quantify injury and evaluate expected restoration gains associated with both cases. Injury for the Certus spill was estimated directly from mussel mortality and incorporated into the REA. Because injury quantification for the LMPI spill was constrained by the broad spatial extent of exposure, predominately sub-lethal effects, and limited historical data, analyses focused on comparing expected restoration gains between cases. Two restoration scenarios were evaluated. The Full Scenario assumed successful establishment of all released mussels at restoration sites, whereas the Reduced Scenario assumed establishment of only 25% of released individuals. Under both scenarios, restoration gains for the Certus case exceeded estimated injury losses, with gain-to-loss ratios of 4.6 and 1.2 for the Full and Reduced scenarios, respectively. However, post-restoration monitoring suggested realized gains were more consistent with the Reduced Scenario. This discrepancy may reflect higher-than-expected mortality, emigration from restoration sites, or excystment of juvenile mussels outside monitored areas. Restoration gains associated with the Certus case were approximately 4.9 times greater than those estimated for the LMPI case. Although injury could not be quantified directly for the LMPI spill, even modest reductions in ecological services across such a large, affected area may translate into substantial long-term injury. Additional refinement of REA methods is needed to better account for sub-lethal effects and variation in ecological services among species and age classes. Nonetheless, the REA framework developed in this study provides a useful tool for future NRDAR applications involving freshwater mussels, particularly acute mortality events.

Keywords: Resource Equivalency Analysis; Natural Resource Damage Assessment and Restoration; freshwater mussels; injury assessment; restoration ecology

Funding: This research was funded by the Office of Restoration and Damage Assessment, Washington, D.C.

Facing an uncertain future - What can we learn from 10 years of research in a drought-prone river system?

Astrid N. Schwalb[1]

[1] Texas State University, Texas, USA

* Corresponding author: schwalb@txstate.edu

Abstract

Freshwater mussels are declining worldwide. Mussels inhabiting river systems that experience regular flash floods and extreme droughts face an especially uncertain future, with both climate change and groundwater extraction posing major threats. This presentation reflects on research findings from the past 5 –10 years in the upper Colorado River basin in Texas, where depauperate mussel communities are remnants of historically dense and thriving mussel beds. This talk examines lessons learned from previous field and modelling studies on the effects of drought, documenting both decline and persistence, as well as the importance of flow and drought refuges across different spatial scales. It also discusses how distinct parts of the river system may represent different potential future scenarios as droughts become more severe, and which factors may contribute to the persistence of mussel populations.

Keywords: Climate change, drought; flow refuge;

Funding: This research was funded in part by US Army Corps of Engineers

Freshwater Unionidae population dynamics in relation to the 2015 pollution incident in the Šešupė River

Grita Skujienė[1,*], Miglė Ragelytė[1] and Jonas Aistis Skuja[1]

[1] Institute of Biosciences, Life Sciences Center, Vilnius University, Lithuania

* Corresponding author: grita.skujiene@gf.vu.lt

Abstract

Freshwater Unionidae are important components of river ecosystems, contributing to water filtration, nutrient cycling, and habitat structure. This study examines freshwater mussel population dynamics in relation to a 2015 pollution incident in the Šešupė River, river flowing through Poland (~27 km), Lithuania (~158 km), the Russian Federation (Kaliningrad region, ~62 km).

The 2015 pollution event near Antanavas (Lithuania) was characterized by a sudden and severe deterioration of water quality, including intense foaming, elevated concentrations of surfactants, and increased levels of nitrogen and phosphorus compounds, accompanied by fish mortality. The incident is considered to have originated from an acute anthropogenic pollution input, most likely associated with accidental or unauthorized wastewater discharge into the river system, although no single responsible source has been formally confirmed.

The Šešupė River basin has been previously studied in Poland, with comprehensive biological and physicochemical assessments, conducted in 1984 and 2019 (Ożgo et al., 2021). In Lithuania, systematic water quality monitoring has been carried out by the Environmental Protection Agency since 2022 and contamination and genotoxity biomarker responses in *Unio pictorum* or *Unio tumidus* were studied (Rybakovas et al., 2020).

Sampling was conducted across 6 sites representing different habitat conditions and levels of anthropogenic impact in 2023 and 2026. Results revealed marked spatial heterogeneity in Unionidae abundance. Among the studied species, *Unio crassus* and *U. pictorum* appeared to be the most sensitive to environmental changes, showing the most pronounced variation in occurrence across sites. It was found that *U. tumidus* individual biomarkers of genotoxicity did not show a consistent trend, but the cumulative criterion of damages revealed a highest impact of pollution near Kalvarija and Šapalai and the lowest one – in Bosai, but compare damages it has no significant differences ($p < 0.05$). Assessing the extent of damage to freshwater mussel populations following the 2015 pollution incident remains challenging due to the lack of detailed pre-disturbance data and the influence of multiple environmental factors. The observed sensitivity of *U. crassus* and *U. pictorum* suggests that these species may serve as useful indicators of ecological disturbance in the Šešupė River system.

Keywords: *Unio*; abundance; contamination; water quality.

Funding: This research was funded by the Research Council of Lithuania, agreement No P-SV-23-424.

Spatial and temporal dynamics of native freshwater mussels in an intermittent Mediterranean stream

Mafalda Gama[1*], Pedro Brandão[1], Filipe Banha[1], and Pedro Anastácio[2]

[1] MARE - Marine and Environmental Sciences Centre/ ARNET - Aquatic Research Network, Departamento de Paisagem, Ambiente e Ordenamento, Escola de Ciências e Tecnologia, Universidade de Évora, 7000-671 Évora, Portugal

* Corresponding author: mgama@uevora.pt

Abstract

Freshwater mussels are key ecosystem engineers in riverine systems, yet they are increasingly threatened by hydrological instability and habitat fragmentation. This study assessed the spatial dynamics of two native unionid species from the Iberian Peninsula, *Unio delphinus* and *Unio tumidiformis*, over a ten-year period in three summer pools of an intermittent stream in southern Portugal. A standardized monitoring framework was used to estimate population density, describe spatial structure, and evaluate the environmental drivers shaping population patterns. Spatial aggregation was quantified using variance-to-mean ratios and kernel density estimation, while interspecific co-occurrence was assessed with the Jaccard index. Temporal and species-specific differences in density were tested using two-way analysis of variance, and the relative influence of environmental, spatial, and temporal predictors were examined using linear models. Both species showed consistently aggregated distributions across all sites, indicating strong clustering within localized microhabitats. Co-occurrence between species was low, suggesting partial habitat segregation. Clear contrasts in population dynamics were detected: *U. delphinus* reached higher densities, occupied a broader spatial range, and showed stronger responses to spatial and temporal predictors, whereas *U. tumidiformis* remained at low density and exhibited greater interannual variability. Although temporal variation was significant for both species, no species-specific temporal response was detected. Hydrological variables had limited explanatory power, suggesting that commonly used environmental descriptors may not adequately capture the processes governing mussels' population dynamics in these systems. Overall, the results indicate that persistence of freshwater mussels in intermittent Mediterranean streams depends strongly on fine-scale spatial heterogeneity, pulse-driven temporal dynamics, and the availability of refuge microhabitats, particularly under stressful conditions. Conservation strategies should therefore prioritize the protection of key microhabitats and incorporate spatial structure and extreme hydrological events into management and restoration planning.

Keywords: freshwater mussels; intermittent rivers; microhabitats; spatial aggregation; conservation

Funding: This research was funded by SOMINCOR/BOLIDEN —Sociedade Mineira de Neves-Corvo through the service contract "Monitorização de bivalves na ribeira de Oeiras (2016–2025)", established with the University of Évora. This work had the support of Foundation for Science and Technology (FCT) through the strategic project awarded to MARE – Marine and Environmental Sciences Centre (UID/04292/2025), and ARNET – Aquatic Research Infrastructure Network (LA/P/0069/2020). The FTC also supports Filipe Banha through an individual contract (CEEC/01896/2021).

Using simulation models as tools for studying the food web and population ecology of freshwater pearl mussel

Sabrina Nykänen[1,*], Jouni Taskinen[1], Timo J. Marjomäki[1] and Anna Kuparinen[1]

[1] University of Jyväskylä, Department of Biological and Environmental Science, 40014 Jyväskylä, Finland

* Corresponding author: sabrina.s.nykanen@jyu.fi

Abstract

Freshwater mussels provide important ecosystem functions but are highly threatened, and key aspects about their ecological roles and recovery potential remain challenging to address empirically. Long lifespans, complex life cycles, and numerous direct and indirect interactions within food webs may limit our ability to observe underlying mechanisms and evaluate management actions within relevant timescales. Simulation models provide powerful tools for understanding such processes and for guiding management. However, their application in freshwater mussel ecology and conservation studies remains limited. We present two modelling approaches that illustrate how simulation models can be used to address different questions. First, a boreal stream food web model, based on allometric scaling laws, is used to examine freshwater pearl mussels as mediators of resource flows via biodeposition. The results imply that mussels do not simply provide subsidies but redistribute energy within the system: the production of biodeposits benefits some organisms while simultaneously reducing resources available to others, generating both competitive interactions and bottom-up effects. The magnitude of these effects is sensitive to mussel assimilation efficiency, highlighting it as an important but poorly studied physiological process in mussel ecology. Second, an individual-based population model is developed to explore freshwater pearl mussel recovery potential following prolonged periods of unsuccessful recruitment, as well as the effectiveness of juvenile stocking in supporting population recovery. Given the long timescales involved, such dynamics are difficult to assess empirically. Preliminary simulations indicate that uncertainties in key aspects of mussel life history, such as survival in early life-stages and recruitment process, induce considerable uncertainty into model outcomes, underlining their importance for both modelling and conservation. Together, the two models demonstrate how simulation models can improve mechanistic understanding, identify key knowledge gaps, and support more informed management.

Keywords: ecosystem modelling; functional role; management; population dynamics

Funding: This research was funded by the OLVI FOUNDATION (SN), the FINNISH FOUNDATION FOR NATURE CONSERVATION (SN), the DOCTORAL SCHOOL OF UNIVERSITY OF JYVÄSKYLÄ (SN), the EUROPEAN RESEARCH COUNCIL, grant number 770884 (AK), and the EU LIFE PROGRAMME, grant number LIFE20/NAT/FI/000611 (JT).

Do size and depth matter – some world records among freshwater pearl mussels?

Juha Syväranta[1*], Panu Oulasvirta[1], Jouni Leinikki[1] and Visa Tolonen[1]

[1] Alleco Ltd, Olarinluoma 7, 02200 Espoo, Finland

* Corresponding author: juha.syvaranta@alleco.fi

Abstract

The long-lived freshwater pearl mussel (FPM, *Margaritifera margaritifera*) is a fascinating species whose presence indicates good water quality. Alleco Ltd has monitored the status of FPM populations over the past 35 years in more than 120 rivers across Finland. The accumulated data include some extremes from the world of FPM, possibly even world records for the species. FPM continues growing throughout its life, although growth slows significantly after the age of 40. The largest individuals are typically 120–140 mm in shell length. In 2023, we found an individual specimen measuring as much as 183 mm in length. As far as we know, this is the largest FPM ever measured, both in the Nordic countries and globally. The pearl mussels in this particular river are generally quite large, and the record size does not necessarily mean that the individual is exceptionally old. In Finland, where forestry dominates much of the landscape, the present FPM populations are mostly found in small, clear headwater brooks where water quality has remained good. On the other hand, large and deep rivers have been studied insufficiently. In 2025, during the bridge construction work on River Emäjoki in northern Finland, we discovered FPM at a depth of 10.4 meters. To our knowledge, this is the deepest reported observation of the species in Finland and worldwide. The finding demonstrates that FPM can also inhabit deep bottoms in large rivers and highlights the need to survey the main channels of large rivers more thoroughly.

Key words: Freshwater pearl mussel, record depth, record size, big rivers

Ecological functions of freshwater mussel shells for the macroinvertebrate community

Marie von Wesendonk[1], Joachim Pander[1], Małgorzata Ożgo[2], Juergen Geist[1*]

[1] Aquatic Systems Biology Unit, TUM School of Life Sciences, Technical University Munich, Muehlenweg 22, D-85354 Freising, Germany

[2] Department of Evolutionary Biology, Kazimierz Wielki University, Ossolińskich 12, 85-064 Bydgoszcz, Poland

* Corresponding author: geist@tum.de

Abstract

The ecological functions of freshwater mussels are widely recognized, as is their role in enhancing the ambient macroinvertebrate community. A comprehensive understanding of species-specific ecological roles constitutes a critical foundation for effective conservation and ecosystem management strategies. However, due to a lack of empirical data, the functional role of dead freshwater mussel shells as habitat for other species remains unclear. Drawing primarily from research in marine ecosystems, we hypothesized that mussel shells enrich riverbed habitat structure by providing diverse microhabitats, especially for macroinvertebrates. We conducted a field experiment in which shells of native freshwater mussel species (*Margaritifera margaritifera*, Unio crassus, Anodonta spp.) were exposed using wire cages in three mussel streams. Colonization by macroinvertebrates was compared to controls without shells. An effect of mussel shells was observed in each stream. Although overall the differences between streams and seasons exceeded the effect of exposing mussel shells on the macroinvertebrates community level, there was a positive trend for a higher abundance of predators and filter feeders in the cages with mussel shells. Notably, there was a clear positive effect of mussel shells on specific species, such as two crayfish species *Astacus astacus* and *Pacifastacus leniusculus*. The findings of this study indicate that dead shells provide important microhabitat functions if a threshold volume of shells (>0.1 m2 shell surface with a surface ratio of 1.6 shell surface/riverbed) is exceeded and shells should therefore be retained in aquatic ecosystems. Additionally, mussel shells can be utilized to promote target species for conservation such as crayfish.

Keywords: Freshwater mussel shell; Macroinvertebrates; Ecosystem engineer; Crayfish; Aquatic microhabitats

Funding: This research was funded by a scholarship from the Hanns-Seidel-Stiftung awarded to Marie von Wesendonk.

Do unionid freshwater mussels incur reproductive costs during the incubation of the bitterling fish?

Anna Maria Łabęcka [1*], **Martin Reichard** [2, 3, 4]

[1] Jagiellonian University, Faculty of Biology, Institute of Environmental Sciences, Life History Evolution Group, Gronostajowa 7, 30-387 Kraków, Poland, ORCID 0000-0002-8810-7093

[2] Institute of Vertebrate Biology, Czech Academy of Sciences, Květná 8, 60365 Brno, Czechia

[3] University of Łódź, Faculty of Biology and Environmental Protection, Department of Ecology and Vertebrate Zoology, Banacha 12/16, 90-237 Łódź, Poland

[4] Masaryk University, Faculty of Science, Department of Botany and Zoology, Kotlářská 2, 611 37 Brno, Czechia

* Corresponding author: anna.labecka@uj.edu.pl

Abstract

Unionid mussels belong to one of the most threatened groups of animals. Their decline is primarily driven by anthropogenic pressures, including habitat transformation and loss, as well as climate change. The role of interspecific interactions in shaping mussel condition and reproductive success remains poorly understood. Therefore, the aim of our study was to assess the reproductive costs imposed on unionids by ostracophilous fishes.

In an in-situ experiment conducted in a Morava River oxbow lake, we tested the effect of the bitterling *Rhodeus amarus* on the reproduction of its host, the swollen river mussel *Unio tumidus*. Bitterling broods were incubated by male, female, and hermaphroditic mussels, although males hosted higher numbers of fish offspring. Bitterling eggs and embryos deformed the gill brood chambers of mussels. Females parasitized by bitterling exhibited reduced fecundity, expressed as fewer ovulated oocytes and more numerous degenerated cells. At the same time, mussel ovaries contained follicles with developing oocytes that may represent a source of subsequent cohorts of germ cells within the same reproductive season.

Our results indicate that the incubation of bitterling embryos imposes substantial reproductive costs on *U. tumidus*. However, the prolonged gonadal activity of mussels, allowing multiple spawning events within a single reproductive season, may partially compensate for the effects of fish parasitism. We suggest that such reproductive behaviour may represent a general response of mussels to environmental stress. Asynchronous oocyte maturation may lead to the sequential deposition of oocytes into brood chambers. This process could favour multiple paternity and potentially enhance the genetic diversity of offspring. In turn, the sequential release of offspring throughout the reproductive season may reduce the risk of reproductive failure under unfavourable environmental conditions.

Keywords: brood parasitism; life history; multiple spawning; reproductive activity

Funding: The research was supported by the Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University (N18/DBS/000003) and Czech Science Foundation (GACR) (21-00788X).

Hidden Manipulators: The Influence of Parasites on the Behavior of Freshwater Mussels

Daria Skibińska[1], Maria Urbańska[1], Nicoletta Riccardi[2] and Sandra Kaźmierczak [1,*]

[1] Department of Zoology, Poznan University of Life Sciences

[2] CNR IRSA Verbania Pallanza, Italy

* Corresponding author: sandra.kazmierczak.kazik@gmail.com

Abstract

Trematodes of the genus *Rhipidocotyle* are among the organisms that parasitize freshwater mussels. Numerous studies have shown that these infections negatively impact their hosts. During the early stages of infection, the parasites invade the reproductive system, leading to castration. In later stages, they migrate to the hepatopancreas and eventually to the gills, considerably decreasing the mussels' chances of survival in their natural habitat. Many publications investigating the interactions between freshwater mussels and trematodes of the genus *Rhipidocotyle* focus mainly on reduced reproductive capacity and host-selection preferences. In contrast, relatively few studies have examined the effects of these parasites on mussel behaviour. To investigate whether *Rhipidocotyle campanula* parasites influence the behaviour of *Unio elongatulus*, experiments were carried out on 100 individuals. Mussels were subjected to valvometry experiment using Hall sensors to measure gapping in the presence and absence of fish species: White Cloud Mountain minnow (*Tanichthys albonubes*) and Zebrafish (*Danio rerio*), In addition, a modified open-field test was also performed with continuous recording method in the presence and absence of above-mentioned fish species. Infected individuals were identified through gonadal biopsies, and the results were later confirmed by dissection. The study demonstrated that parasitized mussels exhibited behavioural differences compared with non-infected individuals when exposed to a potential next intermediate host.

Keywords: trematodes; Hall sensors; mussel behaviour

A Diagnosis of Knowledge on South American Freshwater Bivalves

Agustín Bassó[1,2,*]

[1] Laboratorio de Ecología Molecular Aplicada (LEMA), Instituto de Ciencias Veterinarias del Litoral (ICiVet-Litoral), Facultad de Ciencias Veterinarias (FCV), Universidad Nacional del Litoral (UNL) / Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET).

[2] Escuela Superior de Sanidad (ESS), Facultad de Bioquímica y Ciencias Biológicas (FBCB), Universidad Nacional del Litoral.

* Corresponding author: abasso@fbcb.unl.edu.ar

Abstract

South America harbors one of the world's most diverse yet least studied freshwater bivalve faunas, spanning major hydrographic systems including the Amazon, La Plata, Orinoco, São Francisco, Magdalena-Cauca, and Patagonian basins. Despite their ecological importance as ecosystem engineers, freshwater bivalves remain largely absent from local and regional conservation agendas. This keynote synthesizes current knowledge on the diversity, biogeography, threats, and conservation needs of South American freshwater bivalves while highlighting the foundations for a coordinated continental conservation strategy. The presentation will examine major knowledge gaps in taxonomy, life-history traits, host-fish relationships, and distribution data that hinder effective conservation assessments and management actions. Special attention will be given to the rapid hydro-morphological transformation of South American river systems caused by hydropower expansion, industrial waterways, dredging, pollution, land-use, invasive species, and climate change. These stressors are fragmenting river connectivity and accelerating the decline of native bivalve populations across the continent. The talk will incorporate socio-cultural perspectives between Indigenous and local communities, including their historical use as food, tools, ornaments, ceramic temper, and cultural symbols. These perspectives emphasize that freshwater bivalves represent not only biological heritage, but also biocultural heritage deeply linked to riverine identities. Finally, recognizing that freshwater biodiversity decline is a global process driven by shared pressures, the keynote will emphasize the need for coordinated action at an international scale. In this context, it will explore emerging opportunities for conservation through regional collaboration, ecosystem service valuation, environmental governance, and innovative restoration strategies aimed at strengthening the resilience of freshwater ecosystems.

Keywords: Neotropics; Biodiversity; Conservation; Unionida

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Reproductive mode and hybridisation shape conservation genomic patterns in *Anodonta* freshwater mussels

Ellika Faust[1,2,+], Julie Conrads[1,+], Marco Giulio[1], Claudio Ciofi[3], Chiara Natali[3], Philine G. D. Feulner[2] and Alexandra A.-T. Weber[1]*

[1] Department of Aquatic Ecology, Swiss Federal Institute of Aquatic Science and Technology (Eawag), Dübendorf, Switzerland

[2] Department of Fish Ecology and Evolution, Swiss Federal Institute of Aquatic Science and Technology (Eawag), Kastanienbaum, Switzerland

[3] Department of Biology, University of Florence, Sesto Fiorentino (FI), Italy

[4] Institute of Ecology and Evolution, University of Bern, Bern, Switzerland

* Corresponding author: Alexandra.weber@eawag.ch

[+] Equal contribution

Abstract

Freshwater mussels are among the most threatened animal groups in Europe, yet genomic information is still rarely used in conservation assessments. Genetic indicators such as diversity, inbreeding and effective population size can provide important information on extinction risk, but their interpretation depends strongly on species biology. We investigated this issue in *Anodonta* freshwater mussels in Switzerland, focusing on species that differ in reproductive mode and conservation context. We generated draft genomes for the hermaphroditic *Anodonta cygnea* and the gonochoric *Anodonta anatina*, and analysed whole-genome resequencing data from 421 individuals collected across 31 Swiss localities. In *A. anatina*, population structure largely followed catchment boundaries, and genetic diversity was higher in larger waterbodies, suggesting that populations in small ponds may be especially vulnerable. Although inbreeding was generally low, effective population sizes were consistently small, often below thresholds associated with long-term persistence. We also found strong genomic divergence between *A. anatina* populations north and south of the Alps, pointing to a potentially undescribed *Anodonta* species in Ticino. Beyond population structure, our results revealed two additional complications for conservation: hybridisation between *A. cygnea* and *A. exulcerata*, indicating permeability between species boundaries, and genomic signatures consistent with facultative selfing or parthenogenesis in *A. cygnea*. This reproductive strategy was associated with reduced genetic diversity, stronger population structure, increased inbreeding and lower effective population size compared with outcrossing *A. anatina*. Together, these findings from Swiss *Anodonta* show that genetic indicators cannot be interpreted in isolation. Reproductive mode, hybridisation and species boundaries fundamentally shape genomic patterns and should be considered when setting conservation priorities for freshwater mussels.

Keywords: *Anodonta*; Switzerland; conservation genomics; reproductive mode; hybridisation

Funding: This research was funded by Eawag Discretionary Funds; HORIZON EUROPE Framework Programme (Grant No. 101059492); Swiss State Secretariat for Education, Research and Innovation (SERI) (Grant No. 22.00173, 24.00054) and UK Research and Innovation (UKRI).

Evaluating the three Rs of conservation utilizing population genomics

David J. Berg [1*] and Steven R. Hein [2,3]

[1] Department of Biology, Miami University, Hamilton, OH USA

[2] Department of Biology, Miami University, Oxford, OH USA

[3] Alaska Marine Mammals Management Program, Anchorage, AK USA

* Corresponding author: bergdj@miamioh.edu

Abstract

The US Endangered Species Act requires that listing and recovery of imperiled species be determined using objective and measurable criteria. Such criteria are then incorporated into species status assessments (SSAs) and species recovery plans (SRPs), the science documents used to inform endangered species management in the United States. Both documents attempt to 1) understand the life history of a target species; 2) evaluate current status of the species; and 3) predict the likelihood of persistence into the future using the Three Rs of conservation biology. 1) Resiliency measures population health. It can be estimated using within-population metrics such as number of private alleles, nucleotide diversity, and genetically effective population size (N_e). 2) Redundancy is primarily concerned with maintaining multiple populations and can be evaluated using measures of population divergence such as F_{ST}, population inference, and estimates of migration rates. 3) Representation focuses on the responses of a species to changing environments by estimating adaptive potential at loci that are likely to be under selection. We illustrate the application of population genomics for determining the Three Rs using *Popenaias popeii*, a federally endangered species from the Rio Grande basin. The five extant populations of this species differ in within-population genetic variation which suggests differences in resiliency. They exhibit limited redundancy, with little-to-no gene flow among populations. The five populations compose three adaptive units, which form the basis of representation. This population genomics framework based on the Three Rs not only characterizes the current conditions of the species, but by examining trajectories of the measurable criteria, it also allows predicting the likelihood of persistence into the future. As population genomic methods become more robust and less expensive, approaches such as these should become routine in the management of imperiled species.

Keywords: resiliency; redundancy; representation; *Popenaias popeii*;

Funding: This research was funded by the New Mexico Department of Game & Fish and the US Fish & Wildlife Service

A population genomics approach to understanding the *Unio crassus* species complex in Poland and Croatia

Arianna Lord[1*], Marco Giulio[1], Jasna Lajtner[2], Stjepan Novosel[2], Marina Piria[3], Ivan Špelić[3], Monika Mioduchowska[4], Katarzyna Zając[5], Tadeusz Zając[5], Alexandra A.-T. Weber[1]

[1] Department of Aquatic Ecology, Swiss Federal Institute of Aquatic Science and Technology (Eawag), Dübendorf, Switzerland

[2] University of Zagreb Faculty of Science, Department of Biology, Rooseveltov trg 6, Zagreb, Croatia

[3] University of Zagreb Faculty of Agriculture, Department of Fisheries, Apiculture, Wildlife Management and Special Zoology, Zagreb, Croatia

[4] Faculty of Biology, Department of Evolutionary Genetics and Biosystematics, University of Gdańsk, Gdańsk, Poland

[5] Institute of Nature Conservation, Polish Academy of Sciences, Kraków, Poland

* Corresponding author: arianna.lord@eawag.ch

Abstract

Unio crassus is a critically endangered species found across Europe and has recently been identified as a complex of several cryptic species. Recent increases in mass extinctions within the *Unio crassus* species complex suggest that global warming, particularly heatwaves, significantly contributes to mussel decline. However, while some populations suffer from high mortality rates, others appear tolerant and unaffected despite elevated temperatures. The relative influence of abiotic factors (e.g. elevated temperatures), biotic factors (e.g. pathogens, parasites), and genetic background (e.g. species identity, ancestry, and population diversity), on mussel population mortality is not well understood. Previous studies on the species complex have largely relied upon mitochondrial data or few nuclear markers, but none has examined the genetic structure of *Unio crassus* populations using whole-genome data. Here we focus on genetic background and explore the population structure of the *Unio crassus* species complex across Poland and Croatia by sequencing over 400 individual genomes from 20 populations per country. We use this genomic data to explore species boundaries, admixture, genetic diversity and connectivity among populations. These results will provide conservation practitioners with a genome-informed basis to identify distinct conservation units, prioritize vulnerable populations, and guide future monitoring and restoration efforts.

Keywords: genomics; population structure; admixture

Funding: This research was funded by the Swiss National Science Foundation, grant number 230666 and Croatian Science Foundation, grant number MAPS-2024-9713.

Range-wide analysis of the phylogeography and genetic variation of *Lampsilis cariosa*, a widespread but potentially at-risk freshwater mussel of North American Atlantic Slope drainages

Paul R. Stanley[1], Cassia Busch[2], Aaron Aunins[2], Miluska Hyde[2], and David Zanatta[1]

[1] Central Michigan University

[2] United States Geological Survey

Abstract

The drainages of the East Coast of North America, referred to as the Atlantic Slope, are isolated from one another, causing patterns of genomic structure to resemble those observed among wildlife populations inhabiting geographic islands. The Atlantic Slope is the native range of the Yellow Lampmussel (*Lampsilis cariosa*), a freshwater mussel in decline and facing a variety of threats across much of its range. The sessile nature of the Yellow Lampmussel makes them particularly vulnerable to the effects of isolation, such as reduced genetic diversity and increased genetic divergence among watersheds. The distribution of Yellow Lampmussel populations was also impacted by Pleistocene glaciation, complicating the genetic effects of isolation. Understanding the patterns of genetic diversity and divergence within and among watersheds is critical for developing conservation strategies to prevent federal listing of this species. Yellow Lampmussels (n=130) were non-lethally sampled across 9 Atlantic Slope drainages from Georgia, USA, to Nova Scotia, Canada. Using ddRAD-seq, a high-throughput genomic sequencing approach, a range- and genome-wide SNP dataset for the Yellow Lampmussel was assembled. This dataset will be used to clarify the phylogeny of the Yellow Lampmussel with respect to other closely related members of the genus *Lampsilis* and determine patterns of genetic diversity and divergence across the Atlantic Slope. We expect phylogenetic and population genetic analyses of the Yellow Lampmussel to largely align with the drainage configuration of the Atlantic Slope. Furthermore, we expect low genetic diversity and divergence in northern Atlantic Slope drainages (e.g., Chesapeake Bay drainages and north) due to recent colonization and potential bottlenecking because of the Pleistocene glaciation, and relatively high genetic diversity and divergence in southern Atlantic Slope drainages due to their longstanding, largely isolated populations. Preliminary analyses suggest potential introgression with closely related species and evidence of population structuring across the Yellow Lampmussel's range.

Keywords: freshwater mussel, phylogeography, genomics, SNPs, North American Atlantic Slope

Funding: This research was funded by U.S. Fish and Wildlife Service.

Population-specific phenotypic plasticity of endangered bivalves in response to extreme events

André Gomes-dos-Santos[1*], Manuel Lopes-Lima[2,3], Beatriz Silva[1], André M. Machado[1], Rui Pinto[1], Martin Osterling[4], Magnus Lovén Wallerius[5], Maria Urbańska[6], Janusz Golski[6], Sławomir Runowski[6], Sandra Kaźmierczak[6], Amílcar Teixeira[7], Ronaldo Sousa[8], L. Filipe C. Castro[1,9], Paulo Castro[8], Francisco Carvalho[8], Elza Fonseca[1], Elsa Froufe[1,10*]

[1] Aquatic Ecology and Evolution (AEE) group - Interdisciplinary Centre of Marine and Environmental Research (CIIMAR), University of Porto, Portugal

[2] CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório; Associado, Universidade do Porto, Portugal

[3] BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Portugal

[4] River Ecology and Management, Research Group RivEM, Department of Environmental and Life Sciences, Karlstad University, Sweden

[5] Department of Biological and Environmental Sciences, University of Gothenburg, Sweden

[6] Department of Zoology, Poznań University of Life Sciences, Poland

[7] CIMO, LA SusTEC, Universidade Politécnica de Bragança, Portugal

[8] CBMA – Centre for Molecular and Environmental Biology/ARNET-Aquatic Research Network & IB-S, Institute of Science and Innovation for Bio-Sustainability, Department of Biology, University of Minho, Portugal

[9] Department of Biology, Faculty of Sciences University of Porto, Portugal

[10] ICBAS - Laboratory of Cytogenetics; School of Medicine and Biomedical Sciences, University of Porto, Portugal

* Corresponding authors: asantos@ciimar.up.pt; efroufe@ciimar.up.pt

Abstract

Freshwater mussels are among the most endangered animal groups, highly sensitive to climate change due to their strict dependence on freshwater habitats. While freshwater mussels are often considered ecologically strict, their distribution across broad environmental gradients raises the possibility of population-specific adaptations mediated by phenotypic plasticity.

This study investigates whether geographically and climatically distinct populations of two freshwater mussel species (*Unio pictorum* and *Unio delphinus*) exhibit different transcriptomic responses to prolonged heat stress and whether these responses reveal signs of local adaptation. We exposed northern and southern populations of both species to gradually increasing temperatures in controlled laboratory conditions, simulating a prolonged thermal extreme event, and RNA-seq was used to quantify differential gene expression.

Results showed strong differences between northern and southern populations of the two species, both in the magnitude and functional composition of transcriptomic responses. Southern populations exhibited intense expression shifts involving classical stress pathways,

heat shock proteins, detoxification (cytochrome P450s), apoptosis, and energy metabolism, while northern populations, particularly *U. delphinus*, showed a markedly subdued response. Notably, *U. pictorum*'s northern population relied heavily on the cytochrome P450 family even at moderate temperatures, while the southern populations of both species activated broader proteostasis and immune responses at higher stress thresholds.

These findings demonstrate clear population-specific phenotypic plasticity, shaped by environmental conditions rather than phylogenetic proximity. They underscore the need for conservation strategies to move beyond species-level management, embracing intraspecific variation as a buffer against climate impacts. As climate change accelerates, safeguarding the evolutionary potential encoded within populations, not just species, is essential to preserving biodiversity resilience.

Keywords: Phenotypic plasticity; Differential gene expression (DGE); Climate change; Heat stress; Unionida

Funding: This research was developed under the project EdgeOmics - Freshwater Bivalves at the Edge: Adaptation genomics under climate-change scenarios (PTDC/CTA-AMB/3065/2020) funded by Fundação para a Ciência e a Tecnologia (FCT) through national funds. FCT also supported AGS (2023.07625.CEE CIND/CP2848/CT0010) and EF (CEECINST/00027/2021/CP2789/CT0003). FCT also provided funds within the scope of the Strategic Funding UIDB/04423/2020, UIDP/04423/2020, and LA/P/0101/2020.

From Habitat Restoration to Optimised Reinforcement: Progressing Freshwater Pearl Mussel Recovery in the River Irt

Sarah Raubenheimer[1*], Chris West[2] and Louise Lavictoire[1]

[1] Freshwater Biological Association, The Ferry Landing, Far Sawrey, Ambleside, Cumbria, LA22 0LP, UK

[2] West Cumbria Rivers Trust, Keswick Convention Centre, Skiddaw Street, Keswick, Cumbria, CA12 4BY, UK

* Corresponding author: sraubenheimer@fba.org.uk

Abstract

Recovery of the freshwater pearl mussel increasingly depends on integrating habitat restoration with supportive breeding and population reinforcement. We present outcomes from 19 years of conservation breeding and translocations in the River Irt, demonstrating how a long-term recovery programme has progressed from restoring habitatcondition to optimising reinforcement strategies. Initial efforts focused on reducing fine sediment inputs and restoring riverbed conditions suitable for juvenile survival. Since 2017, more than 5,000 propagated juveniles have been released to reinforce the remaining population which numbered only 300 aging adults. Monitoring of PIT-tagged juveniles has recorded an average post-release retention of 65% across release sites, demonstrating that habitat restoration and supportive breeding can be successfully integrated to initiate recovery in populations in the wild. Building on these outcomes, the programme is now testing whether reinforcement can be delivered more efficiently. Ongoing trials compare the release of smaller and larger juvenile size classes to evaluate whether reduced rearing time and production costs can be achieved without compromising post-release survival. This work shifts the focus from demonstrating successful reinforcement to identifying strategies that maximise conservation benefit while improving the scalability of recovery programmes. The River Irt provides a long-term example of adaptive management in freshwater pearl mussel conservation, demonstrating how quantitative monitoring can guide the continual refinement of recovery strategies and inform evidence-based reinforcement programmes for threatened populations.

Keywords: freshwater pearl mussel; population reinforcement; habitat restoration, adaptive management, conservation breeding

Funding: This work has been funded from a range of sources including most recently the Environment Agency, Natural England and United Utilities.

ORAL PRESENTATION

Freshwater mussel mass mortality events: current knowledge and future priorities

Daniel A. Cossey[1]*

[1] Department of Zoology, University of Cambridge, Cambridge, CB2 3EJ, UK

* Corresponding author: dac89@cam.ac.uk

Abstract

Freshwater mussel mass mortality events (MMEs) can have devastating consequences, potentially wiping out entire populations of highly threatened taxa and impairing ecosystem functions. Despite recent increases in the frequency of mussel MME reports, the causes of these events often remain elusive. Here, I summarise the current state of mussel MME research. I draw on multiple studies, including work on the Clinch River (USA) mussel MMEs, my recent investigations of Scandinavian pearl mussel MMEs, concerning mortality observations across Europe, unpublished laboratory trials attempting to identify MME drivers by fulfilling Koch's postulates, and new protocols for improved MME study. Using these examples, I provide a synthesis of current knowledge and what needs to be done to better understand, respond to, and manage these events moving forward. In particular, I highlight the need for standardised reporting and sampling of MMEs, the development of more sophisticated methods for assessing mussel health in the field, improved protocols around mussel translocations, and increased efforts to understand mussel diseases. The perspective I present provides a potential starting place for future work addressing and responding to mussel MMEs, an important next step in improving the conservation of these essential taxa.

Keywords: Die-off; Disease; Mussel health, Global declines

Funding: Supported by the Woolf Fisher Scholarship and Whitten Studentship.

ORAL PRESENTATION

Multi-Species Biomarker Assessment of Olive Mill Wastewater Toxicity on Freshwater Bivalves

Silvana Costa[1*], Ronaldo Sousa[2], Fernando Miranda[3], Fernando Teixeira[3], Aya Zidouh[3], Conceição Fernandes[4,5], Luís Dias[4,5], Zulimar Hernandez[5], Moisés Canle López[1], Amílcar Teixeira[4,5]

[1] React! Department of Chemistry, Faculty of Sciences & CICA, University of A Coruña, E-15071 A Coruña, Spain.

[2] CBMA – Centre for Molecular and Environmental Biology/ARNET-Aquatic Research Network/ IB-S, Institute of Science and Innovation for Bio-Sustainability, Department of Biology, University of Minho, Campus Gualtar, 4710-057 Braga, Portugal.

[3] Bragança Polytechnic University, Campus de Santa Apolónia, 5300-253 Bragança, Portugal.

[4] Centro de Investigação de Montanha (CIMO), Universidade Politécnica de Bragança, Campus de Santa Apolónia, 5300-253 Bragança, Portugal.

[5] Laboratório Associado para a Sustentabilidade e Tecnologia em Regiões de Montanha (SusTEC), Universidade Politécnica de Bragança, Campus de Santa Apolónia, 5300-253 Bragança, Portugal.

* Corresponding author: silvanatcosta@gmail.com

Abstract

Olive mill wastewater (OMWW) is a major environmental stressor in Mediterranean regions, producing phytotoxic effluents that may threaten aquatic ecosystems. However, the ecological effects of OMWW discharges are rarely assessed, especially in filter feeders organisms such as freshwater bivalves. Given this gap, the present study evaluated the long-term effects of OMWW exposure (14 days) on four native (*Unio delphinus*, *Unio tumidiformis*, *Anodonta anatina*, and *Potomida littoralis*) and one non-native (*Corbicula fluminea*) freshwater bivalve species. Under controlled laboratory conditions specimens from the five species were exposed to three treatments: two OMWW concentrations (C1: 8.77 mg/L and C2: 21.31 mg/L of organic matter) and a control (CTL: 0 mg/L). At the end of the experiment, neurotoxicity (acetylcholinesterase- AChE) and oxidative stress (superoxide dismutase - SOD, Thiobarbituric acid reactive substances - TBARs) biomarkers were assessed in the gills and in the digestive gland. Results demonstrated higher sensitivity of native species—especially *U. tumidiformis*— showing an overall ineffectiveness of antioxidant mechanisms (SOD) to neutralize reactive oxygen species (ROS), leading to TBARs accumulation and neural inhibition (AChE). In contrast, the non-native species *C. fluminea* respond to the lower OMWW concentration used reducing basal activities such as SOD and AChE, which may be interpreted as a reduction in their metabolic rate, leading to minimal energy expenditure. Moreover, *C. fluminea* exhibited a biphasic response characterized by enzymatic downregulation at lower concentrations and enzymatic upregulation at higher levels, suggesting a higher physiological plasticity compared to native species. Overall, this study underscore the ecological importance of bivalves as sentinel species to assess OMWW pollution, supporting the objectives of the EU Water Framework Directive.

Keywords: Agroindustry, sentinel species, aquatic ecosystems, ecotoxicology, oxidative stress.

Funding: This work was supported by NORTE 2020, through the European Regional Development Fund (FEDER), within the scope of project BagaÇo+Valor (FEDER-072124). The authors also acknowledge the Foundation for Science and Technology (FCT, Portugal) for financial support to CIMO (UIDB/00690/2020 and UIDP/00690/2020) and SusTEC (LA/P/0007/2020). The authors are grateful to the University of A Coruña (Spain) and the Bragança Polytechnic University (Portugal) for the resources and infrastructure provided, which allowed the publication of this paper within the framework of the Doctoral Program in Environmental Science and Technology (UDC).

ORAL PRESENTATION

Using high-resolution chemical analysis to explore patterns of trace element distribution in *Actinonaias ligamentina* shells from the Allegheny River, USA

Kristi Dobra[1]

[1]University of Pittsburgh, Geology and Environmental Science Department, Pittsburgh, PA, USA

Abstract

Freshwater mussels are sedentary animals that mineralize an increment of carbonate shell material each year, preserving a multi-decadal record of stream chemistry and mussel health. These shell records could therefore provide valuable insight into the timing and magnitude of stream pollution events, mussel food sources, habitat preferences, or the effects of dam construction, for example. If the date of shell collection is known, one can select particular years of interest within the shell and extract geochemical and growth information from that year. Using analytical techniques with high temporal resolution, we seek to better define the relationships between stream chemistry, biological factors, and shell composition. Our objectives were to assess patterns of trace element distribution in mussel shells over time, and evaluate how shell chemical composition may inform our interpretation of annual shell growth rates. We measured trace elements in the shells of 33 individual *Actinonaias ligamentina* collected from the Allegheny River in western Pennsylvania, USA. Shells analyzed represent both contemporary and historical museum collections dating back to the late 1800's. We selected *A. ligamentina* for our analysis because it is relatively widespread and abundant throughout the Ohio River watershed (USA). Thin-sections of each shell were made, and ages and growth rates associated with each year of life were determined under a microscope (ages ranged from 9-55 years). Major and trace element chemistry was analyzed using laser ablation inductively coupled plasma mass spectrometry (LA-ICP-MS), which provides sufficient temporal resolution such that annual compositional patterns may be discerned. Chemical composition of co-located river water and sediment porewater were also evaluated. Preliminary results suggest that shells of *A. ligamentina* preserve an annual cyclical pattern of manganese, barium, and strontium. Chemical patterns might therefore be combined with standard age and growth rate determinations (i.e. using microscope) to provide greater fidelity on calendar year assignments for each shell increment. Shell chemical patterns also suggest that strontium may be a useful tracer for stream chemical shifts and/or pollution events.

ORAL PRESENTATION

Sublethal responses of Carter's freshwater mussel- *Westralunio carteri* Iredale 1943- to multiple stressors.

Dulmini Perera[1,*], Stephen Beatty[1], Alan Cottingham[1] and Jake Daviot[1]

[1] Centre for Sustainable Aquatic Ecosystems, Harry Butler Institute, Murdoch University, Murdoch, WA 6150, Australia

* Corresponding author: thaveesha2002@gmail.com

Abstract

This study will investigate how multiple climate-driven stressors influence the behaviour and sublethal physiological responses of *Westralunio carteri*, a threatened freshwater mussel endemic to south-western Australia that has experienced major range contractions due to secondary salinisation and ongoing regional drying and warming. To understand how rising temperatures, increasing salinity, and declining dissolved oxygen may affect the species across its distribution, the project will examine population-level plasticity and resilience in mussels sourced from three thermally divergent river systems: Gingin Brook, the Serpentine River, and the Margaret River. Controlled laboratory experiments will be conducted using recirculating aquaculture systems and custom-built respirometers, where mussels will be gradually exposed to elevated temperatures (up to 30 °C), salinity levels up to 3.0 mg/L, and reduced dissolved oxygen to simulate summer refuge pool conditions. Continuous monitoring of valve-gaping behaviour using Hall-Effect Valvometry will provide high-resolution behavioural data to quantify sublethal stress responses. These experiments will be complemented by analyses of in-situ valve-gape activity collected through an ongoing cybernetic water-quality monitoring program, enabling direct comparison between laboratory and natural environmental responses. Behavioural plasticity will be assessed using valve-opening amplitude modelled with Generalized Linear Mixed Models, while survival analysis will be used to evaluate how different stressor combinations influence survival probabilities. By integrating laboratory and field datasets, the study aims to identify population-specific traits that may confer resilience or vulnerability under future climate scenarios, improve understanding of the mechanistic pathways through which environmental stressors affect *W. carteri*, and provide evidence-based guidance for conservation management, particularly in the protection of thermal refuges and mitigation of salinity and hypoxia risks in south-western Australian river systems.

Keywords: *Westralunio*; freshwater mussels; multiple stressors; valvometry; Australia

ORAL PRESENTATION

Divergent behavioral, metabolic and physiological responses of two salmonids to glochidiosis

Joschka Wiegleb[1], Richard Durtsche[1,2], Mladen Avramović[1], Olle Calles[1], Niclas Carlsson[1], Ann Erlandsson[1], Miguel Gomez[1], Mattias Hansson[1], Lefman L. Kan[1,3], Dennis Leandersson[1], Emil Nordström[1], John Piccolo[1], Fahime Rashidabadi[1], Samuel Shry[1], Johan Watz[1], Eyla Wågemark[1], Martin Österling[1], Sebastian L. Rock[1*]

[1] River Ecology and Management, Research Group RivEM, Department of Environmental and Life Sciences, Karlstad University, 65188, Karlstad, Sweden

[2] Department of Biological Sciences, Northern Kentucky University

[3] Institute for biodiversity and ecosystem dynamics, University of Amsterdam, The Netherlands

* Corresponding author: sl.rock.research@gmail.com

Abstract

Unionid mussels are an endangered order of ecosystem engineers which rely on a parasitic life stage (glochidium) that temporarily infests host fish. *Anodonta anatina* is among the most common mussels in Europe, yet it's effects on host fish have rarely been quantified. The effects of glochidia on salmonids are among the best studied, however, direct comparisons between Atlantic salmon (*Salmo salar*) and brown trout (*S. trutta*) are scarce, and none have investigated their response to *A. anatina*. Existing work has rarely employed robust before-after-control-impact designs (BACI), and few studies simultaneously investigate multiple host responses to parasitism. Here, we used a controlled BACI design to compare the impacts of glochidia from *A. anatina* on juvenile salmon and trout. Fish were exposed to glochidia and monitored before, during and after infestation, alongside uninfested controls. We quantified infestation intensity, growth, metabolic rate, behaviour and several biochemical stress markers. We found that trout were significantly more heavily infested than salmon; this difference was accompanied by unequal growth responses, with the more heavily trout growing more similarly to their uninfested counterparts than the less infested salmon. Metabolically, trout but not salmon suffered from reduced maximum metabolic rate while infested, an effect that does not persist post-infestation. Both species expressed altered behaviour following infestation with trout increasing activity significantly during the period of mussel excystment, supporting prior speculations of host manipulation unionids. We found no differences in biochemical stress markers. The interspecific differences glochidia encystment indicate to a potentially adaptive interactions between *A. anatina* and its host fish and suggest species-specific glochidia coping strategies. The absence of a strong biochemical stress response, despite measurable changes in growth, metabolic rate and behaviour, suggests that glochidia infestation likely operates within the tolerable physiological limits of their hosts. This study illustrates the importance of integrative and comparative approaches when investigating the interactions between mussels and their host fish and provide a robust foundation for future studies on this system to better aid in the conservation of this endangered order.

Keywords: Host–parasite interactions, Salmonids, Endangered species

Funding: This study received funding from the EU LIFE Program (LIFE CONNECTS; LIFE18 NAT/SE/000742, Ecostreams for LIFE; LIFE19NAT/SE/000333, Improve Aquatic LIFE; LIFE23 NAT/SE/101148230) and Karlstad University

ORAL PRESENTATION

From Ecological Disaster to Scientific Opportunity: Structural Studies of Mussel Shells from Lake Orta

Kamil Szpotkowski[1], Maria Urbańska[2], Nicoletta Riccardi[3]

[1] Division of Surface Science, Faculty of Chemical Technology and Engineering, Bydgoszcz University of Science and Technology, Profesora Sylwestra Kaliskiego 7, 85-796 Bydgoszcz, Poland

[2] Department of Zoology, Poznań University of Life Sciences, ul. Wojska Polskiego 28; 60-637 Poznań, Poland

[3] CNR Water Research Institute, Verbania, Italy

Abstract

Lake Orta in northern Italy experienced one of the world's most severe human-induced ecological disasters. Between 1926 and 1980, the lake was heavily polluted by the expanding metallurgical and electroplating industries. The wastewater contained high levels of copper, chromium, zinc, and other substances, resulting in severe acidification, with pH dropping to as low as 3.8 in some areas. Although the lake has since been restored, it remains an excellent model system for studying the life-history strategies of organisms developing in a toxic environment.

The aim of this study was to determine the impact of heavy metals on the structure and morphology of the shells of *Unio elongatulus*. Specimens originating from Lake Orta, specimens from Lake Maggiore used as a reference population, and specimens transplanted from Lake Maggiore to Lake Orta were examined.

A range of analytical techniques was employed in the shell investigations, including powder X-ray diffraction (XRD), scanning electron microscopy (SEM), infrared spectroscopy (FTIR), confocal microscopy, and emission spectroscopy. Protein composition was analysed using denaturing gel electrophoresis.

Powder diffraction analysis enabled the determination of the crystallite size of calcium carbonate forming the inorganic shell layer. Mussels developing in Lake Orta were found to possess smaller calcite and aragonite crystallites. This result may be associated with disturbances in calcium metabolism. Scanning electron microscopy revealed that the overall shell architecture remained consistent across all analysed populations. Infrared spectroscopy confirmed the presence of calcite and aragonite and indicated subtle differences in the proteinaceous component of the shells. Analysis of shell proteins demonstrated differences in the abundance of individual protein fractions. ICP analysis did not detect the presence of metals in the shells.

Based on the results obtained, it can be concluded that the toxic environment affects the metabolism of *Unio elongatulus*; however, it does not significantly alter the shell's composition or structural organisation.

Massive die-off in freshwater mussels: indicators and underlying processes in Unio nanus from the Northern Carpathians

Zając K.[1], Ćmiel A.[1], Lipińska A.[1], Florek J.[2], Zając T.[1]*

[1] Institute of Nature Conservation Polish Academy of Sciences, Al. Adama Mickiewicza 33, 31-120 Kraków

[2] Department of Hydraulic Engineering and Geotechnics, University of Agriculture, al. Mickiewicza 24/28, 30-059 Kraków, Poland

* Corresponding author: tzajac@iop.krakow.pl

Abstract

Massive die-offs of freshwater mussels typically occur during summer. They develop rapidly and are difficult to predict, and because mussel soft tissues decompose quickly, such events often remain unnoticed. In common understanding, these events are usually associated with polluted and/or eutrophic waters. However, mussels of the Unio crassus complex, including U. nanus, typically inhabit clean, well-oxygenated running waters, where such phenomena are not expected. Nevertheless, the abundance of this group has declined dramatically across Poland over the past 25 years. A survey of 20 populations conducted in 2025 revealed that, in contrast to lowland waters, mountain rivers experienced sudden die-offs of populations known for at least a quarter of a century, including those that had been regularly monitored.

In four populations studied over multiple years, so-called background mortality increased during the season, effectively shortening the reproductive period. This suggests that the length of the reproductive season may serve as a useful indicator of habitat quality and expected mortality.

Under mountain conditions, U. nanus occurs in spatially isolated, highly dense populations that are particularly vulnerable to increasing temperatures and habitat desiccation. The disappearance of these source populations may be one of the key drivers of population decline, but at the same time provides insight into the extinction process itself. Such unstable populations are primarily characterised by small body size and a short reproductive period. Environmental factors responsible for their decline include low water levels and rapid habitat degradation due to sedimentation and vegetation overgrowth. Increasing background mortality during the reproductive season may act as an early signal of a massive die-off later in the summer. However, even under such conditions, the presence of even small remnants of source populations can lead to rapid population recovery.

These mechanisms indicate that mountain populations operate within a source–sink system, where small source populations are responsible for maintaining mussel occurrence along the entire river continuum.

Keywords: mortality, life history traits, drought, phenology

Funding: This research was primarily funded by the Institute of Nature Conservation, Polish Academy of Sciences, and partly by the Swiss National Science Foundation (grant no. 230666).

ABSTRACTS

POSTER PRESENTATIONS

Beyond Species Detection: Using eDNA for Genetic Diversity Monitoring in Threatened Mediterranean Freshwater Taxa

Nuno Alves[1,2,*], Elsa Froufe[1], Manuel Lopes-Lima[2] and Manuel Curto[2,3]

[1] CIIMAR - Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Matosinhos, Portugal

[2] CIBIO/BIOPOLIS - Research Center in Biodiversity and Genetic Resources, University of Porto, Vairão, Portugal

[3] BOKU - University of Natural Resources and Life Sciences, Vienna, Austria

* Corresponding author: nunofelix301@gmail.com

Abstract

Mediterranean freshwater ecosystems, particularly in southern Iberian rivers, are increasingly threatened by drought, climate change, hydrological fragmentation, pollution and invasive species. Traditional tissue-based genomics remains the most robust approach for characterizing population structure, genetic diversity and evolutionary units, while environmental DNA (eDNA) offers a non-invasive complement to conventional monitoring, enabling biodiversity and, potentially, intraspecific diversity detection and assessment directly from environmental samples. However, protocols for detecting and monitoring genetic variation within freshwater species remain poorly developed and insufficiently validated. The Critically Endangered freshwater mussel *Unio tumidiformis* and fishes of the genus *Cobitis* were selected as complementary models, representing contrasting components of freshwater biodiversity — an invertebrate bivalve and a vertebrate fish. *Cobitis* comprises cryptic lineages of conservation concern, including Guadiana endemics, while *U. tumidiformis* is among the most threatened freshwater mussels in the region. Both taxa exhibit strong population structure, inhabit fragmented Mediterranean systems and are highly relevant for conservation planning. The hydrologically fragmented Lower Guadiana basin, whose tributaries combine permanent and temporary refugia supporting freshwater communities of high conservation value, is an ideal study system for this project. Coordinated tissue and replicated eDNA sampling will be conducted across Mediterranean Portuguese rivers to establish a comprehensive tissue-based genomic baseline for the target taxa, identifying informative loci and characterizing genetic diversity and population structure. Metabarcoding-based eDNA protocols will then be developed, optimized and validated against this baseline, assessing marker recovery, allele and haplotype detection, population assignment and sensitivity to environmental conditions. Finally, validated eDNA outputs will be integrated with detection probability and occupancy modelling to identify priority populations, refugial habitats and conservation strategies. This project will generate genome-wide genetic information for the target taxa, test eDNA approaches against the tissue-based genomic baseline and evaluate their potential as non-invasive tools for characterizing genetic structure and monitoring intraspecific diversity over time.

Keywords: Environmental DNA (eDNA); Population genomics; Intraspecific diversity; Genetic connectivity; Freshwater ecosystems

Funding: This research received no external funding

From disturbance to opportunity: Beaver slides can promote *U. crassus* reproduction in modified streams

Andreas H. Dobler[1], **Michaela Tille**[1], **Juergen Geist**[1]

[1]Aquatic Systems Biology Unit, TUM School of Life Sciences, Technical University of Munich, Muehlenweg 22, D-85354 Freising, Germany

Abstract

Freshwater mussels of the order Unionida depend on specific host fish for successful larval development. To increase the likelihood of host infection, some species have evolved specialized behavioral and morphological strategies. In the *Unio crassus* complex, females exhibit a shoreward movement during the reproductive period and actively release water jets containing glochidia, thereby enhancing encounters with host fish in shallow near-bank habitats. In disturbed environments, the availability of suitable shallow near-bank habitats can be a critical bottleneck for successful reproduction.

In this study, we investigated the role of beaver slides, which are sloped riverbank structures created by the Eurasian beaver (*Castor fiber*), as potential reproductive habitat for *U. crassus* in structurally modified stream systems. Mussel densities were surveyed across 159 quadrats placed at and adjacent to beaver slides in four streams in Bavaria, Germany.

During the period of larval release, 80% of individuals were recorded within 0.5 m of the riverbank, with highest densities occurring in the immediate vicinity of beaver slides. Mussel densities declined significantly with increasing distance from both the riverbank and the beaver slides.

Our results indicate that beaver slides can locally provide key microhabitats for *U. crassus* reproduction by creating shallow, gently sloping near-bank areas, particularly in hydromorphologically degraded systems such as regulated or channelized streams. While the ecological effects of beaver activity on freshwater mussels are context-dependent and species-specific, our findings highlight the potential of beaver-induced habitat structures to support critical life-history stages of endangered unionids.

A tool for the rapid assessment of mussel condition in the field

Daniel A. Cossey[1]*, Sebastian L. Rock[2], Silvia Giorgia Signorini[3], Camilla Della Torre[3], Martin Österling[2], George Palmer[4], Richard Boothroyd[4], David C. Aldridge[1]

[1] Department of Zoology, University of Cambridge, Cambridge, CB2 3EJ, UK

[2] Department of Biology, Karlstad University, Karlstad, 651 88, Sweden

[3] Department of Biosciences, Università degli Studi di Milano, Milan, Italy

[4] Design & Technical Services Workshop, Department of Engineering, University of Cambridge, Cambridge, CB2 3QZ, UK

* Corresponding author: dac89@cam.ac.uk

Abstract

Freshwater mussels (Unionida) are key to the health of many freshwater systems through the ecosystem functions and services they provide, yet their populations are declining across the globe. To address these declines with appropriate conservation actions, it is necessary to apply informative tools for measuring and monitoring mussel health. To do this, a suite of biomarker methods has been applied to mussels. However, baseline biomarker measurements are often not available, no framework exists for the translation of these methods from research into routine mussel health monitoring, and they are impractical for giving rapid measurements in the field due to the extensive time, expertise, cost, and/or lab processing they require. Here, we developed a tool for measuring mussel valve-closure strength (the mussel stress tester, STer) and aimed to show its applicability as a method for assessing mussel condition by comparing it to established, lab-based biomarker methods. The mussel STer is a specially designed pair of tongs with prongs that can bend when opening a mussel. The tongs give a numerical reading of this prong displacement (the STer value), which is indicative of the mussel's valve closure strength. We showed that measurements with the mussel STer were repeatable and found that STer value was associated with established biomarker assays for stress (acetylcholinesterase activity, glycogen content, and ROS content). However, unlike typical biomarker assays, using the mussel STer requires little user training, minimal costs, and only a few seconds per mussel. Thus, the STer can be applied rapidly in the field to provide estimations of mussel condition, which could be integrated into wider health assessments to inform appropriate conservation action. Additional work is required to assess whether the use of the STer, and associated removal and handling of mussels, causes any long-term harm to individuals, but we envision the widespread application of this tool in rapid mussel health monitoring in the future.

Keywords: Unionid health, disease monitoring, stress measurement, valve closure, mass mortality event methods.

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Thermal tolerance of Carter's freshwater mussel - *Westralunio carteri* Iredale 1934.

Dulmini Perera[1,*], Stephen Beatty[1], Alan Lymbery[1], Alan Cottingham[1] and Jake Daviot[1]

[1] Centre for Sustainable Aquatic Ecosystems, Harry Butler Institute, Murdoch University, Murdoch, WA 6150, Australia

* Corresponding author: thaveesha2002@gmail.com

Abstract

Carter's freshwater mussel *Westralunio carteri*, an endemic species in southwestern Australia, has undergone a ~50% range contraction in recent decades, largely attributed to secondary salinisation and reduced water permanency, yet its thermal tolerance has remained unknown despite predictions that elevated summer temperatures in degraded, low-shading river systems may further drive population declines. This study quantified the upper thermal tolerance of *W. carteri* under controlled laboratory conditions and examined whether these thresholds correspond with the species' distribution in the Harvey River, a heavily channelised system with minimal riparian shading. Mussels were exposed to four temperature treatments (20, 26, 32, and 38 °C; 40 individuals per treatment) for ten days following acclimation, with daily monitoring of mortality. Survival remained 100% at 20 and 26 °C, while complete mortality occurred at 38 °C. Estimated lethal thresholds were LT_{50} = 32.8 °C and LT_{95} = 33.4 °C. To assess field relevance, temperature loggers were deployed at 29 sites across the Harvey River during summer 2022/2023, and mussel surveys were conducted at each site. *W. carteri* populations were detected at 11 sites, ten of which exhibited maximum temperatures below the LT_{50}, and mussel abundance declined with increasing maximum temperature. These findings demonstrate that high summer temperatures already approach or exceed the species' physiological limits at multiple sites, indicating that thermal stress is likely contributing to ongoing declines, particularly in rivers lacking riparian shading. With climate warming expected to intensify thermal extremes across southwestern Australia, elevated temperatures are poised to become an increasingly significant driver of population loss. Restoration actions that enhance riparian shading are therefore recommended to mitigate thermal stress and support the persistence of *W. carteri*.

Keywords: *Westralunio carteri;* thermal tolerance; climate warming; freshwater mussels; riparian shading

Funding: This research received no external funding

Prioritising Space and Actions for Freshwater Mussel Conservation in Southern Portugal

Tamara Spielberger[1], Manuel Lopes-Lima[2,3], Rafael Miranda[4], Janine da Silva[5], Ronaldo Sousa[6] and Joana Garrido Nogueira[2,3,*]

[1] Hochschule Weihenstephan-Triesdorf, Landscape Planning, Germany

[2] BIOPOLIS Program in Genomics, Biodiversity and Ecosystems, CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, Vairão, Portugal

[3] BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661, Vairão, Portugal

[4] University of Navarra. Instituto de Biodiversidad y Medioambiente (BIOMA)

[5] University of Coimbra, MARE/ARNET, Department of Life Sciences, Largo Marquês de Pombal, Coimbra 3004-517, Portugal

[6] CBMA – Centre for Molecular and Environmental Biology/ARNET-Aquatic Research Network/ IB-S, Institute of Science and Innovation for Bio-Sustainability, Department of Biology, University of Minho, Campus Gualtar, 4710-057 Braga, Portugal [5] Biota – Estudos e Divulgação em Ambiente, Ramada, Portugal

* Corresponding author: joana.nogueira@cibio.up.pt

Abstract

Freshwater mussels are among the most threatened faunal groups worldwide, facing severe habitat degradation that is largely driven by anthropogenic impacts. However, spatially explicit conservation action for this taxon remains rare, with previous efforts have been mostly limited to local areas or individual river segments. This study investigates how a multi-action conservation planning approach for freshwater mussels can be operationalised at a regional scale. To this end, a systematic conservation planning approach was applied to freshwater mussels and their host fish across southern Portugal, covering the Sado and Mira catchments and parts of the Guadiana. Sub-basins were assessed for species occurrence and presence of four major threats (barriers, cropland, population density, and climate change), while spatial connectivity was incorporated using both global and action-specific Boundary Length Modifiers. The decision-support tool prioriactions was used to identify priority areas for protection and restoration while accounting for spatial connectivity. The resulting prioritisation showed only limited spatial overlap between the proposed protection areas and the existing protected area network. The precision of management actions and associated cost estimates was constrained by the limited availability of data on freshwater mussels and the threats affecting them. Nevertheless, this study provides a transferable framework for translating conservation needs into spatially explicit management plans that integrate protection and restoration actions to safeguard suitable habitats and mitigate existing threats.

Keywords: Freshwater mussels; Conservation; fish; Restoration; Southern Portugal;

Funding: This research was funded by Associação Viridia – Conservation in Action.

About the presence of *Unio tumidiformis* in the Guadalquivir basin

J. Reis[1,2,3], M. Garcia-Alvarez[1], F. Picazo[4], M.R. Martin-Hervas[5], M. Pola[5], F.J. Galindo[6], D. Acosta[7]

[1] MARE - Marine and Environmental Sciences Centre/ARNET-Aquatic Research Network, Faculdade de Ciências da Universidade de Lisboa, Lisbon, Portugal.

[2] Instituto Português de Malacologia, Albufeira, Portugal.

[3] Biota – Estudos e Divulgação em Ambiente, Ramada, Portugal.

[4] Department of Ecology/Research Unit Modeling Nature(MNat), Facultad de Ciencias, Universidad de Granada, Granada, Spain.

[5] Departamento de Biología; Facultad de Ciencias; Universidad Autónoma de Madrid; Campus de Excelencia Internacional UAM; CSIC; Madrid; Spain; Centro de Investigación en Biodiversidad y Cambio Global (CIBC-UAM). Campus de Excelencia Internacional UAM; CSIC; Madrid; Spain.

[6] Agencia de medio ambiente y agua de Andalucía, Gerencia Provincial de Granada, Granada, Spain.

[7] Dirección General de Política Forestal y Biodiversidad. Consejería de Sostenibilidad y Medio Ambiente, Junta de Andalucía, Sevilla, Spain.

* Corresponding author: joaquim.reis@fc.ul.pt

Abstract

The freshwater mussel *Unio tumidiformis* is one of the most threatened species in the Iberian Peninsula. It is considered Critically Endangered by the IUCN and listed in annexes II and IV of the Habitats Directive (as it has previously been identified as *U. crassus* in the Iberian Peninsula). Up to 80% of its formerly known populations in Portugal and Spain have already disappeared, and climate change models forecast a catastrophic decline of suitable habitat (99% reduction) over the next 20 years. Occasional references to populations found within the Guadalquivir basin are known, with identification relying exclusively on external morphological characteristics. Recent projects in southern Spain have revisited these locations, and other not previously sampled, finding freshwater mussels that are morphologically compatible with being identified as *U. tumidiformis*. We revisited all these populations and made an integrative taxonomic study, including external and internal morphology and genetics (mithocondrial COI sequencing). Even though several specimens presented morphological characters typical of *U. tumidiformis*, genetic results have not yet corroborated this identification. *U. tumidiformis* may either be extinct or extremely rare in this basin, but our results do not allow discarding the possibility of an historical misidentification based on extreme morphological variation in *U. delphinus*, widespread in the region.

Keywords: Unionidae; Endemic; Taxonomy; Morhology; Southern Spain.

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Unintentional establishment of *Magaritifera margaritifera* populations through stocking of *Salmo trutta*

Jon H. Magerøy [1]* and Sebastian Wacker[2]

[1] Norwegian Institute for Nature Research (NINA), Sognsveien 68, 0855 Oslo, Norway.

[2] Norwegian Institute for Nature Research (NINA), P.O. box 5685 Torgarden, 7485 Trondheim, Norway.

* Corresponding author: jon.mageroy@nina.no

Abstract

In several rivers and streams in Oslo and Akershus Counties in Norway, *Margaritifera margaritifera* was discovered at new sites or reappeared at sites where it was thought to have gone extinct. The sites had a history of stocking of *Salmo trutta* from the Sørkedalselva Hatchery. The Sørkedalselva River has a substantial mussel population, and it was known that hatchery trout were getting infected with glochidia until 1993-1994. Thus, it was proposed that the mussel was introduced through the stocking of hatchery trout[1]. We undertook a genetic study of the mussel populations at 13 potential introduction sites, the Sørkedalselva River and six reference sites. The analyses were performed based on 15 microsatellite markers[23], as described by Karlsson et al. (2016)[4]. Genetic heterozygosity, allelic richness and inbreeding coefficient were compared, as well as genetic differentiation. Seven mussel populations at the potential introduction sites showed minimal or no genetic differentiation from the Sørkedalselva population, while three populations showed a substantial genetic differentiation. All these populations showed a substantial differentiation from the reference populations. For the remaining three populations from potential introductions sites, sample sizes were insufficient to make comparisons at a population level. However, for one of the sites individual assignment of mussels suggests that the population also originates from the Sørkedalselva population. Thus, 8 of the 13 populations likely originate from the Sørkedalselva population. These eight populations did not differ substantially in heterozygosity, allelic richness or inbreeding coefficient from the Sørkedalselva population. Thus, indicating that the genetic diversity was transferred from the source population to the introduction sites. Overall, our study shows that it is possible to introduce *M. margaritifera* through host fish to new sites without substantial loss of genetic diversity in the process. Thus, the release of host fish infected with glochidia can be a potential conservation strategy.

Keywords: mussel introductions; stocking fish; genetics; *Margaritifera margaritifera*; *Salmo trutta*

Funding: This research was funded by the County Governor of Oslo and Viken.

Save the Southern Naiads: An Integrated Conservation Strategy for Endangered Freshwater Mussels in Southern Portugal

Liu Manchón[1,*], Keiko Nakamura[2], Joaquim Reis [3,4,5] and Manuel Lopes Lima[1]

[1] BIOPOLIS Program in Genomics, Biodiversity and Ecosystems, CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, Vairão, Portugal

[2] Environmental Service Department, Sociedad Aragonesa de Gestión Agroambiental (SARGA), Zaragoza, Spain

[3] MARE – Marine and Environmental Sciences Centre, Faculdade de Ciências, Universidade de Lisboa, Lisbon, Portugal

[4] Instituto Português de Malacologia, Lisboa, Portugal

[5] Biota – Estudos e Divulgação em Ambiente, Ramada, Portugal

* Corresponding author: liumanchon203@gmail.com

Abstract

Freshwater mussels (naiads) are among the most threatened faunal groups worldwide. In southern Portugal, the native species *Unio tumidiformis*, *Unio delphinus*, *Anodonta anatina*, and *Potomida littoralis* inhabit Mediterranean rivers characterized by highly variable flow regimes and prolonged summer droughts. Their complex life cycle, which depends on specific fish hosts for larval development, together with increasing habitat degradation, reduced water availability, and the impacts of climate change, has resulted in severe population declines. Over the past two decades, these species have declined by more than 70% and are now restricted to a limited number of sites within the Sado, Mira, and Guadiana river basins. Recent national assessments classify these mussels as Endangered or Critically Endangered, while predictive distribution models suggest that some populations could disappear within the next two decades if current environmental trends continue.

The “Save the Southern Naiads” project was established to support the conservation and recovery of these threatened species through an integrated approach combining ex situ and in situ conservation measures. The initiative includes the establishment of an ex situ conservation facility ("Ark") and a captive breeding programme at the Mértola Biological Station to safeguard genetically representative populations and support future population reinforcement. At the same time, priority habitats are being identified for protection, restoration, and potential reintroduction, while conservation actions are supported by stakeholder engagement, long-term monitoring, and environmental education programmes targeting local communities and schools.

By integrating scientific knowledge, conservation management, and public participation, this initiative provides a comprehensive framework for safeguarding freshwater mussels in southern Portugal as well as contributing to the long-term conservation of Mediterranean freshwater ecosystems under increasing climatic and anthropogenic pressures.

Keywords: Freshwater mussels; Conservation; Captive breeding; Southern Portugal;

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Evaluation of oxidative stress and neurotoxicity in the Asian Clam as a bioindicator

Natalia Guillén[1*], Eva Elbaile[2], Cecilia Sosa[1], Carlos Salinas[2], Joaquim Boix[2], Keiko Nakamura[2]

[1] Laborator y of Molecular Toxicology, Department of Biochemistry and Cell and Molecular Biology, University of Zaragoza, Zaragoza, Spain.

[2] Environmental Service Department, Sociedad Aragonesa de Gestión Agroambiental (SARGA), Zaragoza, Spain.

* Corresponding author: nguillen@unizar.es

Abstract

Within the framework of the recovery plan for the critically endangered freshwater mussel *Pseudunio auricularius* in Aragon (Spain), the non-native *Corbicula* spp. was utilized as a surrogate species. The objective was to analyse biomarkers of Total Oxidant Status (TOS) and Total Antioxidant Capacity (T-AOC) to determine the oxidative stress levels in these filter-feeding organisms, as well as the enzymatic activity of acetylcholinesterase (AChE). Data were normalized by protein concentration in individuals collected during July 2025 across three locations (M1, A2, and J3) along the Ebro River, upstream from Zaragoza (Spain). Preliminary results revealed significant spatial variations between sites: site J3 exhibited the highest TOS levels, coupled with the highest mean T-AOC values, suggesting a potential metabolic compensatory mechanism. Sites M1 and A2 showed lower TOS values, particularly M1, and a more stable antioxidant reserve. AChE activity also displayed significant differences, with lower activity recorded in M1 and A2 compared to J3. This inhibition indicates a higher exposure to pollutants such as heavy metals or pesticides with potential neurotoxic effects on these organisms. These findings underscore the potential of the Asian clam as a sentinel species and provide critical ecotoxicological baseline data for the conservation and habitat restoration of native unionids.

Keywords: acetylcholinesterase; *Corbicula* spp.; Ebro River; freshwater bivalves; surrogate species.

Funding: This research was partially funded by Government of Aragón and University of Zaragoza.

Effects of degrading freshwater mussel shells on the water chemistry

Marie von Wesendonk[1], Erwin J. J. Kalis[1], Sebastian Beggel[1], and Juergen Geist[1,*]

[1] Aquatic Systems Biology Unit, School of Life Sciences, Technical University of Munich, Freising, Germany

* Corresponding author: geist@tum.de

Abstract

Living freshwater mussels of the order Unionoida are considered important ecosystem engineers for aquatic habitats, but the role of their dead shells in ecosystem dynamics is not yet fully understood. Therefore, we investigated the influence of decomposing dead mussel shells on freshwater chemistry, particularly with regard to their effects on pH and their potential buffering capacity in acidified water bodies through remineralization. We conducted standardized laboratory (28 days) and field (6 months) experiments across gradients of geology (siliceous to carbonate), pH, and conductivity. In the laboratory, freshly dead shells were exposed to nine hydrochemical settings (three media with different ionic strengths × three initial pH levels) to assess their effects on water chemistry. In parallel, shells were deployed in three Bavarian streams with extant mussel populations to monitor shell degradation under natural conditions. In the laboratory experiment, mussel shells increased total hardness, pH, Ca2+ concentrations, and conductivity, which was attributed to the dissolution of CaCO3 from the shells. These effects were stronger in soft than hard water, and in hard water these effects were higher at lower pH values. In the field experiment, the mass loss of the shells was highest in siliceous streams. These findings indicate that dead shells can play a role in buffering pH fluctuations, especially if they occur in high numbers and in acidified siliceous regions with low ionic strength. The stabilizing effect of dead shells on water chemistry should be considered in restoration projects and in decision-making concerning their removal, for example, after mass die-off events.

Keywords: Freshwater mussel shells; calcium carbonate; buffer capacity; acidification; biological remineralization

Funding: This research was funded by the HIT-Umweltstiftung and the Hanns-Seidel-Stiftung, which provided a scholarship to Marie von Wesendonk.

New descriptions of glochidia from the wet-dry tropics of Australia

Michael W. Klunzinger [1,2,3*], Christopher L. Humphrey[4], Emily Poelina-Hunter[5,6] and Hugh A. Jones[7]

[1] Centre for Sustainable Aquatic Ecosystems, Murdoch University, Murdoch, WA 6150, Australia

[2] Department of Aquatic Zoology, Western Australian Museum Collections & Research Centre, Welshpool, WA 6106, Australia

[3] Australian Rivers Institute, Griffith University, Nathan, QLD 4101, Australia

[4] Environmental Research Institute of the Supervising Scientist (ERISS), Department of Climate Change, Energy, the Environment and Water, Darwin, NT 0800, Australia

[5] ARC Centre of Excellence for Indigenous and Environmental Histories and Futures, Monash University, Clayton, VIC 3800, Australia

[6] Madjulla, Inc., Broome, WA 6725, Australia

[7] School of Biological, Earth & Environmental Sciences, University of New South Wales, Sydney, NSW 2033, Australia

* Corresponding author: m.klunzinger@gmail.com

Abstract

Most freshwater mussels (Unionida) are gonochoristic and females brood embryos in interlamellar spaces (marsupia) in demibranchs of ctenidia (gills). The Hyriidae, found in Australasia and South America, have marsupia on the inner pair of demibranchs. Embryos develop to larvae (glochidia in the Hyriidae, Unionidae and Margaritiferidae). Most glochidia attach to the fins and/or gills of fishes as a dispersal mechanism, during which time they undergo metamorphosis to emerge as juvenile mussels. The morphology of glochidia are mechanisms of release from adult females are useful in systematics. In this study, glochidia were collected from live Hyriidae of three species: *Lortiella froggatti* from northern Western Australia and *Alathyria pertexta wardi* and *Velesunio angasi* from northern Queensland. In all three species, glochidia were observed being released as amorphous mucous conglutinates. Specimens were observed under microscopy for 'blinking' behaviour in individuals free of vitelline membranes, indicating maturity. Larval filaments were observed in all three species of live glochidia. Samples were also obtained by dissection and held in river water for 1-2 weeks at room temperature. This allowed glochidia to die naturally and soft tissues to autolyze, leaving empty shells, which were then rinsed with distilled water and transferred to ethanol. Samples of ethanol-preserved glochidia were pipetted onto specimen stubs mounted with double-sided carbon tape, sputter-coated with gold and examined under scanning electron microscopy (SEM). Glochidial shells were measured from scale-imprinted SEM photographs for height, length, hinge length, larval hook length and angle of obliquity (formed between the ventral apex and midpoint of a valve). Glochidia of all three species have sigmoidal hooks terminating to a sharp singular point in each valve and each possess a larval filament. Shells are smooth and dotted with pores, subtriangular isosceles measuring 250-270 µm in length, 220-270 µm in height and 240-260 µm in hinge length. Larval hooks measure 60-70 µm in length. Angle of obliquity measured 9-11°. Overall, there is only subtle morphological difference between the three species of glochidia. This information will be useful in future systematics work.

Keywords: Bivalvia; Hyriidae; dispersal; parasite; fish

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Artificial light at night impacts the behaviour and gene expression of an endangered unionid mussel.

Sebastian L. Rock[1*], Olle Calles[1], Elza Fonseca[2], Elsa Froufe[2,3], André Gomes-dos-Santos[2], Jeroen Hubert[4], Manuel Lopes-Lima[5,6], P. Anders Nilsson[7], Johan Watz[1], Martin Österling[1]

[1] River Ecology and Management, Research Group RivEM, Department of Environmental and Life Sciences, Karlstad University, 65188, Karlstad, Sweden

[2] CIIMAR - Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Terminal de Cruzeiros do Porto de Leixões, 4450-208 Matosinhos, Portugal

[3] ICBAS - Laboratory of Cytogenetics; School of Medicine and Biomedical Sciences, University of Porto

[4] Marine Animal Ecology (MAE) chairgroup, Wageningen University, P.O. Box 338, 6700 AH Wageningen, The Netherlands

[5] CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório; Associado, Universidade do Porto, Vairão, Portugal

[6] BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Vairão, Portugal

[7] Lund University, Department of Biology - Aquatic Ecology, 223 62 Lund, Sweden

* Corresponding author: sl.rock.research@gmail.com

Abstract

Artificial light at night (ALAN) is a global and increasingly recognized ecological stressor that profoundly alters the structure and functioning of freshwater ecosystems. Even at very low levels ALAN can disrupt organism-level processes, which scale upwards, altering ecological processes and destabilizing community structure. Analogously, freshwater mussels are a globally endangered order of well-recognized ecosystem engineers with a variety of ecosystem functions across freshwater habitats. Large mussel assemblages have significant effects on nutrient cycling, provide habitat for benthic invertebrates and alter fish behaviour. As with ALAN, these organism-level effects propagate through ecosystems, scaling upwards, enhancing ecological processes and supporting food webs. Despite their individual ecological significance, the interaction between the two ecosystem-altering forces, ALAN and freshwater mussels, remains poorly understood. We investigated the impacts of constant light exposure on the behaviour and gene expression of the thick-shelled river mussel (*Unio crassus*), one of Europe's most endangered freshwater bivalves. Gravid mussels were brought into laboratory conditions where valve gape and reproductive behaviour could be observed in a controlled setting, after which tissue samples (foot, mantle and gill) were collected to assess differential gene expression between exposed and control groups, requiring the construction of a novel genome map for the species. ALAN-treated individuals lost their natural diel rhythm and had altered gene expression indicative of perturbed cellular communication, structural maintenance, oxidative stress-response pathways, and immune resilience. Our results indicate that ALAN can act as a significant stressor to freshwater mussels, likely reducing their overall ecological impact. Our results demonstrate that ALAN directly affects an important ecosystem engineer. When the effects of ALAN on *U. crassus* are combined with the other effects ALAN has been previously

demonstrated to have on freshwater ecosystems, ALAN becomes further cemented as a pervasive ecological disrupter necessitating further study.

Keywords: Environmental pollution, Genomics, Valvometry, Light pollution, Endangered species

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Parasitism under the spotlight: artificial light at night disrupts circadian and redox balance in fish, enhancing fitness of parasitic glochidia.

Sebastian L. Rock[1†], Sophia Schumann[2†], Elisabetta Piva[3], Olle Calles[1], Franz Hölker[4], P. Anders Nilsson[5], Sara Pacchini[2], Johan Watz[1], Gianfranco Santovito[2*], Martin Österling[1*]

[1] River Ecology and Management, Research Group RivEM, Department of Environmental and Life Sciences, Karlstad University, 65188, Karlstad, Sweden

[2] Technical University Dresden, Department of Hydrobiology, 01217 Dresden, Germany

[3] University of Padova, Department of Biology, 35131 Padova, Italy[4] Marine Animal Ecology (MAE) chairgroup, Wageningen University, P.O. Box 338, 6700 AH Wageningen, The Netherlands

[4] Leibniz-Institute of Freshwater Ecology and Inland Fisheries, Müggelseedamm 310, 12587 Berlin, Germany

[5] Lund University, Department of Biology - Aquatic Ecology, 223 62 Lund, Sweden

[6] University of Padova, Department of Industrial Engineering, 35131 Padova, Italy

* Corresponding authors: gianfranco.santovito@unipd.it & martin.osterling@kau.se

† Authors share first authorship, listed alphabetically

Abstract

Artificial light at night (ALAN) is an environmental pollutant that disrupts natural light-dark cycles and can have negative effects on ecosystems. While it has been proposed that ALAN could affect host-parasite interactions, few have directly studied the interaction. The thick-shelled river mussel (*Unio crassus*) is an endangered and well-recognized ecosystem engineers that temporarily parasitises fish such as the Eurasian minnow (*Phoxinus phoxinus*). We investigated whether ALAN alters host-parasite interactions by inducing oxidative stress and interfering with host fish circadian regulation. We demonstrate that parasite encystment rates were higher under ALAN disturbance than under natural circadian pattens. ALAN exposure, but not glochidiosis, reduced total antioxidant capacity (TAC) and superoxide dismutase (SOD) activity, indicating that oxidative stress responses were primarily driven by light-induced stress rather than parasitism. The decrease in SOD enzymatic activity under ALAN, without corresponding changes in sod1 or sod2 transcription, suggests the involvement of post-transcriptional regulatory mechanisms. ALAN strongly upregulated the circadian gene clocka, consistent with light-induced circadian disruption. Notably, a negative correlation between clocka expression and SOD activity suggests a redox-sensitive interplay between oxidative stress and circadian regulation. Unexpectedly, clocka upregulation was absent in parasitised fish exposed to ALAN, suggesting that glochidia may reduce light-induced circadian disruption. This raises the possibility that parasite infection could counteract ALAN-induced clocka upregulation through yet-unknown physiological mechanisms. The results demonstrate that ALAN functions as a complex ecological driver, presenting a conservation paradox by simultaneously impairing fish populations and enhancing the fitness of endangered mussels.

Keywords: Artificial Light at Night (ALAN); Host-Parasites Interactions; Oxidative Stress; Circadian Disruption

Funding: This study received funding from the EU LIFE Program (Project acronym: LIFE CONNECTS; LIFE18 NAT/SE/000742), European Union Horizon 2020 Research and Innovation Programme under the Marie Sklodowska-Curie Actions (Project acronym: RIBES; Grant Agreement No. 860800), Karlstad University, Lund University, University of Padova & the Leibniz-Institute of Freshwater Ecology and Inland Fisheries.

Behavioural monitoring of Native versus Non-native bivalves exposed to olive mill wastewaters: A Valvometric Comparative Study

Silvana Costa[1*], Ronaldo Sousa[2], Francisco Carvalho[2], Paulo Castro[2], Fernando Miranda[3], Fernando Teixeira[3], Amílcar Teixeira[4,5]

[1] React! Department of Chemistry, Faculty of Sciences & CICA, University of A Coruña, E-15071 A Coruña, Spain

[2] CBMA – Centre for Molecular and Environmental Biology/ARNET-Aquatic Research Network/ IB-S, Institute of Science and Innovation for Bio-Sustainability, Department of Biology, University of Minho, Campus Gualtar, 4710-057 Braga, Portugal.

[3] Bragança Polytechnic University, Campus de Santa Apolónia, 5300-253 Bragança, Portugal.

[4] Laboratório Associado para a Sustentabilidade e Tecnologia em Regiões de Montanha (SusTEC), Universidade Politécnica de Bragança, Campus de Santa Apolónia, 5300-253 Bragança, Portugal.

[5] Centro de Investigação de Montanha (CIMO), Universidade Politécnica de Bragança, Campus de Santa Apolónia, 5300-253 Bragança, Portugal.

* Corresponding author: silvanatcosta@gmail.com

Abstract

The global olive oil industry has experienced a significant paradigm shift over the last decade, characterized by an accelerated expansion of cultivation areas and enhanced processing efficiencies. However, this industrial success is intrinsically linked to the generation of massive volumes of complex waste streams, as olive mill wastewaters (OMWW). Due to their high organic load and phytotoxic phenolic compounds, OMWW discharges, infiltrations and leakages, pose a critical environmental hazard to freshwater ecosystems. While traditional biochemical biomarkers provide insights into chronic metabolic strain, real-time behavioral monitoring offers immediate, non-invasive "early warning" indicators of anthropogenic stress. This study evaluates the efficacy of high-frequency valvometry—utilizing Hall-effect magnetic sensors—to detect the impacts of environmentally relevant OMWW concentrations (C1: 8.77 mg/L; C2: 21.31 mg/L of organic matter) on bivalve gaping behavior. A 14-day laboratory exposure assay was conducted using four native species of high conservation value from Iberian watersheds (*Unio delphinus*, *Unio tumidiformis*, *Anodonta anatina*, and *Potomida littoralis*) and the highly resilient invasive non-native species *Corbicula fluminea*. Behavioral responses, specifically valve gaping frequency and opening amplitude, were continuously monitored under single moderate and severe exposure scenarios to mimic industrial discharges along the year two-way ANOVA with fixed factors Species (*U. delphinus*, *U. tumidiformis*, *A. anatina*, *P. littoralis*, *C. fluminea*) and Treatment (CTL, C1, C2), including the Species × Treatment interaction, to decode species-specific sensitivity thresholds and recovery rates. It is anticipated that OMWW exposure induces significant, dose-dependent alterations in valve movement patterns, contrasting distinct avoidance strategies between sensitive native species and the non-native competitor. By bridging the gap between ecotoxicology and real-time behavioral ecology, these preliminary findings validate high-frequency valvometric platforms as robust, automated tools for environmental impact assessment. Ultimately, this research supports the development of ecological monitoring frameworks to safeguard Mediterranean aquatic biodiversity under increasing agro-industrial pressure.

Keywords: Agroindustry, sentinel species, aquatic ecosystems, hall sensors, valve movements.

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The bivalve *Unio elongatulus* as sentinel of environmental quality: a case study in Lake Orta

Silvia Giorgia Signorini[1*], Gianmaria Lungo[1], Mattia Alessi[1], Adele Meda[1], Cristina Cremonesi[1], Stefano Magni[1], Andrea Binelli[1], Giovanni De Bernardi[2], Sara Castiglioni[3], Noelia Salgueiro-Gonzalez[3], Nicoletta Riccardi[1], Camilla Della Torre[1]

[1] Dipartimento di Bioscienze, Università degli Studi di Milano

[2] Ecomuseo del Lago d'Orta e del Mottarone

[3] Dipartimento di Ricerca Ambiente e Salute, Istituto di Ricerche Farmacologiche Mario Negri - IRCCS

*Corresponding author: silvia.singorini@unimi.it

Abstract

The Orta Lake has historically been affected by severe industrial pollution, which has led to the disruption of its biological communities. Remediation measures, including liming, have significantly contributed to the ecological recovery. However, the ecosystem has not yet been fully restored, and the lake is vulnerable to the introduction of new sources of pollution, that need to be addressed.

Therefore, the INTEGRARE project aims to assess the presence of contaminants of industrial and domestic origin and their biological effects to the benthic communities. To this goal, we carried out an active biomonitoring using the bivalve *Unio elongatulus*, a native species that has recently recolonized the lake.

Individuals from a population of Lake Maggiore were transferred and kept into cages, placed at five sites of the Cusio area: Imolo, San Maurizio d'Opaglio, Pella, Omegna and Bagnera, characterized by different levels of anthropogenic pressure. The bivalves were sampled after 2 and 6 months and heart rate was measured together with a suite of biochemical biomarkers related to: energetic metabolism (electron transport activity), oxidative stress (levels of reactive oxygen species, activity of the enzymes SOD, CAT and GST), oxidative damage (lipid peroxidation), and neurotoxicity (acetylcholinesterase activity). Moreover, the same endpoints were measured in organisms of the resident populations of Lake Orta located at Gozzano and of Bagnera.

The population of Lake Orta and Lake Maggiore showed a different profile of biomarkers, in response to different environmental conditions occurring in the two lakes. The parameters analyzed showed no significant differences among the different sites, suggesting the absence of point sources of contamination in the Orta Lake. The translocation procedures and the analyses of biological responses applied in this study confirmed the suitability of using *U. elongatulus* as a model organism for assessing the quality of lake ecosystems.

Keywords: *Unio elongatulus*; Lake contamination; Biomonitoring; Biomarkers

Funding: This research was funded by Cariplo Foundation Bandi Emblematici Provinciali Novara

Practical guidance for improving captive rearing success in *Margaritifera margaritifera conservation programmes*

Catarina Varela[1]*, Adolfo Outeiro[1] and Paz Ondina[1]

[1] Universidade de Santiago de Compostela; Dpto. de Zooloxía, Xenética e Antropoloxía Física. Campus Terra. IBADER. Spain.

* Corresponding author: catarina.varela@usc.es

Abstract

Freshwater mussels are among the most threatened faunal groups worldwide, with many species undergoing severe declines due to habitat degradation, altered river functioning and widespread recruitment failure. In this context, captive rearing has become an increasingly conservation tool, particularly for long-lived species such as *Margaritifera margaritifera*, whose natural recovery is often constrained by high mortality during early post-parasitic stages.

This study presents practical recommendations derived from 13 years of applied experience in the captive rearing of *M. margaritifera*, with emphasis on improving juvenile survival through a staged, size-dependent culture strategy. After excystment, post-parasitic juveniles are first selected according to vitality and shell size, allowing poorly developed individuals to be removed before subsequent culture phases.

As juvenile mussels undergo progressive morphological and functional changes during early development, rearing systems must accommodate the heterogeneous transition from pedal feeding to effective suspension feeding as gill structures become fully functional. Accordingly, juvenile performance depends on matching each system to the predominant developmental requirements of the cohort.

During the earliest and most vulnerable post-parasitic phase, selected juveniles are maintained in low-disturbance rearing boxes, which provide stable, controlled conditions. As juveniles grow and their functional requirements change, a gradual transition towards systems with higher water renewal becomes necessary.

At approximately 1.0–2.2 mm, transfer to aquaria with suspended sieves operating in a semi open circuit improves water exchange and support continued growth. At later stages, around 3.0–4.5 mm, juveniles can be moved to more open systems, including Buddensiek plates and sediment boxes, which are better suited to advanced juvenile development and provide conditions closer to those encountered before release.

This staged rearing approach can contribute to the production of viable juvenile stock and help overcome the early-life demographic bottleneck limiting recruitment in natural populations. Nevertheless, captive rearing should be regarded as a complementary measure, supporting population reinforcement while restoration of suitable riverine habitat remains essential for long-term recovery.

Keywords: *Margaritifera margaritifera*, Captive rearing, juvenile development, early stages, Freshwater mussel conservation

Funding: This work builds on the captive rearing programme initiated under LIFE MARGAL ULLA project (LIFE09 NAT/ES/000514) and subsequently supported by Fundación Biodiversidad (MITECO) and the Dirección Xeral de Patrimonio Natural, Consellería de Medio Ambiente e Cambio Climático (XG).

Freshwater Gastropod Diversity in Lithuania: A Review of Historical and Recent Records

Laurynas Orla[1,*], **Grita Skujienė**[1]

[1] Institute of Biosciences, Life Sciences Center, Vilnius University, Lithuania

*Corresponding author: laurynas.orla@mf.vu.lt

Abstract

Freshwater gastropods are important components of aquatic ecosystems and are frequently used as indicators of environmental quality and ecosystem condition. Despite their ecological significance, information on the diversity and distribution of freshwater gastropods in Lithuania remains fragmented and scattered across historical publications, regional surveys, monographs, theses and monitoring reports. The present study aimed to summarise and evaluate the currently available literature data on freshwater gastropod species recorded in Lithuania. A total of 51 literature sources published between 1937 and 2025 were reviewed, including faunistic investigations, biodiversity inventories, ecological studies and reports on non-indigenous species. Particular attention was given to species occurrence records, taxonomic composition and the reliability of historical observations. The review also highlights the contribution of the principal researchers of Lithuanian freshwater malacofauna, including P. B. Sivickis, N. L. Zettler, and earlier European malacologists such as H. Schlesch and C. Krausp.

The review revealed that 53 freshwater gastropod species belonging to 30 genera and 14 families have been reported in Lithuania. The families Lymnaeidae and Planorbidae were identified as the most species-rich groups within the country's freshwater malacofauna. Three non-indigenous species were identified in Lithuanian inland waters: *Physella acuta*, *Potamopyrgus antipodarum* and *Lithoglyphus naticoides*. Several species reported in older publications were considered doubtful because of the lack of confirmed recent findings or insufficient documentation of living specimens. These include *Ampullaceana lagotis*, *Anisus leucostoma*, *Anisus septemgyratus*, *Anisus spirorbis*, *Ecrobia ventrosa*, *Gyraulus rossmaessleri*, *Omphiscola glabra*, *Ampullaceana intermedia* and *Theodoxus major*. The results demonstrate that current knowledge of freshwater gastropod diversity in Lithuania is still largely based on a limited number of faunistic studies and historical records. The compiled overview highlights the need for systematic nationwide surveys and updated monitoring programmes to improve the understanding of species distribution and conservation status in Lithuanian freshwater ecosystems. This study provides a basis for future malacological research and biodiversity assessment in the region.

Keywords: freshwater molluscs, Gastropoda, species diversity, distribution, Lithuania

Relationship between number and size of glochidia of the freshwater pearl mussel *Margaritifera margaritifera*

Jouni Taskinen[1]

[1] University of Jyväskylä, Department of Biological and Environmental Science, 40014 Jyväskylä, Finland

*Corresponding author: Jouni.k.taskinen@jyu.fi

Abstract

Freshwater pearl mussel *Margaritifera margaritifera* is an endangered bivalve inhabiting rivers having brown trout *Salmo trutta* and/or Atlantic salmon *S. trutta*, the obligatory—and the only suitable—fish hosts of *M. margaritifera*. Size of the parasitic glochidium larvae is a critical determinant of the success of juvenile *M. margaritifera*. The larger the glochidium larva the better the survival of excysted juvenile of *M. margaritifera* (Denic et al. 2015 Limnologica 50: 67-74; Marwaha et al. 2017 Ecology and Evolution 7: 1375–1383). One of the potential factors affecting growth and size of glochidia is the number of other glochidia within the host fish individual. Growth of glochidia should decrease with their number because of within-host competition, a principle known as crowding effect. Thus, according to the crowding effect hypothesis, there should be a negative relationship between the number and size of glochidia of *M. margaritifera*. We analysed data from a number of our infestations of brown trout with glochidia of *M. margaritifera*. Opposite to the crowding effect principle, size of glochidia was mostly positively related to their number. Possible explanations, and consequences of this finding on conservation of *M. margaritifera*, are discussed.

Keywords: Freshwater pearl mussel, brown trout, host-parasite relationship, number of glochidia, size of glochidia

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Genes or environment? What determines size at maturity, growth rate and shell shape in the thick-shelled river mussel *Unio crassus*?

Adam M. Ćmiel[1], Anna Lipińska, Katarzyna Zając, Karel Douda, Adrianna Kilikowska, Monika Mioduchowska, Anna Wysocka, Agnieszka Kaczmarczyk-Ziemba, Joanna Rychlińska, Povilas Ivinskis, Jerzy Sell, Tadeusz Zając

[1] Institute of Nature Conservation Polish Academy of Sciences, Al. Adama Mickiewicza 33, 31-120 Kraków

*Corresponding author: cmiel@iop.krakow.pl

Abstract

The influence of habitat on shell morphology in Naiads is still far from being explained, and the fundamental question that arises is, how much the shell morphology reflects the phylogeny or whether it rather reflects the habitat influences, concealing the taxonomic status. The aim of this study was to test the differences in size at maturity, growth rates and shell shape in Unio crassus at multiple spatial scales to show how much of variance is determined/explained by either genetic and environmental factors. Obtained results show evidence of high phenotypic plasticity in shell morphologies within rivers of the same drainage and clearly suggest that variation in shell shape, size at age of maturity and individual growth rate in U. crassus are mostly dependent on the environmental conditions in specific rivers and river catchments, and should be attributed to phenotypic plasticity, rather than genotype.

Environmental DNA survey reveals overlooked freshwater mussel diversity and new records of the *Unio crassus* species complex in Luxembourg

Clemens Reuter[1], Stefan A. Fernandes[1]*, Frankie Thielen[1]

[1] Fondation Hëllef fir d'Natur, Haaptstrooss 14, L-9764 Marnach, Luxembourg

* Corresponding author: s.fernandes@naturemwelt.lu

Abstract

Freshwater mussels are among the most threatened aquatic organisms in Europe, yet their detection remains challenging, particularly in large, deep, or poorly accessible rivers. To update knowledge on the distribution of freshwater bivalves in Luxembourg and to improve the detection of remnant populations of the thick-shelled river mussel complex (*Unio crassus* sensu lato), a country-wide environmental DNA survey was conducted in April 2024. Thirty-nine sampling sites across 14 rivers were investigated. At each site, two water samples were collected, one from each riverbank, and 30 L of water per sample were filtered using 0.45 µm eDNA filters. The samples were analysed using metabarcoding approaches, with the eDNA analyses being carried out by the French laboratory SPYGEN, followed in 2025 by an additional genetic analysis designed to resolve taxa within the *Unio crassus* complex. The survey detected 22 native freshwater bivalve species, including six species of the Unionida order and sixteen species of the order Sphaeriida, as well as four invasive species. Unionida diversity was highest in the Sauer, where six native unionid species were detected. The Attert showed the highest diversity of the order Sphaeriida, whereas the Moselle had the highest number of invasive mussel species. *Unio crassus* s.l. was detected at 13 of the 39 sites. Some detections confirmed already known populations, while others indicated previously undocumented occurrences, including first records for the Clerve, Attert, Mamer and Alzette. A field survey in the Clerve later confirmed the eDNA result through the discovery of a live mussel near the sampling site. Further targeted searches at the remaining sites with positive eDNA detections are planned to verify these results through direct mussel records. Species-level analyses further suggested the co-occurrence of *U. crassus* sensu stricto and *U. nanus* in Luxembourg, with both species detected together at eight sites. These findings highlight the value of eDNA as a complementary tool for freshwater mussel conservation and provide a basis for targeted field surveys, population assessments and management actions.

Keywords: environmental DNA; freshwater mussels; *Unio crassus*; *Unio nanus*; Luxembourg

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Twenty Years Advancing the Conservation of the Freshwater Pearl Mussel (*Margaritifera margaritifera*) in Castilla y León, Spain

Pablo Santos Redín[1]*, Esther T. Peñín Rodríguez[1], Nerea Ballesteros Rodríguez[1,2], Alba Robles Merchán[3] and Santiago Robles Claros[3]

[1] Servicio Territorial de Medio Ambiente de Zamora. Junta de Castilla y León.

[2] Empresa de Transformación Agraria S.A.

[3] RIOTERA Agua y Naturaleza S.L.U.

* Corresponding author: espaciosnaturales.za@jcyl.es

Abstract

The freshwater pearl mussel, *Margaritifera margaritifera*, one of Europe's most endangered freshwater bivalves, has undergone a severe decline due to habitat degradation and fragmentation, declines in host fish populations, recruitment failure, and the spread of invasive alien species. Its conservation requires integrated, long-term action based on scientific knowledge and adaptive management.

In Castilla y León (Spain), this regional conservation programme began with the LIFE NÁYADE project (LIFE03NAT/E/000051, 2003–2007), which assessed the conservation status of the known population in the Tera River basin in the north-west of the province of Zamora, identified the main threats, and established the scientific foundations for its conservation. Subsequent surveys conducted by the Regional Government of Castilla y León (2010–2011, 2018, and 2022) identified new subpopulations and emerging threats, while two river restoration projects (2008–2009 and 2021–2022), implemented by the Duero River Basin Authority, improved longitudinal river connectivity.

Between 2023 and 2026, a project funded by the European Union–NextGenerationEU under Spain's Plan de Recuperación, Transformación y Resiliencia (PRTR) consolidated a comprehensive conservation strategy based on field surveys, ex situ propagation, in situ population reinforcement, habitat restoration, invasive alien species control, environmental monitoring, and public outreach. Its main achievements include increased production and release of juvenile mussels, the release of brown trout (Salmo trutta) infested with glochidia, the development of the INREMMARZA Habitat Quality Index to identify river reaches suitable for reintroduction, and the control of invasive alien species such as *Pacifastacus leniusculus*, Lepomis gibbosus, and *Neogale vison*.

This work shows that adaptive management based on long-term monitoring and the integration of complementary conservation actions can provide a robust framework to support the recovery of *M. margaritifera* and can serve as a valuable reference for future river restoration programmes.

Keywords: *Margaritifera margaritifera*; conservation; adaptive management; river restoration; invasive alien species.

Funding: This work was carried out within the framework of the Plan de Recuperación, Transformación y Resiliencia (PRTR) through the Next-Generation EU project "Conservation actions and ex situ and in situ breeding of Margaritifera margaritifera in the Sanabria region, and maintenance and improvement of the infrastructure at the Vegas del Condado (León, Spain) fish hatchery."

LIST OF PARTICIPANTS

Agustín Bassó
Alex Saturday
Alexander Karatayev
Alexandra Weber
Amílcar Teixeira
André Gomes-dos-Santos
Andreas Dobler
Anna Maria Łabęcka
Arianna Lord
Arthur Bogan
Astrid Schwalb
Camila Chacón
Catarina Varela
Clemens Reuter
Daniel Cossey
Daniel Wendesten
David Aldridge
David Berg
David Strayer
Diana Delicado
Dulmini Perera
Elsa Froufe
Emilia Nordfeldt
Erin McCombs
Esther Rodríguez
Fatima Aroumy
Fatima M'Hamdi
Fernando Miranda
Fernando Teixeira
Frans Olofsson
Gorazd Urbanič
Gretchen Rollwagen-Bollens
Grita Skujienė
Hugh Jones
Ilya Vikhrev
Jake Daviot
Jeronimo Silva
Joana Nogueira
Joaquim Reis
John Hyde
Jon Magerøy
Jonathan Lopez
Jouni Taskinen
Juha Syväranta
Jürgen Geist
Katarzyna Zając
Keiko Nakamura
Khadija Elbouhali
Kristi Dobra
Laurynas Orla
Liu Manchón del Peral
Lyubov Burlakova
Mafalda Gama
Manuel Lopes-Lima
María García Álvarez
Maria Urbańska
Maria Villa
Marie von Wesendonk
Martin Österling
Mary Seddon
Matti Mako
Michael Klunzinger
Michaela Tille
Michele Melchior
Nerea Ballesteros
Nicoletta Riccardi
Nuno Alves
Panu Oulasvirta
Patrik Olofsson
Paul Stanley
Paulina Jakubiak
Paulo Cortez
Paz Ondina
Rebecca Höß
Ronaldo Sousa
Sabrina Nykänen
Sandra Kaźmierczak
Sarah Raubenheimer
Sebastian Rock
Silvana Costa
Silvia Signorini
Simone Varandas
Stefan Abreu Fernandes
Stephen Bollens
Tadeusz Zając
Ville Julkunen
Vincent Prié
Visa Tolonen
Yulia Bespalaya

Accompanying persons
Viktoriia Berkun
Joel McCombs
Jonas Aistis Skuja
Saulis Skuja
Martynas Siupienis
Matthew Paper

COLLABORATORS


























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