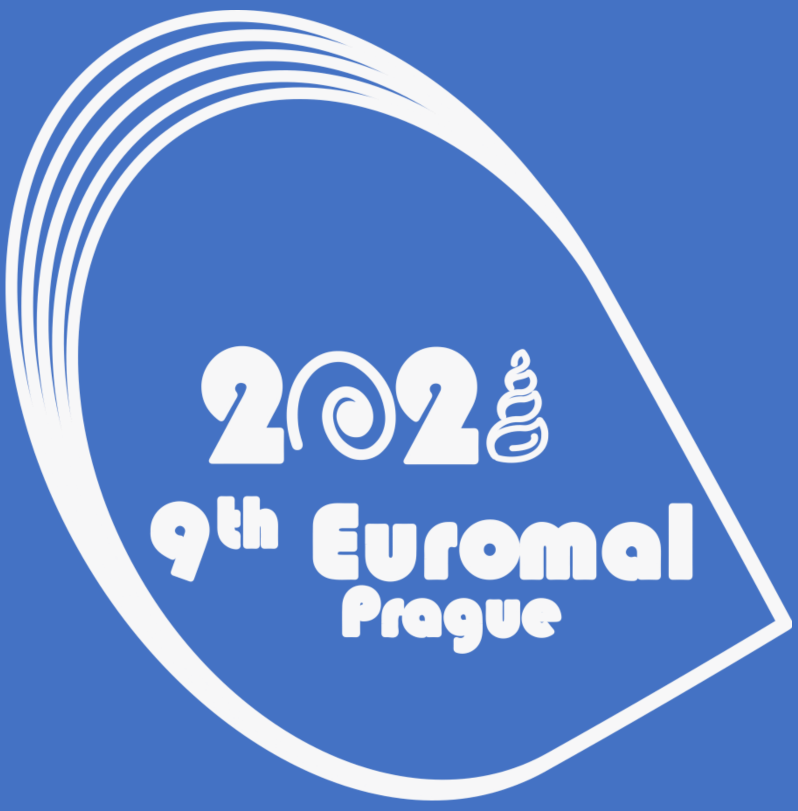
BOOK OF ABSTRACTS

THE EUROPEAN CONGRESS OF MALACOLOGICAL SOCIETIES 2021



Book of abstracts

Edited by:

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Euromal 2021

9th European Congress of Malacological Societies, Prague

5 – 9 September 2021

Hosted by: Czech University of Life Sciences Prague

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Sponsored by:

The Malacological society of London

9th European Congress of Malacological Societies, Prague

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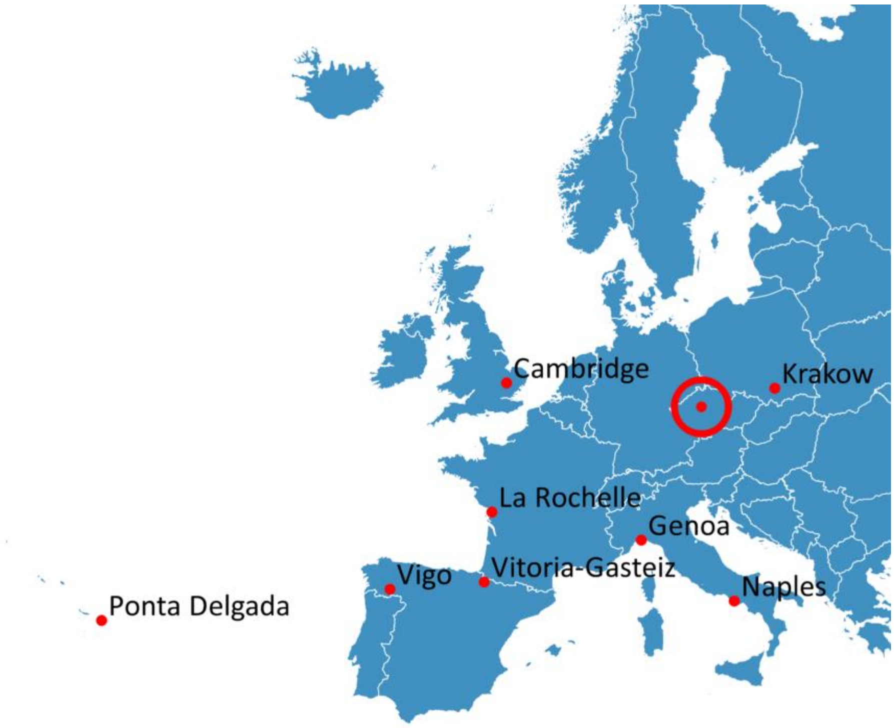
Contents

VENUES FOR PAST EUROMAL CONFERENCES

The European congress of malacological societies is the traditional meeting of mollusk researchers in Europe. Since its beginning in 2000, a total of eight conferences have been celebrated. The conference covers all major topics in malacological research including taxonomy, ecology, evolution, conservation and much more.



- 8th European Congress of Malacological Societies, Krakow, Poland, September 2017
- 7th Congress of the European Malacological Societies Cambridge, United Kingdom, September 2014
- 6th Congress of the European Malacological Societies Vitoria-Gasteiz, Spain, July 2011
- 5th Congress of the European Malacological Societies, 2008 Ponta Delgada, Portugal, September 2008
- 4th International Congress of the European Malacological Societies Naples, Italy, October 2005
- 3rd International Congress of the European Malacological Societies La Rochelle, France, 24-27 June 2003
- 2nd International Congress of the European Malacological Societies Vigo, Spain, 9-13th September 2002
- 1st International Congress of the European Malacological Societies Genoa, Italy, 12-16 November 2000

SCHEDULE

DAY 1 – 5/9/2021

Time	Session	Title	Session	Title	Session	Title
18:00	Welcome presentation: Euromal Organization Committee					
20:00	End of program					

DAY 2 – 6/9/2021

Time	Session	Title	Session	Title	Session	Title
14:00 Day 2	Opening ceremony					
14:30 Day 2	Keynote	Applied malacology: from pure science to environmental monitoring, ecological restoration and aquaculture Dr. David Aldridge				
15:00	Transition to breakout rooms					
15:05 Day 2	Ecology & evolution	Effects of habitat homogenisation on biodiversity associated with mussel beds Dr. Puri Veiga	Invasive species	🐚 Effect of temperature on life history traits and immune status of the invasive tropical freshwater snail *Melanoides tuberculata*. Julie Offerle	Taxonomy and Systematics	In situ identification of cryptic marine invertebrates using molecular markers Dr. Alejandro Centeno-Cuadros
15:15 Day 2						
15:25 Day 2		🐚 "Enemy release" as an explanation for the success of invasive freshwater mussels M.S. Binglin Deng		Testing monitoring method for *Arion vulgaris* and *Krynickillus melanocephalus* (Gastropoda: Arionidae & Agriolimacidae) Dr. agr. Arturs Stalažs		🐚 Molecular phylogeny and species delimitation of the *Felimida dalli* species complex (Nudibranchia, Chromodorididae) Priscila Vilela
15:35 Day 2				Population genetics of an invasive and a resident slug; the races and hybrids of *Arion vulgaris* and *Arion ater* s.l. Dr. John M.C. Hutchinson		

🟦 Standard
🟩 Short
🐚 Student

Time	Session	Title	Session	Title	Session	Title
15:45 Day 2		Ecosystem services of freshwater mussels: elimination of parasite larvae infecting fish Prof. Jouni Taskinen		🐚 Freshwater snails *Gyraulus parvus* (Say, 1817) and *G. laevis* (Alder, 1838): a story of the invasion at the population level Mgr. Erika Šlachtová		The first data on abyssal aglajids Dr. Elena Chaban
15:55 Day 2	Break					
16:10 Day 2	Keynote	Bivalve ecotoxicology: from biomonitoring of legacy pollutants to recent advances to assess the impacts of contaminants on aquatic ecosystems Dr. Camilla Della Torre				
16:40 Day 2	Keynote	Monitoring of mollusks using eDNA and other innovative methods Dr. Vincent Prié				
17:10	Transition to breakout rooms					
17:15 Day 2	Ecotoxicology	Coatings with natural molecules affect the ecotoxicity of Cerium oxide nanoparticles to the mussel species Dreissena polymorpha and *Mytilus galloprovincialis* Lara Nigro	Ecology and evolution	The impact of changes in hydrological conditions and in physicochemical properties of water on mussel populations in euthrophic floodplain Lake Dr. Adam Ćmiel	Taxonomy and systematics	Solenogastres (Mollusca, Aplacophora) diversity in Corsica: findings of the program “La Planète Revisiteé” Dr. M Carmen Cobo
17:25 Day 2				Phenology and reproductive effort in endangered thick-shelled river mussel *Unio crassus* Philipsson, 1788 (Bivalvia: Unionidae) Dr. Katarzyna Zając		
17:35 Day 2		Nanoplastic, Microplastic and Bivalves – physical and chemical perspective Dr. Agnieszka Dąbrowska		🐚 Fish infestation with glochidia of *Unio crassus* 1788, Philipsson in the wild M.Sc. Jacek Dołęga		🐚 Small solenogasters causing big problems: molecular data from the family Meiomeniidae (Aplacophora, Mollusca) Meghan Yap-Chiongco

Time	Session	Title	Session	Title	Session	Title
17:45 Day 2				Freshwater mollusc assemblages in the Bednja River (Croatia) Professor Jasna Lajtner		
17:55 Day 2		Levels of microelements and risks in consumption of soft tissues of mussels collected along South African coast Pavel Nekhoroshkov		🐚 Effect of substrate particle size on burrowing of the juvenile freshwater pearl mussel *Margaritifera margaritifera* MSc Heini Hyvärinen		🐚 Chitons (Class: Polyplacophora) of the Indian coast: Present status and future needs Msc. Liju Thomas
18:05 Day 2	Long Break					
18:50 Day 2	Keynote	Conservation of freshwater mollusks in the Anthropocene Professor Ronaldo Sousa				
19:20	Transition to breakout rooms					
19:25 Day 2	Conservation (dice monitoring)	🐚 The parasitic travel of *Margaritifera margaritifera* in the gills of Atlantic salmon: from glochidium to post-larva Pedro A. Castrillo	Paleonthology	Trends and patterns in the European Cenozoic land snail record Dr. Harzhauser Mathias	Host parasitic relationships	🐚 Field and laboratory evaluation of susceptibility of *Corbicula* spp. clams to *Chaetogaster limnaei* gill parasites Florencia Liquin
19:35 Day 2						
19:45 Day 2		Lagged Response and Gradual Change of a Mussel Community (Unionidae) to Natural Hydrologic Variability Over Two Decades Dr. Garrett Hopper		🐚 Reconstructing Plio-Pleistocene hydrosystems of the Northern Turkana Depression (East African Rift System) from the study of fossil freshwater mollusk communities Msc. Juan David Andrade		🐚 Parasite communities in freshwater mussels: what we know and what we still need to learn M.Sc Joshua Brian
19:55				A taxonomic revision of fossil freshwater pearl mussels (Bivalvia: Margaritiferidae) from Neogene-Quaternary rivers of Southeastern Europe Dr. Artem Lyubas		

Time	Session	Title	Session	Title	Session	Title
20:05 Day 2	Break					
20:10 Day 2	Poster session and discussion					
20:45 Day 2	End of program					

DAY 3 – 7/9/2021

Time	Session	Title	Session	Title	Session	Title
13:20 Day3	Conference with malacological societies	Malac. soc. presentation				
13:25 Day3						
13:30 Day3						
13:35 Day3						
13:40 Day3						
1345: Day3						
13:50 Day3	Break					
14:00 Day3	Keynote	Impact of anthropogenic pressures on marine and estuarine molluscs Professor Rui Rosa				
14:30	Transition to breakout rooms					

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Time	Session	Title	Session	Title	Session	Title
14:35 Day3	Global change	🐚 Biological impacts of ocean warming and acidification on cephalopods: a meta-analysis MSc. Francisco Borges	Biogeography	Comparative phylogeography of amphiboreal Nudibranchia (Gastropoda: Heterobranchia): genetic consequences of historical climatic fluctuations Dr. Irina Ekimova	Ecology and evolution	Correlated loss of shell colour and pattern and vision in deep sea snails Dr. Suzanne Williams
14:55 Day3		Establishing mussel behaviour as a monitoring tool to measure climatic disturbances Ph.D. Vanessa Modesto		Incorporating palaeogeography into ancestral area estimation can explain the disjunct distribution of land snails in Macaronesia and the Balearic Islands Dr. Marco Thomas Neiber		🐚 Collective behaviour and social dynamics during interspecific collaborative hunting between octopus (*Octopus cyanea*) and multiple fish species. MSc. Eduardo Sampaio
15:15 Day3		🐚 Running from climate change: Freshwater mussels' behavioural responses to dewatering events Paulo Castro		🐚 Central-European phylogeographic crossroads and postglacial colonization to the south in *Monachoides incarnatus* (Gastropoda: Pulmonata) Mgr. Tereza Kosová		🐚 Location probing by males complicates sexual dynamics and successful mate-guarding in squid groups MSc. Eduardo Sampaio
15:25 Day3				Mollusc diversity associated to intertidal mussel beds in North Portugal. Dr. Marcos Rubal García		Effect of the elemental content of shells of the bivalve mollusks from Saldanha Bay (South Africa) on their crystallographic texture Pavel Nekhoroshkov
15:35 Day3		🐚 High frequency video analysis as a new method for tracking bivalve filtering behaviour: comparison with traditional methods. Msc. Juan Felipe Escobar-Calderón	Ecology and evolution	🐚 Attacking strategies of malacophagous shell-breaking carabid beetles in laboratory experiments Mgr. Tomáš Němec		You are what (and how) you eat: evolutionary trends in the morphology of nudibranch buccal complex Dr. Anna Mikhlina
15:45 Day3						
15:55 Day3	Break					
16:10 Day3	Keynote	Spring fen habitats as archipelago like systems: Lessons for inland mollusc ecology and paleoecology Professor Michal Horsák				
16:40 Day3	Keynote	Nullius in verba: Bias and error from unverified data. Dr. Jeffrey C. Nekola				
17:10	Transition to breakout rooms					

Time	Session	Title	Session	Title	Session	Title
17:15 Day3	Ecology and evolution	🐚 Land snail assemblages as indicators of regional habitat conservation status of European spring fens M.Sc. Radovan Coufal	Taxonomy and Systematics	A mitogenomic phylogeny for the Western Ghats–Sri Lanka land-snail genus *Corilla* Dr. Dinarzarde Raheem		Free networking space
17:25 Day3						
17:35 Day3		Population collapse in viviparid gastropods of the Lake Victoria ecoregion started before the Last Glacial Maximum Dr. Bert Van Bocxlaer		Convergent evolution of *Amphidromus*-like colourful arboreal snails and phylogenetic relationship of East Asian camaenids Dr. Parin Jirapatrasilp		
17:45 Day3						
17:55 Day3		Extinction probability is linked to lifestyle in freshwater gastropods Dr. Thomas Neubauer		The freshwater gastropods of Greece – preliminary list, conservation and prospects Dr. Elisavet Georgopoulou		
18:05 Day3	Long Break					
18:50 Day3	Keynote	Modern approaches to species delimitation in molluscs Prof. Dr. Thomas Wilke				
19:20	Transition to breakout rooms					
19:25 Day3	Taxonomy and systematics	Molecular phylogeny of the crown snail genus *Taphrenalla* (Stylommatophora, Ariophantidae) from Thailand Dr. Arthit Pholyotha	Ecology and evolution	Feeding behavior in Olividae: more diverse than expected Prof. em. Winfried Peters	Invasive species	🐚 Asian clam explosion and its implication on freshwater mussel populations: the case in the middle Ebro basin, Spain. MSc. Keiko Nakamura
19:35 Day3		🐚 Morphological species of the genus *Belgrandia* Bourguignat, 1870 (Mollusca: Caenogastropoda: Hydrobiidae) in the Iberian Peninsula evaluated using multilocus species delimitation methods Fernando García-Guerrero				
19:45 Day3		🐚 Mollusc biodiversity of Essaouira dunes (Morocco) Fatima Zahra Guennoun		🐚 Function and evolution of high-resolution spatial vision in strombid gastropods Alison Irwin		South American freshwater invasive Bivalvia: patterns emerged by a connectivity analysis Dr. Evangelos Vlachos
19:55 Day3	Invasive species	Studies on the abundance and spread management of invasive slugs in Lithuania Mantas Adomaitis				

Time	Session	Title	Session	Title	Session	Title
20:05 Day3	Break					
20:15 Day3						
20:10 Day3	Poster session and discussion					
20:55 Day3	End of program					

DAY 4 – 8/9/21

Time	Session	Title	Session	Title	Session	Title
13:20 Day 4	Conference with malacological societies	Malac. soc. presentation				
13:25 Day 4						
13:30 Day 4						
13:35 Day 4						
13:40 Day 4						
13:45 Day 4						
13:50 Day 4	Break					
14:00 Day 4	Keynote	From shells to genomes, systematics, phylogeny and biogeography of molluscs Dr. Manuel Lopes-Lima				
14:30	Transition to breakout rooms					

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Time	Session	Title	Session	Title	Session	Title
14:35 Day 4	Genetics	Applying genomic approaches to delineate conservation strategies: a case study using the freshwater mussel *M. margaritifera* in the Iberian Peninsula Dr. Joaquim Reis	Ecology and evolution	Genetic determination of shell-shape variation in *Lanistes* from the Northern region of the Malawi Basin. Dr. Alexis Dollion	Ecology and evolution	The size and shape of parasitic larvae of naiads (Unionidae) – are they optimized Proffesor. Tadeusz Zając
14:55 Day 4		Population genetic trends in the common whelk, *Buccinum undatum*, reveal fine-scale structuring and cryptic speciation within the North Atlantic Dr. Jake Goodall		Assessment of the status of populations of *Unio crassus* Philipsson, 1788 for the establishment of conservation areas in Lithuania Dr. Grita Skujienė		Biodiversity associated with mussel beds as tool to detect anthropogenic disturbances Dr. Puri Veiga Using self–organizing maps and machine learning models to assess mollusc community structure in relation to physicochemical variables in a West Africa river–estuary system Dr. Zinsou Cosme Koudenoukpo
15:15 Day 4		Whole-genome re-sequencing data to infer historical demography and speciation processes in land snails: the study of two *Candidula* sister species Dr. Luis J. Chueca		"Obstetrical dilemma" in viviparous snails Dr. Sulikowska-Drozd Anna		Enrichment of ORFs and UCEs in genomic samples to link microevolution and macroevolution in African freshwater unionids (Parreysiinae: Coelaturini) M.Sc Claudia M. Ortiz-Sepulveda
15:35 Day 4		Inference of DNA methylation patterns in molluscs M.Sc. Lisa Männer		Parallel adaptation of shell morphology across space and time in the land snail genus *Pupilla*(Gastropoda: tylommatophora: Pupillidae) Dr. Martin Haase		Patterns of Trophic Resource Partitioning in Diverse Freshwater Bivalve Assemblages Support Classic Niche Theory MSc. Irene Sanchez Gonzalez
15:55 Day 4	Break					
16:10 Day 4	Keynote	Critically evaluating the functional role of freshwater mussels and their ecosystem services Dr. Carla L. Atkinson				
16:40 Day 4	Keynote	Current advances in propagation methods of endangered mollusks Dr. Frankie T. Thielen				
17:10	Transition to breakout rooms					
17:15 Day 4	Ecosystem services	Ecosystem services of freshwater bivalves: reviewing the global evidence Dr. Alexandra Zieritz	Monitoring	Distribution and DNA barcoding of hydrobioids (Gastropoda) from the	Free networking space	

Time	Session	Title	Session	Title	Session	Title
17:25 Day 4				Kalkalpen National Park (Austria) Hannah Schubert		
17:35 Day 4		Weighing-in: biometric conversion factors as a unifying platform for impact assessment of invasive freshwater bivalves Dr. Neil Coughlan		Effect of professional harvesting on intertidal mussel beds. An experimental approach. Dr. Marcos Rubal García	**Free discussion session:** Microplastics and other emerging contaminants **Dr. Camilla Della Torre**	
17:45 Day 4						
17:55 Day 4	Monitoring	Holoplankton and Meroplanktonic Gastropods from the Celebes Sea, North Sulawesi, Indonesia Dr. Medy Ompi		The rebirth of the Indonesian Malacological Society for mainstreaming mollusks biodiversity, conservation, and sustainable utilization in Indonesia. Dr. Ayu Savitri Nurinsiyah		
18:05 Day 4	Long Break	Long Break				
18:50 Day 4	Keynote	Crowdsourcing: a neglected research approach in malacology Dr. Ivan Jarić				
19:20	Transition to breakout rooms					
19:25 Day 4	Citizen Science	🐌 "Slugs count"; using citizen science to understand terrestrial slug species diversity in UK gardens Ms Imogen Cavadino	Ecotoxicology	🐌 Toxicity associated to exposure and recovery of neodymium in *Mytilus galloprovincialis* exposed to warming conditions M.Sc Carla Leite	Biomaterials	Study of preferred orientation and residual stress of *Sinanodonta woodiana* shells by diffraction methods Ing. Monika Kucerakova
19:45 Day 4	Citizen Science	The Role of Citizen Scientists for the Recent Development of Malacology in Indonesia Dr. Felicia Zahida	Invasive species	🐌 Predation effects of native and invasive crayfish on native and invasive freshwater mussels M.Sc. Andreas H. Dobler	Invasie Species	Massive Northward Expansion of the Alien Asian Pond Mussels (*Sinanodonta* spp.) in European Russia Dr. Ilya Vikhrev
20:05 Day 4	Break					
20:10 Day 4	Poster session and discussion					
20:45 Day 4	End of program					

Day 5 – 9/9/2021

Time	Session	Title	Session	Title	Session	Title
13:20 Day 5	Conference with malacological societies	Malac. soc. presentation				
13:25 Day 5						
13:30 Day 5						
13:35 Day 5						
13:40 Day 5						
13:45 Day 5						
13:50 Day 5	Break					
14:00 Day 5	Keynote	From Mollusks to medicine Dr. Mandë Holford				
14:30	Transition to breakout rooms					
14:35 Day 5	Conservation practice	Hundreds of shells: a time-consuming but useful quantitative approach to malacofauna Dr. Salomé Granai	Ecology and Evolution	Extinction at the fifth and sixth mass extinction – a freshwater perspective Dr. Thomas Neubauer	**Special program:** Popularization of science with games! Killer snails **Dr. Mandë Holford**	
14:45 Day 5		Introducing new project on freshwater pearl mussel conservation: LIFE Revives Dr. Heidi M. T. Kunttu				

🟦 Standard

🟩 Short

● Student

Time	Session	Title	Session	Title	Session	Title
14:55 Day 5		🐚 Spatial distribution of *Unio crassus* linked with environmental variables at a regional scale. Quintia Vaessen		Causes and evolutionary consequences of phenotypic plasticity in land snails of *Trochulus hispidus* complex Dr. Małgorzata Proćków		
15:05 Day 5		Three decades of active protection and population reinforcements of *Margaritifera margaritifera* as the flagship species for oligotrophic rivers in Czechia Dr. Ondrej Simon				
15:15 Day5				Shell microsculpture unmasks convergentshell form witdin four European *Pyramidula* species Mgr. Veronika Horsáková		
15:25 Day 5		🐚 Host-parasitic compatibility of brown trout *Salmo trutta* and freshwater pearl mussel *Margaritifera margaritifera* in central Europe based on fluorescence lipid Ing. Barbora Vodáková				
15:35 Day 5		Mollusks in the rural green belt of Vienna: continuities and changes Dr. Michael Duda		A fragile species in a harsh habitat: a case study of *Vertigo moulinsiana* population in extreme environmental conditions Dr. Anna Lipińska		
15:45 Day5				🐚 Fourier Transform Infrared Spectroscopy used to study glycosylation of proteins in gastropod mucus MSc Edgar Barajas Ledesma		
15:55 Day 5	Break					
16:10 Day 5	Keynote	Biogeography and Quaternary malacology Dr. Nicole Limondin-Lozouet				
16:40 Day 5	Keynote	Islands and snails: unraveling processes Professor Robert A. D. Cameron				
17:10	Transition to breakout rooms					
17:15 Day 5	Biogeography	Phylogeography and potential glacial refugia of terrestrial gastropod *Faustina faustina* (Rossmässler, 1835) (Gastropoda: Eupulmonata: Helicidae) MSc Kamila Stefania Zając	Quaternary Malacology	Mollusc assemblages and paleoenvironmental implications during tde Holocene in tde Elefsis Bay (Saronikos Gulf, Greece) MSc Nikolaos Mavrommatis	Anatomy	Functional micro-morphology of the digestive tract in polyplacophoran molluscs Professor Alexandre Lobo-da-Cunha
17:25 Day 5						

Time	Session	Title	Session	Title	Session	Title
17:35 Day5		🐚 Predicting future range shifts to a critically endangered freshwater mussel in Europe: the importance of including fish hosts M.S. Janine P. da Silva		🐚 Quaternary continental malacology in Spain: new investigations from a Holocene succession at Rio Galera (Andalusia) reveal the biogeographical history of Quentin Wackenheim		🐚 Stuck fast and loose: the impact of ions on gastropod pedal mucus Lauren Eggleton
17:45 Day 5						
17:55	Ecology and evolution	Freshwater mollusc diversity in the Upper Brahmaputra Basin of Assam, India Jyotish Sonowal				Rhipidoglossan radula of Gastropoda: morphology and formation. Dr. Elena Vortsepneva
18:05 Day 5	Long Break					
18:50 Day 5	Invasive species	Occurrence of the parasite and endosymbionts of *Corbicula* clams from native range: Thailand, Korea and Myanmar Ph.D. Yulia Bespalaya	Quaternary malacology	Molluscs of archaeological sites from tde Jabron valley (SE France) dr hab. Marcin Szymanek	Paleonthology and collections	Review and update of the systematics of the malacological collections belonging to the Bonsor Collection (Mairena del Alcor, Seville, southern Spain) Dr. M. Carmen Lozano-Francisco
19:10 Day 5	Invasive species	Shipworms in Lagoon of Venice Ph.D. Irene Guarneri	Conservation	Rare Vertiginidae are absent in the Curonian Spit Benediktas Jukonis	Paleonthology and collections	Crisis or Change? Unlocking biodiversity change from mollusc time series Dr. Frank Wesselingh
19:30 Day 5	Long Break					
	Scientific Committee Meeting (Closed doors)					
20:10 Day 5	Student awards and closing ceremony					
20:40 Day 5	End of the event					

POSTERS SCHEDULING

Day 2: Monday 20:10-20:45

Authors	*Title*	Cathegory
♦ **Altomari L.N., Barros M.R.F., Santos W.C.R., Herrmann M., Chagas R.A.**	*Effect of El-Nino on the growth performance of oyster cultivated on the Amazon coast*	Aquaculture
Babushkin E.S.	*Freshwater bivalve malacofauna of the Taz River basin (Western Siberia, Northern Asia)*	Biogeography
♦ **Bakhtadze N.G., Chakvetadze N.L., Mumladze L.J., Gabroshvili N.Sh., Tskhadaia E.A., Tsiklauri R.S.**	*The chromosome numbers of the family Hygromiidae Tryon, 1866 (Gastropoda: Stylommatophora)*	Taxonomy And Systematics
♦ **Barák V., Jahelková V., Simon O., Bílý M., Douda K.**	*Effects of episodic point-source pollution on survival of caged juvenile Margaritifera margaritifera*	Ecotoxicology
♦ **Benedict A., Geist J.**	*Early life-cycle stages in freshwater mussel conservation and management*	Conservation Methods
Billman-Jacobe H., Haites R. E., Russell D., Watt A.E.	*Tetrahymena rostrata cysts for biocontrol of pest slugs*	Host-Parasite Relationships
Bond C.E., Yap-Chiongco M.K., Hawkins T., Partain R.E., Cobo M.C., Kocot K.M.	*Uncovering the biodiversity of Gymnomeniidae (Aplacophora, Mollusca) in the Norwegian Sea*	Taxonomy And Systematics
♦ **Bonk A., Dąbrowska A., Skawina A.**	*The preliminary results of the nanoplastics and microplastic impact on Unio tumidus and Sphaerium sp.*	Ecotoxicology
♦ **Carvalho de Lima T., Barreto Braga Mello V., de Castro Oliveira C.D.**	*Validation of the most informative descriptors for the species of the gender Cardiomya Adams, 1864 in Brazil*	Taxonomy And Systematics
Castro-Claros J.D., Cobo M.C., Lucena-Serrano C., Checa A., Salas C.	*New record and update of Pruvotia sopita (Pruvot, 1890) (Mollusca, Aplacophora) in the South of Spain*	Taxonomy And Systematics
♦ **Cervera Lara M., Lozano-Francisco M. C.**	*Introduction to the study of the population structure of Cymbula safiana (Lamarck, 1819) on the littoral of the province of Malaga (southern Spain)*	Monitoring Of Mollusc Populations
Ćmiel A.M.1, Zając T., Zając K., Lipińska A.M., Najberek K.	*Comparison of breeding strategies of freshwater Unionidae mussels under stochastic environmental conditions*	Ecology And Evolution
David Andrew A.	*Infestation of commercially reared bay scallops (Argopecten irradians) by the shell boring polychaete Polydora neocaeca on Nantucket Island*	Aquaculture
Doldan M. S., Gimenez L.H., Morsan E.M.	*Environmental forcing on growth and recruitment of marine bivalve species at Northern Patagonia, Southwestern Atlantic*	Global Change
Doldan M.S., Rubilar T., Oehrens Kissner E.M., Kroeck M.A., Morsan E.M.	*Solitary as an oyster? Neighbours, inquinilism, commensals and parasites of Ostrea puelchana*	Ecology And Evolution
Ekimova I.A., Mikhlina A.L., Stanovova M.V., Antokhina T.I., Schepetov D.M.	*New data on nudibranch fauna in the North-West Pacific revealed an astonishing pseudocryptic diversity*	Taxonomy And Systematics

🐚 Gąsienica P., Stec D., Lachowska-Cierlik D., Zając K. S.	*First comprehensive molecular phylogeny reconstruction of the family Milacidae (Gastropoda: Eupulmonata)*	Taxonomy And Systematics
Georgopoulou E., Gkisakis V., Kabourakis E.	*Contribution to the land snail fauna of olive orchards in Crete (Greece)*	Monitoring Of Mollusc Populations
Gomes S., Piteira M., Fernandes C., Varandas S., Saavedra M.J.	*Escherichia coli Isolated from Potomida littoralis and Margaritifera margaritífera: phylogenetic group determination*	Genetics

Day 3: Tuesday 20:10-20:55

Authors	***Title***	**Cathegory**
🐚 Gregarová K., Atkinson C., Zieritz A., Douda K.	*Biomass-clearance rate relationships in freshwater bivalves – introduction of a distributed experimental research network*	Ecosystem Functions
🐚 Guerrero Spagnuoli J., Dop N.S., Pizá J.	*From the Mediterranean to Patagonia: studying Rumina decollata (Linnaeus 1758), a non-native snail in Argentina, through a citizen science project*	Invasive Species
🐚 Guillen C., Marquez-Farias J.F, Avila-Poveda O.H	*Body size variation in an intertidal polyplacophora along a tropical latitudinal gradient*	Ecology And Evolution
🐚 Guillen C., Rodriguez-Dominguez G., Avila-Poveda O.H	*Population growth of the intertidal mollusk Chiton articulatus (Polyplacophora: Chitonida) at its northernmost distribution limit in Mexico, based on length data*	Ecology And Evolution
Guimarães M., Torres A.L.Q., Serra A.C.S., Coutinho R.A., Americo J.A., de Freitas Rebelo M.	*Sex ratio in invasive freshwater bivalve species: a meta-analysis*	Invasive Species
Hajisafarali M., Aaltonen S., Pulkkinen K., Taskinen J.	*Freshwater Mussel Removes Bacterial Pathogen*	Ecosystem Functions
🐚 Inäbnit T., Dennis A.B.	*The mitochondrial genomes of two species within the Melampus bidentatus species complex (Panpulmonata; Ellobioidea)*	Genetics
🐚 Indriksone J.V., Deart Yu.V., Antokhina T.I., Ekimova I.A.	*New data on biodiversity of dorid nudibranchs (Gastropoda: Heterobranchia) in Southern Vietnam*	Taxonomy And Systematics
🐚 Khrebtova I.S., Aksenova O.V., Kondakov A.V.	*A molecular identification of trematodes of the genus Diplostomum in lymnaeid snail from Arctic lakes*	Host-Parasite Relationships
Konopleva E.S., Kondakov A.V., Tomilova A.A., Vikhrev I.V., Lyubas A.A., Bolotov I.N.	*Phylogeography of Depressed River Mussel Pseudanodonta complanata in Russia*	Ecology And Evolution
Książkiewicz-Parulska Z.	*Selected behavioural traits of some European hygrophilous whorl snails (Gastopoda: Eupulomata: Vertiginidae)*	Ecology And Evolution
Kur J., Igliński P., Galant G., Mioduchowska M.	*Study of biofouling on an offshore rig in the Baltic Sea*	Invasive Species
🐚 Lamilla- Tamayo L., Barák V., Mohammadi M., Escobar-Calderón F., Vodáková B., Douda K.	*Evaluation of green algae Ettlia oleoabundans grown under different conditions as food source for freshwater bivalves.*	Conservation Methods

Lewin I., Halabowski D.	*Anthropogenic drivers of molluscs dispersion in tributaries of the Vistula and Odra rivers with different degrees of secondary salinisation*	Invasive Species
Lisova E.D., Stanovova M.V., Ekimova I.A	*Morphological and genetic variability within different populations of amphiboreal nudibranch species Onchidoris muricata*	Biogeography
🐚 **Lisova E.D., Vortsepneva E.V.**	*New data of Nudibranchia rhinophore morphology: case of Onchidoris muricata (Doridina)*	Anatomy
Martín-Hervás M.R., Carmona L., Malaquias M.A.E., Krug P.J., Cervera J.L.	*A new species of non-green sacoglossan sea slug species (Heterobranchia, Gastropoda) from the archipelago of Azores*	Taxonomy And Systematics
Munjiu O.	*Endangered freshwater mollusk Unio crassus Philipsson, 1788 in the Republic of Moldova*	Monitoring Of Mollusc Populations
🐚 **Muñoz Schuler C., Torres V., Aguilera F.**	*Evaluating the putative role of exosomal pathways in the process of shell formation in Crassostrea gigas*	Anatomy
🐚 **Nurhayati P.A., Nurinsiyah A.S., Affandi M.**	*Land snails of Raden Soerjo Nature Tourism Park, East Java, Indonesia*	Monitoring Of Mollusc Populations
🐚 **Paz-Sedano S., Gosliner T.M., Pola M.**	*Who is not Goniodoridella savignyi Pruvot-Fol, 1933? The challenge of Indo-Pacific Goniodoridella species complex (Nudibranchia, Goniodorididae)*	Taxonomy And Systematics
Pereira J.V., Reis J., Magalhães M.F.	*Captive Breeding Techniques for Freshwater Pearl Mussel M. margaritifera – Plastic Boxes vs. Artificial Stream Channels*	Conservation Methods
Pieńkowska J.R., Proćków M., Lesicki A.	*Monacha cantiana (Montagu, 1803) in northern France and the Netherlands*	Taxonomy And Systematics

Day 4: Tuesday 20:10-20:45

Authors	*Title*	Cathegory
Pizá J.	*Self-fertilization depression in an introduced population of the land snail Rumina decollata (Linnaeus 1758).*	Invasive Species
Proćków M., Konowalik K., Proćków J.	*Contrasting effects of climate change on potential distribution of alien species Cernuella virgata and Hygromia cinctella*	Invasive Species
Saavedra M.J.*, Gomes S., Fernandes C., Teixeira A., Varandas S.	*Antibiotic-Resistant Escherichia coli on Asian clam (Bivalvia, Corbiculidea): Case Study in the Tua River, Portugal*	Biosecurity
🐚 **Salles A.C.A., Oliveira C.D.C., Pimenta A.D.**	*Redescription of Rhinus species (Stylommatophora: Simpulopsidae) occurring in the Brazilian Atlantic rainforest: a long-neglected genus amid environmental chaos*	Anatomy

Salles A.C.L., Oliveira J.P.G., Ferreira C.E.L, Padula V.	*Mass stranding of Argonauta nodosus Lightfoot, 1786 (Cephalopoda, Argonautidae) in southeastern Brazil*	Monitoring Of Mollusc Populations
Schell T., Baranski D., Hamadou A. B., Christa G., Galià-Camps C., Greve C.	*Providing a high quality genome for the 'solar powered' sea slug Elysia timida*	Genetics
Simon O. P., Hruška J., Horáčková J., Dort B., Douda K., Švanyga J., Bílý M., Švaříčková J.	*Action Plan for a critically endangered Freshwater Pearl Mussel in Czechia – achievements of semi-natural breeding and population reinforcement in contrast with protracted restoration of its oligotrophic river ecosystems*	Conservation Practice
Sîrbu I., Benedek A.M.	*Saving assets when needed: using spline interpolation functions and integral calculus to assess ecological parameters of mollusk populations and communities*	Ecology And Evolution
Skawina A.	*Narrowing the time of evolution of the eulamellibranch gill anatomy in Unionida - new Late Triassic findings from Poland*	Paleontology
Slavevska - Stamenković V., Hinić J., Shoreva I., Mitić - Kopanja D., Glöer P.	*Towards resolving the mystery about the Balkan endemic freshwater snail Graecoanatolica macedonica Radoman & Stankovič, 1979 in Dojran Lake (R. North Macedonia)*	Conservation Practice
Somoza-Valdeolmillos E., Gómez-Moliner B.J., Caro A., Chueca L.J., Martínez-Ortí A., Madeira M.J.	*Multilocus Molecular Phylogeny of Chondrina farinesii (Gastropoda, Pulmonata, Chondrinidae) in the Iberian Peninsula*	Taxonomy And Systematics
Somoza-Valdeolmillos E., Gómez-Moliner B.J., Caro A., Chueca L.J., Martínez-Ortí A., Madeira M.J.	*Multilocus Molecular Phylogeny of the Chondrina soleri + granatensis + gasulli complex (Gastropoda, Pulmonata, Chondrinidae) in the Iberian Peninsula*	Taxonomy And Systematics
Souza L.S., Costa P.M.S.	*Three new species of Columbellidae (Neogastropoda) from deep waters of the southwestern Atlantic: shell morphology, anatomical data and morphometric analysis*	Taxonomy And Systematics
Teixeira A., Magalhães M.F., Oliveira J.M., Beja P., Lopes-Lima M., Nogueira J., Jesus J., Cortes R., Varandas S., Reis J., Rodrigues P., Pereira J., García Álvarez M., Fonseca C., Barros T., Ferreira E., Teixeira F., Miranda F., Cortez P., Fernandes C., Mesquita E., Pereira A.M., Teiga-Teixeira J., Froufe E., Sousa R.	*Conservation and management of freshwater pearl mussel (Margaritifera margaritifera) and brown trout (Salmo trutta) populations in Portugal*	Conservation Practice
Varandas S., Fernandes C., Ballen A., Teixeira A., Saavedra M.J.	*Freshwater bivalves as reservoirs of multiresistant bacteria: the case of two endangered species (Margaritifera margaritifera and Potomida littoralis)*	Biosecurity
Vázquez A.A., Faugere D., Sánchez J., Alba A., López-Soriano J., Chapuis E., Alda P.,	*Invasion risks of Orientogalba viridis (Lymnaeidae) in Europe: susceptibility to Fasciola hepatica (Trematoda) and life-history traits under experimental tropicalized settings*	Invasive Species

Pointier J.-P., Hurtrez-Boussès S.		
🐚 **Vorobyeva O.A., Mikhlina A.L., Malakhov V.V., Ekimova I.A.**	*Comparative morphology of the cnidosac and related structures in the nudibranch family Fionidae*	Ecology And Evolution
Yang L., Kawaguchi T., Fortunato H.	*Oyster aquaculture and food safety: the microplastics problem*	Aquaculture
🐚 **Yuvero M.C., Lomovasky B., Giménez J.**	*Contour analysis in subtidal and intertidal populations of the mussel Mytilus edulis platensis d' Orbigny, 1842*	Ecology And Evolution
Zaidman P.C., Saldaño M. A., Barrera Fuenzalida E.A.	*What happens to small scale fisheries when new resources appeared: one case of north Patagonia Argentina*	Social Aspects Of Mollusc Research

ANATOMY

STANDARD PRESENTATIONS (2)

Functional micro-morphology of the digestive tract in polyplacophoran molluscs

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Polyplacophorans are benthic marine molluscs, commonly known as chitons, characterized by eight articulated dorsal shell plates. Despite all the investigation made on this class of molluscs, few studies have been dedicated to the digestive system of chitons, which includes a pair of oesophageal glandular pouches known as "sugar glands" and a large digestive gland connected to the stomach. To extend current knowledge about the digestive tract of these molluscs, a histological and ultrastructural study of the oesophagus, stomach and intestine of *Chaetopleura angulata* and *Acanthochitona fascicularis* was carried out. Additionally, stomach content examination revealed the omnivorous diet of these species. In both, the epithelium of the whole digestive tract consisted mostly of thin absorptive cells with an apical border of microvilli. Cilia were also commonly present. Many mitochondria and large electron-dense lysosomes were present in the region above the elongated nucleus. The basal region was characterized by an association of mitochondria, peroxisomes and lipid droplets. Glycogen deposits were also abundant in some cells. The ultrastructural features indicate that the digestive tract epithelium is involved in endocytosis, intracellular digestion and storage of reserves. The association between lipid droplets and peroxisomes suggests that lipid reserves might be mobilised through fatty acid β-oxidation in peroxisomes. Histochemical techniques for polysaccharide and protein detection were employed to characterize the secretory cells that occur along the digestive tract epithelium. In these species, two types of secretory cells were identified in the oesophagus, whereas in the stomach and intestine a single type of secretory cells was recognised. Moreover, basal cells that seem to correspond to enteroendocrine cells containing oval electron-dense vesicles were found along the digestive tract epithelium of both species. The thin outer layer of the digestive tract wall contained muscle cells and nerves embedded in connective tissue.

Keywords: *histology, ultrastructure, oesophagus, stomach, intestine.*

Stuck fast and loose: the impact of ions on gastropod pedal mucus

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Gastropod pedal mucus has two contradictory properties, adhesion and locomotion, which can be seamlessly moved between whenever the functional need arises. The mechanisms behind this transition have not been identified, probably as the two types of mucus are typically studied in isolation. Through the creation of a gastropod locomotion translation device to incite a need for adhesion, a biocrystallisation effect was observed across a range of gastropod species; indicating a potential class-wide fast-acting mechanism used by gastropods to manipulate their mucus' structural composition to meet a specific functional demand.

We propose that this mechanism is activated and moderated through the use of metal ions. We sought to explore the impact both monovalent and divalent ions have on the structure and function of pedal mucus using FTIR, SDS-PAGE and rheology. Additionally, the use of a dilution series provided a greater insight into the concentrations required to incite changes in adhesion and the impact this has on the rheological function of gastropod mucus.

Results indicate a potential fast-acting mechanism based on both divalent and monovalent metal ions which may help explain the apparent contradictory effects of the adhesive and locomotive properties of mucus. Further research linking the various observable crystal structures and compositions to specific metal ions may shed light on the exact mucin structures and molecular motifs used by gastropods to control their mucus to meet a range of seemingly contradictory needs.

Keywords: *mucus, proteins, ions, biocrystallisation, FTIR*

ANATOMY

SHORT PRESENTATIONS (1)

Rhipidoglossan radula of Gastropoda: morphology and formation.

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The radula, comprising a chitinous membrane with teeth arranged in longitudinal and transverse rows, is a characteristic element of the feeding apparatus within the Mollusca. Radular morphology is particularly diverse in gastropods, in which it has been studied in detail and found to be a source of traditionally important taxonomic characters. Rhipidoglossan radula, which is characterized by presence of a central tooth, several lateral teeth, and numerous long marginal teeth in each transverse row, is found in three different subclasses – Vetigastropoda, Neritomorpha and "lower" Heterobranchia. Details of radula formation and its ultrastructure have not to date been studied in any species with a rhipidoglossan radula. Herein we present the data of complex studies of the radular fine morphology and radular formation in two vetigastropod species (*Puncturella noachina* and *Margarites helicinus*), and one species of Neritimorpha (*Nerita litterata*). The radula itself and the radular formation zone were studied using light and electron microscopy (scanning and transmission), as well as confocal laser scanning microscopy. The major peculiarity of Vetigastropoda rhipidoglossan radular formation is posterior bifurcation of the radular formation zone, creating paired horns into which the odontoblasts of marginal teeth extend. Significant morphological difference in the formation of the radula between *Nerita litterata* and two studied vetigastropod species is the absence of external division of the blind end of the radular sac. Nevertheless division of the formation zone in *N. litterata* into two partitions can be seen on histological sections. The marginal teeth of *N.litterata* are synthesized in these horns as well as in vetigastropod species. The adaptive features of the formation zone of rhipodoglossan radula relate to the increase in the secreting surface for the formation of very long and numerous marginal teeth of a wide radula.

Keywords: *ultrastructure, odontoblast, radular formation zone*

Acknowledgments: This research was carried out as a part of the Scientific Project of the State Order of the Government of the Russian Federation to Lomonosov Moscow State University, No 121032300121-0. Support was provided by the Russian Science Foundation No 21-14-00042.

ANATOMY

POSTERS (3)

Evaluating the putative role of exosomal pathways in the process of shell formation in *Crassostrea gigas*

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Most mollusks produce external calcified shells, which are fabricated by specialized epithelial cells on the dorsal mantle. This tissue is underneath the shell and expresses a suite of genes encoding secreted proteins that are delivered into the extrapallial space to finally be embedded into the shell. Recent shell proteomic analyses have revealed that secreted proteins, but also proteins lacking a signal peptide, form part of the shell, raising the question of how these non-secreted proteins reach the mineralization front. Some authors have postulated the hemocytes as possible protein carriers; however, there is not a full understanding of how this could be happening. By performing tough bioinformatics analyses on the genomic resources available for the bivalve *Crassostrea gigas*, we found the majority of components concerning the biogenesis and secretion of exosomes, suggesting that this species has the molecular repertoire required to produce exosomes. We further evaluated the expression patterns of those exosomal components in different tissues of this oyster and found that hemocytes seems to be the main exosome-producing tissue, followed by the mantle. Indeed, gene expression of exosome-related proteins, which have also been reported as embedded in the shell, display high expression in mantle, followed by hemocytes, digestive gland, and adductor muscle. Furthermore, shell-forming genes are expressed in a similar fashion, with a dominant expression in the mantle tissue, followed by digestive gland, male gonad and hemocytes. Our results indicate that genes encoding components of the shell matrix are not only generated in the mantle but also in other tissues, proposing the participation of non-classical biomineralization pathways in shell formation. Altogether, we suggest that molluscan shell formation is probably aided by diverse tissues, with hemocytes, given their high capacity to produce exosomes and infiltrate into different tissues, being the second most important shell-forming tissue.

Keywords: *biomineralization, bivalves, exosome, hemocytes.*

New data of Nudibranchia rhinophore morphology: case of *Onchidoris muricata* (Doridina)

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Rhinophores are important chemosensory cephalic organs in nudibranch mollusks. Morphology of rhinophore are important taxonomic features. In this regard, the external structures of the rhinophore have been described for many species. However, their general morphology has so far been studied fragmentarily. Many details of the internal morphology have not been studied in detail at all. In this work, for the first time, the structure of the *Onchidoris muricata* rhinophore is described in detail.

The collection of material was carried out in the Kandalaksha Bay of the White Sea. The samples were examined by light, scanning electron microscopy, and morphological dissections were also performed.

The large nerve, muscles and the lymphatic cavity are located in the rhinophore center. The large nerve of the rhinophore has branches that bifurcate at the end. The muscular system of the rhinophore is represented by longitudinal muscles retractors, as well as transverse thin strands. The lymphatic canal does not have its own wall and is limited by the rhinophore structural element. The rhinophore wall is reinforced with a large number of spicules. The morphology of the rhinophores spicules differs significantly from the spicules of their body. The spicules are thinner and more curved. The spicule complex of monoaxones and multiaxones looks like a bonfire from a log cabin. A framework of four spicules located along each rhinophore extends around the central part of the rhinophore. Two spicules run directly into the fold of the rhinophore. The rows of spicules are circumferentially displaced relative to each other. The contraction of the rhinophore occurs with the participation of the retractor muscles, the relaxation is passive due to the injection of hemolymph

Our data of the structure of the rhinophore supplement the existing and significantly expand the understanding of the structure of the spicule complex of nudibranchs.

Keywords: *micro-CT, morphology, sclerocyte, spicule*

Acknowledgments: This research was carried out as part of the Scientific Project of the State Order of the Government of the Russian Federation to Lomonosov Moscow State University, No. 121032300121-0. Support was provided by the Russian Science Foundation No. 21-14-00042.

Redescription of *Rhinus* species (Stylommatophora: Simpulopsidae) occurring in the Brazilian Atlantic rainforest: a long-neglected genus amid environmental chaos

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Mollusca phylum is the second most diverse in terms of described species, and it also has the highest documented extinction rate. With the degradation of the environment and the increase in global temperature, terrestrial gastropods are strongly affected, corresponding to about 45% of endemic mollusks in Brazil at risk of extinction. Undoubtedly, this is underestimated by the lack of environmental policies and the demoralization of conservation, a path that Brazil has followed in recent years. The Brazilian Atlantic Rainforest is a biodiversity hotspot and houses more than 8000 endemic plants and faunal species. Unfortunately, its current coverage corresponds to 12.4% of what was originally occupied, with that, many species were extinct even before they were known. There are 19 species of the genus *Rhinus* occurring in Brazilian Atlantic rainforest, only two described based on conchology and anatomical characters. For almost all the remaining species, the literature available is limited to faunal surveys and catalogs, and any descriptive studies are restricted to original descriptions based only on shell. In this work we redescribe 5 species of *Rhinus* based on anatomical and shell morphology and we present the first description of spermatophores for the genus. Specimens of *Rhinus ciliatus*, *R. durus*, *R. evelinae*, *R. heterotrichus* and *R. suturalis* were dissected and pallial cavity and digestive, reproductive and nervous systems were examined in stereoscopic microscope. Details of shell, radula, jaw and when present, spermatophores, were achieved by scanning microscopy. Significant differences were observed in relation to: kidney shape, peripheral glands, connectives between salivary gland ducts, extension of flagellum, position of copulatrix bursa, degree of fusion between ganglia, among other characteristics. We hope this work contributes to a greater knowledge of species of *Rhinus* that occur in Brazilian Atlantic Rainforest by presenting hitherto neglected anatomical details, considering this the first step towards its preservation.

Keywords: *Orthalicoidea, terrestrial gastropods, comparative morphology, spermatophores.*

Acknowledgments: UFRJ, MZUSP, ICMBio and CNPq for financing resources.

AQUACULTURE

POSTERS (3)

Effect of El-Nino on the growth performance of oyster cultivated on the Amazon coast

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The present study aims to analyze the effects of El Niño on the growth of the oyster *Crassostrea tulipa* on the Amazon coast through the Overall Growth Performance (OGP) index. This index compares the general growth functions of von Bertalanffy from several studies, analyzing the growth parameters (K and L_∞) of the species and ordering the data in an auximetric grid. In this experiment, the labeling method using fluorochrome calcein was used. The experiment started in April 2016 (during El Niño 2015/16) and continued for a period of one year. All experimental conditions were based on a previous study carried out (in 2013 – normal year). At each collection, 30 oysters were sampled. In the laboratory, after washing and drying, the shells of the oysters were embedded in crystal resin and cut longitudinally using a diamond saw. After polishing the resulting cuts with different grades of carbide powder and aluminum oxide, the absolute growth rate was determined by detecting calcein marks with a fluorescence microscope. The results of this study indicate a significant difference in the growth parameters of oysters under the influence of El Niño. This influence occurs in a different way, correlated with the strength of the climatic anomaly. In conclusion, there was a negative influence of El Niño on the growth of oysters *C. tulipa*, grown on the Amazon coast, when compared to growth in normal years. It is estimated that oysters grown in El Niño year take approximately three more months to reach their commercial size.

Keywords: *Bivalve mollusk, oyster farming, growth parameters, El Niño.*

Infestation of commercially reared bay scallops (*Argopecten irradians*) by the shell boring polychaete *Polydora neocaeca* on Nantucket Island

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Shellfish farming is quickly becoming the most expansive and profitable sectors of commercial aquaculture but is expected to face several challenges, including diseases. Shell-boring polychaete worms exert considerable stress on both wild and farmed molluscs by boring into the shells of scallops, oysters and abalone, where they weaken the structural integrity of the shell, reduce growth rates, and in cases of heavy infestation, compromises tissue quality. Here, we investigate the identity and infestation levels of shell-boring polychaetes in the last commercially viable wild bay scallop fishery in the world: Nantucket Island, located off the eastern coast of the US. While shell-borers were studied on the mainland US for decades, recent anecdotes by scallop farmers on Nantucket reported unusually high infestation levels of worms over the last few growing seasons, indicating that a potentially new worm may have arrived in the region. To determine the identity of these polychaetes, 30 scallops were obtained from submerged cages at the hatchery and worms were extracted, identified morphologically and DNA barcoded using the COX1 marker. Prevalence and intensity were measured to determine infestation levels. Our results showed that the main culprit responsible for infestation was *Polydora neocaeca* (>90% of infections), a species often associated with gastropod shells. Phylogenetic analyses showed that the Nantucket population formed a distinct North American clade with specimens from New York and Rhode Island (type locality), and were genetically isolated from other global *P. neocaeca*. Prevalence was low (40%) while intensity ranged from 2 – 14. This is the first report *P. neocaeca* infecting commercially reared bivalves from North America and its first detection in Nantucket scallops. The status of the species as an introduced pest will be discussed.

Keywords: *aquaculture, spionid, polydorid,*

Acknowledgements: Funding for this study was provided by the Nantucket Biodiversity Initiative and the Nantucket Shellfish Association.

Oyster aquaculture and food safety: the microplastics problem

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Microplastics derived from anthropogenic pollution have become a major issue in today's society. Available data points to their presence in all terrestrial and marine ecosystems. There is a growing body of literature documenting their presence in many organisms including humans where they may cause serious health problems. Sources of these microplastics are multiple, from trash dumped in rivers and lakes and traveling to the ocean, fishing tools such as nets, ropes, baskets to a range of chemicals dumped in water sources.

Marine organisms often absorb microplastics through food or directly from the water in the case of filter species. Particles are then deposited in the respiratory organs, guts, pallial cavity and other organs. When these species are used as food, these particles are transferred to the consuming organisms where they accumulate.

Oysters are a very important component of Japan's fisheries industry being both consumed inside the country and exported. Therefore, their quality is of utmost importance for the industry's success. This study aimed to evaluate the presence of microplastics in cultivated oysters (*Crassostrea gigas* (Thunberg, 1793)) from four localities in the Pacific coast of Japan.

Oyster soft tissue was digested following a standard protocol, and the dried suspension examined for the presence of microplastics using fluorescence, Raman scattering, and SEM microscopy. Preliminary data showed the presence of a varied amount of microplastics of different coloration (mostly forming red/pink and green fibers) and sizes ranging from 200 - >2000 µm. Raman scattering spectra indicate that the most plausible material is Nylon 66 and urethane, the most frequently used material in oyster aquaculture fishing gear.

We will discuss obtained results in the light of worldwide information concerning microplastics' presence in shellfish. We hope these data help to provide advice to the aquaculture industry and stakeholders.

Keywords: *Japan, aquaculture, oysters, microplastics, food safety*

BIOGEOGRAPHY

STANDARD PRESENTATIONS (4)

Comparative phylogeography of amphiboreal Nudibranchia (Gastropoda: Heterobranchia): genetic consequences of historical climatic fluctuations

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The species delineation is particularly acute in boreal seas, which are often inhabited by species with broad geographic ranges and high degrees of intraspecific morphological and molecular diversity. Environmental conditions in boreal and Arctic regions significantly changed multiply times in recent past, promoting the formation of geographic barriers and leading to allopatric speciation events. Unlike with sympatric species, no separation in ecology happens, and truly cryptic species can be formed with overlapping morphological variation, but significantly distant genetically.

In this study we tested the species identity and observe morphological variation across amphiboreal species of two common nudibranch families: Dendronotidae and Coryphellidae. For this purpose, we used a set of 5 standard mitochondrial and nuclear markers: COI, 16S, H3, 28S and 18S and a large variety of species delimitation (ABGD, GMYC, bPTP) and phylogeographic methods (population analysis; ancestral area reconstruction). The morphological analysis included standard morpho-anatomical examination using the light microscopy and scanning electron microscopy.

Based on our integrative results we identified cases of true amphiboreal species, but also cases of cryptic species being formed allopatrically following Pliocene-Pleistocene Climate Change. Ancestral area reconstruction (AAR) provides evidence for a Pacific origin of both families. Different lineages of *Dendronotus* and *Coryphella* demonstrate different level of genetic differentiation and, according to our molecular clocks calibration, different divergence times. This indicates that the invasion of the Arctic and Atlantic regions occurred multiply times starting from the first opening of the Bering Strait in late Miocene.

Keywords: *Biogeography, Arctic, cryptic species, population analysis, molecular clocks*

Acknowledgments: This study was supported by Russian Science Foundation grant #20-74-10012

Incorporating palaeogeography into ancestral area estimation can explain the disjunct distribution of land snails in Macaronesia and the Balearic Islands (Helicidae: Allognathini)

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The systematics and biogeographical history of the Western Mediterranean and Macaronesian land snail tribe Allognathini (Helicidae: Helicinae) is investigated based on mitochondrial and nuclear DNA sequence data. Our molecular phylogenetic analyses indicate that the genus-group systematics of the tribe needs to be revised. We show for the first time that the narrow-range endemics *Lampadia* and *Idiomela* from the Madeira Archipelago belong to Allognathini and represent together the sister group of the diverse Canary Island *Hemicycla* radiation. We therefore suggest synonymising Lampadiini with Allognathini. Sister to these Macaronesian genera was the Balearic Island *Allognathus* radiation. *Pseudotachea* was not recovered as a monophyletic group and the two currently recognised species clustered in *Iberus*. Similarly, *Adiverticula* was not recovered as a monophyletic group and clustered in *Hemicycla*. We therefore suggest synonymising *Pseudotachea* with *Iberus* and *Adiverticula* with *Hemicycla*. The six genera in Allognathini, which we distinguish here (*Cepaea*, *Iberus*, *Allognathus*, *Hemicycla*, *Idiomela* and *Lampadia*), originated in Western to South-western Europe according to our ancestral area estimation and the fossil record. The disjunct distribution of the Balearic Islands and Macaronesian sister clades and the mainly Iberian *Iberus* clade that separated earlier can be explained by the separation of the Betic–Rif System from the Iberian Peninsula during the Late Oligocene to Early Miocene, along with independent Miocene dispersals to the Balearic Islands and Macaronesia from the Iberian Peninsula, where the ancestral lineage became extinct.

Keywords: *Betic–Rif System, Canary Islands, colonisation, Iberian Peninsula, Madeira Archipelago*.

Phylogeography and potential glacial refugia of terrestrial gastropod *Faustina faustina* (Rossmässler, 1835) (Gastropoda: Eupulmonata: Helicidae)

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Faustina faustina (Rossmässler, 1835) is a mountain species that occurs mainly in Carpathians but it is also present in isolated localities in NE Poland (Romincka Forest) and in Lithuania (Kaunas), where it was probably introduced. The knowledge about this species is limited, however it was recently confirmed that *F. Faustina* should be indeed classified within in the genus *Faustina* contrary to others hypotheses provided in the previous literature. The main aim of the presented study was to investigate the phylogeographic pattern across *F. faustina* distribution range by using multiple molecular markers and species distribution modeling. We detected high level of genetic variability within and between *F. faustina* populations. In case of COI marker, genetic variability ranges from 0.2 to 18.1% between individuals and from 6.3 to 16.6% between clades. Interestingly, only in case of nuclear markers, pattern of haplotype distribution was discovered. Finally, species distribution models indicated a few potential refugia in the Carpathians, with the most climatically stable and largest areas in the Southern Carpathians.

Keywords: *Helicidae, phylogeography, glacial refugia*

Predicting future range shifts to a critically endangered freshwater mussel in Europe: the importance of including fish hosts

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The freshwater pearl mussel *Margaritifera margaritifera* has been suffering major population declines, being listed as critically endangered in Europe. This species is a host specialist and exclusively requires salmonid species (brown trout Salmo trutta and/or Atlantic salmon Salmo salar) to complete its life cycle. In theory, obligatory biotic interactions should deserve special conservation attention, because the loss or massive decline of fish hosts may elicit the extirpation of their affiliated species. While many threats disturbing *M. margaritifera* are similarly affecting salmonids, climate change is particularly alarming, with the potential to significantly change the fish-mussel dynamics. To evaluate the importance of including the occurrence of fish hosts for predicting the current and future distribution of *M. margaritifera* in Europe, three predictor datasets were used to build species distribution models (SDMs) with a maximum entropy (MaxEnt) approach: i) environmental variables (ENV); ii) fish hosts estimated occurrence (FH); and iii) environmental variables and fish hosts estimated occurrence (ENV+FH). The predicted current and future projections were used to evaluate the adequacy of current networks of European protected areas in covering the suitable habitats for *M. margaritifera*. Incorporating data about biotic interactors into SDM procedures improved geographical projections and, to a minor extent, model performance (AUC: ENV = 0.851; FH = 0.848; ENV+FH = 0.867). Large contractions in the distribution of *M. margaritifera* were predicted across the European continent, particularly in central and southern Europe and lowland regions, and current European network of protected areas fail to safeguard the predicted current and future distribution of this species. This study highlights the importance of adopting the use of biotic information about fish hosts in addition to environmental variables to model the distribution of freshwater mussels at a continental scale and supports SDMs as an effective tool for the definition of conservation measures.

Keywords: *Climate change, Conservation, Freshwater pearl mussel, Mussels-fish hosts relationship, Species distribution models*

BIOGEOGRAPHY

SHORT PRESENTATIONS (1)

Central-European phylogeographic crossroads and postglacial colonization to the south in *Monachoides incarnatus* (Gastropoda: Pulmonata)

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Recently, molecular phylogenetics led to re-evaluation of taxonomy and biogeography of several taxa in the Hygromiidae family. The genus *Monachoides* will not be an exception, as phylogenetic data reject the existing system and consequently put its geographic origins to the south of Central Europe instead of the Balkans. Based on results of our phylogenetic analyses, the genus *Monachoides* comprises in addition to the two currently accepted species *Monachoides incarnatus* (O. F. Müller, 1774) and *M. vicinus* (Rossmässler, 1842) also an apparently undescribed species from northwestern Croatia, and some localized lineages related to *M. incarnatus* from the southern Alps, whose status is unclear. One additional species, *M. bacescui* Grossu, 1979, described from the Banat region and is pending revision; three other species reported from the western Balkans in fact belong to the genus *Xerocampylaea*. The most widespread species of the genus is *M. incarnatus*. It is an abundant euryvalent land snail limited longitudinally to Central Europe but extending from Bulgaria and Greece in the south to southern Scandinavia in the north. The first results of phylogeographic analyses indicate a probable origin as well as glacial refugia of *M. incarnatus* south of the Alps. Central Europe was colonized in the Holocene by two divergent haplotype groups from two directions, west and south-east, leading to broad mixing of originally spatially isolated mitochondrial lineages. What is, however, more surprising is the evidence of presumably postglacial expansion from the very northwest of the Balkans or the southeastern Alps southwards, to Bulgaria and along the western Balkan mountains. According to radiocarbon dating, *Monachoides* quickly responded to climate change and spread into Central Europe at the turn of the Late Glacial and the Holocene. This expansion is apparently also responsible for the presence of *Monachoides* in the Balkans.

Keywords: *land snail, phylogeny, postglacial colonization*

Acknowledgments: Thanks to the grant agency of Charles University for funding (GA UK 244120).

BIOGEOGRAPHY

POSTERS (3)

Freshwater bivalve malacofauna of the Taz River basin (Western Siberia, Northern Asia)

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The Taz River basin (TRB) is a large aquatic system in the north of Western Siberia (WS). Information on the bivalves of this basin is scarce and published almost exclusively in Russian. This study aims at giving an overview of the freshwater bivalve fauna of the TRB. Malacological collections of the Zoological Institute (RAS) and the Institute of Plant and Animal Ecology (Ural Branch, RAS), critical review of the scientific literature, and own samples made in TRB were the basis of this work. MolluscaBase (http://www.molluscabase.org/) nomenclature and taxonomy were followed. In total, 26 species of 6 genera from 2 families were identified. The Unionidae was represented by a single species. All other species belong to the genera *Sphaerium* (5 species), *Musculium* (1), *Pisidium* (2), *Odhneripisidium* (2), and *Euglesa* (15) of the Sphaeriidae. The greatest species richness and abundance were noted for the genus *Euglesa* – 15 species and 51.9% of the total number of specimens in the collection. Nine species accounted for more than 80% of the collection. Other species are represented by a much smaller number of specimens. Zoogeographically the core of the fauna is formed by widespread Holarctic and Palaearctic species – 69.2%; European-Siberian and European-Central Asian species composed 30.8%. No invasive species has been encountered. Observed species richness of bivalves in the TRB is more than 80% of all in WS (Babushkin, 2020 a, b), which corresponds to world concepts (Bogan, 2008; Lopez-Lima et al., 2018; Bolotov et al., 2020). In the south of WS, both gastropods and bivalve invasive species were recorded (Vinarski et al., 2015; Babushkin et al., 2021), whose northward spread is very likely explained by the current climate changes. To protect the natural aquatic ecosystems of the TRB, it is necessary to organize ecological monitoring, scientific investigations, and habitats conservation.

Keywords: *Taz River basin, Malacofauna, Unionidae, Sphaeriidae, Species Richness.*

Acknowledgments: The fieldwork, literature review, and examination of museum collections (partially) were supported by the Russian Foundation for Basic Research (project 19-04-00270), Russian Foundation for Basic Research, and Tyumen Region (project 20-44-720008), and the Department of Education and Youth Policy of the Khanty-Mansiysk Autonomous Okrug–Yugra. A significant part of the work on the examination of museum collections was supported by the Russian Science Foundation (project 19-14-00066).

Mollusc diversity associated to intertidal mussel beds in North Portugal.

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Mussels are considered relevant intertidal ecosystem engineers as they provide habitat, food and shelter to many species of invertebrates thus increasing local biodiversity. The Mediterranean mussel, *Mytilus galloprovincialis* is the more frequent and abundant species of mussel along intertidal shores of the Atlantic coast of the Iberian Peninsula. However, the diversity of invertebrate assemblages associated to *M. galloprovincialis* beds in Iberian Atlantic rocky shores has been poorly studied.

The objective of this study was to explore the diversity of mollusc assemblages associated to intertidal mussel beds along the North coast of Portugal. To achieve this objective, six rocky shores were sampled at six dates during one-year period. At each rocky shore and date, a total of 8 quadrats (10x10 cm) were scraped. Molluscs were sorted and identified to the lowest taxonomical level (mainly species). A total of 28 806 individuals and 55 taxa were found. Gastropods were represented by 43 taxa followed by bivalves (9) and polyplacophorans (3). Number of singletons (taxa represented by one individual) were relatively high (11); doubletons numbered only two taxa. The more abundant species was the small bivalve *Lasaea rubra* that amounted for more than 10.000 individuals. Furthermore, six gastropods were also abundant and represented each by >1000 individuals.

In general, our results proved that mussel intertidal beds harboured high mollusc abundances while values of species diversity were similar to those as found in other intertidal ecosystem engineers such as macroalgae.

Keywords: *Molluscs, intertidal, biodiversity, mussel beds.*

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Morphological and genetic variability within different populations of amphiboreal nudibranch species *Onchidoris muricata*

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Nudibranch *Onchidoris muricata* (O.F. Muller, 1776) is a well-known widespread dorid species in the northern Hemisphere. It is characterized by an oval body of white or whitish-yellow colors. The entire surface of the notum is abundantly covered with clavicular and rounded tubercles; rhinophores with two rhinotubercles are located at the anterior end, and unipinate gills are located at the posterior end. *Onchidoris muricata* lacks a shell like other nudibranch, but the body is strengthened by a large number of subepidermal spicules.

In the present work, we study morphological and genetic variability of *O. muricata* from different locations, including the White Sea, the Barents Sea and the Sea of Japan. The samples were examined by light, scanning electron microscopy, and morphological dissections. For all specimens the mitochondrial COI and 16S markers were obtained to reveal the intraspecific population structure.

We confirm species identity of all studied populations, however we detected a distinct genetic divergence between Arctic-Atlantic and Pacific populations and presence of three haplogroups. We also determined conservative and variable morphological characters. Individuals from all studied areas have a reduced plate-like central tooth of the radula, the radular formula (21-30) 1: 1: 1: 1: 1. Internal lateral teeth have a wide base from which the coracoid process departs with or without teeth. The spicule composition is also universal within the species: tetraxon spicules predominate in the body of *O. muricata*; mono-, di- and thriaxon spicules are also found. Features of the reproductive system morphology are variable traits. Significant differences were found in the shape of the ampulla and bursa copulatrix and in the thickness of the prostate.

Keywords: *morphology, Nudibranchia, population genetics*

Acknowledgments: This study was supported by the Russian Science Foundation grant #20-74-10012

BIOSECURITY

POSTERS (2)

Antibiotic-Resistant *Escherichia coli* on Asian clam (Bivalvia, Corbiculidea): Case Study in the Tua River, Portugal

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Antimicrobial resistance (AMR) is a major global health problem. Water use by human activities represent a natural reservoir of AMR, thus a time-integrated approach is required in aquatic ecosystems. Freshwater bivalves are widely applied as accumulation indicators and monitors of contaminant effects on different levels of biological integration once they are suspension feeders that actively filter, retain and concentrates particles from their surrounding water, including free living or particle-bound bacteria. In this study, we aimed to (i) investigate the genetic diversity of *E. coli*, (ii) determine the virulence factors of *E. coli* isolates, and (iii) detect antibiotic resistant *E. coli*. Samples were collected in the middle sector of the Tua River. Isolates were retrieved in Chromocult® Coliform Agar plates (Merck, Germany). Susceptibility testing was performed by the disc diffusion method, according to the Clinical Laboratory Standards Institute (CLSI), and the screening of phenotypic ESBL production was carried out by the double disk synergy test using cefotaxime (30µg), ceftazidime (30µg), and amoxicillin/clavulanate (20/10µg) acid discs. PCR-based assays were designed for phylogenetic *E. coli* groups evaluation, resistance and detection of ESBL genes. The *E. coli* phylogenetic group B1 was the most prevalent (44 %), followed by phylogenetic groups A and D. Phylogenetic groups A and B1 comprised more than half (70 %) of the total *E. coli* isolated. Our results show that *Corbicul*a spp. provide an efficient, time-integrating tool for identifying/quantifying faecal indicators, including multidrug resistant bacteria.

Keywords: *E. coli, Antimicrobial resistance, Corbicula fluminea*

Acknowledgments: This work is supported by National Funds by FCT - Portuguese Foundation for Science and Technology, under the project UIDB/04033/2020 and the I&D project FRESHCO-Multiple implications of invasive species on Freshwater Mussel co-extinction processes (PTDC/AGR-FOR/1627/2014-04/SAICT/2015).

Freshwater bivalves as reservoirs of multiresistant bacteria: the case of two endangered species (*Margaritifera margaritifera* and *Potomida littoralis*)

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Freshwater bivalves (FB), responsible for important functions and vital ecosystem services are sensitive to environmental changes, making them excellent bioindicators. The present study evaluated the dispersion of resistance to several classes of antimicrobials for the first time, simultaneously in freshwater mussels (*Margaritifera margaritifera* and *Potomida littoralis*) and water where they live, in sites subject to different anthropogenic pressures, in an EcoHealth perspective, integrated in the One Health approach. The study was conducted in the river Tua basin, located in northern Portugal. Water samples and individuals of *M. margaritifera* and *P. littoralis* species were collected at four sites in summer of 2018. The isolation of strains from water was performed by the filter membrane method and each bivalve was aseptically opened to get soft tissues, weighted, and diluted on Buffered Peptone Water into sterile stomacher bags. The resultant filters were put on selective and chromogenic media and incubated. The isolates from water and bivalves were tested for antibiotic susceptibility by using a disk diffusion test. Each bacterial isolate was tested for 21 antibacterial agents representing 5 drug classes: β- lactams, fluoroquinolones, aminoglycosides, sulfamides and amphenicos. Among the total of 135 isolates (water and FB), 64.44% were coliforms bacteria and mostly came from water 39.26%, comparing with coliforms bacteria from mussels 25.19%. Among *E. coli* isolates, multidrug resistant (MDR) was exclusively detected at sampling site T4 but for coliforms isolates, MDR was observed at T3 and T4, in both water and FB (*P. littoralis*). MDR level was higher for isolates from FB than from water. We consider that bacterial communities should be a priority for inclusion in the WFD monitoring and evaluation systems, improving programs of measures for the sustainable management of water resources and greater integration with other sectorial policies in order to contribute to the Sustainable Development Goals (SDGs).

Keywords: *Freshwater bivalves, multidrug resistant, bioindicators*

Acknowledgments: This work is supported by National Funds by FCT - Portuguese Foundation for Science and Technology, under the project UIDB/04033/2020.

CITIZEN SCIENCE AND SOCIAL ASPECTS OF MOLLUSC RESEARCH

STANDARD PRESENTATIONS (3)

“Slugs count”; using citizen science to understand terrestrial slug species diversity in UK gardens

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Slugs and snails are notorious horticultural pests, widely detested by gardeners and frequently the most common subject of pest enquiries to the RHS Gardening Advice service. Despite this, very little is known about which species are present in UK gardens or which actually damage plants. This project is engaging with sixty gardeners distributed across the United Kingdom, providing them with the tools and knowledge to identify species of slug found in their gardens during standardised surveys. Surveys, started in October 2020, are being done every four weeks over a twelve-month period using a timed torchlight survey, similar to that of Barnes and Weil (1944 & 1945). Slugs found are identified to species by participants, with all live specimens sent to the RHS to confirm identification. Preliminary results indicate that slug species presence and dominance varies over the seasons and between locations and is likely to be highly influenced by environmental conditions in individual gardens. This data also indicates that some non-native species have become widespread and that other slug species have declined across the UK since the 1940s. The data provide by citizen scientists will help map locally abundant pest and non-pest species across the UK. Ultimately this information will allow control methods to be targeted to problem species, reducing negative impacts on non-pest slug species and other wildlife.

Keywords: *slugs, citizen science, species diversity.*

Acknowledgements: The authors would like to acknowledge the 60 people participating in this project, without which this study would not be possible.

The rebirth of the Indonesian Malacological Society for mainstreaming mollusks biodiversity, conservation, and sustainable utilization in Indonesia.

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Mollusks is one of Indonesian major biodiversity that play a significant role in the diverse tropical Indonesian ecosystems and cultures. Several species are commercially important, which also significantly contribute to the economic sector. However, the information regarding this important resource is still lacking and most people are unacquainted with the importance of mollusks in their life. Therefore, efforts to raise the awareness of Indonesian people on mollusks as a commodity should be conducted. The Indonesian Malacological Society or Masyarakat Moluska Indonesia (MMI) was established in February 2009. Twelve years later, on February 10th, 2021, the society is legalized under the Decree of the Minister of Law and Human Rights of the Republic of Indonesia. The vision of the society is to accommodate students, academicians, researchers, practitioners, and governments in exchanging information as well as competence on mollusks. This covers various aspects, for instance, the discovery of mollusk diversity, conservation, cultivation, sustainable use, etc. In less than one year, approximately 126 amateur and professional malacologists joined the society. They came from no less than 46 institutions in Indonesia, ranging from Aceh to Papua. As a society that aims to mainstream mollusk diversity in Indonesia, MMI published the national peer-review journal, namely, Jurnal Moluska Indonesia (JMI), which is published twice a year for the public, and also Bulletin MMI for internal usage. Additionally, MMI is also active in social media through various platforms. MMI with its members from various backgrounds certainly has the potential to increase public enthusiasm for mollusk resources in Indonesia, which can lead to the management of important assets of commercial value.

Keywords: *Indonesian Malacological Society, MMI, Masyarakat Mollusca Indonesia*

The Role of Citizen Scientists for the Recent Development of Malacology in Indonesia

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Indonesia is well-known as one of archipelago and megadiversity country in Southeast Asia, with more than 17,000 large and small islands, and has the longest coastline in the world, 95,181 km. However, people might rarely know about Indonesia's role in malacology. This article aims to illustrate the role of citizen scientists among other scientists for the recent development of malacology in Indonesia. Method used was gathering information quantitatively from the activities of the citizen scientists which were reflected by their works and compared them with Indonesian national seminars and a sample of world conference in malacology. The results were analysed and presented using graphs and discussed descriptively. Results showed that most of citizen scientists in Indonesia worked in the field of species biodiversity, specifically trying to find new species, and naming them. Some others are trying to maintain species in captivity to understand their nutrition and reproduction habit. Other efforts include recording new findings in the form of a database of Indonesian mollusks, writing reference books on Indonesian mollusks, building networks with communities in the Indonesian archipelago to expand knowledge about local mollusk conditions and proposing an idea of creating a mollusk museum that can physically display collection. Indonesian citizen scientists are best described by Solaris Shell Club members. Most of the active members works as taxonomist and about 50 new species have been named so far.

Keywords: *citizen scientist, mini-survey, quantitative data, qualitative data*

CITIZEN SCIENCE AND SOCIAL ASPECTS OF MOLLUSC RESEARCH

POSTERS (1)

What happens to small scale fisheries when new resources appeared: one case of north Patagonia Argentina

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Small-scale fisheries of the San Matías Gulf, North Patagonia Argentina, based on invertebrates share similar characteristics with other small-scale fisheries such as multi-gear and multispecies. Usually, fishers shift from one and another resource for several reasons, such as profit-earning capacity, depletion, or rise of new resources. In the last decades, purple clam (*Amiantis purpurata*) and southern geoduck (*Panopea abbreviata*) became the main resources for the invertebrates artisanal fishery in the area. But in recent years the emergence of a new resource, shrimp (*Pleoticus muelleri*), in 2012, and the resurgence of a valuable resource, Tehuelche scallop (*Aequipecten tehuelchus*) in 2019, have changed the landscape of fisheries. The objective of the present study was to analyze the effect of new resources in the purple clam and southern geoduck fisheries.

We analyze landings and the number of fishing trips of purple clam and southern geoduck fisheries in the last decade. Also, we analyze if a fisher switched between purple clam, southern geoduck, Tehuelche scallop, and shrimp.

We found that landings and the number of fishing trips did not change significantly with the appearance of shrimp or Tehuelche scallop. Even though two indicators show a marked decrease in 2020 of the two indicators, this was not associated with growth in either the Tehuelche scallop or shrimp fishery. This decrease could be attributed to the pandemic of Covid-19. Although fishers switched between resources, mainly they incorporated the new resources but did not leave those who fished.

Keywords: *small-scale fisheries, Amiantis purupurata, Panopea abbreviate.*

COLLECTIONS

STANDARD PRESENTATIONS (1)

Review and update of the systematics of the malacological collections belonging to the Bonsor Collection (Mairena del Alcor, Seville, southern Spain)

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The Bonsor Collection comes from the exhaustive sampling of malacological materials from different archaeological sites located in the Los Alcores region (Seville, southern Spain) that covers a chronocultural segment from the Neolithic to Roman times, result from the scientific collaboration between George Bonsor Saint Martin, archaeologist, and Robert Ashington Bullen member of the Malacological Society of London at the beginning of the twentieth century. At present this collection is deposited in the Castle of Mairena del Alcor (Seville). It consists of more than 60 specimens of bivalves, gastropods and scaphopods. Malacofauna was initially analyzed by Ashington Bullen. In the present study, the systematics of this collection have been updated, identifying 16 species of marine mollusks and four species of freshwater molluscs. Likewise, four species of fossil mollusks have been identified from the Neogene of the Guadalquivir Basin (Lower Pliocene: Zanclience). The correct identification of the species allows us to reconstruct their area of origin and, especially, the freshwater fauna provides us with important information about the ecosystems from which they come.

Keywords: *Bonsor Collection, Mollusc, Bivalves, scaphopods, fossils*

CONSERVATION METHODS

POSTERS (3)

Captive Breeding Techniques for Freshwater Pearl Mussel *M. Margaritifera* – Plastic Boxes *vs.* Artificial Stream Channels

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The freshwater pearl mussel *Margaritifera margaritifera* (Bivalvia: Unionida) is one of the most threatened freshwater bivalves worldwide mainly due to the lack of recruitment in natural populations. The life cycle of this species is marked by the production of larvae (glochidia) that attach themselves to the gills of salmonids, where they undergo metamorphosis to the juvenile stage. The main objective of this work was to contribute to the optimization of the captive breeding conditions of *M. margaritifera* juveniles by comparing the survival and growth rates of individuals raised under different techniques, namely in artificial systems. Juvenile freshwater pearl mussels were obtained through infection of river brown trouts under controlled conditions and subsequently raised in two different systems: part of the juveniles was kept in plastic containers without water circulation (closed system), while artificially fed, and the rest released into natural substrate of an indoor raceway supplied with river water (open flow-through system) and grew without human intervention. Survival and growth rates were monitored during the captivity period, over 3 months, and compared between different systems. Post-parasitic mussels raised in plastic containers showed a gradual decline in survival rate throughout the experimental period, with only 15% of individuals surviving after 3 months, and reaching a maximum shell length of 452,92 (±48,45) µm. It was not possible to assess survival in the flow-through system. In this system, juveniles reached an average length of 561,49 (±69,99) µm, corresponding to an increase in length three times that observed in the closed system. The individuals raised in the flow-through system had a significantly higher growth rate than juveniles in the closed system. In conclusion, the open system was the most cost-efficient, producing a high number of healthy juveniles with little need for human intervention.

Keywords: *Unionida, conservation, growth, survival, juvenile.*

Early life-cycle stages in freshwater mussel conservation and management

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Rapid climatic and anthropogenic change have led to the global decline of native freshwater mussels, and an increased spread of those which are invasive. Efforts to maintain freshwater mussel diversity have prompted many programs for their conservation and management. One key point to such programs is the collection, maintenance and use of mussel glochidium larvae, which require attachment to a fish host in a sensitive parasitic stage of their life-cycle. Understanding the thermal requirements and host-fish preferences of both native and non-native glochidia can increase knowledge of mussel larval survival and ultimately aid in the development of conservation and management programs. Recent experiments conducted by the Aquatic Systems Biology Unit at the Technical University of Munich investigated the early life-cycle requirements for bivalves currently found in German waterbodies, including the threatened thick-shelled river mussel *Unio crassus*, the native pond mussels *Anatina anatina* and *Anatina cygnea*, and the non-native Chinese pond mussel, *Sinanodonta woodiana*. Results from these studies illuminate the competitive advantages of non-native mussels as threats for native mussel species and underline the importance of species-specific investigations of the mussel life-cycle for developing effective conservation strategies.

Keywords: *conservation, management, life-history, glochidia*

Evaluation of green algae *Ettlia oleoabundans* grown under different conditions as food source for freshwater bivalves.

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Microalgae cultivation plays a fundamental role in rearing filter-feeding organisms for marine and freshwater aquaculture. The produced algal biomass is mostly destined to supply the world demand for marine bivalves, with freshwater species having much less attention. From a nutritional point of view, the quality of microalgae as a food source for freshwater bivalves depends on many components such as essential fatty acids, protein, vitamins, sterols, and carbohydrates. Studying the changes in the algae biochemical characteristics, resulting from the culture conditions in an easily replicable way, could derive in an effective method to formulate better diets for freshwater bivalves in different stages of the life cycle in laboratories and rearing facilities. The green algae *Ettlia oleoabundans*, (S.Chantanachat & Bold) J.Komárek 1989, was the selected species to test the effect of three different culture temperatures on the overall wellbeing of 48 subadults and 480 juveniles of *Sinanodonta woodiana*. For rearing the bivalves, we used a Pulsed Flow-Through experimental system (PFT), in which two different mussel-rearing controlled temperatures were applied, allowing the quantification of the effects of diet components and rearing temperature without the influence of a common holding. Initial results from the analysis on whether changing the microalgae culture conditions and the animal keeping temperature has an impact on bivalves' growth, survival rate, as well as mussel behavioural response will be presented.

Keywords: *Ettlia oleoabundans, microalgae, mussel feeding, diet, Pulsed Flow-Through system.*

CONSERVATION PRACTICE

STANDARD PRESENTATIONS (5)

Distribution and DNA barcoding of hydrobioids (Gastropoda) from the Kalkalpen National Park (Austria)

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The Kalkalpen National Park is situated in Upper Austria and contains more than 800 springs. The international importance of this park is, from the perspective of nature conservation directives, highly significant (European nature reserve Natura 2000, recognized wetland of the Ramsar convention). In the current study the hydrobioid fauna (‘spring snails’) of the Kalkalpen National Park was evaluated. These tiny snails are difficult to determine, however, their investigation is especially desirable, as several species are threatened and as they are important for water quality assessment. The snails of 39 selected springs were examined with classical methods (shell morphology and genital anatomy) and DNA barcodes. Sequences of a approx. 670 bp fragment of the mitochondrial COI gene were generated for 109 specimens and could be compared with already existing DNA sequences. It could be shown that in some springs of the Kalkalpen National Park rare hydrobioids, which are due to their endemic status particularly important to protect, occur in varying frequencies. The species *Bythinella conica*, *Hauffenia kerschneri*, *Hauffenia wienerwaldensis* and *Belgrandiella aulaei* could be clearly identified. For *Bythiospeum nocki*, despite the ambitious collecting effort, until now only empty shells were found (including the locus typicus). The data and analyses obtained can contribute to the assessment of the taxonomic level of the species studied. The present study gives a good baseline for further monitoring of the hydrobioids in the Kalkalpen National Park, which is important to evaluate current and decide on future protection measures for this group.

Keywords: *Hydrobioids, Spring snails, DNA barcoding, National Park, Gastropoda.*

Lagged response and gradual change of a mussel community (Unionidae) to natural hydrologic variability over two decades

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Stream organisms have adaptations to contend with disturbances linked with natural flow regimes but changing climate conditions and human modifications that disrupt hydrologic cycles can be catastrophic to stream species persistence. Unionid mussels are some of the longest-lived stream animals and assemblage structure should be relatively stable for decades in the same location if flow regimes remain within historical boundaries. Few studies have addressed how mussel communities are organized over time scales comprising multiple kinds of natural disturbances. Here, we retrospectively analyze annual surveys for two mussel beds spanning 17 (1999-2016) and 20 years (1999-2019) from a relatively undisturbed portion of the Sipsey River (Alabama, USA), to evaluate the relative importance of “event-driven” and gradual change on assemblage structure. We summarized community data using multivariate statistics and tested for correlations between assemblage structure, hydrologic variables (i.e., precipitation, drought, discharge), and time. Ten species (core community) were found in all surveys and made up ~ 90% of mussels collected. Low or high-flow disturbances occurred in all annual intervals, except three, and assemblage structure at both beds gradually shifted from that of initial surveys. Shifting was not driven by disturbances between annual intervals but were correlated with 5-year time lag fluctuations in maximum annual discharge at one bed. Population declines of six core species comprising all three life-history strategies contributed to assemblage shifts, but underlying reasons are uncertain and require continued monitoring efforts to determine if changes are directional or the assemblage returns to an early state. We show that mussels persist in a river with regular natural hydrologic disturbances, but assemblage responses are lagged in relation to discharge conditions and vary spatially. Our study highlights the value of monitoring long-lived animal communities over relevant time scales.

Keywords: *Long-term data, flow-ecology, disturbance, traits, stability*

Rare Vertiginidae are absent in the Curonian Spit

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The Curonian Spit formed 5,000 years ago as a narrow peninsula (98 km in length and 0.4-3.8 km in width), when the Great Dune Ridge separated the Baltic Sea from the Curonian Lagoon, and it was formed on moraine islands from sand transported by currents, and later covered by forest. Wetlands are also currently being found there, so all sites, although somewhat more similar to possible Vertiginidae habitats, have been specifically inspected in 2021 but rare Vertiginidae listed under Annex II of the Habitats and Species Directive [92/43/EEC] were not found. This highlights once again confirmed the relict status of these Vertiginidae. Meanwhile, in Lithuania, the research of rare Vertiginidae, started in 2019, is successfully carried out and is ending this year, 2021. Overall more than 70 localities in Lithuania were surveyed by a standardised monitoring protocol (Moorkens & Killeen, 2011), adapted for Lithuanian conditions. This protocol included assessment of area of occupancy and quality of habitat, survey and sampling (0.25 x 0.25 x 0.05 m3) along linear transects or spot plots, and analysis of molluscan species (V. geyeri and other) from 1-10 (generally 3-5) samples taken from each locality. Field surveys in Lithuania included habitat assessment and data collection using QField – the mobile GIS app, followed by sieving and identification of mollusc species in the laboratory, and adding all information to the QGIS project stored on the server at the State Service for Protected Areas under the Ministry of Environment. After identification three rare Vertiginidae species were found: Vertigo geyeri, Vertigo angustior and Vertigo moulinsiana. V. geyeri and V. angustior were dominant in wetland habitats with presence of 7230 habitat (Alkaline fens); V. moulinsiana were more abundant in 7140 habitat (Transition mires and quaking bogs). During research over 50 new localities for rare Vertiginidae species were found. These studies have been carried out by the resolution of the Ministry of Environment of the Republic of Lithuania implementing the LIFE Integrated Project "Optimization of Natura 2000 Network Management in Lithuania" No. LIFE16IPE/LT/016 (LIFE-IP PAF-NATURALIT), funded by the European Union for the Environment and Climate Policy Program (LIFE). The research of molluscs in the Curonian Spit have been funded by the Curonian Spit National Park under contract 2021-04-16 Nr.(1.57) 15600-INS-49//BS-13(1.36))/21.

Key words: *Vertigo, Habitats Directive, endangered species*

The parasitic travel of *Margaritifera margaritifera* in the gills of Atlantic salmon: from glochidium to post-larva

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The larval development of the endangered freshwater mussel *Margaritifera margaritifera* (L.) represents one of the most striking parasitism among unionids, in which larva needs to parasite the fish gills for several months. Despite the importance of the developmental and metamorphosis success to culture the juveniles of this freshwater mussel, the larval morphogenesis remains completely obscure in contrast to marine bivalves. To describe the parasitic larval development and metamorphosis of *M. margaritifera*, Atlantic salmon (*Salmo salar* L.) were exposed to glochidia, sampled periodically for over six months to visualize the gills by stereomicroscopy and light microscopy and results were summarized throughout three developmental stages. Once attached to the fish gills, glochidia rapidly changed their morphology within the first three days and acquired an intermediate stage termed mushroom larva due to the presence of the mushroom body and the zip membrane. Both structures were transitory and exclusive of the long-lasting parasitism, and suggest a unique role in the isolation and acquisition of non-particulate nutrients from the fish and accumulation of lipids within the larval mantle. After 200 days or 2000 degree-days, a successful metamorphosis was evidenced by the formation of a complete set of post-larval organs, pointing to the acquisition of different functionality after detachment from the gills, which will be essential for the settlement and deposit-feeding into the riverbed. In conclusion, this study provides an overview of the larval morphogenesis of *M. margaritifera*, from glochidium to post-larva, essential for understanding the parasitic interaction between the freshwater mussel larva and the fish host. Moreover, the morphological techniques and the hallmarks described here (i.e., the lipid content and the presence of the adductor muscle at metamorphosis) might be directly employed to optimize and monitor the larval developmental status during one of the most critical stages of the conservation programmes of this endangered bivalve.

Keywords: *Freshwater Pearl Mussel, larval development, glochidium, post-larva, mushroom body.*

Acknowledgments: This study was supported by Fundación Biodiversidad (Ministerio para la Transición Ecológica y el Reto Demográfico) and Dirección Xeral de Patrimonio Natural, Consellería de Medio Ambiente, Territorio e Vivenda (Xunta de Galicia). P. A. Castrillo held a University Professorship Formation (FPU) grant from the Ministerio de Educación, Cultura y Deporte.

Three decades of active protection and population reinforcements of mollusc *Margaritifera margaritifera* as the flagship species for oligotrophic rivers in Czechia

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Freshwater pearl mussel (FPM) M. margaritifera is a very sensitive freshwater mollusc needed strictly oligotrophic environment especially in juvenile phase of life cycle. The anthropogenic eutrophication has substantial impact on the biodiversity in whole Central-European region since half of 20th Century. The Action Plan for FPM was implemented in the headwaters of the Elbe/Vltava River for over 30 years. In this long-time program, the FPM represents an umbrella species to protect the rests of oligotrophic catchments (for details see poster Simon et all). Three large protected areas (6,9 – 59,6 km2) have been established to protect the FPM rivers and the whole catchment ecosystem. Using bioindication by 1 year old juveniles (started in 1988) was indicated the best natural food, optimal habitats in river networks and monitored anthropogenic disturbances and pollution accidents. More then 50 000 juveniles were released gradually in most perspective localities. These animals established stabile new cohorts and reproduced in some localities now. Many organisms profit on the water's eutrophication decline reached in these protected areas by different measures. However, the other key factors limiting natural reproduction of the FPM (land-use changes, agriculture land draining, excessive erosion, host fish community impairment) have been changed insufficiently still. The current status of natural habitat does not enable the survival of the youngest stages (1–2 years) of mussels nor the sufficient natural reproduction in FPM protected areas. Even though many problems persist, the new semi-natural breeding helped to rejuvenate the overaged Czech populations. Despite the natural reproduction of FPM has not been restored yet, thus the main goal of the Action Plan was not reached, many endangered aquatic, wetland, and terrestrial ecosystems profit from habitat conservation.

Keywords: *freshwater pearl mussel, semi-natural breeding, juvenile*

CONSERVATION PRACTICE

SHORT PRESENTATIONS (4)

Host-parasitic compatibility of brown trout *Salmo trutta* and freshwater pearl mussel *Margaritifera margaritifera* in central Europe based on fluorescence lipid quantification

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The quantification of energetic reserves of juvenile molluscs can provide novel insights into their vulnerability and the survival prospects of populations of threatened species. Freshwater pearl mussel (*Margaritifera margaritifera*) is a strict host specialist and critically endangered Unionid. For its conservation it is crucial to have detail knowledge about its reproduction and host-parasitic dynamics because in many territories there are concerns that the availability and quality of hosts is one of the fundamental limiting factors for reproduction. We tested differences in compatibility between fish hosts and parasitic larvae (glochidia) within national park Šumava (Czech Republic) based on fish population and population of parental mussels as well as the effect of individual fish host. In total we tested six combinations of populations in two years. Except the widely used methods for estimation of the host-parasitic compatibility such as glochidia survival, metamorphosis success rate and juvenile size we also quantified lipid content in individual mussel juveniles tissues with use of fluorescence microscopy technique. In total we quantitated lipids in almost 600 juveniles and our results confirm the advantages of using methods quantifying lipid reserves of larval and juvenile bivalves as an important complementary parameter of larval developmental conditions. Our results have a direct impact on the conservation of *Margaritifera margaritifera* in the tested region.

Keywords: *host-parasitic relationship, Margaritifera margaritifera, lipids*

Hundreds of shells: a time-consuming but useful quantitative approach to malacofauna

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The malacologist is a patient and meticulous observer when listing the malacological fauna living in a given area. Today, environmental DNA provides such a list from a simple soil or water sample. But are these lists sufficient to understand malacological biodiversity and to guide the management strategies of natural areas? The work carried out in recent decades on the malacofauna of the last 12 millennia, corresponding to our current climatic period, i.e. the Holocene, has demonstrated the high value of quantitative malacological studies for the ecological assessment of environments. In Alsatian protected wetlands, this analytical method was applied to modern faunas.Investigative malacological samples were collected in the floor litter of two micro-habitats separated by 34 meters, one mainly composed of reeds and the other of grasses. The quantified analysis of the two samples highlighted significant differences in the composition of malacological assemblages, which were in good agreement with the variability observed in terms of flora. While the reed zone is dominated by marshland and aquatic species, the grassy zone is dominated by molluscs from open environments. The structure of populations (by species) was thus significantly correlated with the diversity of micro-habitats. From an anthropic point of view, only the imprecise sum of these micro-habitats is perceived but, at snail level, this heterogeneity is decisive in explaining the vitality of populations, the diversity of assemblages and the occurrence of rare species in ecological niches. This time-consuming approach should not be used everywhere, but it would be useful for local application in order to assess the vitality of malacological populations, particularly for threatened and vulnerable species.

Keywords: *sampling, quantitative approach, population dynamic, species assemblage.*

Introducing new project on freshwater pearl mussel conservation: LIFE Revives

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European Commission granted 9.5 milj. € for reviving freshwater pearl mussel (*Margaritifera margaritifera*, FPM) populations by improving their – and their host fishes' – habitats in Finland (University of Jyväskylä/JYU; Metsähallitus: Parks and Wildlife, and Forestry; Centres for Economic Development, Transport and the Environment/ELY in South Ostrobotnia, Pirkanmaa and Southwest Finland), Sweden (County Administrative Board of Norrbotten, Swedish Anglers Association, SCA SKOG AB, Sveaskog Förvaltnings AB) and Estonia (Estonia State Forest Management Centre, University of Tartu). This six-year LIFE Revives project, led by JYU, will start in September 2021, and is co-financed in Finland by ELY Centres in Kainuu, Lapland and North Ostrobothnia, Ministry of the Environment, Serlachius and Tuuliainen foundations and WWF, and in Sweden Swedish Agency for Marine and Water Management. Project conservation/restoration actions will be targeted to in-stream habitats, catchment area waters and buffer zones, and they will be carried out in 14 river systems including 69 individual rivers out of which 32 are located in Finland (25 % of the Finnish FPM populations), 36 in Sweden (3,6% of the currently known FPM Swedish populations) and one in Estonia (100% of the Estonian populations). The project impact area of Natura-2000 3210 and 3260 habitats will be more than 2400 ha. To save dying-out FPM population, adult mussels will be revived – and juveniles produced – in captivity. Moreover, specific habitats, "kindergartens", for FPM juveniles will be established in 12 rivers. In addition to standard monitoring method, approaches such as shell opening resistance, drone based aerial surveys and trained dog to find FPM populations will be used for FPM, salmonid and habitat status monitoring. Throughout the project, emphasis is given in sharing good practises among people working with land use and forestry to help forward FPM conservation, and in raising the awareness of FPM importance among public.

Keywords: *freshwater pearl mussel (FPM), salmonids, conservation, captive breeding, FPM kindergarten.*

Spatial distribution of *Unio crassus* linked with environmental variables at a regional scale.

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The thick shelled river mussel (*Unio crassus*, Philipsson 1788) is an endangered european Unionidae. The profuse degradations suffered by rivers (physical, chemical, biological, and hydrological) are as many explanations for the decline of the species. However, it remains uneasy to establish a direct causal link with a quantification of the role played by these deteriorations. In Belgium, *Unio crassus* is evaluated in a conservation status qualified as unfavourable to poor (U2) according to European criteria. It is extinct in Flemish rivers (northern part of Belgium) and only remains in Wallonia (southern part of Belgium), where several functional populations still exist. The species is unevenly distributed in rivers and its decline is equally uneven. The main hypothesis of this research is that the causes of the decline could be identified by observing the current distribution, i.e. by analysing hydro-geomorphological, physico-chemical and biotic factors that could explain the spatial distribution of *Unio crassus* in Wallonia. Hydro-geomorphological characteristics of the streams (bankfull stage, substrate grain size, land cover…), physico-chemical parameters (water chemistry and pollutants), host fishes and predators abondance were compiled and supplemented by field surveys. The ability of these environmental variables to predict the presence or the absence of *Unio crassus* is tested using multiple logistic regression. This method of statistical analysis allows not only to determine which variables have the greatest impact on the species distribution but also to quantify their relative impact to each other. Eventually, key elements for the conservation of the thick shelled river mussel could be identified, and doing so, establish target actions to be undertaken to improve its conservation.

Keywords: *Unio crassus, habitat, GLM, distribution.*

CONSERVATION PRACTICE

POSTERS (3)

Action Plan for a critically endangered Freshwater Pearl Mussel in Czechia – achievements of semi-natural breeding and population reinforcement in contrast with protracted restoration of its oligotrophic river ecosystems

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Even at the beginning of the 20th century, a strong population of freshwater pear mussel (FPM) amounting millions of individuals lived in many Czech rivers. During the 20th century, this bivalve gradually lost up to 95% of its original distribution area as well as many other organisms associated with this type of habitat due to a number of anthropogenic interventions in river ecosystems. At present, its last population is limited to the border area of Bohemia, where the last hundreds to thousands of individuals live in the catchment area of five rivers. At the most of them the species stopped its spontaneous reproduction. Since 1980, due to an alarming decline of FPM population, missing reproduction and the deteriorating quality of entire unique oligotrophic river catchments, the activities to protect them are ongoing. Gradually, declarations of a first action plan for the FPM and its habitats and declaration of protected areas in most of FPM catchments with a detailed plan for the care of the entire ecosystem were being processed. Since 1990, successful semi-natural breeding of FPM and an invading of its host-fish brown trout progressed in order to population reinforcement in individual rivers (for details, see talk Simon et al.). Many rivers have undergone a number of more or less successful river restorations and measures to protect the entire ecosystem and pearl mussels as a flagship species over the last 40 years. Nevertheless, despite of many successes of the action plan, all measures to save and support local ecosystems and their unique habitats are realized too slowly.

Keywords: *freshwater pearl mussel, semi-natural breeding, catchment area*

Conservation and management of freshwater pearl mussel (*Margaritifera margaritifera*) and brown trout (*Salmo trutta*) populations in Portugal

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The project "Recovery and Protection of *Margaritifera margaritifera*" (POSEUR-03-2215-FC-000096) involves a multidisciplinary team with the ultimate goal to protect and restore the freshwater pearl mussel *M. margaritifera* and brown trout *Salmo trutta* populations in Portugal by the implementation of different scientific tasks and conservation measures. Several tasks have been developed in the last 3 years such as: 1) in situ actions that include (a) determination of the extent, detailed spatial distribution and conservation status of the target species; (b) evaluation of the biological and ecological quality of salmonid rivers; (c) analysis of vulnerability to climate change, control of exotics and other threatening factors; (d) increase habitat suitability; (e) design of measures for the management of salmonid watercourses; (f) monitoring of *M. margaritifera* and *S. trutta* restocking programmes; and 2) ex situ actions that include: (g) captive reproduction of *M. margaritifera*; (h) captive breeding of *S. trutta*; (i) genetic characterization of wild populations of *S. trutta*, including selection of several wild stocks for breeding in captivity, according to the strategy defined by the Institute for Nature and Forest Conservation. Overall, scientific results and conservation measures gathered and implemented by this project will be fundamental for the future survival of *M. margaritifera* and its host *S. trutta* in Portugal under a scenario of climate change and increased human disturbance.

Keywords: *Margaritifera margaritifera, host fish, threats, conservation, management*

Acknowledgments: The “Recovery and Protection of *Margaritifera margaritifera*” project is developed by QUERCUS - National Conservation Association of Portugal with the partnership of ICNF – Institute for the Conservation of Nature and Forests of Portugal. The project is financed by POSEUR-03-2215-FC-000096) and the Environmental Fund (Portuguese governmental services).

Towards resolving the mystery about the Balkan endemic freshwater snail *Graecoanatolica macedonica* Radoman & Stankovič, 1979 in Dojran Lake (R. North Macedonia)

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Lake Dojran is one of the priority Key Biodiversity Areas in the Mediterranean biodiversity hotspot, containing Mediterranean, Northern and Eastern floral and faunal elements, but also endemic flora and fauna. Endemic species originate from the relict flora and fauna or have derived through the process of specialisation and adaptation to the specific local circumstances. One of the valuable endemic species from Dojran Lake is *Graecoanatolica macedonica*, described from shells taken from the type locality Kaldrma, on the Macedonian side of Dojran Lake. Unfortunately, its population was noted to have suffered declines in the 1970s when the lake's water levels lowered. As the species was not recorded in the area between 1992 and 2001, it was proclaimed as "Extinct (EX)" on the IUCN Red List of Threatened Species. However, in 2015 and 2016 some fresh-looking shells have been found at the lake by the authors, suggesting the possibility that the species may be still present in the lake. Therefore, detailed and comprehensive survey work was conducted during the summer of 2020 towards revealing whether these shells are 'subfossil' or whether the species survives somewhere at the lake and urgent action in changing its status on the IUCN Red List should be undertaken.

Keywords: *conservation, IUCN, endemic, extinct, Dojran*

Acknowledgments: This research has been conducted under the Critical Ecosystem Partnership Fund (CEPF) funded project "Assessment of an Endemic Freshwater Snail in Dojran Lake - Population Status, Threats and Conservation Measures" implemented by GTI - Geotehnicki Inzenering DOO Skopje, North Macedonia.

ECOLOGY AND EVOLUTION

STANDARD PRESENTATIONS (21)

“Enemy release” as an explanation for the success of invasive freshwater mussels

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An increasing threat to local, native freshwater mussels (Unionida) is the invasion by exotic bivalves. The Enemy Release Hypothesis predicts that introduced species benefit from enemy-mediated competition because they are less likely to be harmed by natural enemies, such as parasites, than their native competitors. We investigated within-site differences in parasitism between sympatric native and invasive bivalves in 8 European waterbodies, harbouring 5 native (*A. anatina*, *A cygnea*, *P. complanata*, *U.pictorum* and *U. tumidus*) and 3 invasive (*S.woodiana*, *D. polymorpha* and *C. fluminea*) freshwater bivalve species, and totally 15 parasite taxa. Large variation between populations and species was evident, but in paired comparisons using within-site averages, the mean number of parasite species in the native bivalves was 2.3 times higher, and the sum of parasites' infection prevalences 2.4 times higher, than in the invasive bivalves. This may lead to enemy-mediated competitive release of invaders and contribute to the success of invasive freshwater bivalves. To test the possible “enemy loss” during the invasion process, we have started investigating parasitism of the invasive bivalves (*S.woodiana*, and *C. fluminea*) in their original region in China. While the invasive clam *C. fluminea* was completely free from parasites in Europe, a total of 6 parasite taxa has been found, so far, in two water bodies in its orginal distribution area in China, indicating parasite loss during invasion. Results support Enemy Release Hypothesis and suggest that parasitism can possibly contribute to success of invasive freshwater bivalves, such as *C. fluminea*. Understanding the factors affecting success of freshwater bivalve invasions, such as parasitism, can aid invasion control and conservation of local, native (endangered) bivalves.

Keywords: *Biological invasion, Enemy release hypothesis, parasite.*

Assessment of the status of populations of *Unio crassus* Philipsson, 1788 for the establishment of conservation areas in Lithuania

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Thick Shelled River Mussel in Lithuania have been inventoried quite successful in 2016 in 236 sites of 58 rivers (not shorter than 20 km). Study sites were distributed across the whole of Lithuania and reached 3955,3 km of rivers length. Specimens were found in 76% (or in 44 rivers) of all investigated rivers. The total average density of molluscs in studied rivers sites suitable for *U.crassus* (889,7 km of the rivers) was 8.7 ind./m2. Only 15 rivers were assessed as good for species. Some rivers had been selected and conservation areas have been established.

In this presentation, we review the results of status of populations of *U. crassus* in some protected areas where the protection objectives have been established to restore or maintain a favorable conservation status for *U. crassus* in an appropriate habitat where species individuals are regularly found. The molluscs were collected by linear transect, where 10 study square meters were arranged per meter. The rivers with such conservation areas have been: Venta, Minija, Alantas, Nemunėlis, Peršokšna, Baltelė, Lakaja, Uošna and Ašva. The two last were selected not only for monitoring but for evaluation of future management work too: are necessary cutting down shoots of trees and shrubs on the shores, removing beaver dams, collecting debris, and naturally fallen or beaver-damaged trees or not. Our results revealed that the mean abundance of molluscs in the studied protected areas is very different and ranges from 1.8 ± 1,7 ind./m2 (Baltelė, min-max 1-5 ind./m2) to 33,5 ± 37,8 ind./m2 (Lakaja, min-max 1-122 ind./m2), therefore, many questions arise why so different rivers were chosen for protection. Also, disputable management measures were selected for last rivers: Uošna and Ašva. After investigation in five sites (total 50 study square meters), the mean abundance of molluscs in Uošva was established 15.4 ind./m2 and min-max reached from 3 to 56 ind./m2. The river is only 17 km long and is drained in front of the protected area. In the section between the unprotected-protected boundary, the beaver dam visibly retains organic particles, so there has been much hesitation as to whether a measure to remove the beaver dam really needs to be applied. There are also doubts about whether it is really necessary to cut bushes-trees and their offspring, because mollusks have been more abundant in those sections of river where there was a forest near the stream and where the stream was deeper and with a less hard bottom - where the area was among other beaver dams. In conclusion we invite share experiences about protection measures.

Keywords: *Unio*, Habitats Directive, endangered species

Attacking strategies of malacophagous shell-breaking carabid beetles in laboratory experiments

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The presence of a shell represents the main defensive structure of land snails. Individual predators have had to adapt strategies to overcome this barrier to reach a retracted soft snail body. It includes crawling into a shell through its aperture or breaking the shell in specific ways. Carabids of the Licinini tribe possess asymmetrical mandibles that are presumably adapted to break the shells by a gradual biting of the dorsal part of the shell whorls starting from the outer lip of the aperture towards the apex, leaving the characteristic spiral furrow. Thus, these morphological adaptations may be related to their obligatory malacophagy. In ongoing experiments, we collected a rich variety of adult carabid beetles that would be potentially malacophagous. All individuals were placed separately in petri dishes together with several snail prey individuals. We aim to find out whether the carabid species would feed on snails and what type of shell-breaking attack it performs. We documented about 350 shell-crushing attacks made by 19 species. In most cases, the carabids fed on snails, but they did not perform the characteristic shell damage. On the contrary, they broke shells in variable manner. Shells were often halved, sometimes their bottom or top parts were broken off to a certain extent. Likewise, the spindle-shaped shells of door snails were broken horizontally or vertically. It is clear that the way of breaking is chiefly different from that of malacophagous specialists. We also observed that juveniles of various snail species represented the most preferred food, especially in case of door snails, i.e. without a fully developed aperture lip. These observations raise a question whether the pattern of shell damage made by carabids is closely related to the level of their feeding specialisation on snails.

Keywords: *land snails, carabid beetles, predation, shell damage, prey*

Causes and evolutionary consequences of phenotypic plasticity in land snails of *Trochulus hispidus* complex

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Phenotypic plasticity modulates selection on populations and can accelerate or inhibit adaptation, divergence and speciation. Ideal organisms to study evolutionary and ecological processes leading to speciation and phenotypic plasticity are land snails from *Trochulus* complex. Its species, *T. hispidus*, *T. sericeus* and *T. plebeius*, are widely distributed and its taxonomy is unclear. We revealed two morphological forms: *T. hispidus* with a flattened shell and a wide umbilicus, and *T. sericeus/plebeius* with an elevated shell and a narrow umbilicus. They do not represent separate biological species because they do not form separate gene pools and can freely interbreed producing fertile offspring. Common garden experiments showed great plasticity of their shells. Laboratory-bred *T. hispidus* changed its shell from flat, wide-umbilicated to high, narrow-umbilicated. The offspring transferred to the natural environment returned to the ‘typical’ shell shape. A similar shape was adopted by originally distinct *T. sericeus* that was transferred to the same environment. The large shell variation within populations significantly correlated with temporal changes in temperature and humidity. Illumination, forestation, isothermality, precipitation and temperature are the most important factors in choosing habitats by snails. *T. sericeus* prefers forests and moist, shaded places but *T. hispidus* more dry habitats and open areas exposed to the sun. The hair durability also correlates with their habitats. Therefore, these forms are considered ecophenotypes. The morphological flexibility of *T. hispidus* corresponds to plasticity in feeding habits and bet-hedging strategy responsible for adaptation to changing environments. The large diversity could allow *T. hispidus* to survive in Pleistocene harsh climate of glacial steppe. These snails can be a good model for studying the interaction between environment and phenotypic plasticity and can help to understand mechanisms responsible for the morphological differences. This work was supported by the National Science Centre, Poland (Narodowe Centrum Nauki, Polska) under Grant number 2016/21/B/NZ8/03022.

Keywords: *land snails, Hygromiidae, Europe, phenotypic diversity.*

Collective behaviour and social dynamics during interspecific collaborative hunting between octopus (*Octopus cyanea*) and multiple fish species.

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In collective behaviour, complex coordination and individual/group decision-making can emerge from simple, localized rules of interaction, considering every individual as identical. However, in biological systems, variation amongst individuals can alter the "weight" of specific individual's decision within a group, creating a dynamic network of attraction-repulsion forces driving individual and group movement. Parallelly, sociality has the potential to drive brain evolution and cognition, but the role of individual cognition on collective movement and group decision-making constitutes a largely unexplored field. Using SCUBA, we recorded interspecific hunting events between *Octopus cyanea* and multiple partners (i.e. various fish species), and obtained animals tracks over a 3D reconstructed habitats, which enables multi-scale analyses gauging novel and key parameters in interspecific collectives, e.g. movement synchrony between *O. cyanea* and fish partners; leader-follower dynamics; habitat, social, and individual level factors influencing leadership; and presence/absence of social rules. From individuals to collective, understanding the underpinnings of these interspecific interactions can potentially deepen our knowledge on cephalopod cognition in a social context, mechanisms of intentional/unintentional communication, and the influence of higher order traits (morphological, behavioural, and cognitive) on collective movement and decision-making in naturally-occurring heterogenous groups.

Keywords: *collective behavior, interspecific hunting, leader-follower, octopus, fishes*

Correlated loss of shell colour and pattern and vision in deep sea snails

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Biological colour plays an important role in species survival. Its roles are diverse; in some species providing camouflage or acting as a warning to predators, in others providing a means for intraspecific communication about sexual status. Colour serves visual functions where the species or its predators have colour vision, however it may also serve non-visual functions such as improving strength or elasticity. In some cases, there is no apparent function for colour. For instance, it has been suggested by some authors that colour in molluscan shells is merely the result of accumulation metabolic waste products. We test this theory, looking at the loss of shell colour in a family of deep-sea gastropods, and compare the evolution of loss of colour, pattern and vision with depth and their pattern of correlation within a phylogenetic framework. Our data suggest that colour and pattern have been lost more frequently than vision, and that colour and pattern are rare in species found in deeper water. We suggest that this indicates that colour serves a visual function in these species (probably camouflage) and that the production of pigmentation is metabolically costly.

Keywords: *colour, shell, deep sea, vision, gastropod*

Effects of habitat homogenisation on biodiversity associated with mussel beds

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The mussel, *Mytilus galloprovincialis* is a very abundant species in the Atlantic coast of the Iberian Peninsula. Aggregates (beds) of mussels provide protection and habitat for many organisms and therefore is considered a relevant ecosystem engineer in the intertidal fringe. Thus, mussel beds enhance biodiversity and can play a significant role to avoid biodiversity loss. Despite its relevance in shaping biodiversity patterns, the factors that influence the assemblage structure of associated fauna are not completely understood.

Here, we aim to explore the effect of level of habitat homogenisation on the associated fauna assemblage. To achieve this, clumps showing very different sized mussels were considered as control and clumps showing closely similar sized mussels were considered as homogenised. Two rocky shores (Muros and Oia) were selected in Galicia (NW Iberian Peninsula). At each shore, two sites were considered and 4 replicates (10x10cm) of homogenised clumps and 4 replicates of control clumps were collected per site. Invertebrates at each replicate were identified to species level. Abundance (N), taxon richness (S) and assemblage composition were compared between treatments by means of univariate and multivariate techniques. N and S showed only significantly higher values in homogenised clumps compared to controls in one site in Oia. Assemblage structure differed significantly between homogenised and control clumps in all sites apart from one site in Muros. The effect of homogenisation of mussel size varied spatially indicating that such effect is context dependent. This could be related to the importance of the surrounding landscape in shaping invertebrate assemblage structure but future manipulative studies will be needed to elucidate which factors are relevant.

Keywords: *Mytilus galloprovincialis, habitat homogenisation, biodiversity, mussel size.*

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Enrichment of ORFs and UCEs in genomic samples to link microevolution and macroevolution in African freshwater unionids (Parreysiinae: Coelaturini).

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A major challenge in facing the current global biodiversity crisis is the study and protection of living species to avoid extinction and ecosystem destabilization. Freshwater mollusks perform important ecosystem services but despite their biological, medical and economic interest these non-model organisms have scarce genomic resources. Despite increasing accessibility of high-throughput sequencing, obtaining high-quality genomic data on non-model organisms without well-assembled and annotated related genomes remains challenging.

Here, we develop a genomic workflow to obtain information on a large set of orthologous markers with the objective to undertake studies on microevolutionary and macroevolutionary drivers and dynamics in understudied African freshwater bivalves. We identified ultraconserved elements (UCEs) for freshwater mollusks via comparative genome analysis and open reading frames (ORFs) from *de novo* transcriptomes for use in high-throughput sequence-capture experiments. We applied our workflow on 96 individuals spanning Coelaturini to assess its performance in characterizing genomic diversity and differentiation in the Malawi Basin as well as continent-wide diversification dynamics. Our results indicate efficient enrichment of our target ORFs (~2MB) in the absence of prior identification of intron-exon boundaries. The enrichment of UCEs was less successful, but the resulting data (~100 kb) still enabled downstream analyses. We also recuperated the entire maternally-inherited mitogenome of the Malawi clade from genome skimming. Exploratory phylogenetic analysis of ORF supercontigs resulted in a fully resolved phylogeny, which was also recovered with the UCEs, albeit with lower support in some branches. Variant calling on our ORF targets from the Malawi clade allowed to identify four population groups with geographic separation, i.e. the northern and southern regions as well as the Shire river and Likoma Island, despite low levels of intrapopulation nucleotide diversity and interpopulation genetic differentiation. Overall, our workflow and results provide exciting perspectives for the development of integrative genomic studies on micro- and macroevolutionary dynamics in non-model organisms.

Keywords: *Unionidae, Coelaturini, phylogenomics, population genomics, mitochondrial genome skimming.*

Extinction at the fifth and sixth mass extinction – a freshwater perspective

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Earth's biodiversity faces a massive decline today. Because of the magnitude of the already observed and future predicted change, many scientists consider the current biodiversity crisis an incipient "sixth mass extinction". The current crisis resembles the previous, fifth mass extinction event at the Cretaceous–Paleogene (K–Pg) boundary 66 million years ago in terms of the rapidity of the change – an asteroid impact paired with extreme weather conditions in the successive months/years vs. anthropogenic impact and climate change. The fifth mass extinction is well understood for terrestrial and marine biota, but little data are available on freshwater biota. Freshwater vertebrate faunas seem to experience a much lesser decline of 10–22% (compared to the global average of 76%). However, vertebrates make up only a minor proportion of freshwater biota, and no comprehensive data are available for invertebrates.

We estimated speciation and extinction rates for a large dataset spanning the fossil record of freshwater gastropods of Europe, with 3,122 species from 24,759 fossil occurrences from Jurassic to Pleistocene deposits. To compare the impact of the sixth versus the fifth mass extinction, we predicted future extinction rates and species loss based on conservation statuses of the extant European freshwater gastropod fauna.

The results were alarming. While our reconstructions show that already the fifth mass extinction has been dramatically underestimated – 92.5% of the gastropod species go extinct and the extinction rate is an order of magnitude higher than the background rate – the predictions for the future are much worse. Our estimates suggest that a third of the modern European gastropod fauna may be lost within 100 years. The estimated extinction rate is approximately a thousand times higher than for the fifth mass extinction event. Our results once more highlight the devasting prospects for Earth's biota and the need for immediate action.

Keywords: *mass extinction events, biodiversity crisis, freshwater gastropods, diversification rates*

Feeding behavior in Olividae: more diverse than expected

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The Olividae (Caenogastropoda) include mostly tropical and subtropical carnivores inhabiting soft sediments in shallow marine habitats. The complex feeding behavior observable in large predatory species, especially the species-rich genus *Oliva* but also *Olivancillaria* and *Agaronia*, includes the grasping of the prey with the anterior foot, followed by its transfer into a pouch formed by the metapodium (posterior part of the foot) in which the prey is killed by suffocation. These predators lack opercula, which has been interpreted as a necessary condition for the ability to form the metapodial pouch. However, we observed similar food handling behavior in *Olivella* species that possess opercula. Foot biomechanics certainly differ between operculate and inoperculate Olividae, which is evident from the movements that occur when the snails withdraw into their shells. Nonetheless, pouch formation for food storage does not seem to be affected.

Concerning their trophic relations, *Olivella semistriata* and *O. columellaris*, which form the subgenus *Pachyoliva*, are remarkable exceptions within the Olividae, as they exhibit pronounced behavioral and morphological adaptations to a suspension-feeding life-style. Both species form dense populations that dominate invertebrate communities on many sandy beaches of the Central and South American west coast. Unexpectedly, we discovered predatory behavior of *O. columellaris* in the wild, and carnivory in both species in captivity. We will discuss possible implications of this unusual switch between suspension-feeding and carnivorous trophic modes for the ecological community structure in the habitats of *Pachyoliva*.

The behavior discussed in this contribution will be documented by video material acquired in the natural habitats.

Keywords: *feeding behavior, Olividae, Pachyoliva, trophic ecology.*

Function and evolution of high-resolution spatial vision in strombid gastropods

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All species within the conch snail family Strombidae possess camera-type eyes of surprising size and sophistication compared to those of other gastropods. Although strombid eyes are known to be structurally complex, very little research on their visual function has been conducted. Here, we use isoluminant looming visual stimuli to test for behavioural evidence of high spatial resolution in a strombid, *Conomurex luhuanus*. Using these stimuli, we show that this species responds to objects as small as 1° in its visual field, which for any invertebrate is very fine resolution vision; for example, this resolution is twice that of a worker bee which uses vision for complex flight. These findings are consistent with calculations of spatial resolution from histological data, and use serial block-face scanning electron microscopy to reconstruct the complexity of the retina structure which gives rise to this high resolution vision. We compare these results to estimates of spatial resolution for the eyes of other families within the superfamily Stromboidea, three of which have much smaller eyes compared to those of strombids such as *C. luhuanus*, and a spatial resolution about five times coarser. This disparity in visual capabilities and eye structures within the superfamily raises exciting new questions about why strombids have such fine spatial resolution. These results also demonstrate Stromboidea to be an excellent group for studying trends in eye evolution; however, a robust phylogenetic framework of the relationships between genera within each family is so far lacking. We therefore use Sanger sequencing data to produce an initial phylogeny of the group, to begin to investigate trends in the evolution of these amazing eyes.

Keywords: *vision, conch, resolution threshold, phylogenetics*

Genetic determination of shell-shape variation in *Lanistes* from the Northern region of the Malawi Basin.

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The East African Great Lakes represent unique, highly diverse freshwater ecosystems with a high degree of endemicity of fishes, snails, crustaceans, and other invertebrates. The species flocks of cichlids are considered classic examples of rapid adaptive radiation, implying that an ancestral species has rapidly diversified into multiple descendant species that are adapted to distinct ecological niches. However, for most invertebrate species flocks the drivers of diversification remain incompletely understood. Examinations of the ongoing radiation of *Lanistes* gastropods in the Malawi Basin have indicated that neutral and mutation-order processes are older and occur mainly between the northern and southern regions of the basin, whereas more recent adaptive processes would drive genetic differentiation within regions. In the southern region, where morphospecies occur parapatric, experimental evidence substantiates adaptive divergence, but no in-depth examinations have been performed on the *Lanistes* populations from the northern region where the nominal species *L. solidus* and *L.* sp. (*ovum*-like) occur often sympatric. Here we investigate determinants of shell-shape variation in these two nominal *Lanistes* species (*L. solidus* and *L.ovum (like)*) from the northern region with a common garden experiment in laboratory conditions and geometric morphometrics. Our results indicate that shell-morphological differences observed in the parents are maintained in the F_1 generation. This result suggests that the main morphological differences among the two morphospecies are heritable rather than driven by plasticity. Although we have currently insufficient ecological data to link morphology to fitness differences and potential microhabitat repartitioning, the positive correlation between phenotypic and neutral genetic differentiation recovered in natural populations suggests a role for divergent selection in speciation. Beyond ecological studies, further in-depth studies of morphological differentiation and genome-wide genetic divergence are required.

Keywords: *Common garden experiment, Geometric morphometrics, Adaptive radiation, Ampullariidae, Heritability*

High frequency video analysis as a new method for tracking bivalve filtering behaviour: comparison with traditional methods.

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Bivalve filtering behavior has been extensively used as a sensitive in vivo indicator of water environment changes. However, greater use of this technique is hindered by the usually complex, invasive, and laborious technical approaches (glued-on sensors) needed to obtain high-resolution data on the movement of bivalve shells. We developed and tested a high-frequency (5 frames per second) video analysis method based in open-source tools for studying the potential for acute behavioral disturbance detection in bivalves. We used this method to monitor the behavioral response of the freshwater mussel (*Anodonta anatina*) to a reference toxicant, and the results were compared to data obtained through traditional valvometric evaluation using magnetic Hall sensors. The video method show consistently higher metrics in comparison with the valvometry approach (Video: 0.97, 95% CI = 0.87 – 1;Valvometry=0.97, 95% CI = 0.17 - 0.97) and specificity (Video: 0.97, 95% CI = 0.82 –1; Valvometry: 0.92, 95% CI = 0.82 - 0.1), accuracy (Video=97.5, Valvometry=95), positive predictive value (Video=97.6, Valvometry=93), negative predictive value (Video=97.4,Valvometry=97.3) and the area under the ROC curve (Video=0.99, Valvometry=0.96) although the difference was not significant according to the statistical tests. A comparison between reaction times in response to stimuli of two reference toxicant concentrations (250 mg/L and 500 mg/L of nitrate-nitrogen) showed that reaction time measured from video data was significantly shorter (mean difference in reaction times=1.56 ± 0.89 seconds, paired t-test: p=0.01) in the 250 mg/L group due to the siphons closing first when exposed to the toxicant. In conclusion the video method showed an equal or better performance in comparison to the traditional valvometry approach, we hypothesize that the difference is caused by the video method being able to track changes in the soft tissue while valvometry approaches can only track movement of the valves. Methods like the one presented here will allow future studies based on video data collection and analysis with a higher resolution than previously possible, complementing traditional gaping frequency measures and increasing our acute behavioral disturbance monitoring capabilities in bivalves.

Keywords: *Valvometry; Image analysis; Bivalve behavior; Siphon.*

Land snail assemblages as indicators of regional habitat conservation status of European spring fens

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The biodiversity is being shaped by anthropic activities across all spatial scales. There is a large body of evidence showing the differences between preserved and damaged sites, however, the knowledge at regional scales is scarce. To address this, four European regions with different habitat conservation status (HCS) were selected and 169 sites were quantitatively sampled for land snail communities. The habitat specialist species richness showed weak associations with local conditions and expressed low variation in the two adequate HCS regions, likely because it was evenly high across the sampled sites. On the other hand, the richness of matrix-derived species, consisting predominantly of habitat generalists, was strongly controlled by local conditions, in particular by moisture. These associations were much weaker in inadequate and intermediate HCS regions as the conditions are less extreme and allow for colonization by matrix-derived species. The two adequate HCS regions also harbored highest population densities of *Vertigo geyeri*, a rare glacial relict protected by EU Habitats Directive. Moisture was shown as key predictor for species composition in regions of adequate HCS, while for the remaining regions, the importance of more anthropic-resilient predictors, such as climate, water chemistry and terrain topography, increased. Our data suggest a complete disruption of community-environment relationships in the inadequate HCS regions as none of the tested predictors was associated with the main compositional gradient. The results indicate that species richness and community patterns can be markedly altered by anthropic pressure, although we cannot exclude the possible effect of some unknown region-specific factor due to inevitably low number of studied regions.

Keywords: *Gastropod communities, Species richness, Species composition, Fens,* Vertigo geyeri

“Obstetrical dilemma” in viviparous snails

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In evolutionary biology the term “obstetrical dilemma” refers to human challenging childbirth, the trade-off between selection for a larger birth canal, permitting successful passage of a big-brained neonate, and the smaller pelvic dimensions required for bipedal locomotion. Antagonistic pressures on offspring size and maternal morphology may also operate in other viviparous animals, e.g. testaceous gastropods, but the problem is understudied. Viviparity and embryo-retention occur in at least 30 families of stylommatophorans, mostly in taxa lacking strong aperture barriers: when shell mouth is broad there is no mechanical obstacle for passage of shelled embryo. In contrast, teeth and/or lamellae in shell mouth were supposed to hinder life birth. Surprisingly, viviparous species appear to be quite common among door-snails, renowned for its complex aperture barriers that include a calcareous plate blocking the shell canal. This intriguing coincidence made Clausiliidae a model group for studying the evolution of viviparity in land snails. Recently it was shown that viviparous clausiliids, subfamily Phaedusinae, represent different phylogenetic lineages which suggested repeated independent evolution of this reproductive mode in this group. Four types of viviparity-related adaptations in Phaedusinae shell has been recognized: 1) reduction (or partial reduction) of clausiliar apparatus including clausilium, 2) widening of the shell canal without reduction of clausilium (clausilium plate becomes very broad to fit the canal), 3) decrease of embryonic shell width, 4) highly flexible organo-mineral structure of embryonic shells. The development of soft and flexible embryonic shell that hardened after parturition has been documented for the first time. Listed types of adjustment that allow for passage of offspring (shelled embryos) through shell canal may occur separately or together in a species. As clausiliids exemplified many ways of overcoming “obstetrics dilemma”, the identification of viviparity in a particular species cannot be based solely on shell morphology, e.g., the width of clausilium plate.

Keywords: *land snails, Clausiliidae, reproduction, evolution, microtomography.*

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Parallel adaptation of shell morphology across space and time in the land snail genus *Pupilla* (Gastropoda: Stylommatophora: Pupillidae)

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If environmental conditions change species have to respond either by dispersal to still suitable habitats or by local adaptation, either genetically or via phenotypic plasticity. We can test the limits of plasticity experimentally, however, the predictability of genetic adaptation is restricted due to its stochastic nature. In particular, studies of parallel adaptation have improved our understanding of evolutionary adaptation, though. Based on molecular phylogenetic inferences (COI, ITS2) and morphological investigations of both recent and fossil shells we tracked the morphological changes in three congeneric species of land snails, *Pupilla alpicola*, *P. loessica* and *P. muscorum*. These species have different habitat requirements as well as historical and extant distributions. In both aspects, *Pupilla alpicola* and *P. loessica* are more similar to each other than to *P. muscorum*. Expecting that the three species reacted independently and individually to the conditions changing throughout the Pleistocene, we hypothesized that *P. alpicola* and *P. loessica* would also be more similar in their changes compared to *P. muscorum*. The results confirmed our hypothesis. Intraspecific differences in shell shape across time were similar in *P. alpicola* and *P. loessica*, which suggests that they transformed in parallel experiencing similar niche shifts. In contrast, extant *P. muscorum* populations could hardly be distinguished from their ancestors. They have probably tracked their ecological niches through time.

Keywords: *adaptive convergence, geometric morphometrics, Palaearctic, Pleistocene, phylogenetics.*

Patterns of Trophic Resource Partitioning in Diverse Freshwater Bivalve Assemblages Support Classic Niche Theory

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Classical ecological theory suggests that resource use differences among co-occurring species promotes coexistence leading to greater resource partitioning and exploitation in communities with more species. Freshwater mussels (Family: Unionidae) are a highly diverse and imperiled group of filter-feeding bivalves that live in multi-species aggregations where interspecific differences in functional traits may drive differences in resource assimilation that promote coexistence. Our goal was to determine isotopic niche variation across species richness gradients and evaluate if patterns of resource partitioning were consistent with niche theory. We quantified niche area for 23 species at 15 sites in the Mobile and Tennessee river basins in the Southeastern United States, using stable isotope analysis (δ13C and δ15N) of soft tissue to calculate standard ellipse area (SEA) for species and total community SEA. Our findings show that mussels assimilate different resources but have variable SEA among sites and rivers. Species SEA declined as assemblage richness increased, meaning that greater species richness led to greater resource partitioning. Even though mean species' SEA was smaller, assemblage SEA expanded with richness. This result suggests that communities are not species saturated and are not constrained by the trophic resource dimensions of the niche but could be controlled by other factors such as habitat. Our study supports classical ecological niche theory, by demonstrating intra- and interspecific variability in resource assimilation that is driven by assemblage richness.

Keywords: *Unionids, stable isotopes, niche space, functional diversity*

Population collapse in viviparid gastropods of the Lake Victoria ecoregion started before the Last Glacial Maximum

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Ecosystems of Lake Victoria and riparian communities have been strongly disrupted by the introduction of the invasive Nile perch and its fishing industry. Beyond this invasion and other recent anthropogenic stressors, the Lake Victoria ecoregion also underwent phases of pronounced aridity over the late Pleistocene, lastly during the Last Glacial Maximum (LGM). The consequences of recent and historic environmental change have been canvassed for the adaptive radiation of haplochromine cichlids occupying the ecoregion, but their effect on freshwater invertebrate diversity remains largely unknown. Here we use 15 microsatellite loci and approximate Bayesian computation to test whether viviparid gastropods experienced a population bottleneck during the LGM, as did cichlids. Clustering analyses support three viviparid gene pools in the Lake Victoria ecoregion, gathering specimens from 1) Lake Albert and the White Nile, 2) the Victoria Nile and Lake Kyoga and 3) Lake Victoria and tributaries. The last group contains the highest genetic diversity, but all groups have a considerable number of private alleles and are inferred to predate the LGM. Examinations of demographic history reveal a 190- to 500-fold population decline that started ~125-150 ka ago, thus substantially before the LGM bottleneck documented in haplochromine cichlids. Population collapses in viviparids are an order of magnitude more severe than declines in cichlids and have not been halted by the re-establishment of freshwater ecosystems since the LGM. Recent anthropogenic ecosystem deterioration is causing homogenization of previously diversified microhabitats, which may contribute to (local) extinction and enhanced gene flow among species within gene pools.

Keywords: *Viviparidae, Bellamya, genetic diversity, demographic history, environmental change.*

Shell microsculpture unmasks convergent shell form within four European *Pyramidula* species

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Cryptic species have been reshaping our knowledge about global biodiversity, nature conservation, and taxonomy. However, in many cases, their existence is supported by just a single data-stream, typically mitochondrial DNA. Many cryptic species have thus neither been empirically tested by other types of data, nor taxonomically described. A minute land snail genus *Pyramidula* provides an excellent opportunity to inspect species crypticity. Previous studies provided a fully resolved phylogeny of European *Pyramidula* species, however, four phylogenetically well-supported species were concluded to lack macroscale diagnostic characters. We therefore conducted a more detailed integrative analysis of these four species using phylogeny reconstruction, multivariate morphometrics, landmark analysis, and previously unexplored microscopic shell traits, to inspect if any diagnostic characters can be found. Our main assumption was that if these species have truly taken their own independent evolutionary paths, each of them is likely to possess species-specific traits. Both multivariate morphometry and landmark analysis separated high-conical *P. rupestris* and *P. jaenensis* from low-conical *P. saxatilis* and *P. pusilla*, but the species within these pairs could not be distinguished from each other. However, they differed in shell microsculpture and angle of growth ridges. Further, although not being the closest relatives to one another, high-conical species were associated with warmer climates, while low-conical species with colder climates. This suggests adaptive advantage of high-conical shell shape in warm climate, and vice versa. Our study cautions against the use of well-detectable shell features such as shell shape, size, and color, which are more likely to be under selective pressure. On the other hand, microscopic surface structures might be highly informative as they are likely to be selectively neutral. We therefore challenge malacologists to combine multiple lines of evidence in phylogenetic and taxonomic studies, as well as to focus on previously underrated shell traits such as shell microsculpture.

Keywords: *Pyramidula, cryptic species, shell microsculpture, morphometry, phylogeny*

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Strong small-scale phenotypic variation in a wide-dispersing marine snail

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Heterogeneous environments pose a particular challenge for organisms because the same phenotype is unlikely to perform best regardless of the variety of encountered stressors. To understand how species meet this challenge, we investigated the extent to which contrasting environmental pressures induced ecological and phenotypic responses in a natural population of a wide-dispersing marine snail at a small spatial scale. We analyzed several traits of *Heleobia australis* (Rissooidea: Cochliopidae) collected from heterogeneous, but highly connected, habitats from the intertidal area of the Bahía Blanca estuary, Argentina. We also conducted molecular analyses by amplifying the COI gene in individuals sampled from each habitat. We found that sympatric subpopulations of *H. australis* exhibited a strong phenotypic divergence in shell characters and body weight in response to thermal, saline, and dehydration stress, crab predation risk, and parasitic castrators. We proved that this differentiation occurred even early in life as most of the characters observed in juveniles mirrored those found in adults. We also found a divergence in penis size in snails collected from each habitat and raised in common garden laboratory conditions. The molecular analyses confirmed that the individuals studied constituted a single species despite the strong phenotypic differences among subpopulations. The small-scale phenotypic differentiation suggests that *H. australis* experienced a fine-grained environment where conditions imposed by different sources of stress favored the expression of beneficial traits. We discuss the role of plasticity in shaping adaptive phenotypic responses that increase the likelihood of persistence of subpopulations facing environmental stress conditions.

Keywords: adaptive plasticity, shell characters, genital morphology, intertidal zonation, planktotrophic snail.

The size and shape of parasitic larvae of naiads (Unionidae) – are they optimized?

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Our study aims to fill the gap in knowledge about important life history stage of naiads – glochidium - by answering the question: do large females of freshwater mussels invest more in progeny size than small females? The trade-off between progeny size and number is commonly regarded as widespread and one of the most important. In naiads it should be very strongly pronounced if we consider the size and number of progeny produced. We analyzed the between- and within- species variation of glochidia size relative to female size in four widespread species of European freshwater mussels (Unionidae): *Anodonta anatina, Anodonta cygnea, Unio crassus* and *Unio tumidus*. Whereas the total reproductive output is collinear with female body size, substantial differences between species in glochidia size were found within genus *Anodonta*, but not genus *Unio* where glochidial size is remarkably consistent. Our results showed, that both glochidium size and shape are constant, regardless of the variation in body size of reproducing females, which suggest that larger females do not invest more in their offspring then smaller females. From evolutionary point of view the uniform glochidia size might be easily explained by very strong optimizing selection on the successful attachment to the host, however, the question remains, why glochidia of *Anodonta* genus differ. The *Anodonta* species inhabit a wide spectrum of habitats and use more than twice the number of fish hosts than *Unio* spp.; that suggests that measures of glochidial variability, aided by modern tools of digital microscopy, may serve as an indicator of host specificity in other naiads, which may prove especially powerful in identifying conservation priorities in poorly studied species.

Key-words: *glochidium, trade-off between offspring size and number, parental investment, maternal effect, body size optimization*

Weighing-in: biometric conversion factors as a unifying platform for impact assessment of invasive freshwater bivalves

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Invasive bivalves continue to spread and detrimentally effect freshwater ecosystems worldwide. Currently, different metrics for body size and biomass are used within the literature to standardise bivalve-related ecological impacts (e.g. respiration and filtration rates). However, the lack of broadly applicable conversion equations has hindered reliable inter- and intraspecific assessment of their impacts. To facilitate improved comparative assessment amongst studies, conversion relationships between body size and biomass metrics, as well as proportional weight-to-weight conversion factors, were determined and tested for six invasive freshwater bivalves: *Corbicula fluminea*, *C. largillierti*, *Dreissena bugensis*, *D. polymorpha*, *Limnoperna fortunei* and *Sinanodonta woodiana*. To achieve this, body size (length, width, height) and biomass metrics of living-weight (LW), wet-weight (WW), dry-weight (DW), dry shell-weight (SW), shell free dry-weight (SFDW) and ash-free dry-weight (AFDW) were collected from a total of 44 globally distributed bivalve populations. Overall, body size measurements tended to be good predictors of biomass (e.g. length to LW, WW, SW or DW: $R^2 = 0.82–0.96$, mean absolute error (MAE): ±9.14–24.19%). Similarly, most calculated conversion factors for proportional biomass relationships were found to be highly reliable (e.g. LW to AFDW: 95%-CI range: 0.7–2.0, MAE: ±0.7–2.0%). Accordingly, the derived biometric conversion equations can facilitate improved comparative assessment amongst studies, as well as the rapid estimation of biologically active biomass. When combined with density data, these equations can be used to estimate biomass per geographic unit-area and contribute to quantification of population-level effects.

Keywords: *Allometric relationships, freshwater invasive bivalves, weight conversion equations*

You are what (and how) you eat: evolutionary trends in the morphology of nudibranch buccal complex

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Nudibranchs are a large order of gastropod molluscs, including about 3000 species. This group is monophyletic and distinguished by a wide range of feeding strategies and feeding apparatus morphology. The evolution of the feeding apparatus (including the buccal complex) is closely related to the diet preferences that follow the phylogeny of nudibranchs. Despite a large amount of data on the feeding apparatus morphology in nudibranchs, there is no clear idea on the ways of adaptation of nudibranchs to various food objects and the ancestral state of the feeding apparatus.

For the first time, we apply the method of reconstructing the ancestral state of the feeding apparatus of nudibranchs, based on extensive morphological and molecular data. We utilized data on the buccal complex's morphology in 95 nudibranch species. More than 45 characters were used in the analysis, which mainly includes a description of the radula (30 characters), as well as the feeding mode and the food object. We also took into account the morphology of the jaws, which provides a valuable insight, since the jaws play a significant role in the feeding process. For our analysis we reviewed the features of feeding biology, which often determines the morphology of the feeding apparatus.

As a result, the main trends of adaptive changes in the feeding apparatus in Nudibranchia were identified. We have determined the characters of the buccal complex, which show a strong correlation with the feeding mode: the morphology of the radular teeth (dentition and shape), the shape of the masticatory processes of the jaws. We also identified the features of the buccal complex that are preserved for a taxon (usually a superfamily) and do not depend on the feeding mode: e.g., the degree of development of rachidian/lateral teeth, the degree of development of the jaw and the shape of the jaw.

Keywords: *prey specialization, radula, buccal armature, Nudibranchia, phylogeny*.

Acknowledgements: This study was conducted in frame of scientific project of the State Order of the Russian Federation Government to Lomonosov Moscow State University No. 121032500077-8 with financial support of Russian Science Foundation, Grant No. 21-14-00042 and Russian Foundation for Basic Research, Grant No. 20-34-70044.

ECOLOGY AND EVOLUTION

SHORT PRESENTATIONS (16)

A fragile species in a harsh habitat: a case study of *Vertigo moulinsiana* population in extreme environmental conditions

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Catastrophes are one of the factors responsible for extinctions of populations or even species. They can lead to a drastic decrease in the population size and irreversible changes in the habitat. Due to limited dispersal/migration capabilities, terrestrial gastropods are particularly sensitive to changes in vegetation structure. We present a case study on a population of endangered (IUCN Red List: VU) and protected (EU Habitat Directive) terrestrial Desmoulin's whorl snail (*Vertigo moulinsiana*) in Poland. The habitat occupied by this species turned out to be quite extreme with heavy winter frost, floods, fires and mowing.

The flood, turned out to be beneficial for the population, it resulted in a significant increase in the number of snails. Surprisingly, the "population boom" did not extend over a perspective longer than the duration of the flood phenomenon itself: in the following year the population significantly decreased.

Our results suggest that there is a freeze-avoidant strategy in this species, with the mean Tc (crystallization temperature) at -9.71°C, and the range between the lowest and the highest recorded Tc from -15 to-5.6°C. The survival rate was the highest in the snails collected in February, whereas mortality was high in the October sample.

The effects of the fire were devastating for the studied population. Although it did survive, there was a sharp decline in the number of individuals, by as much as two orders of magnitude. We found no vegetation-related refugia for this population.

Annual mowing of that area (under the EU agri-environmental scheme; AES) led to the total extinction of this population. The snails were probably removed along with the mowed vegetation. This, in turn, implies that the obligatory removal of the swathe within 2 weeks after mowing, required under the AES, may have a strong negative impact on the population size of *V. moulinsiana*.

Keywords: *endangered species, fire, flood, frost, mowing*

Acknowledgments: This study was funded by the Polish State Committee for Scientific Research (Grant No. NN304236733), National Science Centre (N N304 277940) and partly by the statutory funds of the Institute of Nature Conservation, Polish Academy of Sciences.

Biodiversity associated with mussel beds as tool to detect anthropogenic disturbances

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Biogenic habitats built by *Mytilus galloprovincialis* are considered ecosystem engineers because they maintain useful habitat for other organisms, enhancing biodiversity. In this way, they play a relevant role and should be considered as useful conservational targets. However, marine ecosystems are subjected to increasing human impacts acting at regional and local scales.

The aim of this study was tested if biodiversity harboured by mussel beds could be useful as tool to detect the effects of two common anthropogenic stressors (urbanisation and sedimentation). To achieve this aim, field studies were done in the north Portuguese coast. Different replicates of mussel clumps were collected at urban and non-urban shores and invertebrates at each replicate were identified to species level. Moreover, sediment accumulated among mussel clumps was quantified. Univariate and multivariate analyses were used to test differences between urban and non-urban shores on invertebrate assemblages. Moreover, the relationship between sedimentation with the structure of assemblages harboured by mussels were explored using univariate and multivariate correlations. Results revealed that, the total number of individuals harboured by mussel beds was lower in urban shores regarding those non-urban. Moreover, the structure of assemblages was also significantly different between urban and non-urban shores. Regarding sedimentation, the total number of individuals and richness showed positive and significant correlations with the total quantity of sediment accumulated among mussel clumps, whereas Shannon and Pielou indexes showed significant but negative correlations with the total quantity of sediment. Our results also pointed out that the structure of the associated assemblages with mussels were significantly correlated (almost 75%) with the total quantity of sediment.

In conclusion, the urbanisation and sedimentation seem to shape the abundance, diversity and the structure of invertebrate assemblages associated with mussel beds. Thus, communities harboured by mussel beds could be useful as tool to detect anthropogenic disturbances.

Keywords: *Mytilus galloprovincialis, urbanisation, sedimentation, biodiversity.*

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Development of morphological traits in hatched common whelk (*Buccinum undatum*) juveniles reared in a controlled environment

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The subtidal North Atlantic gastropod common whelk *Buccinum undatum* exhibits considerable phenotypic variation in shell morphology, both with regard to shape and color, across its distribution. Variation in the species' shell morphology has been hypothesized to reflect environmental variation, e.g. variation in hydrological conditions, predation pressure, depth or sea floor temperature. Recent studies on the species have focused on quantifying and analysing these trends at multiple spatial scales, as well as comparing phenotypic and genotypic variation in common whelk populations across the species' distribution.

Considering the observed partial discordance of genetic and morphological patterns for the species, together with the number of various environmental factors that are thought to affect the morphology of the common whelk, it is clear that further study is needed to determine the reliability of assumptions on divergence of populations based on morphological characteristics, and to what extent this truly reflects environmental variation.

In the current study we implement a common garden experiment to study the development of morphological traits of the common whelk under controlled conditions. Using whelk egg-masses from two genetically diverged populations, Iceland and Canada, which allows for relatively independent replicates, juveniles were reared and monitored with regard to color and shape in controlled laboratory conditions from hatching to 19 months of age. Egg-masses were sampled in the Gulf of Saint Lawrence, Canada, and Breiðafjörður, Iceland (same exact sites were also sampled for adults in 2014) and phenotypic traits were also compared to the phenotype of their parental population.

Keywords: *Shell morphology, Shell color, Phenotypic variation, Ontogeny, Common garden*

Ecosystem services of freshwater mussels: elimination of parasite larvae infecting fish

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Increasing number of studies indicate that freshwater mussels can be important ecosystem engineers and provide valuable ecosystem services. Recent results suggest that freshwater mussels can play an important role in restraining the spread of aquatic pathogens, but the ability of mussels to remove free-living stages of macroparasites and reduce their transmission is still understudied. We investigated the influence of the common freshwater mussel (*Anodonta anatina*) on the transmission of a trematode (eye fluke, *Diplostomum pseudospathaceum*), which frequently infects fish in farms and natural habitats, causing blindness of fish. In our experiments, mussels caused a significant decrease in the abundance of trematode's cercarial larvae, from 6520 to 1770 cercariae/L on average (about 4-fold in 2 h). Individual clearance rates of mussels were 0.6–3.7 L per hour (mean 1.9). These tests were followed by experimental infections of rainbow trout (*Oncorhynchus mykiss*) with different doses of *D. pseudospathaceum* cercariae in the presence or absence of mussels. Exposure of fish to cercariae in the presence of mussels significantly reduced the infection intensities in fish (by 30–40%) at all exposure doses. Our results indicate that freshwater mussels 1) can markedly reduce local cercariae densities, and, thus, 2) can potentially affect host-parasite interactions/dynamics in aquatic ecosystems, and 3) could be useful in mitigation of trematodoses harmful to fish farming.

Keywords: *Anodonta anatina, fish, parasites, Diplostomum, eye fluke, ecosystem services.*

Effect of substrate particle size on burrowing of the juvenile freshwater pearl mussel *Margaritifera margaritifera*

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Juveniles of the endangered freshwater pearl mussel (FPM, *Margaritifera margaritifera*) live burrowed in stream substrate for the first years of their life. Fine sediments block water exchange within substrate and may cause juvenile mortality and recruitment failure. To better understand the connection between success of juvenile FPM and substrate particle size, it would be important to understand behavioural responses of FPM to varying substrate sizes at this critical life stage. We placed newly detached FPM juveniles in a 7-mm layer of sieved sand sorted into five sizes (< 120, 120–200, 200–250, 250–500 and 500–650 µm) each with 10 replicate dishes, 10 juveniles per dish, with burrowing status monitored for 96 h. Mean dish-specific proportion burrowed (PB) was significantly affected by substrate size, increasing from 52% in the finest sand to 98% in the coarsest sand. Furthermore, the significant substrate × time interaction was observed due to dropped PB (30-34%) in finest sand at 2–4 h time points. Thus, results suggest a clear behavioural response by juvenile FPM to substrate size, with fine sediments triggering surfacing behaviour. Surfacing may indicate stress, can increase predation risk, and expose juveniles to drift and/or enable drift of juveniles.

Keywords: *early juvenile stage, endangered species, sediment, siltation, Unionida*

Effect of the elemental content of shells of the bivalve mollusks from Saldanha Bay (South Africa) on their crystallographic texture

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In mussels, both wild and farmed in natural conditions, anthropogenic inputs are usually reflected in the increase of the content of specific elements. To determine the possible effect of the elemental patterns of farmed and wild mussels (*Mytilus galloprovincialis*) collected in the Saldanha Bay area (South Africa) on the crystallographic texture of the shells, the content of 20 elements in shells and 24 in the soft tissue of mussels was determined by neutron activation analysis. The crystallographic texture of mussel shells was analyzed using time-of-flight neutron diffraction. According to the neutron activation analysis data, wild mussels from the Danger Bay, which is open to the ocean, lived in stressful natural conditions and contained higher amounts of the majority of determined elements in comparison with mussels farmed in closed water areas (Langebaan Yacht Club and Small bay) with anthropogenic loadings. The changes between the maximums of the same pole figures of the samples are in the range of variability identified for the genus Mytilus. The content of Cl, Sr, and I was the highest in mussels from the open ocean site, which is reflected by the lowest mass/length ratio. The determined crystallographic textures of mussels are relatively stable as shown in the analyzed pole figures despite the concentrations of Na, Mg, Cl, Br, Sr, and I in shells, which significantly differ for wild and farmed mussels. The stability of the crystallographic texture that we observed suggests that it can be used as a reference model. In cases of determination of differences in texture, increased attention to the ecological situation should be paid.

Keywords: *Neutron diffraction, crystallographic texture, neutron activation analysis, trace elements, bivalve mollusk shells*

Extinction probability is linked to lifestyle in freshwater gastropods

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Global change impacts freshwater biota on all levels, and numerous species are threatened with extinction. Many studies over the past years have shown the dramatic biodiversity loss we face today, but typically they focus on entire clades and on a purely modern perspective. In order to provide a deeper understanding of extinction selectivity, we need to i) differentiate extinction threats with respect to differences in the ecology of species, and ii) integrate fossil data to infer whether any observed pattern is only true for today or represents a general rule.

Here we assess differential extinction probability with respect to varying lifestyles and distribution in two major groups of freshwater gastropods, Caenogastropoda (“Prosobranchia”) and Hygrophila (“Pulmonata”). These two groups differ markedly in their reproduction (dioecious vs. hermaphroditic), life cycle (perennial vs. annual), respiration (gills vs. “lungs”) and ecological tolerance (e.g. temperature, oxygen; narrow vs. broad). On average, these traits make Hygrophila better dispersers, and we hypothesize that they have a lower extinction risk accordingly.

We assembled a large dataset of Miocene to extant European lacustrine faunas, covering 27,790 occurrences of 2,109 species. Extinction or survival of modern species was predicted based on IUCN conservation status. Using generalized linear mixed models, we tested for a relationship between extinction probability and systematic clade and geographic range size (estimated using minimum spanning trees), while using time as random effect.

Our analyses show clear differences in the extinction probabilities of the two clades, whereas Caenogastropoda have a higher extinction probability at lower range sizes. This effect is found in the modern fauna as well as in most fossil time intervals, arguing for a general pattern. This increased extinction risk linked to, on average, smaller geographic ranges is likely the result of the comparably poor colonization ability of Caenogastropoda, many of which are endemic species.

Keywords: *conservation, ecological selectivity, long-lived lakes, species distribution*.

Fish infestation with glochidia of *Unio crassus* 1788, Philipsson in the wild

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To complete its ontogenic development, large, bodied freshwater mussels (naiads) have to pass through an obligatory, parasitic phase of larva, which attach to the skin or gills of freshwater fish. This ontogenic transition influences population perspectives and is very important in active conservation projects. The relations between mussel and fish varies in specificity: some species use single species; some have large spectrum of potential hosts. The possibility of successful larvae development is usually verified during artificial infestation of fish in laboratory conditions, whereas the actual (in situ) infestation intensity is rarely studied. We studied the infestation of wild fish by endangered thick-shelled river mussel *Unio crassus*, in natural conditions in the river Warkocz (Świętokrzyskie Mts.) during two breeding seasons. The three sampling plots were selected, where fish were caught and presence of glochidia on their fins was verified. The results demonstrated, that two species were infested with the greatest intensity: common minnow (*Phoxinus phoxinus*) and gudgeon (*Gobio gobio*). Glochidia were attached mostly to fins which are responsible for locomotive functions (pectoral fins and caudal fin). The selection of host species and infestation intensity were different between the study plots. The availability of potential hosts or the mussels abundance did not influence the number of locally infected fish, the most plausible explanation for the infestation intensity is the local composition of functional habitats.

Keywords: *host fish, river habitat, endangered mussels*

Fourier Transform Infrared Spectroscopy used to study glycosylation of proteins in gastropod mucus

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Fourier -transform infrared spectroscopy (FTIR) is a molecular fingerprinting technique well suited towards studying natural materials. It is non-destructive, allows analysis of liquids and solids in real time and helps to identify organic compounds such as proteins or sugars. In particular, the study of glycosylation in proteins is possible, because the sugar residues and protein amide I, produce distinguishable absorption bands at 1024-1135cm^{-1}, and 1645cm^{-1}, respectively, which can be associated to mucins. Given that mucus contains mucins, heavily glycosylated proteins it is somewhat surprising that only a single study covering nine species of gastropod mucus secretions has been carried out to date (Skingsley, White and Weston, 2000). Here we extend this analysis in both number and detail by obtaining FTIR spectra of locomotive mucus from twelve gastropod species: *A. fulica*, *C. aspersum*, *C. nemoralis*, *A. ater*, *A. hortensis*, *L. flavus*, *L. maximus*, *L. haroldi*, *V. sloanei*, *L. stagnalis*, *M. cornuaretis* and *P. diffusa*. Our results show that there is a diversity of protein structures present across these species and that glycosylation may be inferred through the amide I/sugar residues ratio, with the highest corresponding to mucus of the African land snail *A. fulica*, while the lowest corresponding to the tropical freshwater snail *M. cornuaretis*. This study offers a window into the study of gastropod mucus and its structure to better understand how these materials exhibit different compositional properties to keep maintain functionality in different environments.

Keywords: *Locomotive mucus, glycosylation, FTIR.*

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Reference:

Skingsley, D. R., White, A. J. and Weston, A. (2000) 'Analysis of Pulmonate Mucus By Infrared Spectroscopy', *Journal of Molluscan Studies*, 66(3), pp. 363–372. doi: 10.1093/mollus/66.3.363.

Freshwater mollusc assemblages in the Bednja River (Croatia)

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Freshwater molluscs are especially sensitive to anthropogenic and climatic disturbances resulting in species loss accelerating over the past decades. Despite their central ecological role, studies dealing with mollusc distribution and diversity patterns in rivers are insufficient. The main objective of this study was to determine the diversity, trophic structure and habitat preferences of the freshwater mollusc assemblages in the Bednja River (NW Croatia). Macrozoobenthos samples were collected during summer 2015 at 20 localities along the Bednja River, using a bentos hand net. In the laboratory snails and mussels were separated from the other macroinvertebrates and identified to the species level with the exception of the genus *Pisidium*. In total, 20 mollusc species were identified, 15 snails and 5 mussels. The most common species was snail *Holandriana holandrii* which was found at 13 localities. The findings of the mussel *Unio crassus* at 8 localities were especially important because this species is protected by national legislation in Croatia and is listed in the Habitats Directive of the European Union (Annexes II and IV). In the lower part of the river two invasive species were recorded: mussel *Dreissena polymorpha* and snail *Physella acuta*. The analyses of functional feeding groups of snails showed that grazers were prevelant, followed by detritivores, while all bivalve species were active filterers. The Canonical Correspondence Analysis (CCA) showed that the main determining factors of mollusc composition were conductivity, alkalinity and water discharge. The seven analysed environmental variables (water temperature, chemical oxygen demand, oxygen saturation and concentration as well as the three aforementioned) defined over 66% of the total mollusc variability, indicating that environmental conditions are one of the most important factors determining mollusc distribution and variability in the riverine ecosystems.

Keywords: *Gastropoda, Bivalvia, diversity, environmental conditions, trophic structure*

Freshwater mollusc diversity in the Upper Brahmaputra Basin of Assam, India

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A field survey was conducted for four consecutive years, 2015–18 to assess the diversity of freshwater molluscs (Gastropoda and Bivalvia) of the upper Brahmaputra Basin in Assam, India. Altogether, 18 gastropods and 27 bivalve species representing nine families were recorded from 17 sampling stations comprising small to large tributaries and wetlands in the food-plains covering a total geographical area of approximately 3,900 square kilometers. A large fraction (15.55%) of the collected mollusc species are new records from the Upper Brahmaputra Basin of Assam. Rarity in the occurrence of freshwater mollusc was confirmed with singleton and doubleton species accounting for 6.66% and unique species accounting for 35.55% of the total species recorded. It was observed that most of the mollusc species of the upper Brahmaputra Basin are either in the 'Least Concern' or 'Data Deficient' category of the IUCN Red List; except for *Lymnaea ovalior* (Annandale & Prashad, 1921) and *Sphaerium austeni* Prashad, 1921 assessed as 'Vulnerable' and 'Near Threatened', respectively. A significant trend in the diversity in terms of species richness and composition was observed across the sampling stations of the northern basin and southern basin of the river Brahmaputra. The outcome of the present work is firsthand information on the diversity, distribution and status of the freshwater mollusc population of this region and inconsistencies between available data clearly indicate that the taxonomic situation is still a major problem in establishing a database for the planning of species conservation in the region.

Keywords: *Burhi-Dihing, Data Deficient, habitat heterogeneity, species richness, unique*

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Holoplankton and Meroplanktonic Gastropods from the Celebes Sea, North Sulawesi, Indonesia

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Despite being unable to swim against general ocean currents with their weak swimming movements, invertebrate larvae may still be widely dispersed. However, for some reason, some invertebrate larvae are only locally dispersed. This study focuses on determining 1) gastropod species in plankton, and (2) the distribution and density of each gastropod species throughout the Celebes Sea. The gastropods were sampled using an Isac Kidd Midwater Trawl (IKMT) during EWIN 2018 Cruise on the R.V. Baruna Jaya VIII LIPI. Morphological and genetic methods were used to identify the species of gastropod. Three species, *Atlanta inclinata* Gray, 1850, *Reticutriton pfeifferianus* (Reeve, 1844), and *Dulcerana granularis* (Röding, 1798) were identified. These species occurred more often in sites to the North- East of the Celebes Sea than in sites further to the West of the Celebes Sea. The abundance of A. inclinata was 20 - 120 individual's m-3, R. pfeifferianus 20 – 160 individuals m-3, and D. granulatis 20 - 80 individuals m-3. These three species in this study provide the first records of planktonic gastropods in the Celebes Sea. The biological and physical factors influencing the presence of these three gastropod species in the Celebes Sea are discussed.

Keywords: *Distribution, Atlantiidae, Chymitiinae, Bursanidae, meroplankton, holoplankton*.

Location probing by males complicates sexual dynamics and successful mate-guarding in squid groups

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Reproductive fitness is defined by the successful passing of an individual's genes to the next generation. Literature on coastal squids has described mate guarding as the pre- and post-copulatory sole role of males, who are generally observed positioned around the female while she lays eggs in crevices, as well as exhibiting agonistic displays to ward-off rivals in order to prevent insemination by other males' sperm. We observed *Sepioteuthis lessoniana* behavior during mating seasons in two distant geographical locations (Egypt and Indonesia), and found new behavioral elements in the sexual courtship of *S. lessoniana*. Notably, during agonistic bouts, we identified an undescribed display, performed particularly by the dominant male towards rivals, which we named Tentacle Exhibition display. More importantly, we observed that egg laying by females, was preceded by a probing of the same location by males (~87% probability of laying eggs after male probing; exact binomial test: $p = 0.005$). Pre-probing locations carries a clear risk for the male, as he abdicates from mate-guarding momentarily and leaves the female vulnerable to the approaches of competing males, but provides advantages to the female. *S. lessoniana* is considered a species complex composed by several different cryptic species across the Indian and Pacific Oceans, which suggests that either: a) the individuals observed are the same species, or b) these behaviors are shared across cryptic species, either as a conserved trait or as a product of convergent evolution. These results enhance our understanding of the ecological and evolutionary drivers of different reproductive strategies and individual decision-making in squid groups.

Keywords: *communication, evolution, sexual tactics, social behavior, squid.*

Phenology and reproductive effort in endangered thick-shelled river mussel *Unio crassus* Philipsson, 1788 (Bivalvia: Unionidae)

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Reproduction is costly in terms of invested energy and resources. It is strongly affected by habitat conditions, changing along the timing of reproduction, the trait crucial in seasonal environments. In the period of 2013-2021 we studied reproduction of the *U. crassus* in 6 rivers in southern Poland. We defined the stadia of glochidia (larvae) development which could be used to assess current larval developmental stages. We established duration of the brooding period, the number of broods and their size, as well as their changes during the season.

Mussels spawned their first brood eggs from March to May but differed by the river. After fertilization the embryos were brooded, until the developing larvae were ready to infest a fish host in order to complete the obligate parasitic phase of their life. The duration of the brooding period was shortening significantly during the season, from 35 days in early spring to 9 days in summer. The break between consecutive broods was usually short: from almost no break to 17 days. Number of broods raised during the season was variable between rivers and seasons, with varying modal value and the maximum number (max. 6). Both number of broods and the level of marsupia filling were decreasing during the season.

The recorded differences in the spawning time, duration of reproductive activity, number of broods and their size may significantly influence the reproductive output of individuals and population numbers. They indicate strong impact of habitat on reproductive output, which may be affected by both anthropogenic impact and global climate change. The study offers a practical scheme for assessing female reproductive output in *U. crassus*, which may be useful for the future application in conservation measures of this endangered species.

Keywords: *freshwater mussels, conservation biology, phenology, global warming, water temperature.*

The impact of changes in hydrological conditions and in physicochemical properties of water on mussel populations in euthrophic floodplain Lake Pińczów

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The very rapid disappearance of unionid populations is a familiar phenomenon. Nothing is known, however, about why such extinctions should take place so fast, nor is anything known about the mechanisms causing differences in numbers between species. Another widely observed phenomena associated with the disappearance of some freshwater mussels is the lack of juvenile recruitment, but little is known about why this happens.

In the summer of 2018, the massive die-off of approximately one-third of the unionid mussels inhabiting Lake Pińczów took place, within just a few days. Analysis of water samples taken immediately after the die-off revealed extremely high concentrations of phosphates and nitrites, which suggested that motorboat movements must have disturbed the lake sediments, negatively affecting the physiological processes of mussels and thereby causing their mass mortality. The highest mortality was recorded in the rarest species *Pseuanodonta complanata* (81%), followed by *Unio pictorum* (58%), *Anodonta cygnea* (26%), *Unio tumidus* (15%) and *Anodonta anatina* (5%). Mortality was significantly related to the size (age) of the mussels only in *A. cygnea*, and was higher in smaller (young) individuals. The results showed significant differences in levels of tolerance to habitat disturbances between mussel species.

Although eutrophication of freshwaters is a natural process, the human impact often leads to inland waters becoming overloaded with nutrients, impoverishing many valuable and vanishing habitats, such as floodplain lakes. These changes need to be reversed if the occurrence of endangered aquatic species is to be restored. A slight increase in the discharge, following the construction of an additional outflow pipe, positively influenced recruitment in three of the five mussel species inhabiting the Lake Pińczów. Also, after this additional outflow had been built, the niches of *A. cygnea* and Unio spp. juveniles changed, revealing differences in their hydrological requirements. The results suggest that, as in lotic habitats, complex hydraulic parameters are highly significant to unionid mussels in lentic conditions.

Keywords: *Extreme disturbance, extinction, flow velocity, Reynolds number, recruitment*

Using self–organizing maps and machine learning models to assess mollusc community structure in relation to physicochemical variables in a West Africa river–estuary system

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The poor understanding of changes in mollusc ecology along rivers, especially in West Africa, hampers the implementation of management measures. We used a self–organizing map, indicator species analysis, linear discriminant analysis and a random forest model to distinguish mollusc assemblages, to determine the ecological preferences of individual mollusc species and to associate major physicochemical variables with mollusc assemblages and occurrences in the Sô River Basin, Benin. We identified four mollusc assemblages along an upstream–downstream gradient. Dissolved oxygen (DO), biochemical oxygen demand (BOD), salinity, calcium (Ca), total nitrogen (TN), copper (Cu), lead (Pb), nickel (Ni), cadmium (Cd) and mercury (Hg) were the major physicochemical variables responsible for structuring these mollusc assemblages. However, the physicochemical factors responsible for shaping the distribution of individual species varied per species. Upstream sites (assemblage I) showed high DO and low BOD and mineral compounds (i.e., TN, salinity, and Ca), which are primarily responsible for structuring the occurrences of bivalves (*Afropisidium pirothi, Etheria elliptica*, *Sphaerium hartmanni*) and the gastropod Lanistes varicus. Sites along the middle reach (assemblage II) were characterised by a high degree of organic pollution but low heavy metal pollution; we detected no specific mollusc indicator species. Downstream sites (assemblage III) displayed high mineral and heavy metal concentrations and a fauna without specific indicator species. Finally, downstream–associated sites with brackish water displayed important levels of organic and heavy metal pollution (assemblage IV). These sites are dominated by diverse gastropods (i.e., *Bulinus spp.*, *Gabbiella africana*, *Indoplanorbis exustus*, *Pachymelania fusca*, *Radix natalensis*, *Stenophysa marmorata* and *Tympanotonos fuscatus*). Our results highlight that mollusc communities in the Sô River Basin are structured by key physicochemical variables related to the river–estuary continuum. Progressively downstream ward habitats are confronted with increasing anthropogenic stress. Conservation and management plans should focus on downstream habitats.

Keywords: A*rtificial neural network*, *ecology*, *freshwater biodiversity*, *modelling*, *mollusc community*, *tropical river systems*

ECOLOGY AND EVOLUTION

POSTERS (9)

Size-frequency distribution variation in an intertidal polyplacophora along a tropical latitudinal gradient

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The Bergmann's Rule (described first for endothermic organisms, later for ectothermic taxa) established that intraspecifically the organisms of populations which live at colder climate (high latitudes) tend to have larger body sizes than those which live at warmer climate (low latitudes); and the Temperature-Size Rule (which described the relationship between growth of ectotherms and the environmental temperature) established that larger organisms can be found in colder environments and they are going to grow more slowly. For ectotherms inhabiting the intertidal zone such as chitons, temperature and latitude can influence life-history traits as growth. The Polyplacophora mollusk *Chiton articulatus*, is distributed along 8° latitudinal at the Mexican Tropical Pacific, between Sinaloa 23°N (high latitude at 25°C, in mean annual sea surface temperature, SST) and Oaxaca 15°N (low latitude at 28°C SST). Chitons were collected monthly for one year in seven sites along its whole geographic distribution, after scleritome length (mm) was measured and size frequency distributions were generated for all locations (Sinaloa, Nayarit, Jalisco, Colima, Michoacan, Guerrero, and Oaxaca). The chiton population body size was greater at high latitude and decreases towards low latitude, exhibiting a fragmented latitudinal pattern in five areas according to the Kruskal-Wallis test, those were a northern group of SIN that belong to the southern border of the subtropical zone; subsequently, a second northern group of NAY that belong to the northern border of the tropical zone; a middle group conform by JAL, COL, and MIC, which belongs to the Mexican Tropical Pacific ecoregion; the fourth group of GRO; and a southern group of OAX exclusively, belonging to the northern border of the Chiapas-Nicaragua tropical ecoregion. These results follow and support both the Bergmann's Rule and the Temperature-Size Rule, besides the size groups observed of this edible *Chiton articulatus* coincide with each regional SST.

Keywords: *Bergmann's Rule, Temperature-Size Rule, Mexican Tropical Pacific, Chiton articulatus, growth variation.*

Acknowledgments: This research took place within the framework of the Project quitón del Pacífico tropical mexicano (see, DOI: 10.3897/rio.6.e60446); Specimen collection was done under a research permit (No. PPF/DGOPA-130/15) granted by SADER and CONAPESCA.

Comparative morphology of the cnidosac and related structures in the nudibranch family Fionidae

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Nudibranchia is a large taxon of gastropod molluscs that has lost a shell and uses several alternative protection methods. For example, aeolid nudibranchs are well-known for their ability to obtain nematocysts from their prey (different species of Cnidaria), which they incorporate into the specific structures called cnidosacs. While the main features of this process have been studied comprehensively for the last 50 years, little is known about the plasticity of fine morphological traits within the cnidosac across different aeolid lineages.

In this research, we observe the diversity of cnidosac fine structure within different phylogenetic lineages of the family Fionidae, considering the feeding modes and feeding objects of studied species. Members of the family Fionidae are generally characterized by specialized diets. In addition, they have a wide variety of feeding modes and food preferences and a diverse morphology of the buccal complex.

We have studied the fine anatomy of cnidosacs for 13 species of molluscs belonging to 8 genera of the family Fionidae. The material was collected in the White Sea, the Barents Sea and the Sea of Japan in 2017-2020. We performed observations *in vivo*, and used light, transmission and scanning electron microscopy and confocal laser scanning microscopy.

We have shown that the morphology of cnidosacs within most studied genera of the Fionidae is characterized by a specific set of structures common to all species (such as a muscular layer, phagocytic cells in the lining of the cnidosac, proliferation zone). However, we also identified several features specific to each species: the presence of an apical zone, the number and type of selected nematocysts, the presence of different cell types in the cnidosac lining. We suggest that these features are not phylogenetically significant but represent an adaptive character, as their states correlate with mollusc’s feeding mode and particular feeding object.

Keywords: *functional morphology, comparative anatomy, feeding, radula, phylogenetic relationships*

Acknowledgements: The present study was supported by the Russian Scientific Fund, Project No. 20-34-70044.

Comparison of breeding strategies of freshwater *Unionidae* mussels under stochastic environmental conditions

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There are very significant differences in reproductive strategies between unionid populations, manifested by the different numbers of broods produced during the year. We modelled what would happen to a hypothetical mussel population (in terms of population growth rate and the probability of its extinction) that released the same number of glochidia during one to five reproductive events during a season, in unpredictable habitat conditions differing in the probability of host fish infestation. We evaluated how the number of spawning events would affect population parameters that are important from the point of view of population persistence, i.e. its size, extinction rate, coefficient of variation of mean population size and the mean time to extinction. The results suggest that the number of broods is one of the factors strongly affecting the fitness of individual mussels. To date, this factor has not been described even for individual species; it is extremely variable, because of the interaction between mussels and their host-fish species.

Keywords: *Population dynamics, habitat stochasticity, modelling, growth rate, extinction*

Contour analysis in subtidal and intertidal populations of the mussel *Mytilus edulis platensis* d' Orbigny, 1842

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Outline shape in bivalves is a key character that provides information on life habits, and is related with endogenous (genetic and physiological) and exogenous (biotic and abiotic) factors. The mussel *Mytilus edulis platensis* d' Orbigny, 1842 presents a wide distribution from Rio Grande do Sul (32° 2'S; 52°5'W), southern Brazil to Santa Cruz (50° 1'S; 68° 31'W), Argentina. The aim of this study was to compare the subtidal and intertidal populations of *M. edulis platensis* through contour morphology; we hypothesize an association between shell morphology and habitat due to habitat-specific constraints. The subtidal samples were obtained on board the ARA Puerto Deseado, at 35 meters deep, in August 2012 at the Litoral Bonaerense (36º 53' S; 56º 20' W) (n=37); the intertidal samples were collected in August 2019 in Villa Gesell (37° 15'S; 56° 57'W), Buenos Aires province, Argentina (n=33). Left valves were digitized with a digital camera. We studied the overall shell shape with an Elliptic Fourier Analysis (EFA) of the closed contour, with seven harmonics, and carried out a Principal Component Analysis (PCA). Significant differences between contours were tested with a MANOVA. The PCA allowed us to discriminate two morphotypes through the outline data. The first principal component (PC1) accounted for 75.59% of the variability, while the second principal component (PC2) determined 12.93%. We associate the PC1 to differences in the width; globose shapes representing intertidal individuals and narrow shapes related to the subtidal. Differences along the PC2 were related to the angle of ventral displacement of the umbo, evident in the subtidal specimens. Statistically significant differences between contours were defined (MANOVA: Wilk's lambda= 0.31, $F_{2, 69}$= 78.37, $P < 0.001$). All these results suggest that *M.edulis platensis* has developed two ecomorphs with distinct morphological responses to physically stressful conditions registered in the intertidal, as opposed to lower physical stress in the subtidal habitats.

Keywords: *morphometry, EFA, PCA*

Phylogeography of Depressed River Mussel *Pseudanodonta complanata* in Russia

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The Depressed River Mussel *Pseudanodonta complanata* (Rossmässler, 1835) represents an Anodontini taxon (Bivalvia: Unionidae), being considered one of the most rare European unionid species, especially in Central and Eastern Europe. In Russia, *P. complanata* ranges throughout freshwater bodies of the Baltic, Azov, Caspian, and Black Sea drainages and prefers lotic environments such as rivers and streams. Nowadays *P. complanata* as most other taxa of the Russian fauna represents a common species with broad distribution considered as Least Concern (LC). At the same time, IUCN Red List describes *P. complanata* as a 'vulnerable' species, which requires conservation efforts and monitoring globally.

Specimens of *P. complanata* were collected from the Don and Volga river basins as well as from waterbodies of the Baltic Sea drainage in European Russia. We generated 13 new sequences of the *COI* gene, while 11 additional *COI* sequences were obtained from GenBank. To evaluate the phylogeographic patterns, we used a median joining network approach. Our sequence set shares ten unique haplotypes, including six unique haplotypes from Russia. Among them, there is one common haplotype, which is also typical for several European countries (Poland, Ukraine, France, and Sweden). Two unique *COI* haplotypes were found in different parts of the Volga Basin. Three haplotypes from River Khopyor in Russia and River Siversky Donets in Ukraine (Don Basin) belong to a divergent lineage (mean uncorrected *COI* *p*-distance = 2.2±0.5%). Recently, a separate mitochondrial lineage from the Azov Sea drainage was also discovered for Duck River Mussel *Anodonta anatina*. These results support the hypothesis on the existence of a Plio-Pleistocene refugium in the Azov Sea drainage. Our study highlights that freshwater mussel fauna in this drainage should be considered of high conservation priority due to high genetic diversity and the presence of unique phylogenetic lineages (e.g., *P. complanata* and *A. anatina*).

Keywords: *Pseudanodonta complanata*, COI, Plio-Pleistocene refugium, Azov Sea, rare species.

Acknowledgments: This work was supported by the Russian Science Foundation (project No. 21-74-10130).

Population growth of the intertidal mollusk *Chiton articulatus* (Polyplacophora: Chitonida) at its northernmost distribution limit in Mexico, based on length data

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Growth is an important life history trait that can be related to environmental features or can be implemented to characterize populations. This study examined growth by Schnute growth models based on length data for an edible intertidal invertebrate with indeterminate growth: *Chiton articulatus*. The geographical distribution of this species extends within the Mexican tropical Pacific from southernmost Oaxaca State (15° N) to northernmost Sinaloa State (23° N). From the length data of 470 organisms sampled monthly along a year (October 2015 to October 2016), several growth parameters (population size, number of size groups, number of cohorts, growth rate, and longevity) were evaluated for the northernmost adult populations of *C. articulatus* that living on the boundary between tropical and subtropical regions. We hypothesize that growth parameters of this ectothermic intertidal species will display a slow growth rate, with a larger adult body size in this boundary region as compared with the southern one. It was possible to identify: an adult population size between 45.87 mm to 86.06 mm; between one to three size groups per month (with an average of two groups); a total of six cohorts in the year; and estimated longevity of 3.45 years or 41.5 months. The best growth model was the case 2 Schnute model and the growth rate of adult populations in Sinaloa was slow and approached an asymptote. This study complements previous growth assessments of *Chiton articulatus* in their southernmost distribution confirming the previous hypothesis and reinforces the use of length data and Schnute growth models in mollusk studies.

Keywords: *Schnute growth models, indeterminate growth, growth parameters, "sea cockroach", history life parameters.*

Acknowledgments: This research took place within the framework of the Project quitón del Pacífico tropical mexicano (see, DOI: 10.3897/rio.6.e60446); Specimen collection was done under a research permit (No. PPF/DGOPA-130/15) granted by SADER and CONAPESCA.

Saving assets when needed: using spline interpolation functions and integral calculus to assess ecological parameters of mollusk populations and communities

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What can be done when there is a shortage of assets, and a population size of a bivalve species has to be assessed along an extended river's sector? The devoted method has to be replicated periodically by one or two rangers in the future. Another question: how can we explore the similarity or overlap between resource use of several mollusk species, characterizing all the pairs, while taking into consideration also the availability of resources in the environment, when all resources and gradients are varying continuously? The last question might be rephrased as: how to compute a community matrix, between n pairs of species, described by a standardized niche similarity index that considers the species demands as well as the resources' status in the environment, measured along continuous gradients? In an ideal world, we could investigate what is happening with the population or community, step by step, along the whole gradient(s). Most of the time this is not possible. We usually use a network of knots, i.e., select certain values along the gradient's range, and assess the corresponding value(s) of the parameter(s). Then we search for links between these discrete related series, by regression analysis (sensu lato) and/or canonical multivariate ordination methods. Sometimes this is not possible or recommended either. Here we propose an alternative, using cubic spline interpolation functions, which link together the discrete values (counts, densities, or resources used by species or their abundance in the environment) and then we aply integral calculus on the plotted functions. We estimate values and statistics of parameters that we use further for other purposes. For instance, the niche matrix might be used along with functional traits, environment and community data-tables in double-constrained correspondence and variation partitioning analyses. We show how this can be done and illustrated using Mathcad and other software.

Keywords: *ecological methodology, gradient analysis, modeling*

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Selected behavioural traits of some European hygrophilous whorl snails (Gastopoda: Eupulomata: Vertiginidae)

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Whorl snails are superfamily associating tiny land snail species. Most of them demand a high (or very high) humidity for life and reproduction. Therefore, vertiginids may be usually found dwelling in wetlands, humid meadows, or woodlands. Alterations in the natural environment resulting from a human interference and climate crises contributed toward heat waves and droughts. The extreme weather events deteriorate whorl's snails habitats conditions. High temperatures and reduction of water availability may be also a direct threat for snails affecting their activity (including foraging and reproduction) and increasing mortality rates due to exceeded physiological limits. A range contraction of some Vertigo species is already noticeable. However, the behavioural reactions of individuals and its consequences for whorl's snails' population survival in the climatic crisis are poorly explored. Facing a temperature stress and a drought land snails exhibit behavioural responses aimed at reducing negative effects of overheating and dehydration. Confronting the irritants or life-threatening conditions gastropods usually hide in the shell and stay there till the environmental conditions will improve. The aim of my study was to examine some behavioural reactions of whorl snails for different temperatures (6°C, 11°C, 21°C and 36°C) and humidity (30%, 100%) for snails' activity. The studies were carried out for three species: *Vertigo angustior*, *Vertigo moulinsiana* and *Vertigo antivertigo*, two of which are threatened across Europe and are listed in the annex II of the EU Habitat Directive. Results of my investigations shown different reactions of the studied species and age classes for temperatures and humidity.

Summarizing, the climate change may have a diversified impact on the Vertigo species, generating different behavioural responses. Developing the knowledge on the behavioural traits of vertiginids may be helpful for explaining current population trends of European whorls snails.

Keywords: *climate crises, humidity, temperature, Vertiginidae.*

Solitary as an oyster? Neighbours, inquinilism, commensals and parasites of *Ostrea puelchana*

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Oyster species play an important role in marine ecosystems, hosting a wide diversity of organisms. It has been stated that epibiosis entails both benefits and disadvantages for the oysters. However, studies of multiple biological interactions of organisms associated with oyster reefs are scarse. In the Northern Patagonian gulfs, Argentina, *Ostrea puelchana* presents low-density beds; it is not a reef-forming species but it generates a three-dimensional structure as a result of successive settle of oyster larvae on the shells of a "founder" oyster. The aim of this study was to investigate the biodiversity of associated organisms to *O. puelchana* at multiple spatial scales. We described the community associated to the oyster beds of Northern Patagonian gulfs, and performed non-parametric multidimensional analyses to test whether oyster beds were similar in terms of community components. We also tested the effect of biological interactions such as the inquinilism of *Tumidotheres maculatus* -living inside the pallial cavity of the oyster-, the parasitism of *Lithophaga patagonica* –a shell burrower-, and the effect of the grazer chiton *Chaetopleura* sp. We recorded a total of 85 taxa in the community associated to oyster beds, mainly molluscs (30%), crustaceans (20%) and echinoderms (10%). The similitude among beds was moderate (non-transformed < 40%; square root transformation: 40-65%) and was influence by the dominance of the echinoderm *Ophioplocus januarii* and the slipper limpet of the genus Crepidula. A total of 31 taxa were recorded as epibionts, mainly polychaetes and molluscs Crepidula sp. and Tegula sp. Condition index of oysters was significative lower for oysters hosting *T. maculatus* or *L. patagonica*. Chaetopleura density correlated negatively with oyster recruits. Our findings contribute to the knowledge on the functional role that oysters of *O. puelchana* play in benthic ecosystems at San Matías Gulf (Northern Patagonia, Argentina), hosting a diverse assemblage of organisms such as invertebrates and algae via parasitism, symbiosis, inquinilism or commensalism.

Keywords: biodiversity, marine bivalves, biological interactions.

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ECOSYSTEM FUNCTIONS

STANDARD PRESENTATIONS (1)

Ecosystem services of freshwater bivalves: reviewing the global evidence

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The concept of Ecosystem Services (ESs), i.e. the outputs of ecosystems and species that directly affect human well-being, has proven instrumental in galvanising public and political support for biodiversity conservation. Each year, hundreds of papers justify the importance of studying freshwater bivalves (FBs) based on their ESs, yet the available scientific evidence of associations between FBs and specific ESs has never been comprehensively reviewed. We conducted a systematic literature review to (1) develop a list of ESs that have been shown to be associated to FBs; (2) quantify temporal and geographic patterns of this evidence across taxonomic groups, native *vs*. non-native species and types of ESs; and, on that basis, (3) identify current shortcomings in our knowledge and recommend future directions for research. After screening the 6,745 studies retrieved in our search, our final dataset comprised 691 studies and 906 records (i.e. pieces of evidence) from 69 countries and 24 Classes of provisioning (n=189), cultural (n=493) and regulating (n=224) ESs. Evidence came from a total of 91 genera and 191 species, dominated by Unionida (55% of records), followed by Veneroida (21%; mainly *Corbicula* spp.) and Myoida (20%; mainly *Dreissena* spp.). The majority of records originated from either Asia (34%), dominated by nutritional, material and medicinal provisioning ecosystem services, Europe (30%) or North America (23%), both dominated by the cultural ecosystem service "biomonitoring".

About one third of records referred to species that were non-native to the country of study, predominantly those in Europe and the Americas. Whilst annual output of evidence from North America has been relatively constant over the past 20 years, that from Europe and Asia has increased in this period. Future research needs include addressing the severe geographic bias of available evidence, and quantifying the (monetary value of) ESs provided and disrupted by native and non-native FBs.

Keywords: *ecosystem services, freshwater mussels, systematic review, Unionida*

Acknowledgement: EU-COST Action CA18239 - Conservation of freshwater mussels: a pan-European approach

ECOSYSTEM FUNCTIONS

POSTERS (2)

Biomass-clearance rate relationships in freshwater bivalves – introduction of a distributed experimental research network

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Biofiltration by freshwater mussels is recognised as an important ecosystem service and often used as a tool in the monitoring of water quality. The process of biofiltration and therefore, purification of water, can be quantified by measuring an organism's clearance rate, sometimes also referred to as filtration rate. Freshwater bivalve clearance rates and the factors affecting the same have been the subject of many scientific studies over the recent decades. However, the clearance rates quantified for different freshwater mussel species and populations in different studies are generally not directly comparable due to differences in study design and methodologies employed. Here we present the launch of a coordinated research network that will focus on quantifying the spatial, temporal, and methodological sources of variability in clearance rates and other basic freshwater mussel ecosystem function estimates. The initiative will run within the framework of EU-COST Action 18239 (confremus.eu) and will commence with an international training school at the Czech University of Life Sciences, Prague, 14-17th September 2021. Particular focus will be put on developing a standardised protocol for quantifying freshwater mussel clearance rates and the effects of external (e.g. particle concentration) and internal (e.g. genotype) factors on the functional response of bivalves. Further focus will also be on generating equations describing the relationships between mussel biomass and clearance rate, with the aim to improve our ability to estimate the biofiltration capacity of mussel communities across large geographic scales. The first results of a systematic review of published data on the link between biomass and clearance rate data will be presented.

Keywords: *filtration, ecosystem services, ecosystem function, freshwater mussels*

Acknowledgements: COST CA18239 - Conservation of freshwater mussels: a pan-European approach

Freshwater Mussel Removes Bacterial Pathogen

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Decline of freshwater mussels (Unionida) is a global phenomenon, threatening biodiversity and the essential ecosystem services that mussels provide. Freshwater mussels can clear the water by filtering suspended particles, such as phytoplankton, but they can also remove bacteria from the water and therefore decrease the risk of infections in aquatic organisms. Here, we studied if the common freshwater bivalve *Anodonta anatina* (duck mussel) can remove *Flavobacterium columnare* from water. This bacterium is the causative agent of columnaris disease in fish, which causes serious problems in aquaculture. Mussels removed bacteria from the water in two experiments performed, so that after 96-h monitoring, the concentration in mussel treatments was only 0.3–0.5 times that of the controls. Mussel behavior (shell openness, foot position, and movement) was not affected by the presence of bacteria or algae. Biodeposition formation was higher with algal diet than with bacterial diet, and lowest in clean water. The intestines of *A. anatina* that were offered bacteria, harbored *F. columnare*, suggesting that mussels ingested the bacteria. From the ecosystem services angle, present result supports the view that freshwater mussels can have an influence on bacteria, and suggests that freshwater mussels have a potential to mitigate problems caused by aquaculture pathogens as well as to play a role in water quality management.

Keywords: *biofiltration, columnaris disease, duck mussel, Unionidae, ecosystem services*

ECOTOXICOLOGY

STANDARD PRESENTATIONS (3)

Coatings with natural molecules affect the ecotoxicity of Cerium oxide nanoparticles to the mussel species *Dreissena polymorpha* and *Mytilus galloprovincialis*

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The ongoing development of nanotechnology has raised several concerns regarding the potential risk of nanoparticles (NPs) for the environment, in particular to aquatic ecosystems. In this context, the adsorption of biomolecules from the surroundings might affect significantly NP interactions with biological targets. Therefore, we carried out an ecotoxicological evaluation of ceria nanoparticles (CeO_2NPs) with different surface modifications, to assess how this may influence the toxicity towards aquatic organisms. CeO_2NPs were synthetized *ad hoc* with Alginate and Chitosan as coating agents. The impacts caused by CeO_2NPs were assessed using the mussels *Dreissena polymorpha* and *Mytilus galloprovincialis* as biological models representative of freshwater and marine ecosystem, respectively. Mussels were exposed *in vivo* to naked and coated CeO_2NPs. The aggregation and stability in water of CeO_2NPs were measured through dynamic light scattering (DLS) analysis and the levels of Ce in exposure media and in mussel soft tissues were determined by inductively coupled plasma-mass spectrometry. A set of biomarkers related to oxidative stress/damage and energy metabolism was applied to evaluate the biological effects of CeO_2NPs. Results showed a different hydrodynamic behaviour and stability of CeO_2NPs in both the matrices related to the different coatings. Despite this, no differences in the bioaccumulation of CeO_2NPs were observed among the experimental groups in both species. The different coatings affected also the toxic outcomes of the CeO_2NPs. In *D. polymorpha* all the three CeO_2NPs acted as ROS scavenger reducing significantly Reactive Oxygen Species (ROS) level and the activity of the antioxidant enzymes while a different response arose from the exposure of *M. galloprovincialis,* as in this species coated CeO_2NPs triggered oxidative stress and oxidative damage. Our results emphasize the role of environmental modification in determining the NP toxic outcomes highlighting that mussels are suitable model to investigate ecotoxicity of nanoparticles.

Keywords: *Cerium oxide nanoparticles, eco-corona, marine mussels, oxidative stress.*

Nanoplastic, Microplastic and Bivalves – physical and chemical perspective

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The increasing amount of microplastics (MPs) in the freshwater and the ocean environment gradually transforms our Blue Planet into the plastic one. Among various consequences of this phenomenon, one can point out the new ecological niche – Plastisphere (all available surface of MPs). The complex problem of nanoplastics and microplastics interaction with biota needs the interdisciplinary approach. The aim of this research is to present the usefulness of Raman spectroscopy and other physical and chemical methods to characterize the synthetic materials from the environment, and their role in the deeper understanding of the MPs and their behaviour. Furthermore, providing this data will help to properly design the ecotoxicological experiment. The talk will discuss obtained results and future perspectives of research on nano- and microplastic interactions with fresh- and saltwater bivalves.

Keywords: *microplastics, nanoplastics, ecotoxicity, Plastisphere, Raman spectroscopy*

Acknowledgements: The author would like to thank Barbara Pałys for the access to Raman spectroscopy, Aleksandra Skawina, Barbara Urban-Malinga and her group for the fruitful collaboration.

Toxicity associated to exposure and recovery of neodymium in *Mytilus galloprovincialis* exposed to warming conditions

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Several stressors, such as climate changes factors and rare earth elements (REEs), have been identified as contributors of environmental change. However, the toxicity resulting from the combination of both stressors has received little attention. Neodymium (Nd) is a REE that has been widely used in magnets, and the present study aimed to evaluate the responses of *Mytilus galloprovincialis* species to Nd (10 µg/L) under actual (17 ºC) and predicted warming conditions (21 ºC) after a short exposure period (fourteen days) followed by fourteen days of recovery, analyzing Nd accumulation, histopathological and biochemical alterations. The results showed that after exposure mussels were able to accumulate Nd at both temperatures, with higher concentrations at 21 ºC. Increased temperature and Nd did not significantly alter the characteristics of digestive tubules but caused histopathological injuries in gills, although the combination of both stressors did not have a cumulative effect in gills. Contaminated mussels at 17 ºC only activated glutathione reductase enzyme which was not sufficient to avoid cellular damage. Although the highest Nd accumulation under 21ºC, it seemed that the increase in superoxide dismutase activity was enough to avoid damage in membrane lipids and proteins. After the recovery period, mussels at 17 ºC maintained the concentration of Nd, while mussels under warming conditions were able to decrease their Nd content. No improvements in gill's status were found and contaminated mussels at 21 ºC showed more changes in digestive tubules than those from the exposure. Contaminated mussels under both temperatures did not activate their antioxidant and biotransformation defenses, resulting into cellular damage highlighting the impacts caused by a previous exposure to Nd. This study may indicate that mussels were not able to recover from the exposure to Nd and that both stressors compromise mussel's biochemical and histopathological processes and may eventually influence the population maintenance.

Keywords: *Neodymium, climate changes, mussels, biochemical alterations, histopathology.*

ECOTOXICOLOGY

SHORT PRESENTATIONS (1)

Levels of microelements and risks in consumption of soft tissues of mussels collected along South African coast

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The soft tissue of mussels could be used as the main food source, especially in coastal areas. The excess of dangerous elements in mussels could be prejudicial to health because of their constant consumption by the local population.
The content of 23 macro- and microelements was determined in soft tissues of selected sets of mussels (*Mytilus galloprovincialis)* collected in 12 zones from Namibia to the East coast of South Africa, including the pristine and polluted areas. The neutron activation analysis at the REGATA facility of the reactor IBR-2 was used for the simultaneous determination of specific groups of elements of terrigenous (Al, Sc, V, Th, etc.) and anthropogenic (Zn, As) origin.
Dietary risks were assessed by using four different approaches: direct comparison with the maximum permissible levels for food products, estimation of risk quotients by calculating estimated weekly intakes, estimation of the mass of mussels' meat that could be consumed to reach provisional tolerable weekly intakes, assessment of the target hazard quotients for each element and hazard indices for each studied site. The threshold levels of elements in the meat of mussels were calculated based on the risks of their consumption by population and compared with ranges in different pristine areas. It was suggested that the levels of trace elements in mussels from polluted zones could be dangerous for human consumption. In the studied area such elements as Al, Cr, Co, Zn, As and I considered as harmful at the high levels have to be under control in monitoring studies and farming of mussels.

Keywords: *Mytilus galloprovincialis, health risks, neutron activation analysis, South Africa*

ECOTOXICOLOGY

POSTER (2)

Effects of episodic point-source pollution on survival of caged juvenile *Margaritifera margaritifera*

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The effects of contaminants are traditionally considered one of the main reasons of the global declines of freshwater mussels including endangered freshwater pearl mussel *Margaritifera margaritifera* (Linnaeus, 1758) (FPM). The objective of our study was to develop and test a robust design for the *in situ* investigation of the multiple point-source pollution-caused effects on FPM. A declining FPM population occurring in the Malše River (Czech Republic, Central Europe) has reportedly been disturbed by the impact of municipal pollution from a point sources but there is a lack of data documenting these effects due to the inherent episodicity of the pollution events. Therefore, a 30-km-long river stretch was delimited of the impacted and both the upstream and downstream control sections. At each of total 15 sites, 2−4 open water mesh cages with juvenile mussels were located. Five water samples were taken at each site at intervals of 6−8 days during one-month experiment. As it had been assumed, survival rates of FPM within impacted section were lower than at control sites (73–95% and 91–100% of the upstream and downstream control values, respectively). An acute effluent-induced toxicity could be detected within studied river. Several potential stressors (ammonia and nitrite, low DO levels) have been found to be elevated and were associated with the adverse mussel development. This study highlights the importance of freshwater mussel species sensitivity to sudden adverse changes in ambient water quality. The methodology applied here may provide a useful tool for assessing and managing water quality in streams with FPM and possibly other freshwater bivalves.

Keywords: *in situ monitoring, freshwater pearl mussel, water quality, effluent-induced toxicity*

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The preliminary results of the nanoplastics and microplastic impact on *Unio tumidus* and *Sphaerium* sp.

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The presence of diverse plastic particles in aquatic environments and their influence on the ecosystems became a world-scale fact. Although the impact of plastics of different sizes on marine environments is under investigation for several years now, little is known about the presence and influence of these materials in freshwaters even if they are considered as likely places of original plastics' load to the oceans. Several freshwater bivalve species were observed to be contaminated with microplastic fibres and spheres, however, there are currently no data on the presumable impact of this contact on plastic properties.

We treated adult *Unio tumidus* and *Sphaerium* sp. with the 20 µm polystyrene microspheres suspended in *Scenedesmus* algae for 2 hours. After this, bivalves were sacrificed, histological frozen sections were prepared and confocal microscopy used for analysis. Microspheres were detected in the intestine of both species, together with algae. Raman spectroscopy was used for acquiring spectra of both polystyrene spheres - suspended in algae and spheres from intestine content. Furthermore, we treated adult *Unio tumidus* with polystyrene nanoparticles (<20 nm). Although preliminary test on variants of sole polystyrene resulted in obtaining clear spectra, both bivalves' induced samples: pre- and post- intestinal passage occurred as inaccessible for this method, but presumably for different reasons. The spectrum of spheres suspended in algae was presumably hidden in algae spectra, while particles from the intestine were likely precisely covered by the intestine content, which made access to the plastic and its measurement impossible. Nevertheless having in mind these difficulties we look for future methods of removal of biological contaminations to open the possibilities for testing the composition of the plastic particle in different moments of their passage through organisms and ecosystems.

Keywords: *microplastic, freshwater, Unio tumidus, Sphaerium sp, Raman spectroscopy.*

Acknowledgements: We are grateful to Barbara Pałys for the access to Raman spectroscopy, Piotr Maszczyk for sharing the microplastic sample, and to Piotr Bernatowicz for providing *Scenedesmus* algae suspension for these tests.

GENETICS

STANDARD PRESENTATION (4)

Applying genomic approaches to delineate conservation strategies: a case study using the highly endangered freshwater mussel *M. margaritifera* in the Iberian Peninsula

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The understanding of genetic structure and diversity patterns of highly endangered organisms is crucial to guarantee the implementation of effective conservation actions that counteract the current decline of populations and species, ensuring their long-term preservation. We used Single Nucleotide Polymorphisms (SNPs) to address the population structure in the Iberian Peninsula of the freshwater pearl mussel (*Margaritifera margaritifera* L.), a threatened species listed as critically endangered in Europe and included in the European Habitats Directive under Annexes II and V, and in Appendix III of the Bern Convention. A total of 130 individuals of *M. margaritifera* were collected from 26 populations belonging to 16 hydrological sub-basins. We obtained 31,692 SNPs through Genotyping by Sequencing (GBS) and used this dataset to infer the population structure. Pairwise FST comparisons revealed low levels of genetic differentiation among geographically close populations, with the lowest values found between locations within the same river, sub-basin or basin. sNMF and Admixture analyses were consistent and both methodologies showed K=2 and K=3 as the most plausible number of ancestral populations according to cross-entropy (sNMF) and cross-validation error (Admixture) analyses. For K=2, two major genetic clusters, one constituted by the Atlantic and Cantabrian basins and a second cluster including the large Douro basin populations. For K=3, the Atlantic - Cantabrian group was

subdivided into two differentiated genetic clusters: one mainly formed by the Atlantic populations, and another by the Cantabrian ones. The Paiva river showed an even mixture of the three genetic lineages in the individuals sampled closer to its spring, while all the individuals from the downstream end of this river were assigned to the Douro lineage. Our results show that genetic conservation units do not match individual rivers, and that previous knowledge of the genetic structure is necessary before planning recovery plans that may involve relocation or restocking.

Keywords: *Conservation genomics, endangered species, Margaritiferidae, Iberian Peninsula, conservation units*

Inference of DNA methylation patterns in molluscs

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Mollusca are the second largest and arguably most diverse phylum of the animal kingdom. Nevertheless, our knowledge concerning epigenetic mechanisms including DNA methylation in this invertebrate group is still very limited. To get a deeper insight into inferred DNA methylation patterns, we analysed the normalized dinucleotide CG content in protein-coding sequences and identified DNA methyltransferases (DNMT1 and 3) in published transcriptomes and genomes of 140 species across all eight classes of molluscs. Given the evolutionary age and morphological diversity of molluscs, we expected to find evidence for diverse methylation patterns. Furthermore, we suggested that molluscs possess substantial levels of DNA methylation in gene bodies as a rule. However, we did not only find out that (i) the CpG observed/expected distributions indicate a reduction in DNA methylation in certain groups, but also (ii) a reduction in the completeness of the DNMT toolkit. One subclass and one order even lacked DNMT3 completely, usually responsible for de novo methylation, although they showed signs of DNA methylation. Our survey may serve as guidance for direct empirical analyses of DNA methylation in molluscs.

Keywords: *CpG observed/expected distribution, DNA methylation, DNA methyltransferase, epigenetics, molluscs*

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Population genetic trends in the common whelk, *Buccinum undatum*, reveal fine-scale structuring and cryptic speciation within the North Atlantic

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The common whelk, *Buccinum undatum*, is a subtidal gastropod that exhibits clear spatial variation in phenotypic shell traits across its North Atlantic distribution. While multiple studies of spatial phenotypic variation exist for the species, population genetic studies, to date, have been limited to a small number of mitochondrial and microsatellite markers. Here, we present a population genetic study of *B. undatum* using SNP variation obtained from ddRAD sequencing. These data greatly expand the availability of neutral genetic markers for the species, allowing for fine-scale characterization of population trends across the North Atlantic. Our data indicate significant genetic differentiation exists between Canadian and European populations (Iceland, Faroe Islands, and England) consistent with the divergence of populations in allopatry ($F_{ST} > 0.57$ for all pairwise comparisons). Within Europe (Iceland, the Faroe Islands, and England), populations structure is typified by weak but significant genetic structuring following an isolation-by-distance model. Finally, we discuss the suitability of Icelandic populations as models for genotype-phenotype interaction by establishing significant correlations between genetic structuring in Iceland and two phenotypic traits: shell shape and color frequency. The works discussed here enhance our understanding of spatial genetic patterns in *B. undatum*, highlight potential cryptic speciation embedded within species (as currently described), and highlight the potential for ongoing research into genotype-phenotype interactions.

Keywords: *divergence, F_{ST}, genetics, phylogeography, speciation*

Whole-genome re-sequencing data to infer historical demography and speciation processes in land snails: the study of two *Candidula* sister species

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Despite the global biodiversity of terrestrial gastropods and their ecological and economic importance, the genomic basis of ecological adaptation and speciation in land snail taxa is still largely unknown. Here, we combined whole-genome re-sequencing with population genomics to evaluate the historical demography and the speciation process of two closely related species of land snails from western Europe, *Candidula unifasciata* and *C. rugosiuscula*. Historical demographic analysis indicated fluctuations in the size of ancestral populations, probably driven by Pleistocene climatic fluctuations. Although the current population distributions of both species do not over-lap, our approximate Bayesian computation model selection approach on several speciation scenarios suggested that gene flow has occurred through-out the divergence process until recently. Positively selected genes diverging early in the process were associated with intragenomic and cyto-nuclear incompatibilities, respectively, potentially fostering reproductive isolation as well as ecological divergence. Our results suggested that the speciation between species entails complex processes involving both gene flow and ecological speciation, and that further research based on whole-genome data can provide valuable understanding on species divergence

Keywords: *approximate Bayesian computation, demographic history, ecological speciation, Gastropoda, gene flow, whole-genome re-sequencing*

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GENETICS

POSTER (3)

Escherichia coli Isolated from *Potomida littoralis* and *Margaritifera margaritífera:* phylogenetic group determination

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Antimicrobial resistance (AMR) is a major global health problem. Water use by human activities represent a natural reservoir of AMR, thus a time-integrated approach is required in aquatic ecosystems. Freshwater bivalves are widely applied as accumulation indicators and monitoring tools of contaminant effects on different levels of biological integration since they are suspension feeders that actively filter, retain and concentrate particles from their surrounding water, including free living or particle-bound bacteria. In this study, we aimed to (i) investigate the genetic diversity of E. coli strains isolated from freshwater bivalves, and (ii) determine their virulence factors. Samples were collected in the middle sector of the Tua River. Isolates were retrieved in Chromocult® Coliform Agar plates (Merck, Germany). Antimicrobial susceptibility testing (AST) was done by the Kirby-Bauer disk diffusion method against 21 antimicrobial agents, according to the recommendations issued by the EUCAST and CLSI. Antibiotic resistance rates were ticarcillin (TIC) 87.5%, ticarcillin-clavulanic acid (TIM) 87.5%, piperacillin (PRL) 6.3%, cefoxitin (FOX) 18.8%, tobramycin (TOB) 31.3%, gentamicin (CN) 12.5%, and amikacin (AK) 87.5%. Antibiotics whose antimicrobial resistance was 100% belong to β-lactam, namely penicillins and carbapenems. The antimicrobial susceptibility test revealed that 43.75% of the isolates were MDR. PCR-based assays were designed for phylogenetic E. coli groups evaluation. The E. coli phylogenetic group D or E was the most prevalent (50%), followed by phylogenetic groups E or clade I, B1 and A. Phylogenetic groups D or E and E or clade I should be confirmed using E-specific primers. Our results indicated that bivalves provide an efficient, time-integrating tool for identifying/quantifying faecal indicators, including multidrug resistant bacteria.

Keywords: *Phylogenetic groups, E. coli, One Health*

Acknowledgments: This work is supported by National Funds by FCT - Portuguese Foundation for Science and Technology, under the project UIDB/04033/2020.

Providing a high quality genome for the 'solar powered' sea slug *Elysia timida*

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‘Solar-powered’ sea slugs are fascinating! *Elysia timida* belongs to a small group of marine, heterobranch slugs, called Sacoglossa, of which certain species have the ability to incorporate and maintain the chloroplasts of its food algae. These ‘stolen’ plastids (kleptoplasts) are then stored in a functional state in the digestive gland cells of the slugs and presumably allow them to endure weeks or months of starvation. How do they keep the chloroplasts active which continuously produce starch? No one knows! But up to now, this spectacular phenomenon, called functional kleptoplasty, has only been observed among animals in Sacoglossa and few marine flatworms.

In this poster, we summarize the statistics of the first draft genome assembly of *Elysia timida*, using PacBio’s ultra-low DNA input library preparation protocol. The genome assembly of *Elysia timida* has a contig N50 value of 1.08 Mb, a total length of 723 Mb, which is close to the estimated genome size of 650 Mb, and a high percentage of detected metazoan BUSCO genes (95.3%). In general, the ultra-low lib prep enabled efficient sequencing of this species in the first place. With standard lib prep protocols for long-read sequencing platforms it could only be sequenced with a very low sequencing output. Next, we will combine the long-read assembly with proximity ligation data to increase the contiguity of the assembly. Comparative genomics between *E. timida* and the previously published draft assemblies of the sacoglossan *Elysia chlorotica* (contig N50 = 30.5 kb) and *Plakobranchus ocellatus* (contig N50 = 5.5 kb) will give us the unique chance to gain new insights into underlying genomic mechanisms related to kleptoplasty. It will further provide a valuable genomic resource for future genome-wide comparative analyses to organisms with similar life styles, i.e. those stealing useful parts out of their prey and incorporating, instead of digesting them.

Keywords: *Heterobranchia, Kleptoplasty, Long-read genome assembly, Sacoglossa, Ultra-low DNA input library preparation*

Acknowledgements: The project was supported through the program “LOEWE - Landes-Offensive zur Entwicklung Wissenschaftlich-ökonomischer Exzellenz” of Hesse’s Ministry of Higher Education, Research, and the Arts. We thank the Genome Technology Center (RGTC) at Radboudumc for the use of the Sequencing Core Facility (Nijmegen, The Netherlands), which provided the PacBio SMRT sequencing service on the Sequel II platform.

The mitochondrial genomes of two species within the *Melampus bidentatus* species complex (Panpulmonata; Ellobioidea)

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Melampus bidentatus is a complex of three cryptic species that are an important component of the salt marsh communities along the North American east coast and the Gulf of Mexico. We assembled the mitochondrial genome of the cryptic species *M. bidentatus* “North” and “South” from Illumina short read data using NovoPlasty and from PacBio Hifi data using MitoHifi respectively and annotated them using the MITOS webserver. Both mitochondrial genomes contain 37 genes (13 protein coding, 2 rRNA, 22 tRNA), 24 on the forward strand and 12 on the reverse strand, and have an identical gene order. The pairwise difference between the two mitochondrial genomes is 0.333. *Melampus bidentatus* North and South are two of four currently known Ellobioidea species (one, Pedipes pedipes, related, the other, *Myosotella myosotis*, less so) who deviate from the otherwise uniform gene order within the Superfamily (10 sequenced mitochondrial genomes). These four species are also recovered outside the rest of the Ellobioidea in all mitogenome based phylogenies, which is not supported by other phylogenetic or morphological studies. A putative control region was identified for all known mitochondrial genomes within Ellobioidea.

Keywords: *Ellobiidae, mitochondrial genome, genomics, control region.*

GLOBAL CHANGE

STANDARD PRESENTATIONS (3)

Biological impacts of ocean warming and acidification on cephalopods: a meta-analysis

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Cephalopods hold a relevant ecological role in the world's oceans, being widely known for their cognitive and behavioural prowess. Found in almost all habitats, these molluscs play an important role as both predator and prey, while also being economically valuable. The existing literature suggests that this group may be able to cope or even thrive under the ocean's novel conditions, due to their phenotypic flexibility and environmental plasticity. Notwithstanding, a growing body of literature has revealed potentially negative impacts of climate change for several species. In this context, the peer-reviewed literature was surveyed for articles featuring a sustained (≥24h) and controlled exposure of cephalopod species to increased temperature, reduced pH, reduced oxygen levels, and their combination. A comprehensive array of sequential meta-analyses was conducted over 211 control-treatment comparisons, from 57 suitable articles, using a standardized comparative framework to address the potential global effects of these stressors, across lineages (cuttlefishes, octopuses, and squids), climates (tropical and temperate), and life stages (embryo, paralarvae, juvenile, and adult). This analysis was also performed across specific response categories (e.g. Survival, Development, etc.). Temperature was the most influential factor, with significant effects for most categories. Reduced pH exhibited a significant, although comparatively smaller resulting effect size. Despite relatively low article and comparison number, the combination of both stressors further increased the effect size, suggesting potential synergy between both stressors. Overall, the existing literature suggests that temperature and low pH can have significant and pervasive effects on cephalopods, across lineages and life stages. This study also highlights the need for further research in certain taxa (e.g. Sepiida and Oegopsida), and emphasizes the current knowledge gaps on the effects of experimental deoxygenation, and of full factorial designs evaluating the effects of the 'deadly trio' in this class of molluscs.

Keywords: *Climate change, Temperature, Acidification, Meta-analysis, Cephalopods*

Establishing mussel behaviour as a monitoring tool to measure climatic disturbances

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Freshwater mussels (FM) are suitable biological indicators to assess environmental stressors. Behaviour is a good parameter to measure rapid mussel's responses. In this sense, valvometric method, that exploits the Hall sensor (real-time remote monitoring tool), has been used to measure the behavioural responses of mussels (valve opening amplitude and valve opening-closure frequency). During the last two decades, these methodologies have been used to measure the presence of the pollutants in the waterbodies. However, studies that focus on physical disturbances in the environment related to climate changes are lacking. Since future climatic scenarios in Europe predict an increase in temperature and change in the hydrological conditions, the main objective of this study was to evaluate the influence of water temperature increase and water discharge rates (without and with sediment transport) in four endpoints of mussel's behaviour: normal activity, resting, transition and avoidance. Our results suggest, that on experiments with increasing temperatures and high variation in water discharge rates with sediment transport, mussels presented high valve opening-closure frequencies and amplitudes. In this sense, mussels could be used as biological sensors to monitor changes in thermal and hydrological conditions which are increasing with climate changes.

Keywords: *valve gapping, biological sensors, environmental stressors.*

Running from climate change: Freshwater mussels behavioural responses to dewatering events

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Altered hydrological regimes imposed by climate change are one of the major threats to freshwater mussels (FM) conservation. Reduced water flows, as a consequence of warmer and dryer summers, may leave FM especially vulnerable due to their sedentary traits. Therefore, in this study we assessed the response of three native Iberian FM (*Unio delphinus*, *Anodonta anatina*, and *Potomida littoralis*) to climate change by analysing their behaviour, measuring horizontal and vertical movement, in relation to different dewatering scenarios. Nine ramps (simulating riverbanks) were built and placed in three semi-artificial river channels. Each ramp contained three replicates of each species placed side by side and three scenarios were tested: control (no dewatering), slow rate (4cm/day), and fast rate (8cm/day) dewatering.

In general, species responded differently to dewatering treatments. Horizontal movement differed significantly between species, being *A. anatina* more active and *P. littoralis* more sedentary. Vertical movement also differed significantly between species and not by treatments, but it decreased from control to fast rate dewatering. Main differences were observed on *A. anatina* which showed >50% shell exposure. Both *A. anatina* and *U. delphinus* were able to respond to slow and fast dewatering treatments, unlike *P. littoralis* that failed to adapt to declining water levels in both scenarios.

Behaviour may play an important role in the conservation of these species and this study suggest different interspecific movement strategies to climate and hydrological changes. While the less threatened *A. anatina* and the *U. delphinus* seem to be better adapted to water level changes, the lower ability of the endangered *P. littoralis* to avoid fast dewatering poses an additional threat to this species reinforcing the need for future conservation actions to mitigate drought and water abstraction activities. This situation may be especially important considering future climatic scenarios where extreme events such as droughts are predicted to be more frequent and intense.

Keywords: *freshwater mussel, climate change, dewatering, behaviour.*

GLOBAL CHANGE

POSTER (1)

Environmental forcing on growth and recruitment of marine bivalve species at Northern Patagonia, Southwestern Atlantic

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In coastal ecosystems, the recruitment of bivalves is characterized by year-to-year variability. Annual cohorts often differ in the number of recruits, resulting in irregular pulses of high abundance (i.e., successful recruitment) followed by periods of scarcity (i.e., failing recruitment). Environmental forcing likely underlies these pulses as favourable conditions (i.e., temperature, food availability) determine whether larvae settle and whether new recruits survive. As a factor that operates in a large-scale, it can also result in a synchronic recruitment of populations of multiple species within the same area. Sessile organisms represent a continuous record of environmental variability for a given location as a result of changes in annual growth rates. These changes can be seen in the shells as wide and narrow growth increments, representing favourable and unfavourable environmental conditions, respectively. At San Matías Gulf (Northern Patagonia, Argentina) the clam *Glycymeris longior* offers an opportunity to assess the effects of environmental forcing on the recruitment of commercial bivalve species along coastal ecosystems of the Southwestern Atlantic based on the growth anomalies recorded on its shells. In this context, we generated a multi-decadal growth chronology (~60 years) using sclerochronological on *G. longior* live collected individuals. We assessed the relationship between annual standardized growth variability and environmental factors. We also analysed the coherence between *G. longior* growth and successful recruitments reported for three clam populations from the area (*Panopea abbreviata*, *Ameghinomya antiqua* and *G. longior* itself). We found a positive relationship between the sclerochronology and the mean sea surface temperature of autumn (Spearman correlation, $\rho= 0.48$, $p= 0.04$) and the Southern Annular Mode index for winter months (Spearman correlation, $\rho= 0.54$, $p= 0.007$). On the other hand, the successful annual recruitments corresponded to peak values of growth, particularly for the periods 1976-1979, 1982-1983, 1997-1998. Our findings support a geographic large-scale coherence in recruitment for bivalve populations.

Keywords: *environmental forcing, recruitment, marine bivalves*.

Funding: Projects M025 and M026 from Universidad Nacional del Comahue.

HOST-PARASITE RELATIONSHIPS

STANDARD PRESENTATIONS (3)

Parasite communities in freshwater mussels: what we know and what we still need to learn

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The study of parasites in freshwater mussels has largely proceeded on an *ad hoc* basis; in particular, knowledge on what drives the assembly of parasite communities, and the subsequent effects of those parasite communities on host individuals, populations and ecosystems remains scarce. In this talk we describe a sustained three-year program of research on the mussels *Anodonta anatina* and *Unio pictorum* that was designed to address the questions of how parasite communities are assembled in these hosts, and what the effects are of these parasites on their hosts at multiple ecological levels. First, we analyse the factors that contribute to patterns of parasite prevalence and abundance in freshwater mussels across multiple scales, using both observational and experimental field data. We demonstrate that parasite communities are determined by: the wider environment in which the mussel lives; the time of year the mussels are sampled; characteristics of individual mussels (both within species and between host species); and within-host interactions between different parasites. Then, we use field and laboratory studies to show that the effects of multiple parasite species (trematodes and mites) interact to reduce the reproductive output of mussel populations by up to 13%, even at low prevalences. Further, this effect depends on the mussel population being studied, with the negative effects of mites only observed in certain populations. Finally, we use laboratory experiments to show that two parasites (bitterling fish embryos and trematodes) both affect the filtration rates of freshwater mussels, but in different ways, with implications for the ecosystem services they provide. Our study provides clear and significant advances in freshwater mussel parasitology from both community ecology and conservation angles, and highlights key unanswered questions that should set the agenda for studies in the future.

Keywords: *conservation, community ecology, ecosystem services, parasitology, unionid*

Field and laboratory evaluation of susceptibility of *Corbicula* spp. clams to *Chaetogaster limnaei* gill parasites

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The release of natural enemies, in conjunction with relative immunity to potential resident enemies, has often been proposed as an explanation of the success of invasive species in the ecosystems they colonize. Yet parasites of freshwater invasive bivalves have been relatively little studied. *Corbicula* spp. clams are dominant invasive clams in South American freshwater habitats, and parasitological studies on this group are very scarce or altogether lacking. During preliminary sampling, *Corbicula fluminea* and *C. largillierti* populations from Río de la Plata, Argentina, were found to be naturally infected with *C. limnaei* oligochaete worm gill parasites (prevalence 25-40% and mean intensity 2-4), while *C. largillierti* congeners from populations established more recently 1500 km apart in the Salta province were uninfected. To evaluate the susceptibility of Salta populations to infection, we exposed clams of two sizes (shell length ~11 mm and 18 mm) to three oligochaete concentrations (15, 30 and 60 worms per container) in 10-ml containers at 20ºC in the laboratory (five clams per container; n=10 replicates; total of 30 containers and 150 clams). Worms were obtained from naturally infected native snails in nearby waterbodies. At all concentrations tested, we obtained infected clams, and both prevalence and mean intensity of infection increased with oligochaete concentration (prevalence 14%, 32%, and 68%; intensity 0.52, 1.12, and 2.02, at low, mid, and high worm concentrations, respectively). Both in the field (GLM) and at the end of our laboratory experiments (Anova), small clams had a significantly higher worm prevalence than large conspecifics, although this effect was population dependent. These results indicate *C. largillierti* populations have not acquired immunity nor undergo enemy release. Instead, the worm's absence from wild clams is likely related with a low availability of parasites in aquatic habitats occupied by *C. largillierti* in northwestern Argentina.

Keywords: *Corbicula largillierti, Chaetogaster limnaei, susceptibility, experimental infection*

HOST-PARASITE RELATIONSHIPS

POSTER (2)

A molecular identification of trematodes of the genus *Diplostomum* in lymnaeid snail from Arctic lakes

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Trematodes of the genus *Diplostomum* have a complex life cycle which includes the change of two intermediate hosts. At the first stage of development the egg of the trematode turns into a miracidium which infects a freshwater gastropods from the Lymnaeidae family and passes into the sporocyst or parthenite stage. Thus, the metamorphosis of miracidium into cercariae occurs in the mollusk which after maturation leaves the first intermediate host and subsequently infects the second intermediate host, the fish. Infected fish become easy prey for waterfowl which act as the final host for trematodes. The aim of our study was to assess the infestation of lymnaeid snails from Arctic lakes with trematodes of the genus *Diplostomum*. For this total DNA was isolated from the pond snails fixed in 96% alcohol and the internal transcribed spacer 2 (ITS2) was amplified that made it possible to detect the presence of trematodes in mollusks. To identify trematodes the obtained nucleotide sequences were compared with data from NCBI GenBank. During the study, the presence of two species of trematodes *Diplostomum baeri* and *D. spathaceum* in the Arctic waters was confirmed. As a result, of two unique sequences of the ITS2 spacer of *Diplostomum baeri* were identified on the Kola and Chukotka Peninsula different from the widespread haplotype from Germany and Canada by three substitutions. This is the first finding of this trematode species confirmed by a molecular method, which indicates its distribution in the Arctic. Also, our results showed that the *D. spathaceum* distributed in the lakes of Siberia, Central Asia, and Europe.

Keywords: *trematodes, Diplostomum, Lymnaeidae, PCR diagnostics*

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Tetrahymena rostrata cysts for biocontrol of pest slugs

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Tetrahymena rostrata is a facultative parasitic protist which can infect a variety of terrestrial slugs and snails. Infection can be lethal for the Grey Field slug, *Deroceras reticulatum* and *T. rostrata* has previously be proposed as a potential biocontrol agent. *T. rostrata* has several developmental forms including trophonts (feeding cells), cysts (resting cells), and theronts (excysted cells). Previous studies on the capacity of *T. rostrata* to kill slugs were conducted with trophonts which are easily cultured in large quantities in the laboratory.

We have developed methods to efficiently produce *T. rostrata* cysts which could be stored for long periods, which opens the possibility of formulations of products with practical shelf-life. The methods achieve synchronised encystment and excystment, resulting in pure preparations of theronts. Theronts were found to be more effective at producing lethal infection in slugs than trophonts. Infected slugs stop feeding and have reduced movement in the days preceding death. Infection was shown to occur initially in the slug renal tissue. However protists invaded most organs. The susceptibility of a range of pest molluscs has been evaluated.

Keywords: *biological control, terrestrial slugs, protist*

Acknowledgments : This work was funded by the Australian Grains Research and Development Corporation and The University of Melbourne

INVASIVE SPECIES

STANDARD PRESENTATIONS (8)

Asian clam explosion and its implication on freshwater mussel populations: the case in the middle Ebro basin, Spain.

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The Asian clam (*Corbicula* spp.) was first detected in 2004 in the Ebro River (Aragón, Spain). In 2006, it was also found in the Canal Imperial de Aragón (CIA) and in 2007 in the Canal de Tauste (CT). Both artificial canals held large populations of native freshwater mussels and are the main habitat of *Pseudunio auricularius* (Spengler 1793). However, since 2013 this critically endangered species has suffered massive mortality episodes. The high density of the Asian clam has been hypothesized to explain this unusual mortality, so this invasive species received further attention and research. The mean clam densities in the canals in 2016 exceeded 1000 ind/m^2, with a mean shell size of 18 mm. Nevertheless, five years before (2011) in CT, we registered a mean density of just 70 ind/m^2. Also, a decrease in the maximum size of Asian clams was recorded downstream in the CIA, which was not observed in the river. In 2018, The mean clam density in selected invaded areas of the Ebro River where it lives in sympatry with native freshwater mussels, was 981 ind/m^2, with a mean shell size of 22.87 mm. However, during a systematic sampling in 2019 we registered a density of 196 ind/m^2 with an average shell size of just 11.22 mm, suggesting a higher Asian clams' survival and growth, in the same freshwater mussel habitats. The density of alive freshwater mussels (*Anodonta anatina, Potomida littoralis, Unio mancus* and *P. auricularius*) in the CT decreased from 1.53 ind/m^2 in 2011 to almost zero in 2016 (0.01 ind/m^2), and a similar value was registered in the CIA (0.02 ind/m^2). In the river, a density of 0.9 ind/m^2 was registered in 2018.

The implications of the population explosion of the Asian clam in the canals and its possible influence on the disappearance of the freshwater mussels will be discussed and compared with the data collected in the natural environment.

Keywords: *endangered species, massive mortalities, non-indigenous invasive species*

Effect of temperature on life history traits and immune status of the invasive tropical freshwater snail *Melanoides tuberculata*.

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Invasive species cause major losses in biodiversity and alter ecosystem functioning across the globe. Once invaders become established in an ecosystem they are often impossible to remove, which is particularly problematic in isolated, eco-insular systems such as the African Great Lakes. Beyond the intrinsic biological properties of invasive taxa, a crucial factor determining invasiveness and our ability to anticipate, prevent and manage invasions is how anthropogenic modifications of ecosystems alter ecological opportunities for migration and establishment. Here we investigate the influence of temperature on key biological traits, notably fecundity, the size of the juveniles at birth and parental immune status, of the invasive Asian morph of *Melanoides tuberculata* from ancient Lake Malawi. We subjected adults of this parthenogenetic (clonal) lineage to simplified, uniform temperature treatments of 20°C, 26°C and 32°C, standardized feeding and we collected weekly cohorts of juveniles to examine life history traits. At the end of the experiment we evaluated the immune status of the parents by testing their antimicrobial response against a microbial agent from their environment. We anticipated that intermediate temperatures would maximize reproduction and antimicrobial responses whereas other conditions would cause physiological stress. We found no difference in fecundity between treatments, but the size of juveniles at birth increased with temperature, so did the induced antibacterial activity of the female parents. Our results also indicated elevated juvenile mortality at 32°C. In general, it thus seems that adult *M. tuberculata* becomes more competitive in hot environments, at the price of reduced juvenile survival at least under standardized feeding. We observed contrasting responses in the various studied traits, suggesting that *Melanoides tuberculata* adopts compensatory mechanisms to cope with environmental changes at the individual level. These mechanisms likely result in fluctuations of invasion potential with seasonal variation and contribute to the competitive pressure invasive *Melanoides* lineages exert on native taxa at the population level.

Keywords: *Melanoides tuberculata, life history traits, immune defense, climate change, experimental invasion ecology*

Massive Northward Expansion of the Alien Asian Pond Mussels (*Sinanodonta* spp.) in European Russia

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Asian pond mussels are one of the most remarkable invaders among freshwater bivalves rapidly spreading throughout the world. There are two species in the genus documented as alien ones: *S. woodiana* (Lea, 1834) and *S. lauta* (Martens, 1877). The invasion of Asian pond mussels in Russia was firstly discovered in 2017 in the artificially heated section of the Yenisei River, Eastern Siberia. Later, invasive populations of both species were recorded in the Belovo Reservoir, Ob River basin, Western Siberia. Both of these sympatric invasive assemblages are associated with artificially heated waters discharged from thermal power plants (TPP) and further spreading of Asian pond mussels out of these thermal refugia is restricted by unfavorable temperature conditions of surrounding freshwater habitats. In contrast, invasive Asian pond mussels that were found in the downstream section of the Volga River have established rather abundant populations under natural environmental conditions. Furthermore, these species were recorded from the Kama River basin, where they inhabit the artificially heated Karmanovo Reservoir and native habitats in the Buy River. Conversely only *S. lauta* was found in the artificially heated Zainsk Reservoir and the Zay River. It was found that *S. lauta* from invasive populations shares a COI haplotype that is closely related to those from South Korea. Conversely, *S. woodiana* reveals the commonest invasive haplotype being recorded from European countries and northern Myanmar. We propose that the recent invasion of *S. woodiana* and *S. lauta* in Russia was associated with fish stocks imported from Kazakhstan. The rapid expansion of these mussels throughout Russia was caused by a human-mediated dispersal of infested fishes from a site(s) of initial invasion to other freshwater systems: the Lower Volga (at least since 2002), Yenisei (2004), Ob (2007), and Kama (1985) rivers. Our species distribution modeling (SDM) shows that most of European Russia north of the Don and Kuban River basins is unfavorable for *S. woodiana* under the current climatic conditions. This finding stresses the role of artificially heated water bodies in further northward expansion of *Sinanodonta* invasion in Russia.

Keywords: *invasion, alien species, Asian pond mussels, heated waterbodies, species distribution modelling*

Acknowledgments: this study was supported by the Russian Science Foundation under the project No. 21-74-10130.

Occurrence of the parasite and endosymbionts of *Corbicula* clams from native range: Thailand, South Korea and Myanmar

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Asian *Corbicula* clams are one of the most successful invaders of American and European aquatic ecosystems. Owing to their high invasive potential, fresh- and brackishwater clams of the genus *Corbicula* constitute today one of the most popular research objects for scientists from all over the world. Despite the decades of intense studies of the genus *Corbicula*, the reliable data on the parasite fauna and endosymbionts of this genus are relatively poor. Currently, three genera of trematodes have been reported in its native range, as parasites of *Corbicula* clams (*Phyllodistomum, Echinostoma*, and *Aspidogaster*), and two from North America (aspidogastrid and echinostomatid trematodes). The invasive clam *Corbicula* completely free from parasites in European waterbodies.

This study was conducted in 2018, 2020 in Southeast and East Asia. Although these expeditions focused on the phylogenetic and taxonomy studies of freshwater mollusks, we were able to collect representative material on parasite and endosymbionts of *Corbicula* clams. The study presents the first discovery of the trematode *Prosorhynchoides* sp. in the *C. fluminea* and the *C. leana* from the Sheweli River (Myanmar). Trematodes of the *Prosorhynchoides* Dollfus, 1929 (Digenea: Bucephalidae) are a fairly well-studied group of parasites. The definitive host for these parasites is marine and freshwater fish species. Intermediate hosts are freshwater and marine bivalves.

The larvae of *Symbiocloeon* sp. (Ephemeroptera) were found in the cavity of several individuals of *Corbicula* sp. from tributary Lam-Chae Dam Reservoir (Thailand). Finally, larvae of gudgeon (*Sarcocheilichthys soldatovi)* in the cavity of *C. leana* from the Irrigational channel (South Korea, Mangyeong settlement).

In this study, we detected for first time the infected *C. fluminea* and the *C. leana* by trematode *Prosorhynchoides* sp. confirmed by molecular data. In addition, it was established that mayflies and gudgeon can use the *Corbicula* spp. as a host for laying their embryos.

Keywords: *Corbicula* spp., parasite fauna, native range, endosymbionts

Acknowledgments: This work was partly supported by the Ministry of Science and Higher Education of Russia (project No. AAAA-A17-117033010132-2), the Russian Science Foundation supported the molecular and phylogenetic analyses (project No. 21-14-00092).

Predation effects of native and invasive crayfish on native and invasive freshwater mussels

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Freshwater mussels and crayfish are among the most endangered species with globally declines in the last decades. In both groups, non-native species spread increasingly, potentially exerting further pressure on native species. For a successful conservation management, it is essential to understand the ecological interactions among native and invasive crayfish and mussel species, particularly in terms of predation susceptibility.

In controlled laboratory experiments, we investigated the predatory impacts of the native European noble crayfish, *Astacus astacus*, and the invasive signal crayfish, *Pacifastacus leniusculus*, on co-exposed unionids including three native (*Anodonta anatina*, *Anodonta cygnea* and *Unio pictorum*) and one invasive (*Sinanodonta woodiana*) mussel species. In subsequent experiments with the same crayfish individuals, we examined potential learning effects of the crayfish using mussels as prey. In a field investigation of a natural stream, we additionally assessed the *in-situ*-impacts.

Predation effects of *P. leniusculus* on mussels were significantly higher than of *A. astacus*. Over all experiments, native mussels were more strongly damaged than the invasive *S. woodiana*, with the thick-shelled *U. pictorum* being most affected. For both crayfish species, a learning effect could be demonstrated, most strongly in *A. astacus*.

Our experimental results show that crayfish predation may negatively affect mussel populations, even though this could not be confirmed in a field setting. Thicker shells did not protect the mussels from more severe damages, indicating that other factors such as shell shape better explain predation susceptibility. Given that the faster-growing and round shaped *S. woodiana* and the invasive *P. leniusculus* continue to spread, a co-occurrence of both species could boost the decline of native mussels.

Keywords: *Pacifastacus leniusculus, Sinanodonta woodiana, predation, unionids, invasion.*

Shipworms in Lagoon of Venice

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The Venice lagoon has a long tradition in the use of wood, not only for the construction of typical boats, but also for fixed structures such as poles for the signal of the canals (*briccole*, *mede* and *dame* = dolphins, single beacons and poles signalling a canal entrance), mooring poles, piers, bridges, stilts and water gates of the historic buildings. Wood in a marine environment is subjected to degradation due to physical agents such as sun, wind and waves, and biological agents, fungi, bacteria and xylophagous macroinvertebrates. Shipworms belong to this last group of organisms; they are bivalve molluscs highly adapted to living in wood. These bivalves favour the degradation of the wood that reaches the sea, but in an anthropic environment their presence constitutes a problem under various aspects, constituting the main cause of sudden breakage of wooden structures. Drifting pieces of wood are a danger to navigation and this phenomenon has worsened in recent years, leading to reducing the life of an oak post by thirty centimetres in diameter to just one or two years. This contribution will present the studies carried out to promote a sustainable use of wood and the protection of the cultural heritage, the development of protocols and techniques to evaluate the impact of the different shipworm species present in the lagoon, as well as the evaluation of the intensity of their attack. During these studies, the presence of an alien species emerged, much more aggressive than those previously present in the lagoon. Integrated taxonomy techniques were applied for the recognition of the species and for the comparison with species collected in 25 sites distributed on the coast of 15 European countries.

Keywords: *Shipworm, wood degradation, Lagoon of Venice, alien species.*

South American freshwater invasive Bivalvia: patterns emerged by a connectivity analysis

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Previous works have established four hot spots in South America that serve as entry points and distribution foci for non-native mollusk species (NNMS) in the continent: Subtropical-Atlantic, Northern Andes, Central Andes and Southern Andes. In this work we intend to establish the connectivity patterns of the continent, using an application of network theory and methodology. South America has been divided in a grid of 85 squares of 5°x 5° that covers all possible ecoregions. These regions have been connected according to their geographical proximity, and additional connections like river systems, sea-routes, land-routes, and train-routes that could affect the expansion of NNMS in the continent. The conceptualized network helps to establish a connectivity framework that could facilitate or prohibit the invasion and expansion of NNMS in South America. The resulted network metrics allow measuring the integration and importance of each region at a regional and continental level. When the connectivity patterns of the previously established hot-spots are compared, we find significant differences only between the Subtropical Atlantic and the Northern Andes. This difference agrees with the current distribution of the emblematic NNMS *Corbicula fluminea*. Once the Subtropical Atlantic is further sub-divided according to the genetic barriers of *Limnoperna fortunei*, we notice that this difference is actually caused by the connectivity pattern of the Plata Basin, which is significantly different compared to all other regions. The application of network methodology in the distribution of NNMS could offer relevant and complementary information on the management of biological invasions and their socio-ecological impacts. For example, the superposition and the comparison between the current distributions of the NNMS and the recovered connectivity modules could help to establish areas of conservation priorities.

Keywords: *non-native mollusk species, network analysis, Corbicula fluminea, Limnoperna fortunei*

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Study of preferred orientation and residual stress of *Sinanodonta woodiana* shells by diffraction methods

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Study of the preferred orientation of biological materials (bones, shells, etc.) represents the use of crystallographic methods in biophysics to search for new possibilities in material science. Much attention is paid to texture of bivalve mollusc shells. However, for quality systematic investigation of crystallographic preferred orientation of these shells, it is necessary to examine many representatives from different parts of the world. In our work X-ray and neutron diffraction was used to examine the crystal preferential orientation and residual stress of adult shell of the species Sinanodonta woodiana collected from Czech freshwater rivers. The texture of artificially grown young shells was also measured. X-ray pole figure measurements of Aragonite phase (planes 111, 102, 200, 121, 022 and 122) were provided by using high-resolution X-ray diffractometer SmartLab Rigaku with Cu rotating anode X-ray source (Institute of Physic, Prague, Czech Republic). Neutronographic measurements were performed on a KSN2 diffractometer (Rez, Czech Republic) using the constant wavelength method and a SKAT diffractometer (JINR Dubna Russia) using the TOF method. Residual stresses were measured on theta/theta diffractometer X’Pert PRO. Observed data were processed by software packages GSAS, TODF-N, ResMat and X'Pert Texture.

Keywords: *texture, neutron diffraction, X-ray diffraction, residual stress, Sinanodonta woodiana..*

INVASIVE SPECIES

SHORT PRESENTATIONS (4)

Freshwater snails *Gyraulus parvus* (Say, 1817) and *G. laevis* (Alder, 1838): a story of the invasion at the population level

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Most of the non-native gastropods in European inland waters have originated from North America. The planorbid snail *Gyraulus parvus* is one of these species, being first reported from Germany in the 1970s. It has since spread across Central and Western Europe mostly in artificial and highly modified habitats. However, considerable conchological and anatomical similarity exists between it and the native European *G. laevis*, mainly occupying mesotrophic pools and wetlands. Using four other European and one North American *Gyraulus* species as outgroups, separate phylogenetic analyses based on mitochondrial and nuclear DNA sequence showed that *G. parvus* and *G. laevis* are in fact part of the same species-level clade, with *G. parvus* having nomenclatural priority. Moreover, the structure within the mitochondrial tree suggests the North American origin of the invasive populations spreading in Europe even in countries where *G. parvus* has not yet been recorded, such as the United Kingdom. Although native and non-native races in Europe tend to possess some differences in conchology and ecology, the degree of overlap makes it impossible to accurately distinguish between them without the DNA barcode. Our findings change the conservation view on the rare native European race. While interspecific competition among freshwater mollusc species is rare, the invasion on an intraspecific level may represent a serious threat for native populations. Additionally, the spreading of the non-native race of *G. parvus* from North America increases the risk of introducing non-native trematodes as this exotic race is a very common intermediate host of many schistosomes.

Keywords: *molecular data, invasive race, Planorbidae, phylogeny, genotype*

Population genetics of an invasive and a resident slug; the races and hybrids of *Arion vulgaris* and *Arion ater* s.l. in Görlitz, Germany

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The large slug *Arion vulgaris* has spread across much of Europe over the last 70 years, often leading to the local extinction of the resident *Arion ater* s.l. Before this occurs, the two species can hybridise, leading to the hypothesis that the invader may have become increasingly admixed with genes from *A. ater*. We investigated this possibility using slugs from the neighbourhood of Görlitz and Zgorzelec, on the German–Polish border, collected throughout the course of the invasion. Sixteen microsatellite loci as well as COI mitochondrial sequences provided the estimates of ancestry. We confirmed that genitalia intermediate between those of the two species are a fairly reliable indication of hybrids. However, there was little evidence of admixture amongst the *A. vulgaris* present after the invasion was complete. The microsatellite markers also revealed three genetic races within *A. vulgaris* in Görlitz, the consequence of separate colonisations or of founder effects. These races have been slow to mix geographically and genetically. Within *A. ater*, the nuclear genetic variation corresponded to the division into the subspecies *A. a. ater*, *A. a. ruber* and *A. a. rufus*, which was earlier established based on mitochondrial sequences and subtle anatomical differences. *Arion a. rufus*, whose distribution is centred on the British Isles, was common in the German part of the town but absent from the Polish side; this indicates that its introduction dates from after 1945, when the town was divided by the new border.

Keywords: *introgression, hybridisation, microsatellite,* Arion rufus, *introduced species*

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Testing monitoring method for *Arion vulgaris* and *Krynickillus melanocephalus* (Gastropoda: Arionidae & Agriolimacidae)

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Arion vulgaris Moquin-Tandon, 1855 and *Krynickillus melanocephalus* Kaleniczenko, 1851 are highly invasive slug species in Latvia. A monitoring method has been developed for the official monitoring of these slug species. According to this method, slugs are counted in 10 × 2 m area plots and the degree of invasion in score points from 0 to 5 is determined by the number of counted slugs. In daily monitoring, this method is used once a year by recording the accounting time, habitat data and weather data. To test the suitability of this method, the method was tested in the 2020 season by counting slugs for 15 days. The counting was conducted in three localities in Dobele city (Latvia). Slugs were counted three times each evening at 20:00, 21:00 and 22:00. In parallel, temperature on the soil surface as well as the presence of dew were recorded. The counting results showed that the number of snails depended on the counting time. Usually per evening the degree of invasion ranged from 0 to 4, and the highest degree of invasion was usually at 22:00. These results clearly indicate that the tested monitoring method to determine degree of invasion of both slug species needs to be improved, adapting the method to the actual behaviour of slug species.

Keywords: *alien species, invasive species, monitoring, slugs.*

Studies on the abundance and spread management of invasive slugs in Lithuania

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Invasive slugs may cause great ecological and economic impacts both in land ecosystems and agricultural crops. The slug Arion vulgaris Moquin-Tandon 1855 (formerly known as Arion lusitanicus auct. Non-Mabille) was detected in Lithuania in 2008 and later was included in the Lithuanian list of invasive species due to its rapid spread and the loss of crops. Despite the fact that various plant protection products were used by the Lithuanian people, the spread of slugs has not been stopped. In twelve years it has spread to 164 localities and in some settlements the abundance of slugs has reached 80-120 ind./m2. Even worse, they are found in large quantities even in some nature reserves.

In response to people complains, we tested available commercial molluscicides and barrier measures under laboratory and field conditions according description of the using instructions. We repeatedly tested two metaldehyde-based (3% and 5%) and one iron phosphate-based (1%) molluscicide baits and compared the effectiveness of barrier measures for slug control (Schnexagon (SXG), copper strip and galvanized sheet metal). Survival of slugs, consumption of food and molluscicide bait, change of slugs' weight and visual effects on the slugs were evaluated. In addition, we conducted a survey of residents in one settlement and found out the most common mistakes they made in trying to control the abundance of invasive slugs.

Our results showed that molluscicidal baits used against adult slugs changed consumption of food only particularly and some slugs even laid eggs. Also our study did not reveal increased mortality of slugs. The analysis of the different barriers showed different efficiencies. SXG was the most efficient (72%, comparing with control), copper strip was less effective (58%), and the efficiency of galvanized sheet metal was not confirmed at all.

After analysis of all these data we hope that use of baits in early spring with addition of all other measures later can be more effective and prepared a plan for A. vulgaris population testing control in one settlement of Lithuania.

Key words: *Arion, control, invasive, slugs.*

INVASIVE SPECIES

POSTER (7)

Anthropogenic drivers of molluscs dispersion in tributaries of the Vistula and Odra rivers with different degrees of secondary salinisation

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Salinisation that is triggered by human activity within the catchment such as land development, agriculture, discharge of industrial liquid or solid waste and mining, is called secondary salinisation. Secondary salinisation has become a hot spot internationally due to its adverse effects on freshwater ecosystems. In the Upper Silesian Coal Basin (USCB) the extraction of hard coal to the earth's surface is connected with the necessity to pump out underground mine waters that are highly mineralised and contain heavy metals and radioactive nuclides. The survey was carried out in 2010-2021 in the secondary salinised tributaries of the Vistula and Odra rivers (USCB) including the Potok Gromiecki and Potok Goławiecki, currently the most secondary salinised rivers (up to 36.1‰) in the world impacted by hard coal mine waters. The objectives of the survey were to analyse the structure of the mollusc communities including invasive alien species and to determine the most important environmental factors impacted their structure in secondary salinised rivers. Our result showed high concentration of chlorides, nutrients and high conductivity, which is a consequence of the discharge of mine waters from the coal mine dewatering system into the rivers. The unionid mussel *Anodonta anatina* occurred only in one section of secondary salinised tributatry. The maximum density of *Potamopyrgus antipodarum* ranged up to 25130 individuals/m^2 and *Physa acuta* up to 724 individuals/m^2. Canonical correspondence analysis showed that conductivity and concentrations of nutrients in the water were the most predictive parameters impacted the structure of mollusc communities. Tributaries of salinity even up to 25.8- 36.1‰, constitute new habitats for euryhaline species and may create new migration routes for invasive alien species. In secondary salinised rivers, native mollusc species are replaced by invasive alien species, more tolerant to water pollution, including other invertebrates: *Gammarus tigrinus*, native to North America and Ponto-Caspian *Dikerogammarus villosus*.

Keywords: *salinisation, rivers, invasive alien species*

Funding: This research was partially supported by the Ministry of Education and Science, Poland and by the University of Silesia in Katowice, Poland (the Fast Track Grants)

Contrasting effects of climate change on potential distribution of alien species *Cernuella virgata* and *Hygromia cinctella*

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Predicting impact of global climate change on the current and future distribution of alien or endangered species is often a subject in macroecological studies. Only a few were devoted to land snails. Spatial distribution modelling was used to construct European and global potential ranges of *Cernuella virgata* and *Hygromia cinctella* based on current and future climate scenarios. Both species continue to spread northwards from the Mediterranean area. Under the current climate scenario, most presently occupied areas in Europe are also at high probability of future occurrence of these species. However, they will experience contrasting scenarios under four future climatic conditions. *C. virgata* may significantly increase its potential distribution, due to rising temperatures and its weak fluctuations. Global warming, along with morphological and physiological adaptation to dry conditions and the ability to passively disperse, may facilitate the invasion of this species into new regions of the world. In *H. cinctella* no significant change in the geographical distribution of colonisation-prone areas were found. Precipitation in the driest quarter and temperature seasonality will be key factors limiting its future distribution. Understanding of colonisation patterns can help better manage these invaders and formulate policies for their control. This is especially important for *C. virgata*, a serious agricultural pest in southern Australia, where it causes severe economic damage to cereals; yields are reduced, harvest machinery becomes clogged, and grain becomes polluted. Cattle are repelled from grazing plants with contaminated slimy deposits. Effective regulatory strategies focused on reducing human-facilitated propagation and the movement of this species, as well as close monitoring and preventive approaches, are crucial. E.g. in the USA, Canada, China *C. virgata* is on quarantine lists. Shipments contaminated with it are not accepted by other countries. This work was partly supported by the National Science Centre, Poland (Narodowe Centrum Nauki, Polska) under Grant number 2016/21/B/NZ8/03022.

Keywords *bioclimatic variables, emission scenario, range shift, invasive species.*

From the Mediterranean to Patagonia: studying *Rumina decollata* (Linnaeus 1758), a non-native snail in Argentina, through a citizen science project

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Rumina decollata is native to the Mediterranean region but has a worldwide distribution due to accidental or voluntary introductions in several countries of Asia, Africa and America. Its biological characteristics (facultative self-fertilization, high reproductive potential, omnivory and xeroresistance) favored the establishment and colonization in new environments. In Argentina, it was reported in 1988 in Buenos Aires city and had expanded its distribution in the central region. It is considered an invasive species and crop pest in several countries and, although the impact on natural systems is poorly studied, there is evidence that *R. decollata* could negatively affect native fauna. Besides, it was established that *R. decollata* is a potential host of the cat parasites *Toxocara cati* and *Aelurostrongylus abstrusus*. Therefore, *R. decollata* could affect biodiversity, agriculture and health. The aim of our study was to update the distribution of *R. decollata* in Argentina, get information about the impact of this species, and obtain live snail samples for genetic studies. We carried out a citizen science project, publishing a survey on social media asking the general public to inform the location and additional data such as habitat, food preferences, weather conditions, and damage caused. As a result, we got over 600 responses which revealed that it inhabits a broad area of Argentina (16 provinces from Misiones to Patagonia) with 70.61% of the records from Buenos Aires province. Regarding habitat, 82% reported it in peridomiciliary places mainly associated with vegetation (51.2%) and humid conditions (75.2% in rainy days). Concerning food preferences, 33.16% mentioned it consumed plants and 20.19%, cat and dog feces. Our data revealed that *Rumina decollata* is spreading fast in our country. Biological and genetic studies are needed to determine its potential as an invasive species.

Keywords: *non-native snail, invasions, citizen science.*

Invasion risks of *Orientogalba viridis* (Lymnaeidae) in Europe: susceptibility to Fasciola hepatica (Trematoda) and life-history traits under experimental tropicalized settings

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The invasion of freshwater snails, commonly associated to human activities, usually have negative effects on native species or disease transmission. The family Lymnaeidae is a commonly introduced group of freshwater snails with several species displaying a multi-continent distribution. Lymnaeid snails are responsible for fasciolosis transmission worldwide, a parasitic disease that causes severe public and veterinary health problems, also heavily affecting national economies. Recently, the Asiatic semi-amphibious lymnaeid *Orientogalba viridis* was first sighted in Deltebre, southern Spain. We sampled 100 individuals at two different sites and established a laboratory population to test their susceptibility to French *Fasciola hepatica* as well as several demographic parameters using weekly intervals up to 20 weeks. Two different infection settings were applied using amphibious (humid mud, n = 15) and fully aquatic conditions (n = 30). In both cases, *F. hepatica* miracidia were able to infect *O. viridis* with the same prevalence of 73.3% and very similar mean parasite intensity of 20.1±8.1CI (amphibious) and 20.6±5.5CI (aquatic). The experimental population of lab reared *O. viridis* under tropicalized conditions (26-28°C) reached sexual maturity at two-weeks old when egg laying started and remained uninterrupted. At least two reproduction peaks were observed at weeks four and ten with an overall 95% hatching probability. After 20 weeks, the population showed 86% of survivorship and a natural increase rate of 0.85. Our results show that *O. viridis* constitute an actual risk of expanding its distribution in southern Europe. With the temperate-adapted lymnaeid *Galba truncatula* eventually retreating up north in an eventual temperature rise as one of the climate change future scenarios, *O. viridis* may occupy its niche in the transmission of *F. hepatica* in southern Europe.

Keywords: *Lymnaeidae, disease transmission, reproductive capacity, invasion*

Self-fertilization depression in an introduced population of the land snail *Rumina decollata* (Linnaeus 1758).

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Rumina decollata is a hermaphroditic terrestrial gastropod native to the Mediterranean region and introduced in many countries of the world. In Argentina, this species was first recorded in the 1980s. Although the current distribution is restricted to urban and peri-urban areas, it is expanding fast and is likely that it will colonize natural environments where it could affect native biodiversity and agriculture. Its high resistance to extreme climatic conditions and its omnivorous diet, together with its reproductive characteristics, favours the colonization of different environments. *R. decollate* has a high reproductive potential and facultative self-fertilization. The aim of this ongoing work is to study self-fertilization and its effect on fecundity (number of eggs per hatch) and fertility (proportion of eggs hatched) over two generations in an introduced population in Argentina. The parent generation (PG) consisted of 80 juveniles kept isolated until natural death. The 100% of the snails laid eggs by self-fertilization proving the high prevalence of this mode of reproduction in this species. In the F1 generation, 80 hatchlings from self-fertilization of the PG were randomly selected and assigned to different reproductive treatments: T1 (Forced self-fertilization: 40 isolated snails) and T2 (Self or cross-fertilization: 40 snails kept in pairs). The number of eggs per hatch and the proportion of eggs that hatched was significantly lower in the second generation of forced selfing (F1) than in PG. Considering F1, the number of eggs per hatch did not differ between reproductive treatments but the hatching proportion was significantly lower in forced self-fertilizers. The results obtained show evidence of self-fertilization depression in this species. Therefore, cross-fertilization may play a more important role than expected. Improving the knowledge of the biology and reproduction in *R. decollata* is crucial to determine its potential as an invasive species and to develop accurate control strategies.

Keywords: *self-fertilization, cross-fertilization, inbreeding depression, reproduction, invasive potential.*

Sex ratio in invasive freshwater bivalve species: a meta-analysis

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The comprehension of demographic parameters of invasive bivalve species is fundamental to achieve successful management strategies. Sex ratio is a central parameter of population structure, directly influencing survival, reproduction and abundance, and thus, knowledge on the proportion of sexes can help understand populations of invasive bivalves, predict future scenarios and mitigate invasion. We performed a systematic review and meta-analysis to (i) understand how sex ratio varies among invasive freshwater bivalves and to (ii) assess the effects of seasonality and temperature on the sex ratio of the golden mussel, *Limnoperna fortunei*, an invasive species in South America. We examined scientific publications and the gray literature using Dimensions, Google Scholar, Lens and Periódicos Capes with structured and unstructured searches, combining different terms restricted to invasive and wild populations of adult freshwater bivalves. We assessed heterogeneity in articles using I^2 and Q statistics. We compared the proportion of females among species and the effects of seasonality and temperature on the proportion of golden mussel females using GLMM. We found information for five invasive species in 1600 documents. We included 19 articles in the systematic review and 18 in the meta-analysis. Sex ratio was 1:1 in four species of invasive bivalves, *Dreissena bugensis*, *D. polymorpha*, *L. fortunei*, *Sinanodonta woodiana*, and female-biased in *Corbicula fluminea*, which influenced the overall sex ratio (proportion of females = 0.55, CI 0.53 – 0.58). According to the meta-regression, seasonality was important on sex ratio of the golden mussel, with the greatest proportion of females found in the winter and autumn. Temperature presented a negative, but non-significant, effect on the proportion of females. Our results suggest similar proportion of sexes among most freshwater invasive species studied and seasonality influencing the golden mussel sex ratio. Different environmental factors may influence local sex ratio, suggesting space-time variation.

Keywords: *biological invasions, golden mussel, management strategies, population ecology, systematic review*

Study of biofouling on an offshore rig in the Baltic Sea

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Biofouling is called “lessons from nature”. For as long as we can remember, man has struggled with the problem of unwanted biofouling of immersed elements. In modern times, biofouling on artificial structures has become a transfer vector of invasive species. “Artificial islands” become a kind of “hitchhiker’s squats” that allow their further successful dispersion. Currently, governments and industry spend more than 5.7 billion USD annually to prevent and control unwanted marine biofouling. However, this problem has still not been efficiently resolved. The Baltic Sea is defined as a “time machine” for the future coastal ocean, as processes occurring in the Baltic Sea are related to future changes. Our study describes the biofouling community at 12 sites located at different depths on the legs of the “Baltic Beta” oil platform that resulted in finding a maximum of 1,300 individuals on 400 cm-2. We analyzed spatial distribution of dominant marine organisms living on a steel platform surface, their abundance and mass. Biofouling assemblages reached a thickness of about 50 mm at each sampling site as a result of the stratified fouling process. Inner layer was formed by *Mytilus trossulus*. Our work showed no significant difference in the benthic samples mass among different depths or cardinal directions of the rig columns. Finally, our research can help predict offshore biofouling on other devices in the Baltic Sea, control invasive species and estimate environmental load. Ecological and experimental research on existing offshore constructions may be an interesting alternative to studies conducted close to the mainland. The lesson we can learn from our “Baltic studies” is that the level of the Baltic anaerobic zone is really a “dead zone” even for invasive ubiquitous organisms below 50 m in this region.

Keywords: *marine growth, biomass, hydrodynamic efficiency, alien species.*

MONITORING OF MOLLUSK POPULATIONS

STANDARD PRESENTATIONS (2)

Effect of professional harvesting on intertidal mussel beds. An experimental approach.

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The Mediterranean mussel, *Mytilus galloprovincialis* is a frequent and abundant species in the intertidal shores of the Atlantic coast of the Iberian Peninsula. Intertidal beds of *M. galloprovincialis* provide habitat for many species and therefore is considered a relevant ecosystem engineer. Moreover, this mussel constitutes an important economic resource and is cultured extensively in the North-west of the Iberian Peninsula. However, the culture of *M. galloprovincialis* is sustained by the collection of juveniles from natural shores that posteriorly are grown on hanging ropes till they reach the commercial size. Thus, due to the great demand of mussels for cultivation many tons of juveniles are removed from the field every year.

The objective of this study was to explore the effect of professional harvesting on intertidal mussel beds and its associated biodiversity. To achieve this, professional harvesting was simulated on two rocky shores of North Portugal. At each shore, 24 plots (70x70 cm) were selected and mussels were removed from 12 of these plots simulating a harvesting event. The remaining 12 plots were not manipulated and considered as control. Three different sampling dates were considered to follow the recovery of mussel beds and its associated fauna, i.e. 1, 2 and 4 months since the removal date. At each sampling date, the abundance of mussels and other organisms were explored on 4 removal and 4 control plots. Results showed a slow recovery of mussels, with significantly lower percentage of cover on the removal plots than in controls at each date. Moreover, the total number of species remained lower on removal plots than in controls, with many exclusive species on the latter. Short-term recovery of mussel beds (i.e. 4 months) is very limited after harvesting and the diversity of the assemblage is also significantly reduced.

Keywords: *Mytilus galloprovincialis, professional harvesting, biodiversity, mussel abundance.*

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Mollusks in the rural green belt of Vienna: continuities and changes

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The mollusk fauna in the rural green belt of Vienna belonging to areas subjected to the agricultural and rural development program of the EU has been studied from 2020-2021. Vienna potentially inhabits about 180 species of molluscs, 160 of them snails and slugs, another 20 mussels. Samples were taken in about190 sites. Additionally, literature and unpublished data of several working groups of the last 30 years were taken into consideration. The least mollusc diversity was found in arable land in the eastern and southern parts of Vienna. The mollusc fauna there consisted mainly in drought-tolerant euryoecious and invasive gastropods, the latter in some cases only introduced in the last decades, e.g. *Arion vulgaris*. In these areas a higher diversity was only located in semi-ruderal habitats like shelter belts and waysides. The Danubian floodplains, which once inhabited a species-rich mollusk fauna, suffered from massive changes in hydrology caused by stream control, climate change and invasive species. Some typical aquatic and wetland species e.g. *Theodoxus danubialis* therefore became extinct, while others, once wide-spread, are now limited to a few number of sites like *Viviparus contectus*. The gastropod fauna of the river Danube itself changed the most within the last 30 years, as invasive aquatic species like *Corbicula fluminea* became dominant. The highest diversity was found in various habitats of the Vienna Woods and accompanying areas. Within forests, typical east Alpine species like *Aegopis verticillus* could be detected. But also, more specialized species like spring snails, e.g. *Bythinella austriaca* could be recorded. Both wet meadows and spring fens as well as steppe areas and vineyards are home to several endangered species, e.g. *Chondrula tridens*. Therefore, the Vienna Woods and adjacent areas can be assumed as the area with the highest continuity concerning its mollusk fauna in Vienna.

Keywords: *Vienna, City fauna, Mollusca.*

MONITORING OF MOLLUSK POPULATIONS

POSTERS (5)

Contribution to the land snail fauna of olive orchards in Crete (Greece)

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Cultivated land is rarely surveyed for land snails. In this study, we investigated, for the first time, the land snail fauna of olive orchards situated in western Messara valley in Crete (Greece). We surveyed bimonthly, from November 2019 till October 2020, 16 olive orchards located in two agroecological zones, i.e. hilly and plain, regarding the occurrence of land snails. The α-, β- and γ-diversities were recorded and richness differences between agroecological zones were investigated. We found 17 species belonging to 16 genera and seven families, while two more species belonging to the genera *Mastus* (H. Beck, 1837) and *Albinaria* (Vest, 1867) were further identified. The most common species found in all the olive orchards were *Cornu aspersum* (O.F. Müller, 1774), *Cantareus apertus* (Born, 1778) and *Eobania vermiculata* (O.F. Müller, 1774). *Pseudoxerophila bathytera* (Westerlund & Blanc, 1879) was only found in one olive orchard in the hilly zone. *Caracollina lenticula* (Michaud, 1831) was reported for the first time in the area. Three species endemic to the island of Crete were identified. On average, olive orchards in the hilly zone host more species that the plain ones. Species composition (i.e. β-diversity) is mainly shaped by species replacement among the olive orchards. The olive orchards under study host ca. 50% of the land snail species of the wider area. Reported richness differences appears to relate to altitudinal differences, although further investigation is required. Geographic proximity of the studied olive orchards hampers strong differences in species composition. This is a first attempt to understand the impact of human (agricultural/farming) activities on land snails in the Mediterranean region. We highlight the importance of cultivated areas, such as olive orchards, as sites of increased land snail diversity. Further research is required to evaluate land snails as potential indicators of the impact of agriculture on biodiversity.

Keywords: *diversity metrics, agroecosystems, gastropods, cultivations, human impact*

Acknowledgments: This research is co-financed by Greece and the European Union (European Social Fund-ESF) through the Operation-al Programme «Human Resources Development, Education and Lifelong Learning 2014-2020» in the context of the project "Impact of different management systems and spatial factors on the biodiversity of olive agroecosystems" (MIS 5048171).

Endangered freshwater mollusk *Unio crassus* Philipsson, 1788 in the Republic of Moldova

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The *Unio crassus* Philipsson, 1788 is an endangered species (IUCN Red List), inhabiting running waters with high dissolved oxygen content; it is sensitive to water pollution and general degradation of rivers ecosystems. Many synonyms were given to this species due to the high plasticity of shells morphology, caused by biotic and abiotic factors. However, study of mollusks with molecular data from the territory of Ukraine and Russia (Klishko et al. 2017) confirms the validity of the classification by Zhadin (1952). This was applied for Moldova situated between Romania and Ukraine. The sampling was performed during 2009–2020, in main rivers Dniester and Prut, at 14 stations in the Dniester and 17 stations in the Prut, from a depth 0.3–1.5 m by the Petersen and Ekman grabs, bottom scrapers, dredge and by hand. The mussels were determined by standard identification keys (Zhadin, 1952, Starobogatov et al. 2004). The live specimens of *U. crassus* was found in one point of Dniester river and six points of Prut river. Part of the living mollusks were returned to the river, another part (68 specimens) were preserved for detailed analysis and measurements. The highest density and biomass was recorded at Criva in sample collected by grab - 440 ind./m^2 and 6805 g/m^2 correspondingly. The same data for sampling by hand was recorded in Sculeni - 13 ind./m^2 and 224 g/m^2 correspondingly. The maximum frequency - 24% in Sculeni. The length of the shells of live individuals ranged from 4.0 cm to 7.5 cm, with average length 5,31 cm, maximum length of empty shells is 8.5 cm. As in other European countries in R. Moldova there is a declaine of *U. crassus* populations due to pollution and hydrotechnical constractions. Thus, information about distribution of endangered species makes a contribution to conservation of this mollusk.

Keywords: *Unio crassus, Dniester, Prut, distribution.*

Acknowledgements: This study was conducted within the following projects: 09.832.08.07A,11.817.08.13F, 11.817.08.15A, MIS ETC 1150, MIS ETC 1676, BSB165, 15.817.02.27 A, 20.80009.7007.06

Introduction to the study of the population structure of *Cymbula safiana* (Lamarck, 1819) on the littoral of the province of Malaga (southern Spain)

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Cymbula safiana (Lamarck, 1819) is listed as an endangered or threatened species in the Barcelona Convention of 1993; a strictly protected species in Annex II of the Bern Convention and an endangered species in the Red Book of Invertebrates of Andalusia. It is one of the two giant limpets of the Mediterranean. However, its ecology and population dynamics and structure are still unknown. In this study, an approach to the analysis of the populations or subpopulations and their structure of this species on the coast of the province of Malaga (Alboran Sea) was carried out in two areas with differential characteristics: the beach of La Araña and the coastal area of the mouth of the Guadalhorce river. Significant differences were found between the subpopulations in these areas, probably associated with the characteristics of the environment. In addition, new data are provided on its biology and ecology, and on its current distribution area in the province of Malaga.

Keywords: *Cymbula safiana, Alborán Sea, ecology, population structure, distribution area*

Land snails of Raden Soerjo Nature Tourism Park, East Java, Indonesia

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Raden Soerjo Nature Tourism Park is a conservation area located on the slope of Mt. Arjuna-Welirang, East Java, Indonesia. Previous study recorded only three species in the mountain. The present study aims to reveal the land snail diversity in the Raden Soerjo Nature Tourism Park. We collected both live snails and dead shells from 10 plots of 10 x 10 m^2. Sampling was carried out by combining visual observation and sorting-sieving 5kg per plot of soil and leaf litter samples. A total of 159 specimens belonging to eight families and 13 species were collected. They consist of *Bradybaena similaris, Coneuplecta sitaliformis, Helicarion albellus, Japonia ciliocinctum, Kaliella barrakporensis, Landouria* sp, *Liardetia convexiconica, Liardetia platyconus, Microcystina nana, Paraboysidia boettgeri, Parmarion pupillaris, Philalanka micromphala*, and *Philalanka thienemanni.* Shannon diversity index shows 1.99, the dominance index is 0.19, and the evenness index is 0.78. Although the Raden Soerjo Park is a conservation area, the rest of Mt. Arjuna-Welirang's slope is dominated by plantation. Thus the canopy coverage in the Park needs to be maintained or moreover increased, and human activity in this area needs to be minimized. These are efforts to conserve the species diversity in the area and prevent the increase of invasive species coming from the plantations nearby.

Keywords: *Gastropod, Terrestrial, Nature Tourism Park*

Mass stranding of *Argonauta nodosus* Lightfoot, 1786 (Cephalopoda, Argonautidae) in southeastern Brazil

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Argonauta Linnaeus, 1758 is composed by five pelagic octopuses species. The genus is distributed in tropical and temperate regions and characterized by the thin white shell produced solely by females. Specialized tentacles with the function of storing eggs and hydrostatic structures which enable neutral buoyancy are also present. Unlike other molluscs, female argonaut are not attached to the shell, which are popularly known as "paper nautilus". They show extreme sexual dimorphism, males being 10-15 times smaller than females and do not produce a shell. Isolated mass stranding events have been recorded for *Argonauta argo* Linnaeus, 1758 and *A. nodosus* Lightfoot, 1786 in different regions of the world. These are similar species but *A. nodosus* has a shell with more protrusions or nodes with radial and transverse series of intersections while *A. argo* has sinuous radial ridges, narrow branching, and a V-shaped shell opening. Both species are listed from Brazil but based on punctual records and mostly of empty shells. Between January and February 2021, a mass stranding of *Argonauta nodosus* was observed in the upwelling region of Cabo Frio, southwestern Atlantic. Many female specimens were observed alive in groups, many in senescent stage of life. This is the first record of a mass stranding event of *A. nodosus* along more than 40 years of scientific research and marine biodiversity and fishery monitoring in the region.

Keywords: *Octopoda, Coleoidea, argonaut, octopus, paper nautilus.*

PALEONTOLOGY

STANDARD PRESENTATIONS (2)

Crisis or Change? Unlocking biodiversity change from mollusc time series

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Fossil molluscs are an ideal tool to investigate ecosystem and landscape evolution and biodiversity turnover. Species represent a wide spectrum of ecological settings; they are usually well definable and their hard shells preserve well in the fossil record. Furthermore, their shells records information on ambient settings through their isotope geochemical signatures. Hence, they enable us to understand the context and driving processes of past turnover events. Understanding these events is imperative in order to establish whether the nature and rates of turnover today are beyond natural baseline conditions and to assess whether we are in an extinction crisis. However, reconstructing biodiversity turnover from fossil time series is fraught with difficulties as successions are often compromised by uneven preservation and common reworking/time averaging.

In this contribution I will present a novel approach based on taphonomical signatures and ecological compatibility to disentangle mollusc successions from two Late Quaternary successions in order to produce reliable time series of biodiversity change. A Late Pleistocene (MIS5) time series from borehole Castricum (The Netherlands) contains at least three faunas and provide novel insights into the Late Pleistocene evolution of shallow marine biota and ecosystems in the southern North Sea Basin. Unmixed mollusc successions from Late-Pleistocene-Holocene deposits from an offshore core on the Black Sea shelf off Romania shows the dramatic changes in that basin across the basin at the Pleistocene-Holocene transition.

The novel unmixing approach bridges ecological to geological time scales. It has the potential to establish natural baseline rates of turnover, investigate resilience and will shed light on the nature and magnitude of current biodiversity turnover.

Keywords: *molluscs, biodiversity, turnover, resilience, time series.*

Trends and patterns in the European Cenozoic land snail record

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The evolution of the European Cenozoic terrestrial gastropod faunas is characterized by a complex pattern of diversification, turnover, extinction and immigration events. Based on a critical review of a literature-based dataset comprising 1640 species from 609 sites, we calculated net diversity through time (expressed as species, genus and family richness) and β-diversity (as species, genus and family turnover). Within these data, we recognize major disruptive phases, with turnover events at the Ypresian–Lutetian and the Eocene–Oligocene boundaries, as well as extinction events at the Oligocene–Miocene, Burdigalian–Langhian Pliocene–Pleistocene boundaries. Phases of diversification during the Lutetian, Burdigalian and Pliocene, in contrast, seem to be linked to phases of relative climate stability. At least five immigration events are reflected by the appearance of exotic elements in European faunas. Many of them correlate with the formation of terrestrial pathways and major migration events in mammals. The correlation of the observed patterns with global climatic events will be discussed.

Keywords: *terrestrial gastropods, extinction, diversification, immigration*

PALEONTOLOGY

SHORT PRESENTATIONS (2)

Reconstructing Plio-Pleistocene hydrosystems of the Northern Turkana Depression (East African Rift System) from the study of fossil freshwater mollusk communities

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The Turkana Depression of the East African Rift System in Northern Kenya and South-Western Ethiopia holds one of the most complete and well-documented Cenozoic continental fossil records worldwide, including important fossils of early hominins and associated vertebrates. Previous paleoenvironmental reconstructions of the depression were inferred essentially from terrestrial vertebrate faunas and paleolandscapes, leaving freshwater environments and their associated ecosystems largely unaddressed. African Cenozoic freshwater mollusks have left abundant fossils in the Turkana Depression and are considered to be good biostratigraphic indicators. Their shells display periods of faunal stability interspersed with periods of faunal turnover, but to what extent faunal turnover events and morphological changes relate to variation in sedimentary landscapes and lake-level fluctuations remains unclear. Here, we explore this relation. First, we developed a taxonomic framework on Plio-Pleistocene freshwater mollusks to characterize stratigraphically well-constrained fossil assemblages. Second, we analyzed sedimentary facies to independently reconstruct the succession of depositional settings and associated aquatic environments through time. Finally, we linked stratigraphically, and subjected the resulting data to correspondence analysis. Our preliminary dataset, which is still under expansion, contains over 10,000 specimens belonging to 13 genera, attributed to 8 faunistic assemblages that coincide with substantial variation in water level. These initial analyses at the genus level displayed three main groups of assemblages, which largely correspond to different lake stages and reflect the main changes in faunistic composition. Furthermore, they revealed that highstand lacustrine environments with wave-dominated shorelines presented more diverse mollusk assemblages than river-dominated lowstand environments. Nevertheless, further analyses at the species level and at a higher temporal and stratigraphic resolution are required to shed light on key variables that link freshwater mollusk diversity with paleoenvironmental changes in the Turkana Depression, particularly at turnover events.

Keywords: *Paleoecology, East African Rift System, Plio-Pleistocene, Freshwater mollusks*

A taxonomic revision of fossil freshwater pearl mussels (Bivalvia: Margaritiferidae) from Neogene-Quaternary rivers of Southeastern Europe

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Margaritiferidae is a freshwater bivalve family, which has been existing since the Mesozoic. Here, we present a revision of several nominal taxa of fossil freshwater pearl mussels that were described from the Neogene-Quaternary deposits of the Dniester and Prut river valleys. Morphological data and phylogenetic modeling show, that these nominal taxa belong to the genus *Pseudunio* and are junior synonyms of *P. flabellatiformis* (Grigorowitch-Beresowski, 1915). The new synonymy is proposed as follows: *Margaritifera (Pseudunio) moldavica* Chepalyga, 1964 syn. nov., *Margaritifera (Pseudunio) robusta robusta* Chepalyga, 1964 syn. nov., *Margaritifera (Pseudunio) robusta speensis* Chepalyga, 1964 syn. nov., and *Margaritifera (Pseudunio) robusta tirassica* Chepalyga, 1964 syn. nov.

All these fossil nominal taxa were determined on the basis of minor differences in the shell shape and size, hinge structure, and stratigraphic position. Finally, we suggest an updated phylogenetic scheme of the genus *Pseudunio*, which contains five valid species: *P. marocanus* (Pallary, 1918) [Eocene – Recent, Morocco], *P. auricularius* (Spengler, 1793) [Pliocene – Recent, Southern and Western Europe], *P. homsensis* (Lea, 1865) [Pliocene – Recent, Orontes and Orontes and Nahr al-Kabir basins], *P. flabellatiformis* (Grigorowitch-Beresowski, 1915) comb. rev. [Pliocene – Late Pleistocene, Dniester and Danube basins, extinct lineage related to *P. auricularius* and *P. homsensis*], and *P. flabellatus* (Goldfuss, 1837) comb. rev. [Miocene, paleo-Danube Basin, stem lineage, MRCA of *P. auricularius* - *P. homsensis* clade].

Keywords: *Pseudunio, Margaritiferinae, Quaternary, paleo-Danube Basin, paleo-Dniester Basin, Black Sea, Moldova.*

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PALEONTOLOGY

POSTER (1)

Narrowing the time of evolution of the eulamellibranch gill anatomy in Unionida - new Late Triassic findings from Poland

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Phosphatization is a common way of preservation of the soft tissues of animals. Within bivalves this process ensured fossilization of gills in several lineages. The anatomy of gills (the presence of calcium concretions in them) in two related groups – Trigonida and Unionida – likely facilitate their mineralization.

Gills of the members of Unionida serve as the gas exchange and feeding organ and a parental care tool. Marsupia in gills of the females of all Recent unionoids are the place where embryos develop into parasitic larva (a likely adaptation to freshwaters). All the members of Unionida have today eulamellibrach gill anatomy - the tissue transversally connects gill filaments, what result in a basket-like construction (this facilitates parental care). Thus, one may expect this character already existed in their last common ancestor – probably before the Middle Jurassic, when advanced unionoids already existed. Gills which filaments that lack these connections (filibranch anatomy) are present in both: all known, fossil and living trigoniids (the accepted ancestors for Unionida), and early Late Triassic (Carnian) one of the oldest unionoid *Silesunio parvus*. The time period for evolving the eulamellibranchy (possibly followed by parental care) may thus be restricted to between early Late Triassic and Middle Jurassic.

New findings from Middle Norian and Rhaetian of Late Triassic of Poland may complete this picture. Although parts of their gills are preserved, their anatomy is unsolved (possibly due to taphonomy process). They lack typical for eulamellibranchy residues of transverse tissue connections, however they also lack observed in decaying filibranch gills fan-shaped organization of (at least some) filaments.

Keywords: *Unionida, Late Triassic, phosphatization, gills, evolution*

Acknowledgments: All the specimens are stored in Institute of Paleobiology, PAS

QUATERNARY MALACOLOGY

STANDARD PRESENTATIONS (4)

Mollusc assemblages and paleoenvironmental implications during the Holocene in the Elefsis Bay (Saronikos Gulf, Greece)

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The Gulf of Elefsis is a geomorphological embayment located in the northernmost part of the Saronikos Gulf in central Greece. A 342 cm long marine core containing molluscs was retrieved from the deepest part of the gulf. This study focused on assessing the mollusc assemblages and their environmental footprint over time. The methods used included qualitative - quantitative - statistical analysis of the faunal specimens. A total of 10500 specimens were collected, which resulted in 6661 individuals belonging to 45 mollusc genera and 47 species. Four faunal assemblages were distinguished from bottom to the top of the core: the oldest Assemblage D ("fossil") consists of rounded and possibly calcified specimens; Assemblage C (freshwater - oligohaline environment) includes freshwater-brackish living species such as *Theodoxus* sp. and *Hydrobia* sp. and low values of faunal indices (Taxa (S), Shannon-Wiener (H'), Density); Assemblage B (open lagoon) consists of the brackish living species *Cerastoderma glaucum*, *Mytilaster marioni*, *Hydrobia* sp. and intermediate values of faunal indices; Assemblage A (marine) comprises marine living species (mainly *Bornia sebetia*, *Corbula gibba*, *Myrtea spinifera*, *Nucula nitidosa*, *Timoclea ovata*, *Bittium reticulatum* and *Turritella communis*) and high values of faunal indices. The resulted well constrained assemblages provided important ecological data to be considered as a set of environmental indicators. The methodology followed herein could be applied as a valuable alternative or supplementary tool for (paleo)environmental researches.

Keywords: *Quaternary, Elefsis, molluscs, faunal assemblages, paleoenvironment.*

Molluscs of archaeological sites from the Jabron valley (SE France)

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Molluscs from three archaeological sites from the Jabron valley (Var, Southeastern France) were investigated for palaeoecological purpose. The studied malacological remains were collected from Upper Pleistocene and Holocene deposits rich in archaeological artefacts including lithic, bone and charcoal remains. Alluvial deposits were studied at Les Prés de Laure (27-23 ka cal. BP), while lacustrine deposits were identified at Les Condamines-sur-Trigance (c. 18 ka cal. BP). The rockshelter sequence at La Baume de Monthiver is dated from the Late Pleistocene (14-13.6 ka cal. BP) to the Early Holocene (8.2-7.9 cal. BP), however younger deposits may also occur. Standard malacological methods were applied. Shells and shell fragments were collected by hand directly from the trenches and/or were extracted from the deposits after wet-sieved on a 2 mm and 0.5 mm mesh. Altogether 21 mollusc species, 816 specimens and 3332 shell fragments were found in the studied sites, with the richest assemblage noted in Monthiver. Although not abundant, mollusc assemblages from the Upper Pleistocene deposits seem to indicate the predominance of arid and open environments during the deposition. The studied area might have been covered by grasslands and steppe-like vegetation at that time as indicated by numerous *Xerocrassa geyeri* accompanied by *Granaria variabilis*. At Monthiver the most abundant species are *Solatopupa similis*, *Chondrina avenacea* and *Chondrina megacheilos*, as well as *Cepaea* cf. *nemoralis* and *Cepaea* sp. In the lowermost part of the sequence *Pyramidula pusilla*, *Truncatellina cylindrica* and *Pagodulina* cf. *pagodula* were also noted. Dry open habitats and some shrublands and open woods seem to have occurred around the site during the human occupation. The results offer perspectives for further palaeoenvironmental studies within this geoarchaeological context.

Keywords: *Upper Pleistocene, Holocene, palaeoenvironment, geoarchaeology, Southeastern France.*

Quaternary continental malacology in Spain: new investigations from a Holocene succession at Rio Galera (Andalusia) reveal the biogeographical history of humid demanding species

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Non-marine mollusc shells are generally abundant and well preserved in Quaternary carbonate deposits. Continental molluscs represent a relevant bio-indicator for reconstructing local to regional environmental history. Calcareous tufa and alluvial sediments provide excellent sedimentary contexts for palaeoenvironmental studies. In Spain, tufa deposits are widespread and have raised interest of geomorphologists for several decades. However, their malacological content remains rarely studied. In the framework of a German-French collaboration, alluvial and tufa sequences in the Baza basin are at the focus of a multidisciplinary approach which includes the analysis of the mollusc.

At Rio Galera, two continuous sedimentary sequences have been sampled. The Holocene molluscan succession shows a significant diversity including the occurrence of two southern Iberian endemic gastropods: *Iberhoratia morenoi* and *Orculella aragonica*. At its bottom, the malacological succession 1 reveals an unstable and xeric environment, which is followed by marshland. Wetland extension reflects a durable aquatic environment with marshy vegetation in adjacent banks. The occasional occurrence of the stygobiont *I. morenoi* indicates a recurrent influx of groundwater. At the top, the mollusc assemblage records the reduction of the wetland and the palustrine vegetation, progressively replaced by xerothermic vegetation. The sequence 2, is characterised by fluvial sediments forming the lower part of the sequence. They are linked to an Early Holocene age and a badly preserved malacofauna with an increased share of terrestrial elements indicating sediment entry from the catchment slopes. These deposits are covered by clayey layers and tufa formation, pointing to an increase in surface stability. Here we have a well-preserved gastropod fauna with high diversity of aquatic species.

The palaeoenvironmental scheme obtained contributes to the knowledge of local Holocene environmental history. Holocene occurrences of hygrophilous species and two vulnerable taxa (*I. morenoi* & *O. aragonica*) highlight the value of considering fossil malacofauna in a biogeographic perspective.

Keywords: *non-marine molluscs, palaeoenvironment, Holocene, Andalusia, Spain*

Who moves and when? Quaternary palaeobiogeography of land snails: a European project

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Quaternary climatic cycles have strongly influenced the diversity and distribution of the terrestrial gastropod fauna. European territories located at the edge of the Pleistocene ice sheets, were particularly affected by this phenomenon. Since the mid part of the 20th century, studies on Quaternary malacofauna have been widely developed in Western and Central Europe, providing a huge amount of information on species past distributions. The Quaternay record is relevant to the current geographic extensions of European species. In recent years, many papers have focused on the location of glacial refugia and possible recolonization pathways during interglacial periods using alternatively or both Quaternary and phylogeographic approaches. The Quaternary malacological record can provide insight into the evolution of the group diversity and associated causes of these variations over a long period of time, as well as on the timing of both species retreat/extension and extinction rates during climatic cycles. Therefore mapping the expansion of land snails over time is an important key to understanding the current status and distribution of species and helping to predict potential distributions with accuracy.

However, until now, few attempts to compile data in this field of research have been proposed and none on a European scale. The project of a "European Quaternary Molluscan Database" aims to provide maps of species distribution at different periods and tables of reliable well-dated malacological counts recovered from Quaternary deposits across Europe. Particular attention has been paid to the time division table in order to avoid as much as possible regional discrepancies in the interpretation of chronological attributions.

Originally developed at the LGP (Meudon, France) the project has received strong support in recent years from the Czech Quaternary malacology group. Today, the database includes 403 sites with Pleistocene and Holocene records distributed from Ireland to Slovakia. Further contributions from other countries are now highly desirable to improve the database and make it a useful tool for the European malacological scientific community.

Keywords: *Land snails, distribution, Europe, Quaternary, database*

TAXONOMY AND SYSTEMATICS

STANDARD PRESENTATIONS (6)

A mitogenomic phylogeny for the Western Ghats–Sri Lanka land-snail genus *Corilla*

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The land-snail genus *Corilla* (Corillidae) is endemic to Sri Lanka and the Western Ghats of India. Considered to be a putative Gondwanan relict, this genus is represented by 11 described species, of which 10 are endemic to Sri Lanka and 1 to the Western Ghats. We present the preliminary findings of a mitogenomic phylogenetic study that seeks to understand the relationships between the Sri Lankan species and the sole extant Indian representative of the genus, *C. anax*. Our dataset consists of DNA sequence data for the 13 mitochondrial protein-coding genes. The taxa sampled are *C. anax*, 9 of the 10 described Sri Lankan species of *Corilla* and the outgroup taxa *Cornu aspersum* (Helicidae), *Halongella schlumbergeri* (Plectopylidae), *Lissachatina fulica* (Achatinidae) and *Sculptaria damarensis* (Sculptariidae).

Keywords: *Corilla, land snail, phylogeny, Western Ghats–Sri Lanka.*

Convergent evolution of *Amphidromus*-like colourful arboreal snails and phylogenetic relationship of East Asian camaenids

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East Asian camaenids are diverse in terms of genus and species numbers, shell morphology and mode of living. This family also includes colourful conical arboreal snail taxa, the shell of which always regards them in the genus *Amphidromus* Albers, 1850. This is the first study in revealing that not all these arboreal snails from Asia belong to *Amphidromus* of the subfamily Camaeninae. The presence of a dart complex comprising mucous glands, a dart sac, an accessory sac and a proximal accessory sac, along with a pronounced penial caecum and molecular phylogenetic analyses revealed that former "*Amphidromus*" *dautzenbergi* Fulton, 1899, "*Amphidromus*" *roemeri* (Pfeiffer, 1863) and "*Camaena*" *mirifica* (Bavay & Dautzenberg, 1908), and one unidentified species belong to *Aegistohadra* Wu, 2004 of the Bradybaeninae. These species have a conical shell with colourful spiral bands and some species have variegated spiral and transverse banding patterns. DNA sequence analyses also revealed that intraspecific variation of colour and banding patterns could not be differentiated by mitochondrial (COI and 16S rRNA) gene fragments. The phylogenetic position of *Aegistohadra* within the East Asian camaenids revealed that the similar appearance in shell morphology, microhabitat use and diet to arboreal snails in the genus *Amphidromus* was homoplastic. Moreover, the presence/absence of a dart complex is also homoplastic and deems unsuitable for suprageneric classification. In contrast, the presence of flagellum and penial caecum is more informative for the classification.

Keywords: Aegistohadra, *Bradybaeninae, homoplasy, suprageneric classification, tree snail*

In situ identification of cryptic marine invertebrates using molecular markers

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The study of cryptic biodiversity is a major challenge in conservation biology. Genetics has greatly contributed to a better understanding (and disentangling) between and within species complexes providing molecular biology-based tool sets for their identification and description. After decades of work, there is a standardized workflow by which researchers may identify cryptic species by using PCR-based techniques such as barcode or other phylogenetic analyses. However, these techniques require specialized equipment usually restricted to molecular biology laboratories. This constrain limits *in situ* species identification and often implies results can only be obtained after several days since sampling. In this study we will show the optimization procedure to differentiate between two sympatric nudibranch species of *Aeolidia* Cuvier, 1798 (Heterobranchia, Gastropoda) using a loop-mediated isothermal amplification (LAMP) based technique. There are some external morphological differences between *A. papillosa* (Linnaeus, 1761) and *A. filomenae* Kienberger, Carmona, Pola, Padula, Gosliner & Cervera, 2016. However, they require a quite trained eye and, once the individuals are preserved, are also indistinguishable. LAMP is a single-tube technique for the amplification of DNA that synthetizes DNA at a constant temperature and, therefore, does not require thermal cyclers. Our results suggest that the species-specific molecular marker designed to amplify the Cytochrome *c* Oxidase subunit I (COI) in LAMP reaction together with a naked-eye visualization procedure, discriminates between the two target species, although some optimization is required to adapt this protocol outdoors. Consequently, LAMP opens the door to bring the lab to the field to identify *in situ* cryptic biodiversity.

Keywords: *Loop-mediated isothermal amplification, Aeolidia papillosa, A. filomenae*, Heterobranchia, Gastropoda.

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Molecular phylogeny and species delimitation of the *Felimida dalli* species complex (Nudibranchia, Chromodorididae)

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Nudibranchs are marine gastropods with a few centimetres in length and can be found in all marine environments. They do not have a shell in the adult life stage and are hermaphrodites. The taxonomy of nudibranchs is traditionally based on features of body colour pattern and internal structures like the radula and the reproductive system. In the recent years, taxonomic studies using genes and an integrative approach resulted in a better delimitation and identification of nudibranch species. The genus *Felimida* includes 31 species. Among them, four similar species from eastern Pacific and Atlantic: *Felimida dalli* (Bergh, 1879) distributed from California to Galápagos Islands; *Felimida punctilucens* (Bergh, 1890) from Florida; *Felimida ghanensis* (Edmunds, 1968) from Ghana and *Felimida edmundsi* (Cervera, García-Gomez & Ortea, 1989) recorded from the Azores to São Tomé and Príncipe. In addition to these four nominals species an additional morphotype was recently found in the southwestern Atlantic, Brazil. The validity of some of these species and possible synonymies remains doubtful due the absence of a detailed comparative study. The objectives of this project are: 1) to test the monophyly this group of species; 2) to delimitate the species based on morphology, molecular phylogeny (COI, 16S and 28S genes) and a species delimitation analysis (ABGD); 3) to identify and characterize species and their geographic distribution. The preliminary results confirm the monophyly of this group of species, indicate a likely synonymy between *F. edmundsi* and *F. ghanensis*, and that the Brazilian morphotype corresponds to an undescribed species. New analyses will be carried out and the implications of the findings will be discussed.

Keywords: *Gastropoda, Nudipleura, Heterobranchia, Integrative Taxonomy, ABGD.*

Small solenogasters causing big problems: molecular data from the family Meiomeniidae (Aplacophora, Mollusca)

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Solenogastres (Aplacophora) have a reputation for their challenging identification and taxonomy. Most solenogasters are epibenthic using their reduced foot to glide on compact substrate or found epizootically in association with cnidarians. However, at least 23 described species are considered meiofaunal, presenting further complication for identification due to their minute size. Meiomeniidae is a family composed of four described species, all of which are meiofaunal and are described exclusively from interstitial habitats. Published occurrence records from this family are limited to off the coast of the U.S. and Bermuda, but our own observations indicate that they inhabit coarse marine sands across the globe. As a fully interstitial family, Meiomeniidae presents an excellent framework to understand the evolutionary shifts that accompany adaptation to life between sand grains. Standard practices in solenogaster taxonomy combine characterization of habitus, sclerites, internal anatomy through histological sectioning, and DNA barcoding, however, due to the small size of these animals, producing an integrative taxonomic dataset is challenging. Past work provides detailed microanatomical data that highlights the issues with species delimitation within this family as descriptions rely on characters found to be taxonomically unstable. Additionally, habitus and sclerite morphology are uniform across the family, making species identification with Meiomeniidae highly problematic. To begin to address the challenges within this family, molecular data are needed. Here we present the first molecular data from several sampling initiatives in the North-East and Western Atlantic and Pacific Ocean. These efforts re-sampled type localities as well as expand upon the known distribution of Meiomeniidae. Our preliminary phylogeny and molecular species delineation reveal higher species diversity and increases the range for the family. Molecular data will help to uncover the hidden diversity within this group while serving as a case study to aid in our efforts to understand interstitial solenogaster taxonomy and evolution.

Keywords: *Aplacophora, Solenogastres, Meiofauna, Taxonomy.*

Solenogastres (Mollusca, Aplacophora) diversity in Corsica: findings of the program “La Planète Revisiteé”

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Solenogastres are a group of marine molluscs that remain relatively unknown, as they usually go unnoticed or are discarded from research due to the elusive nature of their taxonomical study. Most species are known from well-studied areas such as the Antarctic, NW Atlantic and Mediterranean Sea, with nearly all records from type localities. The discovery of new species is common, but less effort is focused on the redescription of known species. Nevertheless, their finding and study is relevant to obtain molecular and updated anatomical data that will help to clarify solenogaster classification, and to understand the early evolution of the phylum. Additionally, advancing knowledge on the real distribution and diversity of the group adds to an increased understanding of marine biodiversity; a fundamental initial step to create or enhance environmental protection figures in specific regions. Led by the Muséum National d'Histoire Naturelle, in partnership with the Collectivité de Corse and the Office Français de la Biodiversité, La Planète Revisiteé programme in Corsica aims to modernise the inventories of Mediterranean taxa. A collection of 48 Solenogastres obtained from these expeditions were sorted based on the habitus and sclerites (SEM and light microscopy) and were grouped into morphospecies. Four were easily identified based on external morphology: *Dondersia festiva* Hubrecht, 1888; *Nematomenia banyulensis* (Pruvot, 1890); *Anamenia gorgonophila* (Kowalewski, 1880) and *Tegulaherpia myodoryata* (Salvini-Plawen, 1988). However, to appropriately place the remaining eleven morphospecies, study of the internal anatomy may be required. Two of the mentioned species, and likely several of the remaining ones, are new records for the French Mediterranean waters. With DNA barcodes for all species and updated morphological information, the study of this collection is contributing to define the biodiversity of the region while expanding our knowledge of solenogaster taxonomy and distribution.

Keywords: *Solenogastres, Mediterranean, biodiversity, taxonomy*

Acknowledgments: The collection is a loan of the Muséum national d'Histoire Naturelle. We are especially grateful to the participants in the expeditions. Thank you to all the partnerships of the programme La Planète Revisiteé. This work was also funded by the NSF award 1846174.

TAXONOMY AND SYSTEMATICS

SHORT PRESENTATIONS (6)

Chitons (Class: Polyplacophora) of the Indian coast: Present status and future needs

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Faunal groups from understudied regions need to be updated using upgraded techniques for better understanding the biodiversity. India with a coastline of 8,129 kilometres and 0.5 million square kilometres of continental shelf, is bestowed with diverse habitats such as coral reefs, rocky intertidal regions, sandy beaches and mangroves, that supports an extensive diversity of marine fauna. The area extending from the Andaman and Nicobar Islands in the East, to Indian mainland and further to the Lakshadweep archipelago in the west is an area connecting many groups of marine organisms from neighbouring seas in the East and West. Despite the large number of studies rising globally, chitons (Polyplacophora) from Indian coast are poorly represented in literature. A literature survey on studies on chitons from the Indian coast is done to assess the history and present status of chitons recorded from the coast. Since the first discovery of chiton in 1906 several novel species and new records of chitons have been discovered from the Indian coast. More than 80 percentage of the studies from the region were based on museum collections and literature. Other studies appear to be opportunistic as part of general faunal surveys. There are no comprehensive works available on taxonomy and distribution studies of chitons from the coast in the past four decades, which can be attributed towards the lack of expertise on chiton taxonomy from the region. Our analysis identifies the shortfalls in chiton research in the country and emphasises on carrying out extensive field surveys, use of integrated taxonomy using SEM and molecular techniques, understanding the ecological dynamics in their microhabitats, and collaboration with global experts will facilitate developing local expertise and better understand this group and their characteristics.

Keywords: *chitons, India, taxonomy,*

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Molecular phylogeny of the crown snail genus *Taphrenalla* (Stylommatophora, Ariophantidae) from Thailand

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Thailand has been recognized as biodiversity hotspots which harbor highly diversity and endemism of land snails. Among Thai malacofauna, the ariophantid snail genus *Taphrenalla* Pholyotha & Panha, 2020 exhibits the peculiar “Crown” shell characteristics in performing the dorsal deep suture and radial channels. As from the surveys in more than 200 localities in Thailand, *Taphrenalla* was found only from southern part of the country and showed high variations of shell sculpture by having varied depth degree of sutures and radial channels that cause doubtful identification. To test the hypothesis whether the shell variables are corresponding with systematic classification and geographic relationships, we analyzed both genital morphology and two mitochondrial (COI and 16S rRNA) plus the nuclear 28S rDNA gene sequencing. Based on morphological results, we found that species diversity of the “Crown Snails” seems to present 11 morphospecies. Interestingly, molecular phylogeny (ML and BI trees) confirmed all morphotypes that were formed as a crown snail clade. Moreover, all members of *Taphrenalla* showed high endemism and were found in limestone areas along the two main mountain ranges in southern Thailand (the Phuket Mountain and Nakhon Si Thammarat Mountain).

Keywords: *Southeast Asia, limestone karst, diversity, endemism, phylogeny*

Mollusc biodiversity of Essaouira dunes (Morocco)

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The Site of Biological and Ecological Interest of Essaouira dunes has an exceptional ecosystem biodiversity, characterized by rich and diversified flora and fauna species with a high rate of endemism and rarity. Our study focuces on a qualitative malacological survey to compare actual inventory with last records, since few studies about mollusc biodiversity were conducted in this site.

In order to cover the majority of the site, 18 stations were chosen according to the variation of ecological factors, such as substrate, type of vegetation, and sea effect. Sampling was done by hand on plants, soil, and litter. Identification was made based on the morphological characters of the shell and the morpho-anatomy of the genital organs of living species collected.

The examination of the malacological inventory revealed the existence of 25 species of terrestrial molluscs; belonging to 21 genera and 11 families. Geomitridea's family is the most dominant by the presence of 11 species. We have also noticed the presence of two groups of species: the first one group is not exigent to the ecological parameters notably *Theba pisana* and the second group includes species that are characteristic of a well-defined ecological parameter; for example: *Xeroleuca turcica*, *Truncatellina cylindrical* and *Theba subdentata* which are respectively related to the type of calcareous substrate, sandy substrate, and sea effect.

Keywords: *Terrestrial molluscs, morpho-anatomy, biodiversity, Essaouira dunes, Morocco.*

Morphological species of the genus *Belgrandia* Bourguignat, 1870 (Mollusca: Caenogastropoda: Hydrobiidae) in the Iberian Peninsula evaluated using multilocus species delimitation methods

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The genus *Belgrandia* Bourguignat, 1870 includes 30 extant species of freshwater snails distributed in continental Europe. Most species have been described essentially based on conchological characters, since their small size challenges the study through anatomical data. Here we re-assess the taxonomic identity of the seven nominal species occurring on the Atlantic and Mediterranean slopes of the Iberian Peninsula through the use of molecular tools. Mitochondrial (mtCOI and 16S) and nuclear (28S, 18S and H3) sequences of 22 specimens collected from nine Iberian localities were phylogenetically analysed by Bayesian Inference (BI) and Maximum Likelihood (ML). In addition, populations of the type species *B. gibba* and other two species from southern France were included in this study. For species delimitations, we used the methods: ABGD, bPTP, mPTP and ST-GMYC. The ML and BI analyses showed strong phylogenetic support for the morphologically recognised species, but the mean sequence divergence (measured as uncorrected pairwise distances) among them was low (from 0.2 to 4.1% for COI). Besides, both inferences grouped the Iberian species according to their Mediterranean and Atlantic distributions. The species delimitation methods suggested three (ST-GMYC) to ten (ABGD) species-groups, being the ABGD the one that best fits the number of described taxonomic species (match ratio = 0.70). In conclusion, the diversity scheme suggested by our novel phylogenetic results needs to be verified and compared with anatomical data to correctly identify the Iberian species of *Belgrandia*.

Keywords: *Taxonomy, freshwater gastropods, ABGD, PTP, ST-GMYC*
Acknowledgements: To Jordi Corbella that provided samples of *B. gibba*, to Beatriz Arconada that provided a sample of *B. boscae* and financial support of Fauna Ibérica Projects: PGC2018-095851-B-C61, CGL2014-53332-C5-1-P, 202030E213 Intramural project and a German Science Foundation (DFG) grant (DE 2605/1-1).

The first data on abyssal aglajids

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In this study we examined an enigmatic new deep-see genus of the family Aglajidae, comprising two new species from abyssal zone of the Sea of Okhotsk and the Pacific slope of Kuril Islands. For the descriptions and phylogenetic analysis, we used an integrative approach, including a molecular phylogenetic analysis based on four gene markers (cytochrome *c* oxidase subunit I, 16S rRNA, histone H3 and 28S rRNA) and a morphological analysis based on traditional anatomical dissections and scanning electron microscopy. The new genus has a well-developed radula and an internal bulloid shell. The new genus is recovered as a member of *Nakamigawaia–Philinopsis* clade. According to our molecular phylogenetic analysis, our results clearly indicate that the new genus possesses several plesiomorphic characters and is likely a deep-sea relic representing the ancient aglajid fauna. It retained the ancestral *Philine*-like shell and radula with marginal teeth, lost by their shallow-water relatives. The morphology of the new genus is markedly similar to that of the cephalaspidean family Laonidae, whereas a molecular phylogenetic analysis has firmly placed them within the Aglajidae. This suggests that more aglajid taxa can be found among species sharing internal and external similarities to the Laonidae for which no molecular data are yet available. Our findings support the recent view that within Aglajidae the radula loss and the shell reduction occurred independently in different phylogenetic lineages. A discovery of the group, which was previously considered exclusively as shallow water one, at abyssal depths highlights how understudied the deep-sea Cephalaspidea are.

Keywords: *abyssal zone, Aglajidae, phylogeny.*

Acknowledgements. This study was conducted with financial support of Russian Science Foundation grant no. 20-74-10012.

The freshwater gastropods of Greece – preliminary list, conservation and prospects

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Greece is a hotspots for freshwater biodiversity. In particular, freshwater gastropods are a diverse but rather neglected group. Recent efforts have focused on documenting the distribution of selected species, the description of new species and resolving the phylogenetic relationships of certain taxa. Here, for the first time, we report on the freshwater gastropods of Greece based on an extended bibliographic review of published works spanning from the 19th century up to 2021. We assembled distribution and habitat data for the species and we recorded their IUCN Red List conservation status. A richness map based on 10*10 km grid was created. In total, we counted 201 species, belonging to 58 genera. 130 species and ten genera are endemic to Greece. Approximately 29% of the species has been documented at least from lakes, while the remaining 71% has been recorded from springs, rivers, ephemeral waters etc. The most speciose genera are *Bythinella* Moquin-Tandon, 1856 and *Pseudamnicola* Paulucci, 1878 with 34 and 18 species, respectively. Both genera inhabit almost exclusively springs. Only 39 species are listed in the IUCN Red list as vulnerable, endangered, critically endangered or extinct. The richest grid cells correspond to lakes, e.g. Trichonis, Pamvotis and Prespa. Most species are recorded from a single locality.

Our results highlight that Greek lakes are hotspots for freshwater gastropod diversity, as they are inhabited by a plethora of endemic species. Nonetheless, springs also host a high number of endemic species with restricted ranges. Although our knowledge of the Greek freshwater gastropods is gradually increasing, we are still missing information. Considering the vulnerability of freshwater biotas and the global freshwater biodiversity crisis we are facing, it is urgent to document and evaluate the Greek freshwater gastropods. Intensive research effort is necessary and the (re-)evaluation of the conservation status of species is pressing.

Keywords: *species richness, species distribution, biodiversity, habitat, Greek freshwaters*

TAXONOMY AND SYSTEMATICS

POSTERS (13)

A new species of non-green sacoglossan sea slug species (Heterobranchia, Gastropoda) from the archipelago of Azores

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A new sacoglossan species, belonging to the genus *Elysia* Risso, 1818 is described from Faial Island (Archipelago of the Azores, Atlantic Ocean). This new species is easily recognizable by its bright and translucent orange colour, visible digestive gland through the skin, and presence of opaque white rounded papillae along the edge of the parapodia. The external morphology of this species resembles the Atlantic *E. flava* Verrill, 1901 and the Indo-West Pacific species *E. obtusa* Baba, 1938, but the colouration depicts subtle differences. The two aforementioned species have an overall translucent pale-yellow body colour with a greenish inner surface and white spots on the tips of the rhinophores, while the new species is orangish with uniform orange rhinophores. In addition, *E. flava* and *E. obtusa* have a broader bright white line on the margins of the parapodia formed by white papillae, which may also be found in small clusters on the pericardial swelling. In some cases, white patches appear scattered on the outer side of the parapodia, not visible in the species here described. Finally, COI uncorrected *p*-distances clearly distinguish this species from all closely related *Elysia* species, with a minimum distance of 10.6 %.

Keywords: *Sacoglossa, species discovery, phylogeny.*

First comprehensive molecular phylogeny reconstruction of the family Milacidae (Gastropoda: Eupulmonata)

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Milacidae, is a family of slugs, which include medium-sized species. Currently, more than 50 species belonging to this family are grouped into two genera: *Milax* Gray, 1855 and *Tandonia* Lessona & Pollonera, 1882. Until now, the GenBank database contains sequences for only one species of the genus *Milax* (*M. gagates*, four COI sequences) and for five species of the genus *Tandonia* (*T. budapestensis*, *T. kusceri*, *T. rustica*, *T. sowerbyi*, *T. marinelli*). To date only one study presented phylogeny of these Milacidae taxa based on the sequences of the mitochondrial COI fragment. Therefore, the relationships between members of the genera *Milax* and *Tandonia* are not well recognized and knowledge on this subject is extremely residual. To fill a large gap in the knowledge regarding taxa relationships within these groups, we reconstructed phylogeny of the family Milacidae based on multiple molecular markers (16S, COI, H3, 28S rRNA) combining it with morphological data. Moreover, besides resolving the relationships between taxa within the investigated family, this study will also greatly contribute to the species identification, thanks to creation of the DNA library for newly obtained barcodes.

Keywords: *integrative taxonomy, slugs, museum collection, phylogeny*

Acknowledgements: We thank Jolanta Jurkowska and the Museum of Natural History, Wrocław University (Poland) for making the collection of Prof. Andrzej Wiktor available for us. This work was supported by a grant from the Jagiellonian University (DS/D/WB/INoŚ/8/2019).

Monacha cantiana (Montagu, 1803) in northern France and the Netherlands

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On the basis of integrative analysis of molecular (gene sequences) and morphological (shell and genitalia) features Pieńkowska et al. (2018, 2019) recognised six distinct lineages of *Monacha cantiana* s.l.: CAN-1 – CAN-6. *M. cantiana* CAN-1 which occurs in the United Kingdom, Spain and the Latium region in Italy was assigned to *M. cantiana* s.str. Lineage *M. cantiana* CAN-2 occurs in northern Italy (Venetum and Lombardy), CAN-3 in northern Italy (Emilia Romagna and Friuli-Venezia Giulia) and also in Austria (Waldviertel and Vienna), CAN-4 (recognised as *M. cemenelea*) in southern France (Sainte Thecle near Nice). The lineages CAN-5 and CAN-6 with narrow distributions in Apuan Alps (Italy) represent different species, however selection of their names requires further studies.

We continue the analysis of distribution of *M. cantiana* in Europe using molecular markers (sequences of selected mitochondrial and nuclear genes). DNA obtained from foot tissue of specimens collected in ten localities in northern France and two in the Netherlands was a template for standard PCR amplification for 5’end of mitochondrial *COI* gene (barcode sequence). Neighbour Joining and Maximum Likelihood analyses of 597 bp long *COI* haplotypes were performed with MEGA7. Four *COI* haplotypes: COI 1 – COI 4 were identified among 44 new sequences. Haplotype CAN-1 was common in specimens from all studied populations. On the contrary, haplotypes COI 2, 3 and 4 were rare, found in single specimens in one French and two Dutch populations. Sequences of these four haplotypes were compared with sequences representing all *M. cantiana* mitochondrial lineages and some other *Monacha* species. Haplotypes COI 1 – COI 4 clustered in ML/NJ tree with sequences of *M. cantiana* CAN-1. Molecularly, it proves that *M. cantiana* s.str. occurs in northern France and the Netherlands, however further analyses of nuclear genes as well as the structure of shells and reproductive tract are in progress.

Keywords: Monacha *genus, species distribution, Europe*

Multilocus Molecular Phylogeny of *Chondrina farinesii* (Gastropoda, Pulmonata, Chondrinidae) in the Iberian Peninsula

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The genus *Chondrina* is distributed through the West of Eurasian continent. Currently, it includes 46 species of land snails, 33 of them living in the Iberian Peninsula being its main center of speciation. The classification of the taxa included within *C. farinesii* complex is still controversial and many taxa are placed within this complex by having an extreme reduction of teeth in the shell aperture, a character that has been shown to be subjected to convergent evolution. Gittenberger (1973) considered three subspecies: *C. farinesii arigonis, C. f. farinesii and C. f. sexplicata*. Later on, Kokshoorn et al. (2010), based on DNA sequences of the *COI* gene fragment separated *C. aguilari*, *C. arigonis*, *C. dertosensis* and *C. massotiana* (including *C. m. massotiana* and *C. m. sexplicata*), previously considered within *C. farinesii*, with full species status. With the aim to progress in the resolution of the taxonomy and phylogenetic relationships of this complex of species we have analysed two mtDNA gene fragments (*COI* and *16S* rRNA), another two nDNA gene fragments (*ITS1-5.8S* and *5.8S-ITS2-28S*) and three species delimitation analyses (ABGD, BPP and Stacey). This study included all the taxa mentioned above. Besides, we included some other taxa closely related to them or with reduced teeth in the shell aperture, including *C. ascendens* and specimens belonging to *Chondrina* spec. 1, *C.* spec. 5 and *C.* spec. 6 following the nomenclature of Kokshoorn and Gittenberger (2010). The new results allowed to reconstruct the phylogenetic relationships of all these taxa and to update their taxonomy. One new undescribed species is here considered.

Keywords: *Chondrina, Iberian Peninsula, multilocus DNA, Phylogeny, species delimitation analyses*.

Acknowledgements: Somoza-Valdeolmillos E. was supported by a PhD fellowship awarded in 2015 by the University of the Basque Country (UPV/EHU).

Multilocus Molecular Phylogeny of the *Chondrina soleri* + *granatensis* + *gasulli* complex (Gastropoda, Pulmonata, Chondrinidae) in the Iberian Peninsula

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Chondrina is a highly diverse genus of terrestrial molluscs currently including 46 species. It is distributed through North Africa, central and southern Europe, from Portugal in the West to the Caucasus and Asia Minor in the East. Approximately 70% of species are endemic to the Iberian Peninsula constituting its main center of speciation with 33 species. The classification of the taxa included within *soleri* + *granatensis* + *gasulli* complex is still controversial. Based on the morphology of the shell, Gittenberger (1973) described *Chondrina gasulli*, while considered *C, soleri* within *C, farinesii* s.l. Later on, Alonso (1974) described *C. farinesii granatensis*. Recent molecular studies have demonstrated that the number of species inside this complex has been underestimated. Kokshoorn et al. (2010), based on morphology and DNA sequences of the *COI* gene fragment separated *C. aguilari* and *C. guiraoensis*, with full species status, and described four new species: *C. arigonoides*, *C. ingae*, *C. marjae*, *and C. pseudavenacea*. They proposed another 2 species within this clade (*C.* spec. 2 and *C.* spec. 3). With the aim to progress in the resolution of the taxonomy and phylogenetic relationships within this complex of species we have analysed two mtDNA gene fragments (*COI* and *16S* rRNA), and another two nDNA gene fragments (*ITS1-5.8S* and *5.8S-ITS2-28S*). The results were analysed by different species delimitation methods (ABGD, BPP and Stacey). We included all the taxa mentioned above and some other adjoining populations. Phylogenetics and species delimitation analyses showed that another nine new species have to be considered within this complex. The new results allowed to reconstruct the phylogenetic relationships of all these taxa and to update their taxonomy.

Keywords: *Chondrina, Iberian Peninsula, multilocus DNA, Phylogeny, species delimitation analyses*.

Acknowledgements: Somoza-Valdeolmillos E. was supported by a PhD fellowship awarded in 2015 by the University of the Basque Country (UPV/EHU).

New data on biodiversity of dorid nudibranchs (Gastropoda: Heterobranchia) in Southern Vietnam

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Nudibranchia is a group of shell-less and strikingly-colored marine molluscs, encountering more than 4000 species. They are distributed worldwide with the highest diversity in the Indo-West Pacific region. Despite there are a lot of researches dedicated to regional fauna composition and distribution, some regions still remain poorly studied. Vietnamese fauna is one of the less studied within the Coral Triangle region. Only three revisions were conducted, and all of them are based on traditional morphological examination and lacks molecular data. Moreover, they were based on material from very restricted areas. To date in total of 150 heterobranch species are registered in Vietnam. At the same time, the biodiversity in adjacent regions (Philippines, Indonesia) is much higher. The main goal of our study was to revise diversity of the suborder Doridina in Southern Vietnam using both modern molecular (COI-based barcoding) and traditional morphological methods. The material was collected in 2016-2019 from Nha Trang Bay and Spratly Islands using SCUBA diving and snorkeling. Of 48 studied species 12 are registered in Vietnam for the first time. All of them were widespread in the Indo-West Pacific, none were endemic. A cryptic diversity was shown within several genera in the family Phyllidiidae, e.g., the species *Phyllidiella pustulosa* (Cuvier, 1804) includes nine clades, and four of them were recognized in our material.

Keywords: *taxonomy, distribution, barcoding, Indo-West Pacific.*
Acknowledgments: This study was supported by Russian Foundation for Basic Research grant # 20-34-70044.

New data on nudibranch fauna in the North-West Pacific revealed an astonishing pseudocryptic diversity

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The North Pacific region is one of three major marine biodiversity origin hotspots, with high numbers of endemic taxa. However, while the North-East Pacific fauna is studied quite well due to contemporary USA and Canadian research programs, the biodiversity studies of another Pacific coast are much more scattered, especially in case of Russian coastal waters. Although preceding comprehensive surveys and expeditions revealed extremely rich fauna in this region, not every taxonomic group was covered in these studies. In particular, data on nudibranch molluscs of the North-West Pacific are permanently updated, and many new taxa have been described during last 30 years, but for many regions like deep-sea waters only a handful of species descriptions exist, scattered across several taxonomically focused papers.

In the present study we analyzed samples collected in 2017-2021 in different regions of the North-West Pacific: The Sea of Japan (Vladivostok, Rudnaya Bay), off Sakhalin Island, the Okhotsk Sea and coastal waters of the Kuril Islands. Molluscs were examined using standard anatomical dissections with help of the light microscopy and scanning electron microscopy. The identifications were supported by sequencing of standard barcoding marker COI and nuclear gene histone H3.

A total of 69 nudibranch species was found. Among them 23 species represent newly discovered undescribed taxa. The highest undescribed diversity (18 species) was found in the Kuril Islands area, in both shallow and deep waters. This region is characterized by high productivity, and deep straits between islands in the Kuril archipelago and hydrological conditions promote mosaic pattern of habitats and their restriction to island coastal waters. Our results highlight the necessity of further biodiversity studies of this region.

Keywords: *Biodiversity, new species, pseudocryptic species, endemism*

Acknowledgments: This study was supported by Russian Science Foundation grant #20-74-10012|

New record and update of *Pruvotia sopita* (Pruvot, 1890) (Mollusca, Aplacophora) in the South of Spain

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Due to their small size and specific habitat, many species are associated to cnidarian colonies, Solenogastres (Mollusca, Aplacophora) often go unnoticed during sampling. Additionally, their identification involves the study of mantle sclerites and the internal anatomy, which requires the use of a specific methodology, that sometimes leads to discarding them for research. Thus, there are around 300 known species but it is considered that their real diversity is underestimated. Remarkably, most of them are only known from their type locality and many were described from one or very few specimens. Besides, although most of the recent described species came from remote locations, new species are still found in well-known areas, where new records are expected to be common. Therefore, there are still many open questions about their actual distribution and interspecific variability. And even if the general anatomy of this group is relatively well-known, the advance in the deep study of some organs it is important for a better knowledge of this interesting group of molluscs.

Here we present the preliminary results of an integrative taxonomic study (histology, SEM and DNA barcoding) of several specimens of Solenogastres collected in bay of Málaga (Southern Spain) on colonies of the hydrozoan *Sertularella* sp. and tentatively identified as *Pruvotia sopita* (Pruvot, 1891). The specimens were previously identified based on their habitat and external appearance. The general study of the histological sections confirmed this identification and provides new data that improves the description of the species. New data on the mantle sclerites and cuticle is also addressed. For the first time barcodes of this species were obtained. This species has only been formally reported from its type locality (Banyuls-sur-Mer), so this constitutes a new record.

Keywords: *Aplacophora, Biodiversity, histology, Solenogastres, Taxonomy*

The chromosome numbers of the family Hygromiidae Tryon, 1866 (Gastropoda: Stylommatophora)

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Our own and literary chromosome number data on the Hygromiidae are summarized. The Hygromiidae is a highly diverse family of terrestrial pulmonate gastropod mollusks with about 570 species and subspecies described. Forty-one of them are recorded from Georgia (Caucasus region). In total, 21 species and subspecies of hygromiids, belonging to 14 genera, 7 tribes of the subfamilies Hygromiinae, Leptaxinae, and Trochulininae are currently known karyologically. Georgian representatives account 14.3% of all karyologically studied species. The haploid chromosome number ranges from 21 to 26 in the Hygromiidae in general. Four different haploid values n=21, n=23, n=24, and n=26 are characteristic for the family. So far, only one of them-23 is detected in the Georgian leaf snails (subfamily Trochulininae). The lowest haploid value n=21 occurs in a more basal taxon of hygromiids (tribe Hygromiini in subfamily Hygromiinae) and is an ancestral character state (plesiomorphy) within the family. n=23 is the modal haploid chromosome number for the subfamily Trochulininae and family in general. n=23 looks like a plesiomorphic character for the subfamily Trochulininae. n=24 is registered in the separate lineages of hygromiid land snails (subfamilies Hygromiinae and Trochulininae) and is a case of homoplasy within this group. For now, n = 26 is the highest haploid chromosome number in the Hygromiidae. It is observed in a more advanced taxon-tribe Cryptosaccini (subfamily Leptaxinae) and seems to be a derived, apomorphic character for this tribe. The diploid chromosome number and some other karyotype details are available only for nine hygromiids, including Caucasian endemic species *Circassina frutis*. Four diploid values 2n=42, 2n=46, 2n=48, and 2n=52 occur in these species. Karyological data show that the Hygromiidae is not conservative concerning the chromosome number at the family level. In the evolution of the family, a tendency to increase the chromosome number is detected.

Keywords: *chromosome number, phylogeny, Hygromiidae.*

Three new species of Columbellidae (Neogastropoda) from deep waters of the southwestern Atlantic: shell morphology, anatomical data and morphometric analysis

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The family Columbellidae is very diverse, with about 900 valid extant species and 74 genera, known from tropical to temperate waters worldwide and from a wide bathymetric range. In Brazil, there are several taxa awaiting to be described. Herein, we studied three new species potentially new to science and provisionally included in *Amphissa* H. & A. Adams, 1853. The latter genus currently encompasses eight species, three are known from the Atlantic but the genus is probably restricted to cool waters of the northeastern Pacific. The material examined was collected mainly during the cruise MD55 (1987) in Southeast Brazil. We analysed the shells, soft parts and radulae of several specimens. A total of 261 shells (sp. A= 61; sp. B= 100; sp. C= 100) were also measured for a morphometric analysis to aid the discrimination of taxa. Taxonomic identifications were made prior to the measurements to identify each taxon. The following variables were measured: length, width, body whorl length, aperture length and aperture width. The ratio length/width was also calculated. All standardized data was included in a Discriminant Analysis (DA). The three '*Amphissa*' species could be distinguished from each other and from other similar species mainly by the protoconch morphology, development of teleoconch sculpture, penial morphology and shape of seminal vesicles. The DA also supported the distinction of these three taxa (Wilks' Lambda= 0.2013631; $F_{12,506}$= 51.80118) with 87% of the specimens classified correctly. The first axis explains about 96% of the distinction between groups and the most important variables were width and aperture length. The three taxa are known from Southeast Brazil. A further revision of the literature may help us erect a new genus for this particular group of species, since they have consistent differences in relation to the eastern Pacific species of *Amphissa*.

Keywords: *Amphissa, Buccinoidea, Deep-sea, Gastropoda, radula.*

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Uncovering the biodiversity of Gymnomeniidae (Aplacophora, Mollusca) in the Norwegian Sea

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Aplacophorans are small vermiform molluscs with a world-wide distribution. Divided among two classes, Solenogastres (= Neomeniamorpha) and Caudofoveata (= Chaetodermomorpha) there are less than 500 formally described species although the true diversity of this group is estimated to be far greater. The biodiversity of solenogasters in the Norwegian Sea was thought to be well characterized, with 18 species described from this region. Here we present the preliminary result of the study of specimens obtained in 2011 and 2013 from the Icelandic marine Animals: Genetics and Ecology (IceAGE) expeditions. The family Gymnomeniidae was selected as five out of eight formally described species were described from the Norwegian Sea. Samples were sorted by morphotype based on habitus. Whole individuals for each morphotype were imaged via light and scanning electron microscopy and used for whole animal DNA extraction and amplification of 16s, COI, and Hsp 90 genes. Phylogenetic analyses were conducted with maximum likelihood analysis on a supermatrix of the three genes in IQ-TREE2 using the best fitting model and 1000 rapid bootstraps. Species delimitation using iPTP and Phylomap indicated between 25 and 38 different species within this region. To begin to unravel this unexpected diversity and confirm species delimitation, the morphology of the epidermal sclerites and characterization of important internal structures are necessary for formal description. Individuals within the same morphotype will be divided into three parts. Semi-thin sectioning of the anterior and posterior ends will be conducted for reconstruction of internal anatomy. The middle piece will be used for SEM under low-voltage for further characterization of the sclerites and used subsequently for DNA barcoding for placement on the tree. This work highlights the necessity for understanding of the true diversity of solenogaster aplacophorans as we continue to find new species, even in well characterized regions such as the Norwegian Sea.

Keywords: *Aplacophora, Solenogastres, Norwegian Sea, Biodiversity, Taxonomy.*

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Validation of the most informative descriptors for the species of the gender *Cardiomya* Adams, 1864 in Brazil

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Cardiomya Adams, 1864 is a genus of septibranch bivalves normally found in deep water. Morphological characters of *Cardiomya* include a rostrate shell and radial sculpture composed by radial ribs. Despite being strongly indicative for generic differentiation, for specific identification, these same characters are extremely plastic and uninformative. Added to this, the rarity of the specimens and the difficulties in collecting make this genus a group full of misidentification and underestimated diversity. Currently, approximately 50 species of the genus are known, of which six have registered occurrences in brazilian waters: *Cardiomya cleryana* d'Orbigny, 1842; *Cardiomya ornatissima* d'Orbigny, 1853; *Cardiomya striata* Jeffreys, 1876; *Cardiomya perrostrata* Dall, 1881; *Cardiomya striolata* Locard, 1897 e *Cardiomya minerva* de Lima, Oliveira & Absalão, 2020. In order to select and test the smallest and most efficient set of characters that are efficient in classifying these species, 29 variables of approximately 200 specimens were selected and measured. To test whether the variables were informative, a discriminant analysis was performed, the average accuracy was 88%. After that, we use the Bayes Information Criterion (BIC) to select the most informative variables within the initial set. Of the 29 initial variables, a set of five was selected as being the most efficient, and a new discriminant analysis was performed using only these five variables in order to test if they were really efficient in discriminating species. Discriminant analysis obtained an average accuracy of 90%, demonstrating the efficacy of these variables even when used alone. This dataset is entirely related to the contour of the shell, demonstrating that these characters should be given greater attention when examining specimens.

Keywords: *Septibranchia*, *Morphometry*, *Taxonomy*, *Biodiversity*.

Who is not *Goniodoridella savignyi* Pruvot-Fol, 1933? The challenge of Indo-Pacific *Goniodoridella* species complex (Nudibranchia, Goniodorididae)

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Goniodoridella Pruvot-Fol, 1933 is a small genus belonging to the family Goniodorididae. The genus was erected from specimens collected in the Red Sea, describing the species *Goniodoridella savignyi*. Since its original description, this species has been found throughout the Indo-Pacific Ocean. In 2015, Martynov, Sanamyan & Korshunova described the species *Goniodoridella borealis*. The authors claimed that *G. savingyi* could include different cryptic species and, in fact, *G. borealis* was previously confused with *G. savingyi*. Thus, the specimens identified as *G. savingyi* reported from the Sea of Japan are *Goniodoridella borealis*.

In order to study the biodiversity of the genus *Goniodoridella* and investigate possible cryptic species, specimens collected from Philippines, Australia and Papua New Guinea were studied. Partial gene sequences of Cytochrome Oxidase c subunit I, 16S ribosomal RNA and Histone H3 were included for six specimens. Bayesian Inference and Maximum Likelihood phylogenetic analyses were performed. Moreover, the external morphology of the specimens was studied using photographs of live animals and laboratory observations. The internal anatomy of some specimens was studied by dissections. Photographs of the radulae were taken under the Scanning Electron Microscope.

Specimens were initially identified as *Goniodoriella* cf. *savignyi* based on the coloration and external morphology. However, the molecular results differentiate at least four different species. The results obtained shows that i) the lack of information in the original description of the species, ii) the lack of specimens collected from the Red Sea and, iii) the great similarity between the specimens studied, makes *Goniodoridella savignyi* a species difficult to determine.

Keywords: *cryptic species, phylogeny, Indo-Pacific, Goniodoridella.*

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