



18th ICA

INTERNATIONAL
COLLOQUIUM
ON AMPHIPODA

Dijon – France

26-30 August 2019

Book of abstracts



BIOGÉOSCIENCES

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Foreword from the co-coordinators

This 18th edition of the International Colloquium on Amphipoda (ICA) is following a long lasting tradition which started 50 years ago. It is an exciting forum for scientific exchanges around all aspects related to Amphipoda (Taxonomy, Phylogenetics, Biogeography, Ecotoxicology, Ecology, etc.)

This 18th edition of ICA is welcoming 130 participants from 27 countries.

The Colloquium includes:

- Three **Plenary Lectures (PLs)** from 3 invited speakers *Dr NICOLAS PUILLANDRE (MNHN, France)* ; *Pr ALEX FORD (Univ. of Portsmouth, UK)* and *Dr JOSE MANUEL GUERRA GARCIA (Univ. of Sevilla, Spain)*.
- Fifty eight (58) **Oral Communications (OCs)**
- Fifty four (54) **Posters (Ps)**.

The present book of abstract includes:

- The programme
- Abstracts of **PLs, OCs** and **Ps**.
- The list of participants

The co-coordinators are grateful to the following Sponsors: NHBS (100 €), SUEZ (tote bags), Centre National de la Recherche Scientifique – CNRS (note pads, pencils and bookmarks), University of Burgundy – uB as BQR - Bonus Quality Research (2000 €), Head of Unité Mixte de Recherche – UMR 6282 Biogéosciences (2500 €), *Evolutionary Ecology* and *Samba* research teams of UMR 6282 Biogéosciences (2150 €) and The Crustaceans Society (800 €).

Most of the collected money has been allocated to 18 Master and PhD Students grants and reduced fees for 8 colleagues from countries with limited funds. The remaining money greatly helps us in keeping fees as low as possible (especially for students) and the balance right.

Thierry Rigaud & Rémi Wattier, co-coordinators



Committees

Organizing committee

The co-coordinators of the Organizing Committee, Thierry Rigaud and Rémi Wattier would like to thank all the students and staff members of the UMR Biogéosciences for their unvaluable involment in organizing the 18th ICA.

Aude Balourdet
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Loïc Bollache (France)
Oliver Coleman (Germany)
Filipe Costa (Portugal)
Cene Fiser (Slovenia)
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Ilona Muskó (Hungary)
Alan Myers (Ireland)
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Wim Vader (Norway)

Programme of sessions

Tuesday August 27th

Plenary Lecture 1 (09.15-10.00)

Chairperson: Rémi Wattier

PL1 DNA Barcoding, DNA taxonomy and integrative taxonomy: separating the wheat from the chaff (**N Puillandre**)

Session 1a: Phylo-bio-geography (10.00-10.30)

Chairperson: Rémi Wattier

10.00-OC1 Molecular phylogeny, habitat shifts and the evolutionary timescale of the Amphipoda (**D Copilas-Ciocianu**, Š Borko & C Fišer)

10.15-OC2 The oldest record of Amphipoda: a 260-million-year old fossil from Brazil (**PG Pazinato**, C Haug, JT Haug, R Rohn, K Adami-Rodrigues, M Cardoso Langer & R Pirani Ghilardi)

Session 1b: Phylo-bio-geography (11.00-12.30)

Chairperson: Cene Fiser

11.00-OC3 Cryptic diversity and ancient divergence in two species of amphipods from central Mediterranean Sea (**R Cimmaruta**, C Abbattista, B Bellisario, F Camisa & G Nascetti)

11.55-OC4 Comparative molecular diversity and historical demography of two gammarid species as indicators of "Atlantification" in the High Arctic (M Grabowski, **A Jabłońska**, A Weydmann-Zwolicka, M Gantsevich, P Strelkov, M Skazina & JM Węśławski)

11.30-OC5 Morphological and molecular comparison between populations of scuds from *Hyaella* genus from two States in Mexico: Veracruz and Ciudad de Mexico, Mexico (**A Marrón-Becerra**, M Hermoso-Salazar & G Wellborn)

11.45-OC6 Bathymetric and geographic patterns of amphipods from Kuril-Kamchatka Trench and adjacent abyssal plain (**A Jażdżewska** & T Mamos)

12.00-OC7 Genetic diversity and connectivity of the *Eusirus perdentatus* species complex (Amphipoda, Crustacea) on the Antarctic continental shelf (**ML Verheye**, C d'Udekem d'Acoz, L Salabao, I Schön & A Van de Putte)

12.15-OC8 First glance at molecular diversity and phylogeography of Periadriatic freshwater gammarids (**M Grabowski**, T Mamos, K Hupalo, W Wrzesinska, M Jelic, K Zganec, A Wysocka & R Wattier)

Session 1c: Phylo-bio-geography (14.00-15.30)

Chairperson: Anne-Nina Lörz

- 14.00-OC9** The phylogeography and classification of the Talitroidea (Amphipoda, Senticaudata) (AA Myers & JK Lowry)
- 14.15-OC10** Phylogeography of the invasive amphipod *Pontogammarus robustoides* (Crustacea) in native and colonized range (T Rewicz, K Baćela Spsychalska, N Berezina & M Grabowski)
- 14.30-OC11** Exploring introduction events and temporal genetic variation of the exotic *Caprella scaura* in Southern Spain (G Martínez-Laiz, M Ros, JM Guerra-García, AM Santos & MP Cabezas)
- 14.45-OC12** Origin, diversity and distribution of freshwater amphipods in Northern Africa (K Ayati, R Hadjab, H Khammar, S Dhaouadi & C Piscart)
- 15.00-OC13** Diversification underground: adaptive radiation in genus *Niphargus* (Š Borko & C Fišer)
- 15.15-OC14** Dispersal of subterranean amphipods during marine regressions (T Delić, F Stoch, Š Borko, J-F Flot & C Fišer)

Session 1d: Phylo-bio-geography (16.00-17.15)

Chairperson: Filipe Costa

- 16.00-OC15** Freshwater amphipods of Mediterranean Islands – fascinating findings and exciting perspectives (K Hupało, F Stoch, I Karaouzas, T Mamos, T Rewicz, Z Csabai, J-F Flot & M Grabowski)
- 16.15-OC16** Connectivity and putative native ranges of the two “cosmopolitan” biofouling amphipod species, *Jassa marmorata* and *Jassa slatteryi* (A Hall-Mullen, A Desiderato, C Havermans, C Held & J Beermann)
- 16.30-OC17** Amphipoda from the Reykjanes Ridge, Iceland, with a focus on their coral associations (AN Lörz, M Schwentner, AH Tandberg, J Taylor & S Brix)
- 16.45-OC18** Persian Gulf as a hotspot or coldspot of biodiversity; evidence from *Ampelisca* (Amphipoda: Ampeliscidae) diversity from PGGOOS expedition (F Momtazi)
- 17.00-OC19** The biodiversity of deep-sea scavenging Amphipoda in the Pacific Ocean (T Patel, H Robert, C d'Udekem d'Acoz, I De Mesel, K Martens, S Degraer & I Schön)

Poster session (17.15-20.00)

- P1** Evaluation of the antioxidant potential of Baikal endemic amphipod *Eulimnogammarus verrucosus* (DV Axenov-Gribanov, YA Lubyaga, ES Protasov, ME Krasnova, EV Pereliaeva, UA Vasileva, XX Shatilina & MA Timofeyev)
- P2** Effect of diet on growth and fatty acid profile of the marine amphipods *Echinogammarus marinus* and *Gammarus locusta* (H Alberts-Hubatsch, MJ Slater & J Beermann)
- P3** Do intersex amphipods get a bad rap? (TL Brown)

- P4** Long-term observations of high frequencies of intersex females in two populations of the freshwater amphipod *Gammarus minus* (Say, 1818) (**TL Brown**, DS Glazier, RA Downer & AT Ford)
- P5** A first in depth look at the Amphipod fauna of the Easter Island (**C Caurant**, L Hughes, M Thiel & J Beermann)
- P6** Inter-/intra-specific variability in contaminant sensitivity in *Gammarus fossarum-pulex* (**A Chaumot**, R Wattier, T Rigaud & O Geffard)
- P7** Thiothrix–amphipod symbiotic relationships) (**C Chauveau**, D Weber, EJ Fleming, SM Sarbu, T Brad & J-F Flot)
- P8** Be my guest: amphipods living in tubes of Ceriantharia (**H Ceriello** & SN Stampar)
- P9** Shadings in digital taxonomic drawings (**CO Coleman**)
- P10** Functional morphological and trophic niche differentiation in a community of freshwater amphipods (**D Copilaş-Ciocianu** & B-V Boros)
- P11** Combining molecules and morphology to describe cryptic new species – the *Bathyceradocus* genus case (L Corbari, A Jazdzewska & **A Ziemkiewicz**)
- P12** Effect of substrate and seagrass habitat complexity on detritus colonization and decomposition in a Mediterranean coastal lagoon (Thau Lagoon, France): a focus on amphipod community (**V Costa**, D Iacofano, S Lo Brutto & F Rossi)
- P13** Coloring outside the lines: cryptic diversity in podocerid amphipods (**BC Cummings** & G Paulay)
- P14** DNA sequencing and morphological analysis of an undescribed *Salentinella* species (Amphipoda, Salentinellidae) from an anchialine cave in Peloponnese, Greece (D Davolos, C Calcari, **E De Matthaeis** & C Di Russo)
- P15** On the evolution of terrestrial talitrid amphipods from Atlantic volcanic archipelagos, with a new species from the islands of Graciosa and Flores, Azores. (D Davolos, **E De Matthaeis**, L Latella & R Vonk)
- P16** ToxMate: an autonomous online biomonitoring tool of water effluent quality based on the video analysis of the locomotor behaviour of the amphipod *Gammarus fossarum* (A Decamps, **A Chaumot**, M Dauphin, N Delorme, A François, L Garnero, F Moulin, H Quéau, D Neuzeret & O Geffard)
- P17** Phenotypical and genetic characters of the giant Antarctic *Eusirus* of the *perdentatus* complex, with the presentation of a new species (**C d’Udekem d’Acoz** & ML Verheye)
- P18** Insights into the ecology of *Cryptorchestia garbinii* on the shores of the urban Lake Tegel (Berlin) (**L Fanini**, CO Coleman & JK Lowry)
- P19** Anxiety-like state and fear in gammarids: coupled or dissociative emotions? (**M Fayard**, MJ Perrot-Minnot & F Cézilly)
- P20** Do artificial structures create a functional shift in coastal benthic communities? (**M Florido**, F Espinosa, C Navarro-Barranco & F Sedano)
- P21** The deep-sea Eusiridae from Papua New Guinea waters (SW Pacific Ocean) (**I Frutos**, JC Sorbe & L Corbari)
- P22** What do parasites do when their hosts diverge and meet again? Diversity of microsporidian parasites in central European lineages of the *Gammarus fossarum* species complex (**M Gajdošová**, E Hendrychová, M Hylíš & A Petrusek)

- P23** Diversity and distribution of freshwater amphipods from Algeria (**R Hadjab**, K Ayati, H Khammar, D Merzoug & C Piscart)
- P24** Pacific species of *Epimeria* (Amphipoda: Amphilochidea, Epimeriidae) with a description of a new deep-sea species from SW Mexico (**M Hendrickx** & I Winfield)
- P25** Two new species of the rare, deep-sea genus *Vemana* (Amphipoda: Vemanidae) from the northeast and southeast Atlantic (**EA Hendrycks** & MH Thurston)
- P26** Historic Peracarid Crustacea collections in The Natural History Museum, London (A Herdman, **LE Hughes** & M Lowe)
- P27** A project's blueprint: drivers of cryptic species coexistence in freshwater gammarid communities of Sicily (**K Hupało**, A Weigand, M Weiss, F Altermatt, D Fontaneto, M Grabowski, D Grabner, B Sures & F Leese)
- P28** New insights on the deep-sea amphipods from the sea of Okhotsk (NW Pacific) (**A Jażdżewska** & I Frutos)
- P29** Barcoding of deep-sea Northwest Pacific Oedicerotidae (A Jażdżewska & **K Kapuścińska**)
- P30** Integrative evidence for hidden species diversity and long-term divergence within *Gammarus balcanicus* Schäferna 1923 morphospecies in the northernmost part of the Carpathian Arc (**K Jażdżewski**, T Mamos, Z Čiamporová-Zaťovičová, F Čiampor & M Grabowski)
- P31** Active biomonitoring using the freshwater amphipod *Gammarus fossarum*: an operational method to monitor chemical contamination and ecotoxicity in watercourses at the French national scale (G Jubeaux, R Recoura-Massaquant, **A Chaumot** & O Geffard)
- P32** First insights into the deep-sea scavengers at hydrothermal vent fields along the Southeast Indian Ridge (**K Kniesz**, A Jażdżewska, TC Kihara & PM Arbizu)
- P33** *Gammarus lacustris* (Sars, 1863) sexual behavior in small brackish lakes of West Siberian Plain southwest part (**OV Kozlov**, SV Arshevsky, OV Arshevskaya & AV Pavlenko)
- P34** Combining artificial substrates, morphology and DNA metabarcoding for investigating marine amphipod communities in NW Iberia (BR Leite, **PE Vieira**, JS Troncoso & FO Costa)
- P35** First records of two hyperiid amphipods *Phronima atlantica* and *Oxycephalus clausi* from Korea (B-J Lim & **M-H Shin**)
- P36** Stable indicators of energy metabolism and non-specific stress response as a strategy of biochemical adaptation in eurybathic Baikal amphipods of the genus *Ommatogammarus* (EV Madyarova, YA Shirokova, DV Axenov-Gribanov, DS Bedulina, VA Emshanova, ZM Shatilina & **MA Timofeyev**)
- P37** Temporal variation of the amphipod assemblage on sandy sediments at the Ría de Ferrol (Galicia, NW Iberian Peninsula) (**J Moreira**, G Santos De-La-Fuente, C García-Rodríguez, G Díaz-Agras & C Navarro-Barranco)
- P38** Spatial patterns of coastal amphipods collected by light traps in South Spain (**C Navarro-Barranco**, A Irazabal & J Moreira)
- P39** Amphipod response to host-complexity along an environmental stress gradient (**C Navarro-Barranco**, PE Gribben, J Ledet & AGB Poore)
- P40** A faunistic description of the Amphipod-fauna of Hjeltefjord, Western-Norway. (**CH Østensvig**, AHS Tandberg & HT Rapp)

- P41** Syntopic coexistence of gammarid cryptic lineages: rule or exception? (**A Petrusek**, T Rutová, PK Bystřický, M Gajdošová, A Beermann, P Pařil, M Horsák, D Copilas-Ciocianu & F Leese)
- P42** Amphipod inhabiting the invasive macroalgae *Sargassum muticum* in the English Channel (**J-P Pezy**, A Raoux & J-C Dauvin)
- P43** Interaction of species, temperature and parasitism may facilitate replacement of native amphipod by invasive species, impacting vital ecosystem process of detritivory (**B Pile**, C Hassall, L Brown & AM Dunn)
- P44** Amphipod diversity assessment of fish-farming environmental impact (W Plaiti, D Podaras, K Mylona & **L Fanini**)
- P45** Reconstructing population histories and biogeography of Antarctic *Charcotia* (Amphipoda, Crustacea) (**T Plevoets**, H Robert, M Kochzius & I Schön)
- P46** Trophic differentiation of *Niphargus* amphipods (**E Premate**, C Touchet, Š Borko, T Delić, F Malard, L Simon & C Fišer)
- P47** Microsporidian infections in the *Gammarus roeselii* species complex (Amphipoda) over its geographic range (**A Quiles**, K Bacela-Spychalska, M Teixeira, N Lambin, M Grabowski, T Rigaud & RA Wattier)
- P48** Estimating the actual biodiversity and evolutionary history of the amphipod genus *Eusirus* in the Southern Ocean (**L Salabao**, B Frédéric, G Lepoint, ML Verheye & I Schön)
- P49** Sediment: Amphipod relationship in a tropical intertidal habitat, South Andaman Islands, India (**K Satyam**, G Thiruchitrabalam, RK Lakra, M Savurirajan & J Equbal)
- P50** First records of amphipod species in the Gulf of Naples (Italy, Mediterranean Sea) (**MB Scipione**, M Lorenti, R Guglielmo & FP Patti)
- P51** First impressions on the Amphipoda of Dronning Maud Land, Antarctica. Results from the Norwegian 2019-cruise (**AHS Tandberg**, T Falkenhaus, A Sveistrup, T Ulvatn, JH Simonsen & S Ambroso)
- P52** Amphipods in macrofouling communities of the port of the area of Livorno (northern Tyrrhenian Sea) (**J Tempesti**, J Langeneck & A Castelli)
- P53** Distribution patterns of amphipod assemblages along the Iberian Atlantic rocky shores (**PE Vieira**, A Desiderato, FO Costa & H Queiroga)
- P54** When one becomes 15: Morphological vs. molecular species delimitation in the “*Niphargus aquilex*” complex (**D Weber**, T Brad, A Weigand & J-F Flot)

Wednesday August 28th

Plenary Lecture 2 (09.00-09.45)

Chairperson: Thierry Rigaud

PL2 Amphipod ecotoxicology: endocrine disrupting pollution and endocrine disrupting parasites (A Ford)

Session 2a: Ecotoxicology (09.45-10.30)

Chairperson: Thierry Rigaud

- 9.45-OC20 Molecular omics resources and tools for amphipod investigation (Y Cogne, D Gouveia, O Pible, A Chaumot, D Degli-Esposti, O Geffard, C Almunia & J Armengaud)
- 10.00-OC21 From proteogenomics to systems biology in the freshwater amphipod *Gammarus fossarum* (D Degli Esposti, N Koenig, Y Cogne, D Gouveia, A Chaumot, C Almunia, J Armengaud & O Geffard)
- 10.15-OC22 Transcriptional profiles and differential exposure in response to abiotic stressors in endemic Lake Baikal amphipods *Eulimnogammarus verrucosus* and *E. cyaneus* compared to that in a common Holarctic species *Gammarus lacustris* (P Drozdova, L Rivarola-Duarte, D Bedulina, T Luckenbach, M Timofeyev & PF Stadler)

Session 2b: Ecotoxicology (11.00-12.15)

Chairperson: Lauren Hughes

- 11.00-OC23 Effects of injection of non-biodegradable polyelectrolyte microcapsules into the amphipod circulatory system (A Gurkov, E Shchapova, A Nazarova, Y Rzhechitskiy, A Saranchina & M Timofeyev)
- 11.15-OC24 The use of amphipods as biomonitors of environmental health change using trace element analysis (RA Peart, M Handler, R Wysoczanski, M Holmes & C Seabrook)
- 11.30-OC25 First approach to the use of an index based on a polychaete/amphipod ratio to detect pollutant in marinas (A Fernández-Romero, J Moreira & JM Guerra-García)
- 11.45-OC26 Responses of *Orchestia gammarellus* (Amphipoda, Talitridae) to copper contaminated soil (R Jelassi, H Khemaissia, C Ghemari, A Ayari, M Raimond, C Souty-Grosset & K Nasri-Ammar)
- 12.00-OC27 Effect of organic and metallic pollutants on the density of micro-amphipods in northeastern Tunisia: case of some coastal localities (M El Gtari & F Charfi-Cheikhrouha)

Thursday August 29th

Plenary lecture 3 (09.30-10.15)

Chairperson: Rémi Wattier

PL3 Fifty years of amphipod meetings. Taxonomical, ecological and behavioural patterns of the amphipodologist community (**JM Guerra-García**)

Session 3: Public outreach (10.15-10.30)

Chairperson: Rémi Wattier

10.15-OC28 Amphipod-based public outreach: a dream or a possibility? (**AH Tandberg**)

Session 4a: Ecology (11.00-12.30)

Chairperson: Jan Beermann

11.00-OC29 Functional ecology of the genus *Niphargus* (**C Fišer**, F Altermatt, D Copilas-Ciocianu, T Delić, Ž Fišer, A Jemec-Kokalj, S Kralj-Fišer, E Premate, P Trontel, M Zagmajster & V Zakšek)

11.15-OC30 The impact of pelagic food falls on an amphipod dominated scavenger community in the Deep Norwegian Sea, an experimental approach (**SL Scheer**, K Sweetman, U Piatkowski & HJT Hoving)

11.30-OC31 Density-dependent leaf litter consumption in experimental amphipod communities (**R Alther**, A Krähenbühl, CJ Little & F Altermatt)

11.45-OC32 Large seaweeds and small consumers: the role of amphipods in Arctic food webs (**J Beermann**, L Gutow & B Lebreton)

12.00-OC33 Abundance and food preferences of amphipods (Crustacea: Amphipoda) in the Eastern Gulf of Finland, Baltic Sea (**NA Berezina** & AA Maximov)

12.15-OC34 Scavenging amphipods of the abyssal and hadal Wallaby-Zenith Fracture Zone in the East Indian Ocean (**J Weston**, RA Peart, H Ritchie, SB Piertney, H Stewart, T Linley & AJ Jamieson)

Session 4b: Ecology (14.00-15.30)

Chairperson: José Guerra Garcia

14.00-OC35 Disparity in oxygen demand of native *Gammarus lacustris* and invasive *Pontogammarus robustoides* – which is superior under deteriorating environment? (**E Šidagytė-Copilaş** & K Arbačiauskas)

- 14.15-OC36** Adaptation to cold as a possible advantage of Lake Baikal endemic amphipods *Eulimnogammarus verrucosus* and *E. cyaneus* compared to a potential invader *Gammarus lacustris* (**KP Vereshchagina**, ES Kondrateva, AD Mutin, DV Axenov-Gribanov, EV Madyarova & MA Timofeyev)
- 14.30-OC37** Are all cryptic gammarid hosts a constant resource for their acanthocephalan parasites? (**A Bauer** & T Rigaud)
- 14.45-OC38** Cryptic diversity, mate discrimination and cannibalism among amphipod lineages: if you can't mate with them, eat them! (**C Lagrue**, M Galipaud & L Bollache)
- 15.00-OC39** Fouling amphipods, testing correlations with port effect and salinity gradient while facing taxonomic impediment (**A Desiderato**, J Beermann, JP Bozina Pine, L Sandrini-Neto, C Havermans, C Held & MA Haddad)
- 15.15-OC40** *Cleonardopsis carinata* K.H. Barnard, 1916: a Capbreton 'canyon indicator species' questionably reported all around the world ocean (**I Frutos** & JC Sorbe)

Session 4c: Ecology (16.00-17.30)

Chairperson: Anne-Helen Tanberg

- 16.00-OC41** From local to global: the network architecture of amphipod biodiversity in the Mediterranean Sea (**B Bellisario**, F Camisa, C Abbattista & R Cimmaruta)
- 16.15-OC42** A standardized methodology for monitoring and assessing fouling amphipod assemblages across spatio-temporal scales (**M Ros**, AT Revanales, V López de la Rosa, A Spinelli, A Fernández-Romero, JL Cervera-Currado & JM Guerra-García)
- 16.30-OC43** Are coastal defense structures shaping amphipod assemblages? (**F Sedano**, C Navarro-Barranco, JM Guerra-García & F Espinosa)
- 16.45-OC44** Effects of the amphipod *Gammarus insensibilis* in *Seriola dumerili* culture: growth, lipids profile and pigments (**P Jiménez-Prada**, S Jerez, JA Pérez, C Rodríguez, I Hachero-Cruzado & JM Guerra-García)
- 17.00-OC46** Small-scale phenotypic divergence highlights the underestimated value of amphipods as a model to study (contemporary) evolutionary divergence (**J Jourdan**, K Piro, A Weigand & M Plath)
- 17.15-OC47** Shape variations in *Parhyale darvishi*, the primary step of speciation (**Y Layeghi**, F Momtazi, A Bagherian Yazdi)

Friday August 30th

Session 5a: How many taxa? (09.00-10.30)

Chairperson: Ed Hendryck

- 09.00-OC48** Progress in the discovery of amphipod crustaceans (**T Arfianti**)
- 09.15-OC49** Talitraits: a taxonomic backbone for talitrid amphipods' traits (**L Fanini**, O Defeo, AF Bessa, LE Hughes, D Iacofano, R Cardoso, X Zafeiropoulos, S Lo Brutto, L Vandepitte, B Vanhoorne, W Decock & J Lowry)
- 09.30-OC50** French marine amphipod taxonomists: from the taxonomy to physiology (**JC Dauvin**, RA Kaïm-Malka & D Bellan-Santini)
- 09.45-OC51** Non-native marine amphipod species in the English Channel (**J-P Pezy**, A Baffreau & J-C Dauvin)
- 10.00-OC52** A new genus, new species and new records of Phoxocephalidae Sars, 1891 for the southeast and southern Brazil (**LF Andrade** & AR Senna)
- 10.15-OC53** Taxonomic study of lysianassid amphipods in Korean waters (**J-H Heo** & Y-H Kim)
- 10-30-OC54** First revision of UK caprellid amphipods in 75 years (**LE Hughes**)

Session 5b: How many taxa? (11.15-12.15)

Chairperson: Michal Grabowski

- 11.15-OC55** DNA barcode reference library for European freshwater malacostracans: getting there (**T Mamos**, T Rewicz, K Bacela-Spychalska, K Hupalo, A Jablonska, K Zganec, M Jelic, A Wysocka, L Sworobowicz, D Copilas-Ciocianu, A Petrusek, R Wattier, J Hinić, V Slavevska-Stamenković & M Grabowski)
- 11.30-OC56** Broad-scale DNA barcode-based meta-species analyses of patterns of molecular variation in Amphipoda from world's oceans (**PE Vieira**, C Gonçalves, P Soares, H Queiroga & FO Costa)
- 11.45-OC57** DNA barcode availability for European groundwater macrocrustaceans (**M Zgmajster**, Š Borko, T Delić, C Douady, D Eme, C Fišer, F Malard, P Trontelj & A Weigand)
- 12.00-OC58** What public data can tell us about current practices in DNA barcoding amphipods (**AE Radulovici**)

Abstracts

Plenary Lectures

DNA Barcoding, DNA taxonomy and integrative taxonomy: separating the wheat from the chaff

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The DNA Barcoding revolution started in 2004, and soon after had to face severe criticisms, mainly from taxonomists. Among other deadly sins, they accused the DNA barcoders to ignore the traditional approaches, and, by doing so, to reinforce the taxonomic impediment, instead of reducing it. But most of the controversy was based on misunderstandings, and if clarifications have been proposed about what DNA Barcoding can and cannot do, it remains sometimes difficult to conciliate it with traditional taxonomy. During my talk, I will thus (re-)define what is DNA Barcoding, in its restricted sense but also in its expanded applications, such as DNA taxonomy, and, when combined with other characters, criteria and methods of species delimitation, integrative taxonomy. I will insist on the differences between specimen identification and species delimitation, and will also elaborate on recent advances in the so-called "species concept debate". I will conclude with several examples, to illustrate why apparent contradictions between different characters, such as DNA and morphology, actually help not only to reinforce the species hypotheses, but also to propose hypotheses on the processes at their origin.

Amphipod ecotoxicology: endocrine disrupting pollution and endocrine disrupting parasites

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Our understanding of amphipod biology and ecology has a rich history extending back over a century. This coupled with their ecological importance and species diversity has meant they have been used extensively in ecotoxicology to assess the health of aquatic ecosystems. Since the late 1990s scientists have become concerned that a variety of different pollutants have the capacity to alter the endocrine systems of wildlife resulting in reproductive abnormalities and intersexuality. Despite this concern, our understanding of endocrine disrupting chemicals in crustaceans is still relatively poor. Many amphipods are prone to infections by parasites which can alter sex ratios and behaviour along endocrine mediated pathways. These parasites, despite sometimes ignored or considered an inconvenient 'noise' in environmental monitoring have the capacity to inform and conceptualise the impacts of endocrine disrupting chemicals. For example, incomplete feminisation by parasites can sometimes leave populations with a very high prevalence of intersexuality. Intersex specimens carry of burden of altered growth, reproduction and immunity. In addition, behaviour altering parasites utilising serotonin mediated pathways can leave organisms with increased likelihood of predation. For the past 15 years we have been researching amphipods which have feminising and behavioural altering parasites that are being used to determine adverse outcomes (AOs) for reproductive and neurological endocrine disruption. Using the marine amphipod (*Echinogammarus marinus*) as a model, we have determined the differential gene expression of male vs female specimens and organisms with parasite and non-parasite mediated intersexuality. We have created a toolbox of sex 'specific' genes and highlight that existing vertebrate biomarkers of feminisation should not be applied to crustaceans, as orthologous genes are not induced in feminised amphipods. Moreover, we have used behavioural and serotonin altering parasites to develop behavioural tests to inform serotonin altering pollutants such as antidepressants. These in tern have revealed insightful biological pathways using molecular approaches. All these reproductive and behavioural costs have been used to parametrize a dynamic deterministic population model over 10 year scenarios striking effects on long-term populations. These studies have provided the necessary information and tools to better understand the risk posed to pollution and underscore the importance of understanding parasites in ecological systems.

Fifty years of amphipod meetings. Taxonomical, ecological and behavioural patterns of the amphipodologist community

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In this ICA in Dijon we commemorate fifty years of Amphipod meetings, since the first one in Verona in 1969 organised by Sandro Ruffo and Traudl Krapp-Shickel. The amphipod family is growing: in the last 10 years the number of participants in ICAs has triplicated and the number of represented countries has duplicated. Regarding the topics addressed in ICAs, there has been increasing interest in molecular systematics, physiological aspects and applied research (e.g. toxicology, aquaculture). Since 1969 the annual rate of newly described amphipod species has also significantly increased, with a higher proportion of species now described by multiple authors instead of single ones, including not only taxonomical information (both morphological and molecular) but also ecological and behavioural data. The active participation of amphipodologists in WoRMS is also remarkable. Important advances using amphipods as models in proteogenomic, transcriptomic and mitogenomic studies have been achieved throughout the last decade, and detailed studies dealing with invasive species, life histories, behaviour and trophic ecology have also been presented in ICAs and published. The progress in the use of amphipods as bioindicators and as resource in aquaculture (live food for several species of commercial interest and also elements of Integrate Multitrophic Aquaculture systems) is especially interesting. Amphipods have also attracted the attention of different media during the last few years, and two amphipods, *Liropus minusculus* and *Epimeria quasimodo* have been among the top ten new species, in 2014 and 2018 respectively, selected from a total of ca. 15,000 species described annually. Despite the increasing interest in amphipod research, there is still a long way to go to understand and convey the importance of this group. Amphipod meetings are a great opportunity to highlight the importance of amphipods in ecosystems and the relevance of their applications in our society and thus convince authorities, governments and funding agencies that it is worthwhile to invest in amphipods. But above all, ICA meetings remind us that Amphipoda represent a way of life that is shared between these creatures and ourselves. With this presentation we will discover that we amphipodologists are not so different from our beloved amphipods...

Abstracts

Oral Communications

In alphabetic order

Density-dependent leaf litter consumption in experimental amphipod communities

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Amphipods are among the main shredders of leaf litter in freshwater habitats, particularly in the northern hemisphere. As such they play a key role for ecosystem functioning. However, amphipod communities are currently rapidly changing due to anthropogenic influences and biological invasions, with hitherto largely unknown consequences for subsequent ecosystem functioning. Here, we experimentally investigated how leaf litter processing by freshwater amphipods varies with changing population density and community composition. We used *Gammarus fossarum* as a native species and *Gammarus roeselii* as a non-native competitor, varying their density by two orders of magnitude, both in monocultures and pairwise mixtures. Results from 252 mesocosms show, that individual-based leaf processing rates are strongly depending on population density in monocultures. Adding a community context by interspecific competition reinforced this relationship, strongly affecting processing rates but also survivorship of the individual species. The density-dependent consumption rates possibly arose due to both intra- and interspecific interference competition. Our work demonstrates the need to account for nonlinear density-dependent processing rates and pairwise species interactions when predicting ecosystem functioning changes due to community changes.

A new genus, new species and new records of Phoxocephalidae Sars, 1891 for the southeast and southern Brazil

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The family Phoxocephalidae Sars, 1891, is one of the most diverse taxa in terms of taxonomic characters, being grouped in the suborder Amphilochidea Boeck, 1871. They are benthic, living mostly buried in the substrate, and are widely distributed bathymetrically, being found from shallow waters to the deep sea. The material examined was collected off the Atlantic coast of South America, from the states of Rio de Janeiro to Rio Grande do Sul, from 1969 to 1972, at depths ranging from 20 to 500 meters. The campaign was organized by the Instituto Oceanográfico from Universidade de São Paulo (IO-USP), using the R/V Prof. W. Besnard within the scope of the MBT (Mini Biological Trawl) project. All specimens are preserved in ethanol 70% and will be deposited at the Crustacea Collection of the Universidade do Estado do Rio de Janeiro (UERJ). For the taxonomic study, the appendages and mouthparts were dissected and mounted in glycerin gel slides, drawn under an optical microscope with camera lucida, Motic-BA 310, and digitalized with CorelDRAW X8. After the analysis of samples from 26 stations, it was possible to identify 12 taxa of Phoxocephalidae to date, grouped into 5 known genera, plus the description of a new genus belonging to the subfamily Phoxocephalinae. From this total, only *Microphoxus uroserratus* Bustamante, 2002 and *Pseudharpinia tupinamba* Senna & Souza-Filho, 2011 were previously recorded for Brazil. New records for Brazilian waters were found to the Argentinean species *Metharpinia dentiurosoma*, Alonso de Pina, 2003, *M. grandirama* Alonso de Pina, 2003 and *M. iado* Alonso de Pina 2003, besides seven new species grouped in the following genera: *Cephalophoxoides* Gurjanova, 1977; *Heterophoxus* Shoemaker, 1925; *Limnoporeia* Fearn-Wannan, 1968; Phoxocephalinae gen. nov; and *Pseudharpinia* Schellenberg, 1931. Identification keys to the world were created to all genera of Phoxocephalidae found in the campaign.

Progress in the discovery of amphipod crustaceans

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At present amphipod crustaceans comprise 9,980 species, 1,664 genera, 444 subfamilies, and 221 families. Of these, 1,940 species (almost 20%) have been discovered within the last decade, including 18 fossil records for amphipods, which mostly occurred in Miocene amber and are probably all freshwater species. There are more authors describing species since the 1950s and fewer species described per author since the 1860s implying greater taxonomic effort and that it might be harder to find new amphipod species, respectively. There was no evidence of any change in papers per author or publication life-times of taxonomists over time that might have biased apparent effort. Using a non-homogeneous renewal process model, I predicted that by the year 2100, 5,600 to 6,600 new amphipod species will be discovered. This indicates that about one-third of amphipods remain to be discovered which is similar to the proportion for other taxa. To increase the prospect of discovering new amphipod species, studying undersampled areas and benthic microhabitats are recommended.

Origin, diversity and distribution of freshwater amphipods in Northern Africa

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Northern Africa, although one of the world hotpots of biodiversity, is poorly studied and the freshwater fauna living in this part of the world remains partly unknown. In this study, we are interested in the diversity and the distribution of the poorly known freshwater amphipods. We performed an exhaustive analysis of the literature and we sampled more than 150 additional localities from the eastern part of Algeria, Morocco and in Tunisia. Our results showed a high diversity with 25 species (including the presence of at least three new undescribed species) and a very high rate of endemism with 52% of species being located on only 1 or 2 sites. The distribution of species between Europe and Northern Africa and between the western part and the eastern part of Northern Africa allow us to discuss some hypotheses about the factors underlying this endemism and about the biogeographical origin of species. Unfortunately, our study revealed the lack of knowledge, especially in the Southern Morocco and Algeria which remains largely unknown. More information are hence necessary to propose adapted conservation strategy for freshwater fauna in Northern Africa.

Are all cryptic gammarid hosts a constant resource for their acanthocephalan parasites?

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Multi-host parasites may use various host species differing in abundance and susceptibility to infection. These hosts will therefore contribute unequally to the transmission and the fitness of the parasites. The "key hosts" are those contributing significantly more to the completion of the parasite life cycle. Many parasites with a complex life cycle have developed the ability to manipulate several aspects of the phenotype of their intermediate hosts, including behaviour, thus increasing the probability of transmission to their definitive hosts. Several species of acanthocephalan manipulative parasites use *Gammarus* species as intermediate hosts and various vertebrate aquatic species as definitive hosts. It has recently been shown that many cryptic species of *Gammarus pulex* or *fossarum* live in sympatry in the rivers of eastern France, bringing a new vision of the spectrum of intermediate hosts that acanthocephalans can use, and their relative contribution. A field temporal monitoring of the relative frequencies of the different cryptic species of *Gammarus* was performed on two rivers during two years. The aim of the study was to know whether these frequencies are stable over time (allowing simultaneous use of all host resources by parasites), or whether they vary over time (allowing sequential use of hosts by parasites). Prevalence in various acanthocephalans was also measured, to detect eventual preferred hosts. We showed that even if the *Gammarus* frequencies vary over time, all species are present at each sampling date, indicating the possibility of simultaneous use by parasites. The analysis of prevalence showed that the preference for some host species are not the same for all parasites. Furthermore, we confirmed here that taking into account all developmental stages of parasites is fundamental for the study of manipulative parasites prevalence in natural populations.

Large seaweeds and small consumers: the role of amphipods in Arctic food webs

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Benthic seaweeds contribute substantially to the total primary production in Arctic fjords but only few consumers have been identified that are able to make use of the excessive algal biomass. However, herbivorous consumers at the base of the foodweb are crucial for channelling energy from benthic primary production towards organisms from higher trophic levels. Here, we tested 3 common consumers of the ecosystem of Kongsfjorden (Svalbard) for their capabilities to use seaweed biomass: the suspension-feeding amphipod *Caprella septentrionalis*, the biting/cutting omnivore *Gammarus oceanicus* and a surface-scraping gastropod. Specimens were collected in the field and were then offered diets of either fresh or aged algal detritus in controlled laboratory experiments over a period of 14 days. All consumers showed higher consumption rates for aged algal detritus than for fresh algal tissue. High amounts of fecal material produced by all consumers suggest an overall poor digestibility of algal food. We present first results on C/N ratios of the algal food and the fecal material to evaluate if the observed patterns were the result of either higher palatability of the detritus corroborated by increased bacterial colonisation and/or compensatory feeding on poor quality food. Our findings underline the role of amphipods for the flow of energy from detrital matter from Arctic macroalgae belts to higher trophic levels. Knowledge on the fate of macroalgal detritus in marine foodwebs will help to understand future changes of Arctic ecosystems in the context of global warming.

From local to global: the network architecture of amphipod biodiversity in the Mediterranean Sea

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Advances in the integration between different disciplines allowed for the development of brand-new approaches in the study of biodiversity patterns across different taxonomic realms. Among many, network analysis (i.e. the formal representation of species/habitat patches as nodes linked by any ecological relationship) has proved useful to deepen our knowledge of the ecological and evolutive constraints in the structure and functioning of ecological communities, and to identify critical scales in conservation ecology. Here, we applied a network approach in the study of Mediterranean crustacean amphipods associated with *Posidonia oceanica* meadows. Spatial co-occurrences of amphipods at different scales, from local assemblages to whole Mediterranean basin, were used as building-blocks to: i) uncover the role of species-specific traits (i.e. body size) as drivers for habitat selection in community assembly and, ii) identify bioregions in the distribution of Mediterranean amphipods. A general framework based on the integration between classical statistics and network theory has been implemented to infer local (species level) and global (community level) network structures on which to measure the modularity (i.e. a measure of the strength of subdivision of a network into modules, *aka* clusters or communities) and the topological roles of nodes. At local scale, our findings suggest the usefulness of including key species' traits in the reconstruction of association networks, highlighting the role of body size in micro-habitat selection as a main mechanism for community assembly. At global scale, the biogeographic module subdivision and the identification of source-sink communities suggest the role of complex interactions between present and past geographic barriers, local species adaptation, and the biogeography of the host plant in explaining the distribution of amphipod diversity on *P. oceanica*. We advise for an ecophylogenetic approach able to explicitly include phylogenetic information in community ecology, to capture elements of trait matching and evolutionary divergence among species during community assembly, and test for the hypothesis of a convergence between the ecological and evolutionary outcomes of amphipods and seagrass in the Mediterranean basin.

Abundance and food preferences of Amphipods (Crustacea: Amphipoda) in the Eastern Gulf of Finland, Baltic Sea

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The estuary part of the Gulf of Finland, formed at the confluence of the Neva River, is an area of high risk for penetration of invasive species to the Baltic Sea from the basins of the White, Black, Azov and Caspian Seas, the large lakes (Ladoga, Onega, Saimaa) and rivers (Volga, Don, Dnieper and Danube). This paper focuses on the estuarine Baltic amphipods and discusses their abundance and food habits in this part of the Gulf of Finland. From the 19th century until the 1960s, four species, *Gammarus pulex*, *Gammarus lacustris*, *Monoporeia affinis* and *Pallaseopsis quadrispinosa*, were common in the estuary of the Neva River. In 2013-2015, ten amphipod species were found. *Corophium volutator* and *M. affinis* were recorded the deep parts at salinity > 2, while the boreal *Gammarus zaddachi*, *G. oceanicus*, *G. duebeni* and *Bathyporeia pilosa* in the littoral areas. The coastal amphipod biomass was five times higher than the bathyal amphipod biomass. Invasive species such as *Pontogammarus robustoides*, *Gmelinoidea fasciatus* and *Gammarus tigrinus* were dominated by biomass (40 % of the total benthic biomass) and occupied an important position in the coastal food chains of the gulf attributing to be omnivorous or carnivorous animals, changing their food habits during ontogenesis. Adult males of these species preyed actively upon coexisting species of invertebrates reducing their abundance. At the same time, young and middle-sized individuals of amphipods, consuming a significant amount of detritus and algae, promote their rapid transformation, making this resource more available to the other consumers.

Diversification underground: adaptive radiation in genus *Niphargus*

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Adaptive radiation, a rapid monophyletic species proliferation accompanied by ecological diversification, was hypothesized to be the most important mechanism generating global species diversity. Several amphipod clades presumably adaptively radiated; however, a complete test for the adaptive radiation hypothesis was never conducted. We filled this gap in a comprehensive analysis of evolutionary history of the genus *Niphargus*. The genus, counting over 400 species, comprises one of the most speciose clades of freshwater amphipods in the World. Despite limited to subterranean environment, *Niphargus* successfully colonized and morphologically adapted to all subterranean aquatic microhabitats. Most of the genus diversity is concentrated in Southern Europe, and presumably evolved relatively recently. We hypothesized that uplift of major montane massifs, with emerging subterranean microhabitats in Eocene yielded an ecological opportunity that grounded one or more subterranean adaptive radiations. To test this hypothesis, we assembled a dataset of molecular, ecological, morphological and distributional data of more than 300 species. Using time-calibrated multilocus phylogeny and ancestral character reconstructions, we analyzed diversification patterns of species richness, morphological disparity and ecological changes. Additionally, we reconstructed ancestral distributions, and explored which evolutionary model of speciation and morphological disparification most likely explains *Niphargus* evolution. On a genus level, the results follow the predictions of adaptive radiations. We identified a dramatic switch in speciation and diversification patterns that temporally and spatially coincide with the uplift of major European mountain massifs. In this period, rates of speciation and morpho-ecological diversification accelerated, as predicted by the model of adaptive radiation. Moreover, models describing the evolutionary history of morphological traits switched from a neutral evolution to a model of stabilizing selection with multiple adaptive optima. On a clade level, we identified diverse evolutionary scenarios. Some clades followed patterns typical for adaptive radiations while others did not deviate from expectations for neutral evolution. The study has important implications. First, adaptive radiations seem to be a universal mechanism generating biodiversity also in extreme environments. Second, groundwater as fragmented, replicated “island” habitat, may be an interesting model system for studying macroevolutionary processes.

Cryptic diversity and ancient divergence in two species of amphipods from central Mediterranean Sea

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A phylogeographic analysis was carried out on two species belonging to the genus *Apolochus*, widely distributed in Mediterranean *Posidonia oceanica* meadows. Both mitochondrial (COI) and nuclear (H3) markers were used to verify: 1) if a pattern of high genetic differentiation associated to cryptic diversity is recovered, as suggested by both morphological stasis and a genetic architecture favouring high speciation rate observed in marine amphipods; 2) if high haplotype and nucleotide diversity associated to high geographic structuring and to lack of population expansion characterized species structure, so suggesting their survival in localized refugia; 3) if deep or recent splits occurred, with species origin pre- or post-dating the Messinian Salinity Crisis (MSC).

Our results showed: 1) a high cryptic diversity, with six MOTUs (putative species) in the Mediterranean Sea, three in *A. neapolitanus* and three in *A. picadurus*. The geographic distribution of these MOTUs showed that at least some of them were able to cross main Mediterranean barriers and to distribute in different seas over the time; 2) a remarkable level of genetic structuring was observed both between and within the different biogeographic areas, suggesting that the levels of ongoing gene flow are low or absent. This geographically structured pattern was coupled with high haplotype and nucleotide diversity and lack of signs of recent expansion at the population level; 3) the diversification within each *Apolochus* morphospecies was ancient, starting during the Terminal Tethyan Event (TTE, 18-12 Mya) and bearing the signature of the main Mediterranean paleogeographic events, such as the MSC (5.9-5.3 Mya) and the onset of ice cycles during Plio-Pleistocene ages (since 3.7 Mya).

These results provide insights into the usefulness of studying poorly vagile marine organisms to assess the biogeographic history of the Mediterranean Sea, since limited dispersal ability allows avoiding the loss of the signature of ancient events because of the superimposition of contemporary high gene flow. Our results suggest that amphipods are among these organisms and that their study may contribute to change the perception of the Mediterranean biodiversity from having a recent, post-Messinian origin, toward a more ancient derivation thanks to species survival along MSC.

Molecular omics resources and tools for amphipod investigation

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Objectives. Gammarids are key animal sentinels for *in situ* ecotoxicological biomonitoring of fresh water. Molecular biomarkers representative of key physiological parameters may be defined for gaining insights into the response of organisms to toxicants and measuring the anthropogenic impact in the environment. Recently, proteogenomics, a novel approach intimately combining next-generation sequencing and proteomic methodologies, has emerged as a straightforward strategy for discovering relevant proteins in non-model organisms. This opens the possibility to analyze the molecular players from any amphipod, and even to investigate its microbiota and parasites.

Methods. We sequenced the transcriptomes of a male and a female for seven different taxonomical groups: *Gammarus fossarum* A, *G. fossarum* B, *G. fossarum* C, *Gammarus wautieri*, *Gammarus pulex*, *Echinogammarus berilloni* and *Echinogammarus marinus*. These taxa were chosen to explore the molecular diversity of transcribed genes of genotyped individuals from these groups. Transcriptomes were *de novo* assembled and annotated. We optimized the *de novo* assembly strategy and constructed an impressive collection of protein sequences for these fourteen gammarids that can be used for interpreting proteomics data. In parallel, we recorded shotgun proteomics data on more than a hundred gammarid individuals to explore several key questions. We also developed several pipelines to investigate their proteogenomes and their microbiota.

Results. For example, we analysed two regional *Gammarus pulex* populations to characterize the potential proteome divergence induced in one site by natural bioavailable Cadmium contamination compared to a non-contaminated site. We have shown that the intra-population proteome variability of long-term exposed *G. pulex* was inflated relatively to the non-contaminated population. While remaining a challenge for such organisms with not yet sequenced genomes, taking into account intra-population variability is important to better define the molecular players induced by toxic stress in a comparative field proteomics approach.

Conclusion. The fourteen RNA-seq derived protein sequence databases proposed here are an important resource for proteogenomics on these non-model organisms. This work illustrates the relevance of omics for development of multiplexed biomarkers. Interestingly, the tools and strategies developed in this project are transposable to any amphipod.

Molecular phylogeny, habitat shifts and the evolutionary timescale of the Amphipoda

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Amphipods are one of the most taxonomically and ecologically diverse crustaceans, playing key roles in all aquatic ecosystems. However, they are also among the least known malacostracans, with an estimated two thirds of undiscovered species. Furthermore, widespread homoplasy has hindered their long-disputed phyletic classification and only recently morphology-based phylogenies provided a modern evolutionary perspective. Here, we present a first global molecular phylogeny aiming at providing an evolutionary timescale for this poorly fossilized group, assess its eco-evolutionary transitions, and complementing current systematics. We reconstructed phylogenetic relationships among 107 of the 226 recognized families using publicly available nuclear (H3, 18S and 28S) and mitochondrial (COI) sequences. Divergence times were estimated using the amphipod and decapod fossil record. The results revealed several well supported large clades: 1) one consisting of the majority of Senticaudata, the Lysianassidira, and the polyphyletic Hausotriidira and Synopiidira, 2) a clade consisting mainly of Amphilochidea, Colomastigidea and Hyperiidea, and 3) a clade comprising the Talitrida. Several Hadzioid genera have uncertain phyletic affinity, and the primitive family Atylidae is strongly recovered as a sister to the remaining amphipods. The order Ingolfiellida, although distinct, is moderately supported as a sister to Amphipoda. Time estimations revealed that amphipods split off from ingolfiellids in the Permian (~280 Ma), and started radiating shortly after the major Permo-Triassic extinction (~250 Ma). Ecological diversification into freshwater, terrestrial, pelagic, symbiotic and deep sea niches occurred after a long period of ecological stasis from a marine littoral ancestor. This ecological radiation seems to have been driven by global continental reorganization, oceanic deepening, transition to thermohaline circulation, and climatic cooling between the Late Jurassic and Late Cretaceous periods (160 to 80 Ma). Our study provides a solid, time-calibrated, eco-evolutionary framework for future research and sheds new light on the higher amphipod classification.

Combining molecules and morphology to describe cryptic new species – the *Bathyceradocus* genus case

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The deep-sea floor is supplied with a very small amount of organic matter. Sunken wood or plant remains have long been known as a valuable source of energy. Plant remains are widely distributed on the seabed and is found in all oceans and at all depths. Sunken wood make unique habitat that is considered as ephemeral but is inhabited by specialized fauna. After mollusks, the second largest invertebrate group inhabiting wood remnants are crustaceans including amphipods. Ten-odd species of wood-associated Amphipoda belonging to five families and six genera were hitherto identified. Four of them belong to the genus *Bathyceradocus* – *B. stephenseni* Pirlot, 1934, *B. iberiensis* Andres, 1977, *B. wuzzae* Larsen & Krapp-Schickel, 2007 and *B. hawkingi* Jażdżewska & Ziemkiewicz, 2019. The Tropical Deep Sea programme (ex MUSORSTOM) started in 2004 a series of surveys focused on the exploration of the sunken wood environments in the Solomon Islands, Vanuatu Archipelago and Papua New Guinea and specifically targeted sunken vegetation to further characterize its fauna. Material from these surveys supplemented by material from other parts of the World resulted in the collection of 141 individuals assigned to the genus *Bathyceradocus*. Molecular study of COI and 18S genes revealed very high diversity of the group and allowed to identify more than 15 putative species. The majority of them are species closely related to *B. stephenseni* suggesting a species complex and the assignation of them as new to science. The morphological characters that distinguishes the species are among others, the shape of propodus of gnathopod 1 and 2, the shape of coxa 4 as well as the shape of basis of pereopods 5-7 and armature of mandibular palp. These results suggest a revision of the genus *Bathyceradocus* and related species.

French marine amphipod taxonomists: from the taxonomy to physiology

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The role of the French taxonomists on the marine Amphipod knowledge along the French metropolitan coasts, and in other areas of the World wide Ocean is presented and commented. Latreille and Bosc described the first marine amphipod genus *Talitrus* in 1802, and de Savigny described the first species *Cymadusa filosa* in 1816. The taxonomic studies were amplified by Chevreux (1846-1931) with his descriptions of marine amphipods collected in Atlantic Ocean, Mediterranean sea, from the French Polynesia (Gambier Islands), and during the Prince Albert 1st de Monaco expeditions, in the Mediterranean Sea and the Atlantic Ocean. For a long time, the Chevreux and Fage Fauna of amphipods (1925) was used for the identification of amphipods. Another important step was the Mediterranean fauna of amphipods Bellan-Santini et al. (1982, 1989, 1993, 1998). Ledoyer with the Madagascar Fauna of amphipods (1982, 1986) gave important contributions to the knowledge of the amphipod fauna. Furthermore, Bellan-Santini and Ledoyer participated actively to the Amphipoda Fauna of the Mediterranean Sea. Along the time, both authors contributed to numerous amphipod species description from the Mediterranean Sea, Antarctic Ocean, sub-Antarctic area and Pacific Ocean. Nowadays, more than 900 species were described by French taxonomist, which represented about 9% of the known marine amphipod species (10,206 species) in the worldwide Ocean. Moreover, studies on taxonomic knowledge were the occasion to improve other researches on phylogeny, biology, physiology, ethology and ecology of amphipods and to develop numerous international collaborations.

From proteogenomics to systems biology in the freshwater amphipod *Gammarus fossarum*

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Objectives. Next generation sequencing and mass spectrometry technologies have recently expanded the availability of whole transcriptomes and proteomes beyond classical model organisms in molecular biology, even in absence of an annotated genome. These advancements are paving the way to explore the molecular physiology and the mechanisms of toxicity in environmentally relevant species, such as the amphipod *G. fossarum*. Here we present the results obtained combining systems biology and proteogenomics approaches to get functional insights in the reproductive system of *G. fossarum* and to identify different mechanistic effects of toxicants in the amphipod’s testes.

Methods. We performed co-expression network analyses (based on the R package Weighted Gene Co-expression Network Analysis, WGCNA) on shotgun proteomics data obtained from i) male and female gonads at different maturations stages and, ii) from testes of males exposed during their spermatogenesis at different concentrations of cadmium (Cd), methoxyfenozide (MET) or pyriproxyfen (PYR).

Results. We identified groups (*modules*) of co-expressed proteins (*i.e.* whose expression is highly correlated) significantly associated with biological processes, such as the secondary vitellogenesis in the female ovaries, and spermatozoa morphogenesis and energy metabolism in the testes. In particular, we identified taxonomically restricted proteins that may play a central role in the oocyte maturation. Moreover, we found that specific modules of testicular proteins were significantly associated with the exposure to the different contaminants we studied. These results show the interest of systems biology approaches for identifying distinct modes of action even in the presence of similar toxicological responses.

Conclusion. We showed that co-expression network analysis are a powerful integrative tool to investigate the –omics data issued from a proteogenomic approach in *G. fossarum* and that provide functional information about many unknown proteins and mode of action of environmental contaminants. In view of these results, it appears that mechanistic studies in amphipods can be carried out without waiting for the availability of genomes for our species of interest. In the perspective of this presentation we will also discuss the strategy currently in place to sequence the genome in *G. fossarum*, which will benefit from these upstream functional studies in the next future

Dispersal of subterranean amphipods during marine regressions

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Fluctuations of sea level have been considered as a major force shaping distribution patterns of terrestrial and freshwater fauna. Dispersal routes established during marine regressions and terminated during marine transgressions, yielded an interplay of dispersal and vicariant events. We tested the interchangeable role of dispersal and vicariance using a clade of subterranean amphipods of the genus *Niphargus*. The clade is distributed across the Western Balkans and the Apennine peninsula, the so called trans-Adriatic distribution. We assumed that the clade originated in the Balkans, and during one or more marine transgressions colonized the emerging Apennine peninsula, followed by vicariant speciation. We tested this hypothesis using multilocus calibrated phylogeny, and modelling of ancestral ranges. First, we analyzed the taxonomic structure of the trans-Adriatic clade using unilocus species delimitation. The clade, counting 101 putative species, indeed originated in the Balkans and dispersed independently across the Adriatic basin multiple times. The first two independent dispersal events were related to the establishment of two little known land bridges between the Balkans and the southern Italian peninsula, approximately 13 Ma. The third dispersal event corresponded to Messinian Salinity Crisis (Miocene, 5.9-5.3 Ma), when an Italian clade colonized an archipelago in the Eastern Adriatic Sea. The last dispersals presumably took place during Pleistocene Adriatic regressions and included between-island dispersal and colonization of islands from the Balkan Peninsula. All dispersal events were best explained by a biogeographic model hypothesizing jump dispersal, which is in agreement with relatively short time frames enabling dispersal via land bridges. We conclude that trans-Adriatic distribution reflects an unexpected and complex history of dispersal-vicariance events, which significantly increased species diversity of the clade.

Fouling amphipods, testing correlations with port effect and salinity gradient while facing taxonomic impediment

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Fouling communities are mainly composed of pioneer species that overgrow any kind of hard substrate immersed in water. In contrast to the sessile fauna of these communities, which is widely studied with respect to engineering issues and the introduction of alien species, their mobile portion is understudied. Amphipods constitute one of the most ubiquitous and diverse taxon of the fouling fauna, but little is known about their community patterns and status. We performed a hierarchical experiment in four southern Brazilian estuaries - two of which with international ports and one included in the Lagamar Biosphere Reserve. Polyethylene plates were deployed in the cold/dry and warm/wet season and retrieved with their fouling communities after three, six and twelve months. The amphipod assemblages were studied with an integrative taxonomy approach: an initial morphological identification was followed by an analysis of CO1 DNA barcodes of selected specimens for each species via Sanger-sequencing. Multivariate analyses of the community were performed in order to explore and test the effect of ports and salinity on the presence of species. Using general linear models, the environmental variables that best described the richness of total, native, cryptogenic and non-indigenous species were identified. The fouling communities of the estuaries with ports differed significantly in terms of species diversity and richness from those without ports, with higher alien and overall species richness. Our analyses also elucidated the influence of salinity and dissolved oxygen on community patterns. Furthermore, the molecular analyses confirmed several new records for the Brazilian coasts and, on the other hand, exhibited a high number of cryptic species in some presumably cosmopolitan species such as *Monocorophium acherusicum* and *Jassa slatteryi*. Our study underlines that the Brazilian marine fauna, and amphipods, in particular, are still far from being fully described. This shows that ecological research on fouling communities at southwestern Atlantic coasts is likely subjected to a taxonomic impediment. Further research should implement this hurdle, in order to prevent biased information for stakeholders to correctly manage biodiversity.

Transcriptional profiles and differential exposure in response to abiotic stressors in endemic Lake Baikal amphipods *Eulimnogammarus verrucosus* and *E. cyaneus* compared to that in a common Holarctic species *Gammarus lacustris*

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Lake Baikal is the oldest and deepest lake on Earth. Abiotic conditions in the lake have remained stable over millions of years. It is strongly oligotrophic, cold, has high concentrations of dissolved oxygen and low mineral content. Baikal is home to a unique freshwater fauna of endemic amphipods comprising about 350 species and subspecies. Interestingly, in contrast to the endemic species dwelling only in the lake, a widely distributed Holarctic species *Gammarus lacustris* inhabits small water bodies around Baikal and its shallow-water gulfs, but not the lake itself. This phenomenon is termed immiscibility of Baikal and non-Baikal faunas. In this work, we explored gene expression profiles in two Baikal endemic species, *Eulimnogammarus verrucosus* (Gestf. 1858) and *E. cyaneus* (Dyb. 1874), and in a Holarctic species, *Gammarus lacustris* Sars 1863, to understand if the differences in the stress response pathways could explain the immiscibility barrier between Lake Baikal and non-Baikal environments. To model the situation of *G. lacustris* invasion in Baikal, we acclimated the individuals of all species to the same conditions (Baikal water at 6 °C) and subsequently subjected to abiotic stressors. Subsequent RNA sequencing allowed us to obtain high-quality reference transcriptome assemblies for these species and perform inter- and intraspecies comparisons of expression profiles. These comparisons revealed that *G. lacustris* appeared to be already stressed by acclimation to the conditions typical for Lake Baikal and was then capable of very limited response to additional stressors, while both Baikal species provided a clear and similar response to elevated temperature and cadmium treatment. Among the gene families with the most pronounced response to both stressors were predictably heat shock proteins/cognates 70. Previous works in these species have only revealed a transcript, expression of which was moderately further induced by protein-destabilizing conditions. Here we described heat-inducible *hsp70s* in these species. Thus, this work provided insight into the molecular mechanisms of stress response in related Baikal and non-Baikal gammarids.

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Effect of organic and metallic pollutants on the density of micro-amphipods in northeastern Tunisia: case of some coastal localities

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Amphipods are one of the most common taxonomic group in aquatic ecosystems. They have been studied on several topics (ecological, genetical, biological, behavioral, etc.) They have been used as biotest in several studies and also as bioindicators of the "health condition" of their environments.

In the present study, six coastal localities affected by different sources of pollution and more or less anthropogenic activities are investigated. Sidi Ali Mekki (SAM) and Rimel (RML) exhibit the less anthropogenic pressure. Sidi Salem (SDS) is the most important tourist area of Bizerte city. Zarzouna (ZZP) is a port. Raoued beach (RB) and Khelij canal (KCE) are the most affected localities by organic and urban pollutants.

Sediment and water samples were collected from each locality. They were analyzed to measure organic (NO_2^- , NO_3^- , NH_4^{3+} , PO_4^{3-} , etc.) and metallic (Cu, Cd, Co, Fe, Pb, Mn, Ni, Mg, Hg, etc.) pollutants. The assays showed that the sediment in ZZP was the most affected by trace metals while the sediment and water of KCE and RD presented the highest organic components.

Regarding biological analyzes, our results showed that, among the microzoobenthos particularly crustaceans, the lowest density of amphipods was recorded in four localities. They also showed that organic and urban pollutants have an important effect on amphipods density (RB). The total absence of amphipods at ZZP will be proved by their sensitivity to trace metals recorded at high concentrations in this locality.

Talitraits: a taxonomic backbone for talitrid amphipods' traits

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Organisms' traits are increasingly being targeted to describe systems and their functionality. In ecological studies, analysis of traits' as units are largely applied to communities, while the application of traits to taxonomic levels is receiving less attention. The project "Talitraits" was launched to target: 1) a relatively low taxonomic level, the family Talitridae and 2) a well-defined ecological level, marine coastal zones. The selection of these levels drives the focus towards a set of traits that characterises talitrid species resident in coastal zones worldwide.

The project was supported by the E-Science European LifeWatch Infrastructure for Biodiversity and Ecosystem Research through LifeWatch Belgium. The Infrastructure targets different aspects of biodiversity research, and the Taxonomic Backbone of LifeWatch aims at bringing together taxonomic and species-related data and at filling the gaps in our knowledge, expanding the content and enhancing the quality of taxonomic databases. "Talitraits" thematic editors met to select a set of traits, consistent with the attributes already present in WoRMS on one hand, and sufficient to define coastal talitrids on the other. Traits were prioritized and addressed, using the published literature. Size, diet and relationship with substrate were set as initial priorities. Being the focus restricted to coastal organisms, distribution records were inserted as Country name - Exclusive Economic Zone. Traits specifically targeted by other thematic datasets (e.g. AMBI species, introduced species) were also prioritized.

The analysis of traits at family level and for a specific environment at global scale tightly connects to the species-environment perspective. It highlights the relevance of the local level within a global scale, and implies a connection of single species with environmental features (including human-driven ones). A set of additional traits, e.g. behavioural ones, will be a forthcoming priority area to address this specific theoretical frame. The Talitraits project highlights the issue of unbalanced literature within the Talitridae family, hence the dataset can be used to plan further gap-filling research.

First approach to the use of an index based on a polychaete/amphipod ratio to detect pollutant in marinas

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The implementation of the European Water Framework Directive (WFD, 2000/06/EC) has encouraged the use of biotic indices to determine the quality of European waters. We propose to reexamine the opportunistic polychaete/amphipod ratio suggest by Dauvin & Ruellet (2007), modifying and applying it for epifaunal communities associated to marine infrastructure such as harbors and marinas. This new ratio, called *epifaunal fouling opportunistic polychaetes and amphipods index* (EFOPA) follows the same calculations as the BOPA index: $\text{Log}_{10} (fp/(fa+1)+1)$, where fp is the opportunistic polychaete frequency and fa is the amphipod frequency but also including opportunistic amphipods (e.g. the genus *Jassa*).

To test the efficiency of EFOPA index, data obtained from 14 marinas sampled along the Iberian Peninsula (7 in the Atlantic and 7 in the Mediterranean coast) were used. For each marina, three colonies of *Bugula neritina* (the dominant fouling substrate) were collected and three random measurements of different environmental parameters were made. At the laboratory, all macrofauna was identified at major taxonomic levels and individuals of each group counted. To explore significant differences among marinas and significant correlations among environmental variables and EFOPA values, the SPSS v.22 package was used. Furthermore, a PCA was performed on abiotic data (PRIMER-e v.6).

PCA results indicated that Mediterranean marinas presented higher pollutants concentrations than Atlantic ones. After applying the EFOPA index for the studied marinas, significant differences between Atlantic and Mediterranean were detected ($p < 0.05$). Overall, index values were lower in more polluted marinas at the Mediterranean (between 0.003 to 0.01) and they increased in Atlantic marinas with less pollutants levels (between 0.01 to 0.06). There were significant correlations for Salinity, Temperature, Phosphorus, Sulfur, Chrome and Copper. Finally, EFOPA index seems easy to use because is based on the principle of “taxonomic sufficiency” and provides information about common pollutants in marinas. Anyway, it should be tested it in other human-impacted environments before being considered eventually for environmental management. Although taxonomical expertise is mandatory to properly identify species in ecological studies, environmental agencies, companies, local governments and authorities usually demand alternative easy indexes (such as EFOPA for marinas) as tools to address monitoring programs.

Functional ecology of the genus *Niphargus*

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Understanding the function of traits is a cornerstone of evolutionary ecology. Function is an outcome of a concerted action of one or more heritable traits, such as morphology, physiology or behavior, and is critically linked with an organisms' performance and fitness. The relationships between heritable traits, their function and organisms' fitness are essentials of adaptive biology, whereas organisms' performance, realized through specialized functions, is central to community ecology. Here we review studies on the genus *Niphargus* to 1) identify functionally relevant traits, 2) revise the functional correlates of these traits, 3) identify the tradeoffs they are subjected to, and 4) identify and discuss main research gaps. Virtually all *Niphargus* live in subterranean environments. Despite being eyeless, some of these species living at the subterranean-surface boundary detect light and show a strong photophobia, a presumed habitat choice mechanism. Body size is a complex trait; its upper size is controlled by void size. Comparative correlational studies suggest that it positively and negatively correlates with fecundity and metabolic demands, respectively. Appendages, such as antennae and pereopods, have sensory and locomotory functions. Aesthetascs-bearing antennae could be important in chemoreception, although the evidence for this claim is merely anecdotic. Pereopods' lengths relate to locomotion. Correlational analyses imply that the large species walking in upright posture with long pereopods move faster than short-legged species that crawl on their sides. Field observations suggest that the appendage length is controlled by water flow velocity. Gnathopods are important for grooming, feeding and digging. Although observations are mostly lacking, species with different gnathopods tend to co-occur more frequently than species whose gnathopods are similar in shape. The mouthparts have not been studied. Finally, a series of species in the Dinaric Karst, living together with olm, display strong pleonal spines. According to correlational analyses, these spines might have an anti-predatory function. Our review identified two major fields in need of further investigation. First, the functional evidence for most traits is indirect, correlational or qualitative. Second, the heritability of the traits has not been studied. We conclude with a proposal for systematic experimental work, and development of a database of functional traits.

***Cleonardopsis carinata* K.H. Barnard, 1916: a Capbreton 'canyon indicator species' questionably reported all around the world ocean**

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The amathillopsid *Cleonardopsis carinata* is the single species known in the genus *Cleonardopsis*. Originally described by K.H. Barnard in 1916 from Atlantic bathyal bottoms off South Africa, it was subsequently recorded in E Indonesia, W Greenland and SE Iceland. In the last decades, this species has been reported on bathyal bottoms of the Bay of Biscay (depth range: 366–3020 m). During several surveys, *C. carinata* was sampled by means of multi-net suprabenthic sledges, in the Cap Ferret area (canyon and southern margin), in the Capbreton area (canyon and adjacent open slope), on the Le Danois Bank and in the Meriadzek Terrace. Its near-bottom vertical distribution shows that 96.1% of the individuals live in close contact with the sea floor. Although its morphology suggests that it could be an inquiline species (maybe on the erected tubes of the foraminifer *Bathysiphon*), it is also a good swimmer (powerful pleopods), able to perform horizontal/vertical migrations. Specimens were generally sampled in low abundance (≤ 6 ind./100 m²), although an unusual abundant population was detected in the upper part of the Capbreton Canyon (up to 232 ind./100 m²). Such exceptional abundances were used to carry out a demographic analysis of the canyon population at a seasonal level (composite year). Brooding females (5.9–8.5 mm BL=Body Length) were bigger than mature males (5.7–6.4 mm BL) and showed a relatively low fecundity (maximum recorded: 15 ind./marsupium). Juveniles were dominant (68.4% of total abundance), demonstrating a strong autumnal recruitment in the canyon population. As previously observed for some other shelf and bathyal peracarids from the southern Bay of Biscay, the reproduction of this amphipod is probably a continuous process all year round. In the last years, specimens ascribed to the genus *Cleonardopsis* have been also recorded in the N Atlantic Ocean (Irminger and Icelandic basins) and in the SE Australian waters (Tasman Sea). The detailed comparison of all these recently collected specimens with the 'historical' ones, recovered from several museum collections, will allow us to verify if *C. carinata* is as widespread as it seems through literature.

First glance at molecular diversity and phylogeography of Periadriatic freshwater gammarids

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Recent studies reveal presence of very high level of cryptic diversity and local endemism in many freshwater taxa. The Mediterranean, including the Periadriatic Region, is among the key biodiversity hotspots on the global scale. However, majority of studies upon gammarid crustaceans of the region focused mostly on marine species, leaving aside the freshwater fauna. Extensive sampling in the years 2005-2016 yielded a very large collection of gammarids encompassing more than 40,000 individuals gathered from over 500 inland and insular locations in the Periadriatic region. Molecular analyses revealed extremely high level of cryptic diversity, largely exceeding the number of morphospecies already described from the region, i.e. forty molecular species within *Gammarus balcanicus* group, at least twelve species within *Gammarus roeselii*, around ten cryptic species in *Gammarus italicus*, as well as ten molecular species of *Gammarus* from the Peloponnese and high cryptic diversity including a few dozens of species within *Echinogammarus* in the Apennine Peninsula. The collected data greatly aid to reveal the biogeographical affiliations and the diversification time frames of the local gammarids and will eventually help to update the taxonomy within the family Gammaridae. We also hope that the knowledge about the real level of biodiversity will largely aid planning reasonable and effective strategy preventing or at least minimalizing the rapid loss of freshwater biodiversity, due to the extensive anthropogenic degradation of the local freshwater ecosystems.

Comparative molecular diversity and historical demography of two gammarid species as indicators of "Atlantification" in the High Arctic

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One of the regions with particularly noticeable global climate change is the Arctic, where the rate of warming is estimated as three times faster than the global mean value. The process of sea ice coverage reduction, melting of glaciers at large scale, ocean and air temperatures rise as well as transport of warm waters from Atlantic northwards to European Arctic with the West Spitsbergen Current is so called "Atlantification" of the Arctic.

Two common amphipod species, *Gammarus oceanicus* and *Gammarus setosus*, were sampled and studied in the intertidal zone of coastal area in Svalbard Archipelago (Norway). The total of 15 sampling sites were designated in three islands: Spitsbergen, Prins Karls Forland and Barentsoya. Genetic analysis showed geographical homogeneity of *G. oceanicus* with only one molecular operational taxonomic unit (MOTU) and much higher diversification of *G. setosus* (5 MOTUs) in the studied area. Only two MOTUs of *G. setosus* are widespread along the whole studied Svalbard coastline, whereas the remaining three MOTUs are present mainly along the northern and eastern parts of archipelago's largest island, Spitsbergen. Distribution analysis indicates that the demographic and spatial expansion of *G. oceanicus* in the northern Atlantic has started already during the Last Glacial Maximum (LGM, ca. 20 ka), while *G. setosus* seems to be a long-persistent inhabitant of the Arctic, possibly even through the LGM, with slower distribution dynamics. Combining the results of our molecular study with the knowledge upon the direction of ocean currents around the Svalbard Archipelago, it can be assumed that *G. oceanicus* is a typical boreal Atlantic species that has recently migrated to the north due to the warming of the Arctic and has partly displaced *G. setosus*, that used to be the only common gammarid of the Svalbard intertidal zone.

Effects of injection of non-biodegradable polyelectrolyte microcapsules into the amphipod circulatory system

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Microcapsules prepared by layer-by-layer assembly of oppositely charged polyelectrolytes can be used as convenient carriers for targeted delivery of different substances into specific organs. In particular, this possibility can be useful for study of the targeted influence of chemicals on specific tissues, prolonged vaccination, and measurement of physiological parameters *in vivo* using fluorescent molecular probes. Previously, semipermeable microcapsules carrying a pH-sensitive fluorescent dye has been shown to mirror changes in hemolymph pH inside amphipods.

In the current study, we analyze the behavior of non-biodegradable microcapsules coated with polyethylene glycol and their influence on adult amphipods *Eulimnogammarus verrucosus* (Gerstfeldt, 1858) after injection into the circulatory system. The composition of microcapsules was chosen to decrease recognition by the amphipod immune system using polyethylene glycol cover and increase their overall stability for sensing purposes. At least single fluorescent microcapsules were observed in the circulatory system in all segments of the amphipod. Their concentration in the central hemolymph vessel was high only during the first days after injection and significantly decreased already in a week, while in the head the microcapsules were visible up to five weeks. In future, high deposition of microcapsules nearby the head ganglion potentially can be used for targeted delivery of various substances to the nervous system. The number of microcapsules that was necessary to detect their fluorescence in the central hemolymph vessel showed no toxicity during six weeks after injection and did not induce stress response of the amphipods. The injection wound was shown to heal in approximately one month. The activity of phenoloxidase did not react to the injection of microcapsules, but amphipod hemocytes in the primary culture started to significantly aggregate around them in a few hours after contact and isolated them from the media.

So, we conclude that polyelectrolyte microcapsules can be used for measurements of hemolymph parameters only during the first hours after injection due to the relatively quick decrease in their visibility in the central hemolymph vessel and immune response.

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Connectivity and putative native ranges of the two “cosmopolitan” biofouling amphipod species, *Jassa marmorata* and *Jassa slatteryi*

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Little is known about the invasion history of most small marine invertebrate species. Accordingly, it can be difficult to determine whether a species is native to an area, dispersed into the area as a result of natural dispersal mechanisms, or as a result of human facilitation. Two marine amphipod crustacean species, *Jassa marmorata* and *Jassa slatteryi* are typical components of marine biofouling communities and have long been considered to have cosmopolitan distributions, with no reliably assigned native range. Although possible historical invasion pathways of the two species cannot be reconstructed, I hypothesized that due to the species' biology the current “cosmopolitan” distribution of these species is the result of invasive events, probably mediated by transoceanic shipping activities that started centuries ago. This case study aimed to collect detailed information through molecular analyses (CO1 gene) on these two globally distributed *Jassa* species in order to evaluate their genetic structure and to attempt to determine their putative former native ranges. Overall, *Jassa marmorata* exhibited both a lower haplotype and nucleotide diversity than *J. slatteryi* despite a higher sample count. The highest genetic diversity measures (accounting for both haplotype and nucleotide diversity values) in *J. marmorata* were found in the NW Atlantic region, and in *J. slatteryi* from the NW Pacific region. An overall higher genetic variation was detected within populations of *J. marmorata* (47.88%), with a slightly smaller percent variation among populations within the different marine regions (44.98%). In contrast, the overall genetic variation was markedly higher within populations of *J. slatteryi*, (56.89%). Variation among marine regions was the lowest for both species. The results of this study indicate that the likely former native range of *J. marmorata* is the NW Atlantic region, whereas the likely former native range of *J. slatteryi* is the Northern Pacific (NW and NE) region. Shipping appears to be the more successful vector of *Jassa* species dispersal on a global scale as compared to natural dispersal, which exemplifies one of the major threats that human-mediated bioinvasions pose to the maintenance of biodiversity and ecosystem functioning in marine systems.

First revision of UK caprellid amphipods in 75 years

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The marine North Atlantic and UK invertebrate fauna is considered to be the most well-known, with a long established and relatively stable taxonomy in comparison to other marine regions, however genetic approaches are showing high levels of unrecognised diversity. For UK caprellid amphipods, the majority of the fauna were described in the late 17 to early 1800s beginning with Slabber, Linnaeus, Montagu and Leach. Many of these historic species are now listed with large synonymies and world-wide distributions within the literature. This project begins to revise the nomenclature and type description of UK caprellids from the late eighteenth century to current records based on museum specimens and literature, including confocal microscope of historic specimens. Despite modern grey literature citing only 15 species of caprellid amphipods for the UK, 34 species and subspecies are listed in the historic literature which have potential bearing for modern genomic research and applied nomenclature. Scientific names are an essential reference point for conservation management and planning. As vouchered tissue repositories for high quality genomic and transcriptomic research, and custodians of traditional type collections, this project showcases museums as have a unique selling point, supporting hypothesis driven science.

Freshwater amphipods of Mediterranean Islands – fascinating findings and exciting perspectives

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The Mediterranean Islands are known as one of the most speciose biodiversity hotspots in the world, serving as natural laboratories of evolution. Even though, the Mediterranean fresh waters house nearly 6% of global freshwater taxa, being also subject to heavy anthropogenic pressure, still little is known about its freshwater biota, with very few studies focusing on the diversity and phylogeography of the insular fauna. Similarly to continental habitats, gammarid amphipods are vital component of the insular lotic macrozoobenthic communities, however neither biogeographical studies nor molecular bioassessments have been done so far on the insular freshwater gammarids. The multi-marker dataset composed of nearly 1000 individuals belonging to *Gammarus* and *Echinogammarus* genera from more than 100 sites from the Mediterranean Islands including Sicily, Crete, the Aegean Islands, Sardinia and the Maltese islands. The reconstruction of time-calibrated phylogeny revealed a complexity of evolutionary histories, usually dating back to the major geological events and island isolations. The results also indicated that the colonisation of the insular inland waters, depending on the species, took place either from the continent waters or directly from the Tethys. Moreover, all MOTU delimitation methods applied in our study support the extremely high level of overlooked diversity, ranging up to 15 distinct lineages within one morphospecies. Our results from Sicily and Crete indicate a connection between evolutionary history of the freshwater gammarids and the geological history of the Mediterranean Islands. The high level of formerly overlooked insular freshwater biodiversity combined with strong local lineage endemism stress the importance of using DNA-oriented methods in freshwater biodiversity surveys. Moreover, the new, preliminary results from *Gammarus* species from the Aegean Islands and Sardinia as well as from Maltese *Echinogammarus* provide a starting point for unfolding yet unknown evolutionary histories and indicate the strong connectivity between the evolutionary patterns of the insular freshwater gammarid fauna from Mediterranean Region.

Bathymetric and geographic patterns of amphipods from Kuril-Kamchatka Trench and adjacent abyssal plain

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The exploration of the deep sea has vitalized in the recent years. Various regions were intensively sampled and the results considerably increased our knowledge about deep-sea diversity. However, there are several questions that still remain opened, concerning for example bathymetric or geographic ranges of deep-sea species. One of the most abundant abyssal invertebrate groups are amphipods but only 400 benthic species were hitherto identified below 2000 m worldwide of which 50 were recorded from the abyssal of NW Pacific. Recent molecular study of the Northwest Pacific abyssal and hadal Amphipoda identified 135 Molecular Operational Taxonomic Units (MOTUs) representing putative species, of which many are new to science. The aim of the present study is to characterize depth and geographic ranges of the recognized putative species.

The samples were collected during two German-Russian expeditions (KuramBio I and II) to the Kuril-Kamchatka Trench and adjacent abyssal plain. The stations were situated in the trench itself as well on its both sides, covering the depth range from 4800 till 9500 m. The species recognition was based on the analysis of the cytochrome oxidase I (COI) gene. To identify the bathymetric and geographic patterns the MOTUs that were found at three or more stations (28) were chosen.

The bathymetric ranges of the studied MOTUs showed three groups of taxa: typically abyssal (20) and hadal (4) species as well as the ones that inhabit the abyssal zone but extend their distribution into the hadal depths (4). The geographic ranges varied between MOTUs but seven species were recorded at the most remote stations that were situated 1000 km apart and were separated by the Kuril-Kamchatka Trench. They belonged to Eusiridae (2), Pardaliscidae (1), Vemanidae (1), Phoxocephalidae (1), Synopiidae (1), and Lysianassoidea (1). This proves that the trench does not constitute the barrier for certain species distribution. However, it may limit the constant gene flow in case of others.

Responses of *Orchestia gammarellus* (Amphipoda, Talitridae) to copper contaminated soil

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This study deals with the evaluation of copper bioaccumulation and its effect on the hepatopancreas ultrastructure and the locomotor behaviour of the supralittoral amphipod *Orchestia gammarellus* (Pallas, 1766).

Adult specimens were collected from the banks of the Bizerte lagoon (37°13'8"N/09°55'1"E). Then, they were exposed to copper contaminated soil during 14 days and where three concentrations were prepared. Individuals were weekly weighed and metal concentrations in the metabolism of talitrid were measured. The concentration factor (CF) which provides an estimation of Cu contamination in the amphipod was calculated. The locomotor activity rhythm of this species was also studied under controlled laboratory conditions for the control as well as for the contaminated individuals using only the low concentration (C1) under constant darkness (DD).

The obtained results showed that from the first week until the end of the experiment, some fluctuations in the body mass were observed with a highly significant difference between nominal concentrations. The determined CF revealed that *O. gammarellus* was a macroconcentrator of copper.

The hepatopancreas of untreated animals showed histological and ultrastructural features similar to those described in other amphipod species. However, the different concentrations of Cu induced significant changes both in the general morphology and in the ultrastructural organization of the different cells of the hepatopancreas.

Otherwise, this study of locomotor activity rhythm showed the existence of a circadian component for control as well as for contaminated individuals. The locomotor behaviour of these last was characterized by the shortest circadian period.

The present findings suggest the usefulness of the talitrid *O. gammarellus* as a bio-indicator species that might be employed in future biomonitoring programs.

Effects of the amphipod *Gammarus insensibilis* in *Seriola dumerili* culture: growth, lipids profile and pigments

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Three of the relevant areas to research in aquaculture are: i) the investigation of the potential of novel aquatic organisms as live feed, ii) the progress in 'Integrated Multi-Trophic Aquaculture' (IMTA) and iii) the aquaculture diversification in species highly appreciated by consumers. The present study showed the potential use of the amphipod *G. insensibilis*, in the aquaculture rearing of *Seriola dumerili*, a fish with commercial interest, during two distinct stages of development. Two experiments were done with *S. dumerili* larvae of 22 and 44 days after hatchery respectively. Larvae of *S. dumerili* were fed with the amphipod *Gammarus insensibilis*, collected from a terrestrial pond, and one formulated diet. Survival, biometry measures and chemical profile of the fish larvae were measured. In the first experiment, *G. insensibilis* treatment showed better survival, although the other parameters were no different. On the other hand, in the second experiment the survival was similar, the growth was better with formulated diet, and *Gammarus insensibilis* treatment had the best chemical profile. *G. insensibilis* treatment showed higher values of ARA ($5.53 \pm 0.18\%$) and DHA ($19.07 \pm 0.19\%$), low level of TAG ($2.18 \pm 0.5\%$) and a coloration similar to that in wild juveniles of *S. dumerili*. In fact, the fish larvae feed with the amphipod presented 5 times more thunaxanthin, the pigment which give the common name to *S. dumerili* (greater amberjack).

Small-scale phenotypic divergence highlights the underestimated value of amphipods as a model to study (contemporary) evolutionary divergence

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Selective landscapes in rivers are made up by an array of selective forces that vary from source to downstream regions or between seasons. Selective forces are not only of natural origin, but also anthropogenic activities act as selective agents. Local and temporal variation in fitness maxima can result in gradual spatio-temporal variation of phenotypic traits. While many invertebrates disappear at a certain threshold disturbance level, most river ecosystems still harbor at least some amphipod species, rendering them ideal model organisms to investigate adaptation in a dynamic environment. We examined phenotypic responses of non-native *G. roeselii* that occurred at various ecological conditions in the Rhine catchment. We quantified key parameters related to morphological and life-history evolution, including naturally selected (e.g., gill surface areas) as well as primarily sexually selected traits (e.g., male antennae). Acknowledging the complexity of selective regimes in streams and the interrelated nature of selection factors, we collected several potential abiotic (e.g., temperature, flow velocity) and biotic selection factors (e.g., conspecific densities or sex ratios) and condensed them into four principal components (PCs). We found pronounced intraspecific divergence in most of the traits investigated herein, and components of the stream gradient (PCs) explained parts of the observed divergence. Depending on the trait under investigation, phenotypic divergence could be ascribed to gradual variation in abiotic conditions, anthropogenic disturbance by the influx of thermally polluted water, or effects of population parameters. For example, female fecundity showed altitudinal variation and decreased with increasing conspecific densities, while sexual dimorphism in the length of male antennae—used for mate finding and assessment—increased with increasing population densities and towards female-biased sex ratios. Phenotypic divergence over small geographical scales may partly reflect phenotypic plasticity (as evidenced by seasonal variation, e.g., in gill surface areas). Still, divergence of certain morphological traits likely reflects small-scale evolutionary divergence, highlighting the potential of using freshwater amphipods to study local adaptation. Moreover, the fact that *G. roeselii* invaded Central Europe approx. 150 years ago and most of the present anthropogenic disturbance started even later illustrates that questions related to contemporary evolution can be addressed in amphipods.

Taxonomic study of lysianassid amphipods in Korean waters

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This study aims to reveal the specification of Korean lysianassid amphipods through morphological characteristics. In 1991, *Orchomenella obtusa* (G. O. Sars, 1891) was newly reported by Kim and study on Korean lysianassid amphipods began. To date, 10 species of lysianassid amphipods have been reported in Korean waters, and the current status of these studies show that Korean lysianassid amphipods studies are still insufficient. The lysianassid amphipod specimens were collected by fishing net, bait trap, and light trap from 1989-2019. The morphological description was performed using an optical microscope and drawing tube. As a result, we have added 3 new species (*Microlysias* n. sp. 1, n. sp. 2 and *Opisa* n. sp.) and 4 newly recorded species (*Anonyx schefferi* Steele, 1986; *Opisa takafuminakanoi* Narahara-Nakano, Kakui & Tomikawa, 2016; *Orchomenella littoralis* Nagata, 1965; *Socarnes bidenticulatus* Spence Bate, 1858). Three new species are small groups, consisting of two and four species. The *Opisa* group is known as epi-parasitic species, and *Opisa* n. sp was collected from flatfish to identify hosts. Furthermore, we are going to verify morphologically derived results through mitochondrial COI sequence analysis.

Cryptic diversity, mate discrimination and cannibalism among amphipod lineages: if you can't mate with them, eat them!

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The freshwater amphipods *Gammarus fossarum* and *Gammarus pulex* are widespread in Europe and show high cryptic diversity, even at a small spatial scale. In natural amphipod populations containing sympatric but morphologically cryptic amphipod lineages or molecular operational taxonomic units (MOTU), pre-copulatory pair formation was random among MOTUs diverging by less than 4%. However, pre-copulatory pairs involving amphipod individuals from MOTUs diverging by more than 4% were rare, suggesting mate discrimination between sympatric, highly divergent MOTUs.

We tested mate discrimination, pre-copulatory pair formation, egg production and cannibalism among cryptic MOTUs ranging from 0 to 17% genetic divergence in laboratory settings to control for female size and time before reproduction, two traits previously recognized as important in male mate choice. Males generally preferred females from their own MOTU when offered a choice and consistently won the competition over pairing with females of their own MOTU, revealing a strong influence of genetic divergence on mate recognition and reproductive isolation among sympatric MOTUs.

Interestingly, when offered no alternative female and no competition, males still paired with females from highly divergent MOTUs. However, these pre-copulatory pair formations resulted in cannibalism of the female in up to 25% of cases depending on MOTU combinations. Cannibalism occurrence varied with genetic distance between males and females but not exclusively. We observed MOTU specific tendencies to cannibalism in males but also in female abilities to escape pairing and cannibalism.

Overall, our results reveal a strong influence of genetic divergence on mate recognition and reproductive isolation among sympatric MOTUs. Furthermore, the asymmetrical tendencies of different MOTUs for cannibalism may have significant implications for the long-term co-existence of cryptic MOTUs occurring in sympatry. It has long been recognized that intraguild predation in amphipods could lead to species exclusion. Here we show that inter-MOTU cannibalism could significantly influence the success of weaker MOTUs and the co-existence of sympatric *Gammarus fossarum* and *Gammarus pulex* MOTUs.

Shape variations in *Parhyale darvishi*, the primary step of speciation

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Parhyale darvishi Momtazi & Maghsoudlou 2016 is the most frequent amphipod species in the coastal line of the Persian Gulf and the Gulf of Oman. The shape and characters of propodus of first and second male gnathopods, and third uropod have taxonomic value in this genus. Geometric morphometric method is a useful method for detecting shape variations in small scale. In the current project the shape variations of 99 specimens of *P. darvishi* from 10 stations with different environmental characters were studied with semilandmark method. The shape of propodus in first and second male gnathopods and third uropod was digitized with 180, 180 and 150 semilandmarks respectively. Analyses of allometry inter and intrapopulations is shown that there is no significant relationship between size and shape of taxonomical parts in *P. darvishi*. The results of PCA analysis revealed shape variations in all three studied parts. The results also show a significant shape differences and cryptic diversity between studied populations. These results suggest the process of speciation in the genus *Parhyale* in the region.

Amphipoda from the Reykjanes Ridge, Iceland, with a focus on their coral associations

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During RV MS Merian expedition MSM75, an international, multidisciplinary team explored the Reykjanes Ridge SW Iceland in June to August 2018 in four sampling areas.

In the area 1, Steinahóll region (Reykjanes Ridge) ~2000 peracarid individuals were sampled in total between 200-350 m. Of this 65% were Amphipoda, comprising 38 families. The Steinahóll region contains multiple habitat types, including lava talus/pillows, sedimented plains, sponge fields and hydrothermal vent sites. Epibenthic Sledge (EBS) and van Veen Grabs (vVG) sampled soft sediment areas, and Remotely Operated Vehicle (ROV) dives sampled the harder substrates. We do observe significant differences in the amphipod composition via gear type. Our preliminary findings suggest that hydrothermal activity does not significantly influence the amphipod composition.

In the areas 2 and 3 an unexpected density and diversity of cold water corals was discovered. Special attention is given to the amphipods living on colourful hardcorals, mainly collected in 750 to 1450 m depth. There were 10 ROV dives conducted at areas 2 and 3, resulting in over 72 hours of video material. Once again many habitat types are visible, with these areas including locations of coral coverage. Real time interactions between Amphipoda and their associated corals can be observed in the obtained video material. Many hundreds of taxonomically challenging Pleustidae await being scientifically illuminated. To better resolve the diversity of these Pleustidae we combine analyses of COI with next-generation sequencing data (ddRADseq). Species diversities, compositions and species-specific associations with certain corals are studied.

DNA barcode reference library for European freshwater malacostracans: getting there

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The factual diversity of European freshwater malacostracans is scarcely known. Recent molecular studies upon decapods, amphipods, isopods and mysids show that their real diversity largely exceeds the number of already described morphospecies. Yet, its large scale spatial pattern and onset are still weakly understood. So far we obtained ca. 10,000 COI DNA barcodes for malacostracan crustaceans from all over Europe and combined them with barcodes already existing in BOLD and GenBank. We covered the traditionally recognized Mediterranean biodiversity hotspots, the northern post-glacial regions, lowland and alpine areas, lakes, rivers and spring systems. We discovered presence of very high cryptic diversity and numerous molecular operational taxonomic units (MOTUs) endemic for mountain ranges, even in relatively high latitudes, as well as for more southern lowland areas. On the other side, we observed presence of several widespread MOTUs with dynamic demography in post-glacial regions. With aid of other molecular markers we could attribute the observed diversity patterns, even at the species level, to a series of geological and climatic processes ranging from Neogene to the retreat of Pleistocene Ice Sheet as well as to very recent anthropogenic factors. Our effort is a first attempt to construct the comprehensive and publicly available COI DNA barcode library for freshwater malacostracan crustaceans in Europe on a continental scale. Proper identification of MOTUs as well as mapping and understanding their distribution is of utter importance when using crustacean models in evolutionary/ecological studies, biomonitoring and risk assessments.

Morphological and molecular comparison between populations of scuds from *Hyaella* genus from two States in Mexico: Veracruz and Ciudad de Mexico, Mexico

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Hyaella genus is a freshwater taxa of epicontinental crustacean amphipods with few studies in Mexico. In the past, it was accepted *Hyaella azteca* (De Saussure, 1858) as a single species with wide distribution over the America Continent, nevertheless several studies in South America discovered new species, distinguished by the morphology. On the other hand, in the United States there are more than 40 provisional species identified by partial mitochondrial DNA sequences but without a formal description. *Hyaella azteca* was considered as a morphological cryptic species and it was the unique species in genus described and recorded for Mexico. With the objective to know the taxonomic state of the complex *H. azteca* in Mexico there were collected 692 amphipods in three lakes from Mexico City (Chalco, Xochimilco & Chapultepec), and in three lakes in Veracruz State (Catemaco, La Encantada & San Julián). We compared the morphology with SEM images and compared partial mitochondrial DNA sequences from the COI gen. We used a morphotaxonomic approach, and we could identify five morpho-species from Veracruz and one from Mexico City and then we could validate this species with DNA-based delimitation methods with an analysis of gen COI. As results we could identify two clades that belong to Mexico City clade and Veracruz clade, this last one is similar to *H. azteca* by the telson form, according to the redescription by Gonzalez & Watling in 2002 from the syntypes, collected by De Saussure, from Veracruz. The presence of seven morphologically distinguishable species and the confirmation by molecular analysis suggest that the scuds biodiversity in Mexico, especially *Hyaella* genus, is underestimated in the Country, and we need more studies than join the DNA studies with its morphology in order to understand its evolutionary and recent history.

Exploring introduction events and temporal genetic variation of the exotic *Caprella scaura* in Southern Spain

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The amphipod *Caprella scaura*, considered native to the western Indian Ocean, is a successful invader of Atlanto-Mediterranean waters, travelling in association with fouling communities in vessels hulls. In the Mediterranean Sea, and concretely in the Iberian Peninsula, it has been widely spread by means of recreational boating. The present study focuses on several introduced populations associated to fouling communities of marinas in the Atlantic-Mediterranean transition zone (hotspot for introductions in the Mediterranean Sea). We used mitochondrial (COI, 16S) and nuclear (ITS1) markers in order to determine the putative patterns and pathways of introduction for this species in this region; as well as to address, for the first time, the genetic variation of the introduced populations over a 7-year period. Haplotypes dominating southern Iberian marinas show a clear linkage with Canary Islands, Brazil, Mediterranean and Australia populations; supporting the existence of multiple introductions events. Preliminary analyses also suggest diverse patterns of temporal genetic variation among marinas. Indeed, dramatic fluctuations of caprellid populations were observed and seem to characterize these highly instable environments (*i.e.* driven by numerous factors such as propagule pressure, competence, substrate availability, etc.). Ongoing analyses are being conducted in order to draw some more light into the prospective of *Caprella scaura* populations in its introduced range.

Persian Gulf as a hotspot or coldspot of biodiversity: evidence from *Ampelisca* (Amphipoda: Ampeliscidae) diversity from PGGOOS expedition

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The common view about diversity and endemism of the Persian Gulf beloved on the region is a coldspot diversity based on stressful environmental conditions in the region. Poor knowledge is the main reason for primary judgment about the Persian Gulf diversity. Recently, this hypothesis was debated due to some studies. The PGGOOS expedition was provided a chance for studying amphipod diversity of the Persian Gulf. The fourth leg of PGGOOS expedition was conducted in 19 stations from Bandar Dayer to Khajeh Abdollah in the northwestern part of the Persian Gulf. The collection is composed of 19 species from 4 parvorders and 7 families. Local distribution of amphipod species was mapped via GIS software. *Ampelisca* with seven species was the most abundant taxon in the collection and six of them are new for science. The results show that *Ampelisca* density was higher in the center of the Persian Gulf. Water temperature was between 17-18°C. The high number of new *Ampelisca* species as a main part of benthic amphipods in compare with adjacent waters align the evidence of decapod (Naderloo, 2017) verifies the the hypothesis of Price and Izsac hypotheses (2005) which regards the Persian Gulf as a hotspot for marine biodiversity and a center of speciation.

The phylogeography and classification of the Talitroidea (Amphipoda, Senticaudata)

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A morphological cladistic study of world Talitroidea is reported on. The study utilised in the main, previously published descriptions and illustrations. Our methodology involved careful in-depth assessment of each synapomorphy revealed by each successive branch-swapping iteration, in order to minimise the effect of homoplasies.

Until now, only a single family of talitroids, the Talitridae was recognised. We erect three new families, the Uhlorchestiidae, the Caribitroididae and the Austrotroididae. The latter family is comprised almost exclusively of terrestrial forms almost entirely confined to the southern hemisphere. The superfamily Talitroidea probably originated in Pangaea. The Austrotroididae would have been widespread in Gondwana during the Cretaceous. At the breakup of Gondwana, masculopod austrotroidids became isolated in post-gondwanan continents and gave rise independently to femipods in Zeylandia (New Zealand, New Caledonia and Lord Howe Island) on the one hand and in Australia/South Africa on the other. Today, the greatest extant diversity of austrotroidids is in New Zealand and the moist southern regions of Australia and South Africa. Unlike the austrotroidids, talitrids are widely distributed from North America, across Europe to China and Russia as well as in New Zealand, Australia, South America and North America. They have been able to colonise many oceanic islands such as Hawaii and the Society Islands, places that austrotroidids have not been able to colonise. Terrestrial austrotroidids probably evolved from marsh-hoppers, while terrestrial talitrids probably evolved from beach-hoppers, which are found exclusively in the Talitridae.

The Biodiversity of deep-sea Scavenging Amphipoda in the Pacific Ocean

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The abyssal deep sea (3000 - 6000 m) is one of the largest and most unexplored ecosystems on the planet. As part of the Mining Impact “Ecological aspects of deep-sea mining” project, we are studying and comparing the long-term ecological impacts of mining of ferro-manganese nodules on deep-sea crustaceans in two basins; (1) the Clarion-Clipperton fracture Zone (CCZ) a manganese nodule province NE Pacific and (2) the DISTurbance and Re-COLONisation (DisCOL) Experimental Area (DEA), a disturbance proxy in the SE Pacific. More than 60,000 specimens of Amphipoda were collected using a free-fall baited trap lander, from which 19 morphospecies have been identified, including several undescribed species. At the disturbance proxy site, the scavenging amphipod community shows reduced diversity and is dominated by a single species *Abyssorchomene gerulicorbis* indicating that extended time is needed for post-disturbance recovery. Two target species *Paralicella caperesca* and *Abyssorchomene gerulicorbis* were selected for molecular analysis of potential genetic connectivity and dispersal. For 200 specimens, we successfully obtained DNA sequences of part of the mitochondrial COI gene. The molecular results provide evidence for cryptic diversity in both species and also demonstrate a previously unknown genetic connectivity between these two basins (3000 km apart). Here, we also present our first nuclear DNA sequence data for these species. Developing a suitable protocol of population genomic techniques (ddRAD-seq) for these species with unknown genome sizes and also heavy metal/PCBE analysis is in progress (with the KU Leuven and VUB). The CCZ will be revisited for an extended sampling campaign in March 2019, to obtain further scavenging amphipod samples with video guided methods, and also to obtain complimentary abiotic data from these sparsely studied habitats.

The oldest record of Amphipoda: a 260-million-year old fossil from Brazil

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Amphipoda is a large group of worldwide distributed crustaceans, occupying almost all aquatic environments. There are about 10.000 species of extant amphipodans described, representing around ¼ of all eumalacostracan species. Despite this impressive number of known extant species, the fossil record of Amphipoda is very poor, comprising circa of only 25 species so far, almost all from Eocene–Oligocene amber inclusions (50–30 million years). These Cenozoic fossil representatives present the same principle body organization as the extant ones, a laterally compressed body divided into three tagmata: 1) the cephalothorax or functional head, including the ancestral eucrustacean head and the first thoracic segment, 2) the pereion, including the posterior seven thoracic segments, and 3) the pleon with six segments and telson. The pleon is further differentiated into two units: 1) the metasoma including the anterior three pleon segments, which bear natatory pleopods, and 2) the urosoma including the posterior three pleon segments, which are rather short in anterior-posterior dimension and additionally bear more or less styliform appendages, collectively termed uropods, although they are neither in the same position or fulfill the locomotory function expected of a uropod. We present the oldest record of a true amphipodan, from the Lower Permian of Brazil, nearly 260 million years old. The principle body organisation includes three tagmata, yet the pleon is not differentiated into a metasoma and a urosoma as in the extant species. Instead, all pleon segments are of equal shape in dorsal view, being around five times broader than long, and they relatively increase in size in a way that the sixth pleon segment is approximately 1.5 larger than the first one. Apparently, there is no differentiation of the pleopods 1 to 5, all of them are well-developed and natatory, and only the last pair of pleopods is modified into uropods. This more plesiomorphic morphology, with the posterior region of the pleon similar to the ground pattern of Eumalacostraca, in which there is a tail fan composed of strongly developed uropods and telson, suggests that the specialization of the pleon of extant amphipodans may have occurred during the Mesozoic.

The use of amphipods as biomonitors of environmental health change using trace element analysis

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Biomonitors provide a mechanism for assessing the chemical health of the marine environment. Crustaceans such as amphipods take up potentially toxic trace metals into their tissue and exoskeleton, and hence become recorders of their chemical environment. Importantly, they reflect the bio-available fraction of metals in the environment and trace their uptake into different levels of the food chain.

A recent project based on the shallow water, New Zealand coastal environment has found that amphipods are useful indicators of environmental health change when compared across sites and time. Using specialized analysis of thirty trace elements, selected marine amphipod species were examined using a variety of treatments. Including comparisons between species, between sites and a case study of a specific area. The trace element data allow us to evaluate natural variations among specimens from single localities and effects of parameters such as specimen size on accumulation of metals. Specimens from different localities show distinct trace element accumulations reflecting regional (local) differences in their chemical environment. Species, size and distributional influences will be discussed with an emphasis on the use of this method of analysis for assessing environmental health change.

Non-native marine amphipod species in the English Channel

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During the last decades, marine Non-Native Species (NNS) colonized most of the shallow and coastal European waters. Three main origins have been identified: shipping including discharge of ballast waters, biofouling, and through voluntary introduction in aquaculture. In the English Channel, the main site of introduction is Le Havre harbour. During an inventory of the NNS in Normandy, from the Mount St Michel Bay to Le Tréport, 139 species were documented. Among them, seven amphipods were recorded: *Caprella mutica* Schurin, 1935, *Cryptorchestia cavimana* (Heller, 1865), *Monocorophium acherusicum* (Costa, 1853), *Monocorophium sextonae* (Crawford, 1937), *Dikerogammarus villosus* (Sowinsky, 1894), *Grandidierella japonica* Stephensen, 1938 and *Platorchestia platensis* (Krøyer, 1845). Only the caprellid *C. mutica* appeared invasive in the Seine estuary. *Ptilohyale littoralis* (Stimpson, 1853) was recently found at Wimereux (Opal coast). Moreover, ten others species were considered as potential in the English Channel due to their presence in the Bay of Biscay or in the southern part of the North Sea: *Ampithoe valida* Smith, 1873; *Aoroides curvipes* Ariyama, 2004; *Aoroides longimerus*; *Aoroides semicurvatus* Ariyama, 2004; *Caprella scaura* (Templeton, 1836); *Chelicorophium curvispinum* (G.O. Sars); *Gammarus tigrinus* Sexton, 1939; *Incisocalliope aestuarius* (Watling & Maurer, 1973); *Melita nitida* Smith, 1873, and *Monocorophium uenoi* (Stephensen, 1932). Maps of the occurrence of the more current species were presented and discussed in the framework of the Descriptor 2 of the Marine Strategy Framework Directive. Future observations in Normandy marinas during a new research programme (ENBIMANOR, 2017-2021) will be expected to record new NNS including amphipods. In the autumn 2018, nine, 25 × 25 cm polymethyl methacrylate panels, were deployed in 19 sites around the Normandy from Granville in the Normand-Breton Gulf to Le Tréport in the north-eastern border with 'Hauts de France Region'. Results of panels exposed three and six months are presented. Bibliographic inventory and currently observations appear indispensable to obtain an actual view of introduced and invasive species in coastal zone in European waters.

Interaction of species, temperature and parasitism may facilitate replacement of native amphipod by invasive species, impacting vital ecosystem process of detritivory

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Freshwater ecosystems are particularly vulnerable to anthropogenic impacts due to their relatively limited volume, connectivity and proximity to human development. Invasive species are one of the main drivers of biodiversity loss, with introduced Ponto-Caspian amphipods, such as the killer shrimp *Dikerogammarus villosus*, altering freshwater community structures across Europe. Parasites, which are often overlooked, are important community members that can affect host survival as well as host trophic interactions. Furthermore, climate change is increasing the frequency and intensity of extreme weather events, with heatwaves having major consequences for ecosystem structures and productivity. It is important to understand how combined stressors of invasive species, parasitism and climate may interact to affect communities and ecosystem processes.

The main basal resource in temperate freshwater ecosystems is riparian leaf litter, which is broken down by microbial decomposers and invertebrate shredders, providing resources to the rest of the community through shredded leaf mass and biomass growth of consumers. Amphipods are often the dominant shredder species in freshwater communities. We study how this key ecosystem function of shredding is affected by the combined stressors of biological invasion, temperature and parasitism and may thus affect the energy flow and productivity of the ecosystem.

We compared the survival and leaf shredding rate of the UK native amphipod *Gammarus pulex* and the invasive *Dikerogammarus villosus*, exploring the effect of temperature and parasitism. The native amphipod species had a higher shredding rate than the invasive species, but was less tolerant of extreme heatwave temperatures, suffering higher mortality. The invasive amphipod benefitted from predator release from microsporidian infection. In contrast, shredding behaviour and survival of *G. pulex* was negatively impacted by the acanthocephalan parasite *Echinorhynchus truttae*.

The higher tolerance of *D. villosus* to elevated temperatures, as well as its escape from parasites may facilitate their replacement of the native species in the changing climate. Furthermore, the lower detritivory by this invader may negatively impact energy flow and productivity in invaded freshwater ecosystems.

What public data can tell us about current practices in DNA barcoding amphipods

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The last decade saw the rise and establishment of DNA barcoding as a reliable tool for specimen identification during all life stages. The method has seen a wide range of applications due to fast turn-around time (from unknown specimens to known species) and cost-effectiveness. However, DNA barcoding has not been implemented as a regulatory tool in biodiversity conservation, remaining a method of choice mostly in the academic environment. One of the barriers in the wide implementation of DNA barcoding-based specimen identification is the lack of complete reference libraries (i.e., databases of DNA barcodes linked to taxonomically verified morphological vouchers). In the case of amphipods, the World Amphipoda Database (<http://www.marinespecies.org/amphipoda/>) currently holds ~10,000 species of marine and freshwater taxa. The largest barcode database, Barcode of Life Data Systems (BOLD, <http://www.boldsystems.org>) currently holds ~23,500 amphipod public records assigned to 1,500 species and ~3,200 BINs (Barcode Index Number; genetic clusters largely used as proxy for species). About half of public data was originally uploaded to GenBank and then mined to BOLD, while the other half was generated by BOLD users. An investigation of the quality of the public data revealed that ~8% of BINs (4,500 records) showed discordance (i.e., multiple taxa in one BIN), 40 barcodes were flagged as contaminated with human or bacterial DNA, seven barcodes were flagged as having stop codons, and 270 records were flagged as (cross-)contaminated or misidentified. While the impact of these findings on the original studies is not trivial, it is not assessed here. The statistics provided here are revealing the urgent need for an upgrade of current practices in barcoding amphipods to increase data quality and coverage. Establishing a set of best practices in generating, curating and publishing barcode data, to be presented and discussed during the 18th ICA (and if agreed upon, to be followed in subsequent studies), would be of great help in providing valuable data for various stakeholder. This call for best practices is even more stringent now, in times of technological advances allowing a shift in molecular inventories from DNA barcoding to metabarcoding, and from physical specimens to environmental DNA.

Phylogeography of the invasive amphipod *Pontogammarus robustoides* (Crustacea) in native and colonized range

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Pontogammarus robustoides is one of the successful invasive Ponto-Caspian amphipods in European waters. In its native range it inhabits lower courses of the rivers entering Caspian, Azov and Black seas, as well as fresh and brackish water coastal lakes and limans. This species was introduced in the 1950s to dam reservoirs on the Daugava and Nemunas in the Baltic States. It spread, most probably, along the coast of the Baltic Sea to the number of Baltic Sea lagoons (e.g. Vistula and Szczecin Lagoons) and entered many inland waters including Vistula, Oder, Mazurian Lakes, Mitteleand Kanal, Mecklenburg Lake District and lately in the Rhine delta. It was also recorded in the Gulf of Riga and Finland. The main objectives of our studies are to reveal: (1) species phylogeography in native and invaded area, (2) historical demography of populations, (3) source population for first introduction in the Baltic States. We amplified ca 650 bp long portion of the mitochondrial cytochrome oxidase I (COI) marker from ca. 600 specimens collected in 86 locations all over Europe, including 44 locations from the native and 42 from invaded area. Based on mtDNA results, we selected some representative specimens for sequencing for additional nuclear marker ITS2.

The obtained results allowed us to determine the genetic population structure of *Pontogammarus robustoides*. Spatial distribution of clades occurring in the native region is structured geographically. The source population for introductions to Baltic States were populations from the Lower Dnieper, as identical haplotypes were found in both regions. We observed a reduction of genetic diversity connected with the founder effect. In the newly colonized area only three haplotypes were found comparing to seven detected in native Dnieper clade. The species continues invasion to western Europe and the secondary bottlenecks were detected in its westward progress. In the Baltic States three haplotypes were identified, in Poland two, while in Germany only one. Demographic analysis has shown a stable growth of native population in the 8-28k BP which can be associated with sea level and the salinity fluctuations in this area during the Pleistocene.

A standardized methodology for monitoring and assessing fouling amphipod assemblages across spatio-temporal scales

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Anthropogenic modification of habitat through the addition of artificial structures is among the largest current threats for biodiversity conservation and ecosystem functioning. Some of the most dramatic alterations of coastal habitats are the development of harbours and recreational marinas. These artificial habitats have the potential to modify local ecological and environmental conditions and constitute critical entry points for the introduction of non-native species. Understanding the effect of this habitat alteration in global biodiversity patterns of amphipod assemblages requires large-scale, long-term monitoring. However, this is severely hampered by a lack of taxonomic experts but also by the absence of a standardized methodology specifically designed to detect this group of animals. In this study, we developed standardized microhabitats made of two types of commercially available plastic meshes folded three-dimensionally (hereinafter type A and type B) to implement a standardized protocol for collecting fouling amphipods. The type A had a higher volume, less compaction degree and required more processing time to extract the amphipods from the mesh than the type B. These types of artificial microhabitats were tested simultaneously in three marinas of the Bay of Cádiz (Spain) and compared with a commonly used non-standardized methodology consisting in collecting potential fouling basibiont species. Among the organisms collected, amphipods were always the dominant group, followed by polychaetes. Both type A and type B were more efficient in collecting amphipods than the non-standardized methodology used as control. After the first month, the type A had already collected an average of 1785 ± 1683.87 (mean \pm SD) amphipods per unit while the type B collected 547.31 ± 385.73 amphipods per unit. Based on their high efficiency and different physical properties of the two types of artificial microhabitat tested, its use as a sampling unit in the new designed protocol is discussed. This study provides scientific community with a standardized, easy-to-apply, low-cost and quantitative sampling protocol that ensure spatial and temporal comparability for monitoring and assessing epifouling amphipod assemblages associated with artificial habitats.

The impact of pelagic food falls on an amphipod dominated scavenger community in the Deep Norwegian Sea, an experimental approach

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Food falls are carcasses of larger pelagic organisms that are deposited on the seafloor and create areas of high organic enrichment. Especially in the deep sea, where benthic communities mostly depend on indirect or direct organic input from the overlying water column, energy and nutrient transfer via food falls play a crucial role in fuelling the surrounding benthic community. However, the local impact of food falls on benthic scavenging communities remains unknown for many oceanic regions. Natural food falls are rarely observed, which makes it difficult to analyse their exact impact on deep-sea food webs in general and on local scavenging communities in particular. We deployed baited landers to mimic natural food falls and to investigate the impact of different species of medium sized invertebrate and vertebrate food falls on Atlantic deep-sea benthic communities. Landers with fish *Scomber scombrus*, jellyfish *Periphylla periphylla* and squid *Illex coindetii* were deployed in the southern Norwegian Sea for 9-25 hours at depths between 1360-1440 m. Each lander was equipped with a food plate, a time lapse camera (one image per 2.5 minutes), CTD, ADCP and an Aquadopp Current Profiler. Images of the time-lapse camera were analysed to reveal potential differences related to the bait types regarding scavenger composition, abundances, successional stages as well as consumption rates. Preliminary results show rapid scavenging rates (approximately 24.5±8 g/hour). While the scavenging community was dominated by amphipods on all three baits, other crustaceans and fish were also observed and there were differences in composition and abundances between the types of bait. The most prominent differences were found between jellyfish and fish/squid carcasses. While fish and squid carcasses were mostly attended by at least two species of the amphipod genus *Eurythenes*, a smaller, yet to be identified amphipod species, brittle stars and decapod shrimps dominated the jellyfish food falls. Jellyfish was consumed considerably slower (20-25 hours) than the other two food fall types (9-12 hours). Based on this, we will predict potential consequences of shifting pelagic communities and the possible subsequent impact on benthic deep-sea communities.

Are coastal defence structures shaping amphipod assemblages?

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Urban growth in coastal areas is leading to the introduction of multiple artificial structures into the marine environment. These structures differ from natural hard substrates in composition, age, complexity, inclination and even colour. Such factors affect the establishment and development of benthic communities, and it is mostly agreed that these communities are different from those associated to adjacent natural hard substrates. However, amphipod assemblages are usually overlooked in studies comparing artificial and natural hard substrates. In order to assess the effects of artificial structures and to identify the main factors involved, amphipod assemblage structure was studied in the anthropized Algeciras Bay (Southern Spain). Four different artificial structures (seawall, cubes, acropods and rip-raps) and the nearest natural hard substrate were sampled. Three sites were randomly selected for each substrate and nine random 20x20cm quadrats (three per site) were scraped at low intertidal level. Sessile communities were volumetrically measured, and the associated amphipods were counted and identified to species level. Abiotic measurements of each substrate (complexity, rock composition and age) were also measured to relate ecological patterns with different abiotic factors. Differences in assemblage structure were evaluated using PERMANOVA based on a Bray-Curtis similarity matrix. Relationships between abiotic data and biological assemblages were explored by using dbRDA. Twenty-one amphipod species were found, and community structure significantly differed among substrates except for cubes and acropods. dbRDA yielded a significant model of abiotic variables that accounted for 65,7 % of the total inertia, although only complexity measurements were significantly correlated with the biotic data. This suggests that physical attributes, rather than rock composition, are the main factors driving the development of amphipod assemblages, and it should be considered in future eco-engineering actions. Amphipod assemblages were also greatly affected by the secondary substrate (sessile). In fact, dbRDA using the sessile community as explanatory variables, yielded a highly significant model that accounted now for 82,3 % of the total inertia, suggesting that artificial structures are indirectly shaping amphipod communities through the effects over the secondary substrates. Future research should scrape the same secondary substrate in different artificial structures in order to avoid hindering of direct effects.

Disparity in oxygen demand of native *Gammarus lacustris* and invasive *Pontogammarus robustoides* – which is superior under deteriorating environment?

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Oxygen availability is the most important factor limiting the distribution of aquatic invertebrates. When a Ponto-Caspian amphipod *Pontogammarus robustoides* was introduced in Lithuania starting from 1960s, it was observed that it mostly occupied large rivers and mesotrophic lakes. Smaller lakes with higher nutrient enrichment, on the other hand, retained populations of the native amphipod *Gammarus lacustris*. Such macrohabitat partitioning suggested higher oxygen demand of the invader. However, the only previous study involving both species, conducted back in the 1970s, witnessed the opposite trend in oxygen consumption. Thus, the aim of this study was to thoroughly investigate the oxygen demand of the two species. First, using closed chambers, we compared survival (inactivation) of the two species under limited oxygen supply. Secondly, using common-garden cultures, we measured their respiration rates as functions of oxygen saturation, covering a range of body sizes. Both study parts were conducted at 18°C. In the survival experiment, *P. robustoides* lasted significantly shorter and its inactivation rate over 0.2 mg L⁻¹ was significantly higher in comparison to *G. lacustris*. Respirometry also revealed that *G. lacustris* is a more efficient oxyregulator. Allometries of oxygen consumption under normoxia indicated typical scaling exponents (¾) for both species, but the 25% difference in standardization constant uncovered the higher oxygen demand of *P. robustoides*. Critical oxygen saturation (P_c) of *P. robustoides* was significantly higher (36% O₂) than that of *G. lacustris* (28% O₂), as well. The strengths of our study include measuring under full oxygen availability range, controlling for habitat and maternal effects, and adjusting the data for body size. We consistently confirmed that *P. robustoides* has a higher oxygen demand than *G. lacustris*, and therefore oxygen availability can be considered a legit driver for initial macrohabitat partitioning in freshwater temperate lakes. The results have important implications for management the invasion of *P. robustoides*, and use of the species within macroinvertebrate-based metrics of eutrophication and organic pollution.

Amphipod-based public outreach: a dream or a possibility?

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The focus on the necessity of public outreach for all science-projects is becoming more and more present, with most funding-bodies declining grants to projects that do not outline such activities. The general audience has at the same time become more and more vocal on their right to know what public research-money are being used for, and public relations offices of both public and private funding bodies are interested in getting “good PR” for their money. How is this possible with projects focussed on i.e. biosystematics, faunistics or population genetics?

The present focus on social media might present such forums as an easy and not least cheap way to get the outreach “done”. What does a “good science-project presence” on social media involve, and how much effort is needed? How does this compare with other means of outreach?

The talk will go through several examples of public outreach at several levels all describing amphipod based research including blogging, short-burst social media, kindergarden-activities, lectures, newspaper opinions, films and museal exhibits, with a discussion about how they have worked and how much effort needed to go into the work. The talk will draw on the experience from two different projects: one lab- and museum-based and one expedition-based.

Adaptation to cold as a possible advantage of Lake Baikal endemic amphipods *Eulimnogammarus verrucosus* and *E. cyaneus* compared to a potential invader *Gammarus lacustris*

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In the present study, we aimed to evaluate energy metabolism and the mechanisms of non-specific stress response in Baikal endemic and Holarctic amphipod species during long-term temperature acclimation. The investigation hypothesizes that Baikal endemic amphipods have a unique advantage for maintaining high physiological activity at low temperatures compared to Holarctic species.

As the object of the study we chose two of the most abundant endemic Baikal amphipods, *Eulimnogammarus verrucosus* (Gerstf. 1858) and *E. cyaneus* (Dyb. 1873), and *Gammarus lacustris* Sars, 1863, a ubiquitous gammarid of the Holarctic. Animals were exposed under long-term (1 month) acclimation at the temperature near to the freezing point (1,5°C) and at optimum temperatures of each species: 6°C for *E. verrucosus*, 12°C for *E. cyaneus* and 15°C for *G. lacustris*. Antioxidant enzymes (peroxidase, catalase and glutathione S-transferase), as well as energetic metabolites (glucose, glycogen, ATP, and lactate), were chosen as the markers for the study.

According to our results, Baikal endemic amphipods have higher basic activity levels of antioxidant enzymes compare to Holarctic *G. lacustris*. Low temperatures have a significant effect on energy metabolism of thermotolerant Baikal endemic *E. cyaneus* and the potentially invasive species *G. lacustris*, which is mirrored in changing ATP, glycogen and lactate levels. It was shown that the mechanisms of antioxidant defense, as well as energy metabolism strategies, at low temperatures, are species-specific.

Low temperatures have a significant effect on the mechanisms of non-specific stress response and energy metabolism in the potentially invasive species *G. lacustris*, which is currently one of the main advantages of Baikal endemic species.

The work was supported by the Russian Science Foundation / Helmholtz Association of German Research Centres (grant number 18-44-06201).

Genetic diversity and connectivity of the *Eusirus perdentatus* species complex (Amphipoda, Crustacea) on the Antarctic continental shelf

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The Southern Ocean is experiencing environmental changes happening at an unprecedented rate, across broad temporal and spatial scales. Climate change–related stressors (hydrodynamic changes, environmental shifts) can disrupt gene flow between populations of benthic organisms, thereby altering their genetic diversity. Ultimately, the absence of gene flow may lead to population divergence and speciation. Identifying contemporaneous and past population connectivities in key benthic species along the continental shelf will contribute to our understanding of how climatic changes affect the Antarctic benthos. *Eusirus perdentatus* Chevreux, 1912 is a giant amphipod species, very abundant and widespread on the Antarctic shelf. Previous genetic studies based on COI, CytB and ITS2 markers revealed potential cryptic diversity within this nominal species. In the present study, species boundaries within the complex are reassessed, using both morphology and DNA-based methods. Two putative species within this complex are circum-Antarctic and can be readily distinguished based on their coloration pattern: the “marbled” and the “spotted” *perdentatus* species. A third putative species appears endemic to the Ross Sea. Newly developed nuclear microsatellite markers are used along with the mitochondrial COI data to investigate and compare genetic population structuring in both the marbled and the spotted species, in order to evaluate their connectivity along the shelf and assess their dispersal abilities. Molecular signatures of bottlenecks and recent demographic expansions, characteristic of organisms surviving the last glacial maximum in refugia, are investigated to study the impact of past climatic changes (glacial cycles) on the genetic structure of these species. The interpretation of all results will help identifying historical, environmental and biological variables responsible for the observed geographical distributions and genetic structure of these two species of the *perdentatus* complex.

Broad-scale DNA barcode-based meta-species analyses of patterns of molecular variation in Amphipoda from world's oceans

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Large-scale global initiatives, such as the Barcode of Life, have been promoting the generation of vast amounts of DNA sequence data directly comparable across numerous animal taxa. This creates an unprecedented opportunity for extensive investigation of core aspects of molecular evolution in whole taxonomic assemblages, like the Amphipoda. Here we conducted a comprehensive investigation of available cytochrome oxidase I (COI) sequence data, in order to gain insights into evolutionary rates and patterns of molecular evolution among the Amphipoda.

A curated dataset of the world's marine and brackish waters amphipods was compiled on Barcode of Life Data Systems (BOLD; on 01/03/2019) and a suite of filters was applied to ensure the quality of the records, including sequence length and quality, sampling location and taxonomic identification. Only 5559 of the 23551 publicly available DNA barcodes in BOLD, fulfilled our quality criteria. These barcodes belong to 458 valid morphospecies (209 genera and 80 families) and 651 Barcode Index Numbers (BINs). The families Talitridae and Ampithoidae comprised the highest number of morphospecies (29 and 28 respectively), while the family Hyalidae had the highest proportion of BINs compared to morphospecies (216%). The overall mean intra-specific distance was 1.92% (max. 27.77%), congeneric 23.37% (max. 45.49%) and confamilial 26.99% (max. 50.22%). The family Oxycephalidae displayed the highest mean congeneric values (35%), while the family Hyperidae the lowest (14.60%). The mean GC content was 37.88% [26.67-50.49%], with the first codon position with higher values (46.19%) than the second (42.40%) and third (25.06%). The families Haustoriidae and Iulopididae displayed the highest and lowest GC content, respectively (40.45% and 30.14%). COI sequence data suggested an impressive amount of hidden diversity among marine amphipods, adding circa 50% more suspected species in relation to morphospecies. The most notorious taxa contributed disproportionately to the total number of potential new species, surpassing 10 hidden taxa in some cases and contributing with 1/3 of additional suspected species. GC content and genetic distances, in particular congeneric, varied considerably among families, suggesting appreciable differences in molecular evolution rates. Some families were phylogenetically divergent from the remaining, which brings insights about taxonomic differences in evolutionary rates within this order.

Scavenging amphipods of the abyssal and hadal Wallaby-Zenith Fracture Zone in the East Indian Ocean

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Presently, our knowledge of scavenging amphipod communities from hadal depths (> 6000 m) is focused on large subduction trenches. The Wallaby-Zenith Fracture Zone (WZfZ) in the East Indian Ocean offers a unique location to test drivers of hadal endemism and community structure, as it is not a large subduction zone but does technically extend over the abyssal-hadal boundary. Using free-fall baited landers, scavenging amphipods were collected from the six depths between 4932 to 6546 m in June 2017. By combining traditional taxonomical identification and DNA barcoding of the 16S rDNA and COI mitochondrial regions, ten lysianassoid amphipods species were identified from the WZfZ, with two species new to science. Of those 10 species, *Eurythenes maldoror* was prevalent at abyssal depths, but with a depth record of 6546 m. *Bathycallisoma schellenbergi*, a lower abyssal but more typically hadal amphipod, dominated depths greater than 6500 m with no exhibition of ontogenetic stratification. Evidence of competitive exclusion between these two larger species was observed. The presence of hadal species in a relatively small and isolated feature with little geomorphological similarities to large subduction trenches suggests that depth is the primary driver separating the abyssal and hadal diversity. With the WZfZ results, we can infer that hadal communities are not exclusively found in the large trenches, but they are capable of sustaining populations in very small and isolated fracture zones, and perhaps other depressions interspersed across abyssal plains. This further alludes to a stepping-stone mechanism for connectivity between large subduction ecosystems and potential for a far larger distribution of hadal species than previously thought.

DNA barcode availability for European groundwater macrocrustaceans

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Crustaceans are the most common invertebrate inhabitants of groundwater. Although groundwater is often considered as extreme and species poor environment, crustacean diversity in European groundwater surpasses diversity of its surface counterparts. However, due to demanding sampling techniques (e.g. Bou-Rouch pump, deep vertical caving, cave diving) and shortage of taxonomist, study of groundwater fauna remains challenging. In addition, species abundances are low, and complete inventories require multiple visits. Finally, subterranean habitats are characterized by strong, directional selection, which induces morphological convergences. Consequently, cryptic species are common. These issues hinder fundamental studies of distribution and biodiversity of groundwater species, but also applied studies such as biomonitoring of groundwater quality. Recent application of molecular tools may substantially accelerate all aspects of groundwater research. A cornerstone of successful implementation is reconciling traditional and molecular taxonomy and development of reference libraries, linking diagnostic barcodes with species names and, finally, specimen vouchers. In this contribution, we evaluated the completeness of DNA barcode libraries for routine identifications of different classes of groundwater crustaceans, with an emphasis given to amphipods. In Europe, amphipods represent approximately one third of groundwater crustacean species, and reflect local and regional groundwater species richness. We used information on distribution of macrocrustaceans, taken from the European Groundwater Crustacean Dataset, and collected all available DNA sequences, that could be used in identification of species or operational taxonomic units. We compared number of species with number of DNA sequences and present the coverage of both on the continental scale. We identified the insufficiently explored regions and crustacean taxa that should be prioritized in future molecular analyses, in order to make DNA barcodes an operational tool for further studies of groundwater biodiversity and routine monitoring of groundwater.

Abstracts

Posters

In alphabetic order

Evaluation of the antioxidant potential of Baikal endemic amphipod *Eulimnogammarus verrucosus*

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In the current study, the antioxidant potential of Baikal endemic amphipod related to species *Eulimnogammarus verrucosus* was evaluated. It was aimed to assess the stress-induced changes of low-weight secondary metabolites that can contribute to the protection of aquatic organisms to elevated oxygen content. Amphipods of *E. verrucosus* species were exposed to hyperoxia at the high concentration of oxygen (40 mg/l). Control group of organisms was fixed before the beginning of the experiment. The experimental group was fixed after 3 days of the experiment and then, after 7 days of experimental hyperoxia.

After exposure, alive amphipods were homogenized in the ethyl acetate. The upper fraction was collected for subsequent evaporation and dissolution in the methanol (10 mg/mL). Crude extracts were analyzed by assays of liquid chromatography-mass spectrometry (LC-MS) with following dereplication analysis of natural products using the Dictionary of natural products database (CRC-press, 2018).

It was established that experimental hyperoxia leads to the change in the content of low-molecular natural products. Experimental hyperoxia-induced activation of synthesis of three metabolites with molecular weight [M+H] 359.15 Da, 318.32 Da, and 637.40 Da after 7 days of exposure. At the same time after 3 days of the experiment, we observed a decrease of two metabolites content with molecular weights [M+H] 313.31 Da, and 568.33Da. Also, we detected a short-term increase in the content of the metabolite with a molecular weight 852.65 Da.

Thus, the materials of the study indicate that increased oxygen content in the environment leads to the activation of specific metabolic reaction in endemic organisms that naturally adapted to environmental hyperoxia. Dereplication analysis indicates a high similarity of the analyzed compounds with chemical molecules isolated from sea sponges and described as sex pheromones.

The study was carried out with the main financial support of Russian Science Foundation grant 18-74-00018, with the partial financial support of Russian Foundation for Basic Research grant 18-29-05051, 18-34-00294, the base part of Goszadanie project 6.9654.2017/8.9, Lake Baikal Foundation.

Effect of diet on growth and fatty acid profile of the marine amphipods *Echinogammarus marinus* and *Gammarus locusta*

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Rapidly expanding fed aquaculture demands high quality, sustainable nutrient sources for diets. Marine gammarids may be an excellent source of essential fatty acids, however, their aquaculture using formulated diets remains untested in terms of survival, growth and nutritional value of cultured product. Two marine gammarid species, *Gammarus locusta* and *Echinogammarus marinus* were maintained in controlled feeding experiments with four formulated diet treatments, *Ulva* spp., *Fucus* spp., lupin meal and carrot green. *Gammarus locusta* exhibited significantly higher growth performance and survival rates than *E. marinus*, particularly when fed terrestrial carrot green. Growth results, along with fatty acid profiles of resulting gammarid product optimally suited to marine fish nutrition, indicate high suitability of *G. locusta* as an aquaculture diet source. In contrast, *E. marinus* may provide beneficial fatty acid profiles for aquatic animal nutrition, but poor growth performance seems to make it less suitable for application as an aquaculture species. Results indicate, for the first time, that marine gammarids are capable of trophic upgrading and can use non-marine diets for healthy growth in culture. Suitability as feed for specific fish or crustacean species needs to be investigated individually. Future research should include the development of optimal large-scale production as well as investigation of optimal methods of inclusion of gammarids in target species diets.

Do intersex amphipods get a bad rap?

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The phenomenon of intersex, defined as an organism possessing both male and female primary and/or secondary sex characteristics, exist throughout the animal kingdom. The condition is well established and widespread throughout many crustacean populations, including Amphipoda, however, the intersex condition found in the freshwater amphipod *Gammarus minus*, occurs in extremely low frequencies, or not at all. Interestingly, a study conducted over 40 years ago in Virginia (USA) discovered two separate populations of the amphipod *G. minus*, where 100% of the females displayed intersex characteristics. Such high levels of intersexuality are atypical amongst gonochoristic crustaceans and theories regarding sex allocation suggest that intersex forms should be selected against, resulting in a populations' extinction. Based upon these findings, this study focused on investigating the populations' continual intersex condition by utilizing the following objectives, population's phenotypes, sex ratios, and amphipod lengths and maturation.

In Falling Branch Road (site 1), and Falling Branch Cave (site 2) a total of 2,961 adult animals were collected via the standard kick-net method and subsequently sexed as male, female or either intersexed male or intersexed female. Organisms were further classified with respect to body length, and phenotype.

The results of this study confirmed these populations may have maintained the highest incidence of intersexuality in amphipods (60 – 100%) over time (40+ years). There were no normal females in site 1. Within site 2, proportions of intersex females remained static over the sampling period (65 – 75%). Furthermore, intersex females in both populations maintained similar growth patterns. Populations were male-biased and intersex females were consistently larger (mean 6.0mm:5.1mm) and outnumbered normal females (66%:34%).

The high prevalence of female intersexuality and male-biased populations provide a unique opportunity to observe behaviors and the overall effect at individual and population levels. The assumption that normal females are ultimately more successful than intersex females is not supported and these populations may even challenge the long standing theory of sex allocation and evolution. The overall importance and contribution of this research may be applied towards the plasticity and adaptation qualities of the animal kingdom, while potentially endorsing a new norm within both FBR and FBC.

Long-term observations of high frequencies of intersex females in two populations of the freshwater amphipod *Gammarus minus* (Say, 1818)

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Intersexuality (possession of both male and female sexual traits by individual organisms) occurs throughout the animal kingdom, including amphipod crustaceans, though usually at low frequencies within populations. Sex-allocation theory predicts that intersex individuals should be rare within populations because they have lower evolutionary fitness than normal males and females. However, two populations of the amphipod *Gammarus minus* in Virginia (USA) exhibit surprisingly high frequencies of intersex females. The first censuses carried out by Arthur Buikema and colleagues during 1977 and 1980 showed that the percentage of females with male genital papillae was 60-100% in these two populations. Our later surveys during 2005-2006 and 2010-2014 have verified these high frequencies: 60-75% in the Falling Branch Cave population, and 100% in the Falling Branch Road population. Therefore, these high frequencies have persisted for over 40 years. This striking finding has important implications for sex-allocation theory and our understanding of mate choices. Consequently, a 4-year population study was conducted to determine the cause(s) and possible fitness cost(s) of the unusually high frequencies of intersex females. To establish the cause(s) of female intersexuality, we investigated factors known to influence sexual development (i.e. pollution, parasitic infections and seasonal effects such as, photoperiod) plus, any unusual water quality measurements (i.e. pH, temperature, DO, hardness, and alkalinity). Acquired data were analyzed seasonally and between sample sites. Reproductive fitness was examined by comparing offspring production (fecundity) between normal and intersex females. Significant relationships between the tested factors and intersex development of females included photoperiod (intermediate daylight 13 – 14.5 hours), increased stream temperatures ($\geq 13.8^{\circ}\text{C}$) and higher pH (7.8 – 8.0). Parasitic infection (microsporidian) was significant between intersex versus normal females (10% intersexes and 0% normal females); however, the vast majority of intersexes (90%) weren't infected. To our knowledge, the microsporidian that we detected is the first documented in *G. minus*. Reproductive fitness (fecundity) was significant (i.e. 23% fewer eggs in intersexed females). Although the causes and fitness consequences of intersexuality are still not well understood, our study populations offer an excellent model system for studying the ecology and evolution of sex determination.

A first in depth look at the Amphipod fauna of the Easter Island

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The remote island of Rapa Nui (Easter Island) represents an isolated outpost of the Indo-West Pacific fauna. The marine invertebrate fauna of the island is impoverished but few specific studies published to date acknowledge a high level of endemism. Accordingly, the amphipod fauna of Easter Island was still largely unknown. In a recent effort to capture the island's fauna, various intertidal habitats were sampled in three consecutive campaigns at different locations. Here we present a first overview and description of the amphipod fauna found on Easter Island, and relate community patterns to selected environmental conditions. At least 9 different amphipod species could be distinguished in Easter Island's rocky intertidal. As hypothesized, Rapa Nui's amphipod fauna seems to be characterized by a high level of endemism and select morphological characters as well as respective species descriptions are highlighted.

This project was financially supported by the Chilean Millennium Initiative through Millennium Nucleus Ecology and Sustainable Management of Oceanic Islands (ESMOI).

Inter-/intra-specific variability in contaminant sensitivity in *Gammarus fossarum-pulex*

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Objectives: Ecotoxicology is based on the use of organisms from controlled populations, which raises the question of the representativeness with regard to the sensitivities of natural populations. We questioned the existence of differences in sensitivity in *Gammarus fossarum-pulex* 1/ between naïve populations 2/ between naïve populations and cadmium historically exposed ones 3/ as well as the possibility of genetic selection of tolerance.

Methods: 1/ About twenty populations have been selected from the eastern half of France. These stations were chosen as not exposed to chemical pressure and covering a diversity in terms of habitats, environmental conditions (hardness, water regime, organic matter richness...) and phylogeography of the *G. fossarum-pulex* species complex. We evaluated their sensitivity to exposure to two model compounds (methomyl insecticide, cadmium) in the laboratory, following feeding inhibition, AChE inhibition, and mortality. 2/ Differences in cadmium sensitivity between cryptic lines in *fossarum* were also assessed in 8 populations of Müller types A, B and C (COI barcoding). 3/ the cadmic sensitivity of populations historically exposed to cadmium (4 populations) was evaluated on organisms collected in situ and on their offspring in the laboratory. 4/ The characterization of *in situ* chemical exposure was conducted through the study of bioaccumulation in naïve organisms transplanted on site (active biomonitoring).

Results: On the set of reference populations we conclude to an homogeneity in sensitivity to methomyl and cadmium, particularly between the *G. fossarum* cryptic types and a slightly higher sensitivity of *G. pulex*. We demonstrated a negative correlation between cadmium contamination of sites and susceptibility to this element in *G. fossarum*, but the acquired tolerance remains very limited. This tolerance is transmitted in uncontaminated conditions to the first cohorts of offspring, but sensitive individuals are produced again from the 3rd cohorts.

Conclusions: Overall, the toxicological sensitivity appeared very similar within the *pulex-fossarum* group. However, we were able to highlight a slight heterogeneity in the cadmic sensitivity between the two morpho-species. Moderate changes in population sensitivity can nevertheless occur in the event of long-term exposure and the role of parental effects seems to be key in determining the plasticity of sensitivity.

***Thiothrix*–amphipod symbiotic relationships**

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The genus *Thiothrix* comprises filamentous gamma-proteobacteria that are ecologically important chemoautotrophic sulphur-oxidizers. They are found in a variety of marine and freshwater aquatic environments ranging from sulfide-containing natural waters to wastewater-treatment plants. *Thiothrix* bacteria different from free-living ones have been documented growing as epibionts on spines and setae of amphipod legs in the sea (on *Urothoe poseidonis*, Urothoidae, Amphipoda) and in groundwater (on *Niphargus* spp., Niphargidae, Amphipoda); the specificity of this association suggests it is a symbiosis, but its physiological and evolutionary significance is still unclear. Such ectosymbioses are often regarded as the first forms of symbioses to have appeared in the history of life. Using 16S sequencing, metagenomic chromosome conformation capture and fluorescence in situ hybridization, we will explain our plans for elucidating the History and evolution of this symbiotic-relationship *Thiothrix*-Amphipoda. Thus, we present the current state of knowledge about *Thiothrix*–amphipod symbioses and the outline of the Ph.D. project about to start at the Université Libre de Bruxelles (ULB), Belgium.

Be my guest: amphipods living in tubes of Ceriantharia

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In this study we report amphipod species inhabiting tube species of Ceriantharia and discuss the characteristics of these occurrences. A total of 7 tubes of *Ceriantheomorpha brasiliensis*, *Ceriantheopsis lineata* and *Isarachnanthus nocturnus* from Argentina and Brazil were assessed. All tubes were longitudinally cut with surgical carbon steel scalpels and then opened and fixed using acupuncture needles. Both the inner and the outer wall of all tubes were analyzed. The fauna found anchored on the tubes was removed, photographed, and measured using a Zeiss AxioCam MRc5 and Zeiss AxioVision SE64 Rel 4.8 imaging software. Afterwards, the associated fauna was morphologically identified with specific taxonomic keys. Analyses revealed 5 amphipod species (n= 18) (*Ampelisca burkei*, *Cymadusa filosa*, *Elasmopus pecteniscrus*, *Monocorophium acherusicum* and *Photis sarae*) using ceriantharian tubes as anchoring points. Based on literary review and analyses of the sampled material, we reported a new location record for the species *Photis sarae* and extended its distribution from Rio de Janeiro to São Paulo State. Nonetheless, we observed that amphipods use filaments of ptychocysts as both protection and anchoring mechanism. Lastly, we suggest that ceriantharian tubes can provide protection, shelter and food resources to amphipods anchored on it, especially for tubicolous and infaunal species that usually burrow into sediments or anchor on fixed or mobile habitats seeking shelter.

Shadings in digital taxonomic drawings

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The use of computers for taxonomic drawings helps to speed up the documentation and at the same time improves the quality of these line drawings. Compared to the traditional use of ink pens, the digital drawing method with Adobe has advantages: e.g. corrections are easy, it is possible to create complex structures like setae in an elegant and rapid way and the arrangement of plates is quickly achieved (Coleman 2003, 2006, 2009).

The poster describes how shadings can be applied to taxonomic line drawings created with vector graphics software. The line drawings created with the vector graphic software are saved in vector format and then also in bitmap graphics format. The bitmap version is opened in a bitmap graphics program and the areas for shading selected. A new layer is then created and clouds of pixels are 'sprayed' onto these areas. The pixel clouds are saved and later placed onto the outlines in the vector graphic software as a new layer. The results combine the advantages of vector graphics, perfectly smooth lines and the greyscales of bitmap graphics (Coleman 2018).

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Functional morphological and trophic niche differentiation in a community of freshwater amphipods

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The link between functional morphology and trophic niche is elusive in many amphipod lineages. This is also the case for most freshwater taxa which, despite considerable phylogenetic and morphological diversity, are frequently lumped into the shredder (omnivorous) functional group. Here, we examine the connection between trophic niche and functional morphology in a phylogenetically diverse assemblage of three species (*Niphargus valachicus*, *Synurella ambulans* and *Gammarus dacicus*) widespread across the middle and lower Danube. We measured 45 morphological traits related to food acquisition, processing and digestion, as well as sensory function, locomotion and jet propulsion, and quantified the proportion of food items in the gut. Multivariate analyses revealed significant trophic differences among the focal species, with *N. valachicus* being mainly predatory, *G. dacicus* largely herbivorous and *S. ambulans* intermediate. This trophic differentiation was well reflected in the examined functional morphological traits, with the predatory *N. valachicus* having a smaller molar surface and stomach length, larger gnathopods, longer antenna I, pereopod VII and pleopods than the herbivorous *G. dacicus*. *Synurella ambulans* was morphologically intermediate in many of these traits, in accordance with its trophic niche. Such differences are in agreement with the patterns observed in other amphipod groups, as well as in other crustaceans or even vertebrates, paving the way towards a better mechanistic understanding of the link between niche and morphology. Therefore, it seems that functional morphology can accurately reflect trophic niche in freshwater amphipods, although more species from different taxonomic groups need to be studied to generalize this conclusion. Furthermore, we hypothesize that the trophic and morphological distinctiveness of the troglomorphic *N. valachicus* among its epigeal counterparts allowed it to occupy an empty niche. Thus, its ecological transition from subterranean to surface habitats was facilitated by reduced competitive pressure.

Combining molecules and morphology to describe cryptic new species – the *Bathyceradocus* genus case

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The deep-sea floor is supplied with a very small amount of organic matter. Sunken wood or plant remains have long been known as a valuable source of energy. Plant remains are widely distributed on the seabed and is found in all oceans and at all depths. Sunken wood make unique habitat that is considered as ephemeral but is inhabited by specialized fauna. After mollusks, the second largest invertebrate group inhabiting wood remnants are crustaceans including amphipods. Ten-odd species of wood-associated Amphipoda belonging to five families and six genera were hitherto identified. Four of them belong to the genus *Bathyceradocus* – *B. stephenseni* Pirlot, 1934, *B. iberiensis* Andres, 1977, *B. wuzzae* Larsen & Krapp-Schickel, 2007 and *B. hawkingi* Jażdżewska & Ziemkiewicz, 2019. The Tropical Deep Sea programme (ex MUSORSTOM) started in 2004 a series of surveys focused on the exploration of the sunken wood environments in the Solomon Islands, Vanuatu Archipelago and Papua New Guinea and specifically targeted sunken vegetation to further characterize its fauna. Material from these surveys supplemented by material from other parts of the World resulted in the collection of 141 individuals assigned to the genus *Bathyceradocus*. Molecular study of COI and 18S genes revealed very high diversity of the group and allowed to identify more than 15 putative species. The majority of them are species closely related to *B. stephenseni* suggesting a species complex and the assignation of them as new to science. The morphological characters that distinguishes the species are among others, the shape of propodus of gnathopod 1 and 2, the shape of coxa 4 as well as the shape of basis of pereopods 5-7 and armature of mandibular palp. These results suggest a revision of the genus *Bathyceradocus* and related species.

Effect of substrate and seagrass habitat complexity on detritus colonization and decomposition in a Mediterranean coastal lagoon (Thau Lagoon, France): a focus on amphipod community

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In the Mediterranean Sea, *Zostera noltei* (Hornemann, 1832) meadows constitute an important part of the intertidal shallow ecosystems in estuaries, bays and lagoons. Most of the primary production of these ecosystems is not directly used but is channelled to higher trophic levels as detritus. Acting as a faunal magnet, the seagrass detritus hosts an abundant community of mesograzers that use it as food source and shelter. Despite the important role of detritus quality and the surrounding environment, in term of habitat complexity, in shaping the associated mesograzer community, our understanding of their effects remains limited. We assessed the importance of changes in substrate and habitat complexity in structuring the amphipods community associated with natural and artificial seagrass detritus in three different *Z. noltei* density meadows (high, medium and low density).

Detritus decomposition, expressed as loss in detritus weight, and colonization were analyzed in Thau Lagoon (South France). 30 litterbags filled with a known amount of natural and artificial seagrass detritus were deployed in April 2018 and retrieved after 22 days. Mesograzers were separated from the detritus and amphipods were then counted and identified.

Results revealed no differences in seagrass decomposition during the experiment. A total of more than 2,800 amphipods were found in the samples. We identified 11 different species: *Amphitoe ramondi*, *Aora gracilis*, *Dexamine spinosa*, *Erichthonius argenteus*, *Gammarella fucicola*, *Gammarus insensibilis*, *G. subtypicus*, *Microdeutopus anomalus*, *M. gryllotalpa*, *Monocorophium insidiosum* and *Phtisica marina*. Both the natural and the artificial substrate were colonized by the same species with, in general, no differences in number. Half of the species identified showed significant differences related to the complexity of the habitat with higher values in the high density condition.

Despite the short duration of the experiment, the consistency in the results provides new information about the importance of substrate and habitat complexity in shaping complex communities. Results showed how the habitat complexity, in this particular case seagrass density, is far more relevant than the substrate type in structuring detritus amphipods community.

Coloring outside the lines: cryptic diversity in podocerid amphipods

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Podocerus cristatus (Caprelloidea, Podoceridae) is a cosmopolitan amphipod that exhibits striking color polymorphism in part of its range. Many individuals are inconspicuous and camouflaged against algal, hydroid, or other benthic substrata, however, brightly pigmented specimens have only been recorded along the west American coast from California to British Columbia (Goddard 2016, and unpublished observations). The enormous geographic range and potential color adaptation necessitates a reevaluation of this group for cryptic diversity. Since there has been virtually no genetic assessment of podocerid species, my research assesses the phylogenetic placement as well as potential cryptic differentiation of *P. cristatus* by generating a broad phylogeny of the Podoceridae. Specimens of *P. cristatus* were collected from four NE Pacific sites from British Columbia to Los Angeles, CA, in addition to outgroup specimens *P. spongicolus* and *P. brasiliensis*. Additional specimens of this species and other podocerids from other geographic regions were obtained from collaborating museums and institutions (e.g. FLMNH, UCSB, Natural History Museum (London), Australian Museum). Pereopod tissue will be sequenced for COI, 16S, cytB, H3, ITS, and used to reconstruct a phylogenetic tree with maximum likelihood, Bayesian, and coalescence methods. It is expected that phylogenetic analysis will reveal well-supported clades and inform the degree of cryptic diversity within Podoceridae. I will also use photographs to assess the geographic distribution of color morphs and whether different color morphs are conspecific. Since color polymorphism may be associated with Batesian mimicry of local aeolid nudibranch species (Goddard 2016), I will also assess how color pattern relates to the local color environment. This project serves as an exciting preliminary exploration of a poorly explored amphipod group, thereby providing a guide to future sampling efforts for comparative research.

Reference: Goddard JHR. 2016. *Mar. Biodiv.* 46: 535. <https://doi.org/10.1007/s12526-015-0402-0>

DNA sequencing and morphological analysis of an undescribed *Salentinella* species (Amphipoda, Salentinellidae) from an anchialine cave in Peloponnese, Greece

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The species of the genus *Salentinella* Ruffo, 1947 (Amphipoda, Bogidiellida, Salentinellidae) are known from the Mediterranean region and generally were found in groundwater environments and cave habitats. In this study, we report on a new *Salentinella* species collected in 2016 and 2018 from the anchialine water of the Koukouri cave, 85 m asl, in Peloponnese, Greece. The cave, 500 m from the seashore, develops with a gallery long about 70 m and ends with a large circular lake 4,5 m depth (23° French, pH = 8.2), which is connected with the sea. Morphological analysis indicated specimens (ca. 1.6 mm) belonging to an undescribed *Salentinella* species but related to *Salentinella angelieri* Ruffo et Delamare–Deboutteville 1952. We carried out a molecular analysis of this putative new taxon using mitochondrial (mt) and nuclear gene sequences, cytochrome oxidase I (COI), and histone H3 (H3), respectively. For the first time in amphipod phylogeny, we deal with the Bayesian analysis of multiple molecular sequences from a *Salentinella* species. DNA sequences of mt and nuclear genes from other families of Bogidiellida and infraorders (Talitrida, Hadziida, Corophiida, Gammarida) of the suborder Senticaudata were included in the analysis. Evolutionary questions relative to anchialine cave isolation and in situ speciation are here discussed.

On the evolution of terrestrial talitrid amphipods from Atlantic volcanic archipelagos, with a new species from the islands of Graciosa and Flores, Azores

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The terrestrial talitrid amphipods from the Atlantic volcanic islands live in humid, evergreen broadleaf laurel forest. Currently, six autochthonous talitrid species from the Canary Islands (4), Madeira (1), and Azores (1) are validly described. Here, we propose a new terrestrial species, collected from the islands of Graciosa and Flores, Azores, with a small lobe on the merus of male gnathopod 1, a variable character within talitrid genera. To determine the evolutionary relationships, Bayesian phylogeny was carried out on the new taxon in relation to other talitrid species belonging to different genera including *Canariorchestia*, *Cryptorchestia*, *Macarorchestia*, *Orchestia*, *Palmorchestia*, and *Speziorchestia*. Our phylogenetic tree, inferred from a mitochondrial and nuclear gene dataset, supported major clades. The *Macarorchestia* taxa formed an independent monophyletic lineage. Our molecular analysis revealed the neotenic *Palmorchestia*, endemic to La Palma, Canary Islands, as the closest genus of the new Azorean taxon. They formed a clade with *Canariorchestia canariensis* and *Cryptorchestia stocki* (*sensu* Lowry & Myers 2019), both endemic to Gran Canaria, and *Canariorchestia monticola* endemic to Madeira. Notably, our data confirmed *C. canariensis* and *C. stocki* as closely related species, indicating that the latter belongs to *Canariorchestia*. The phylogeny indicated another clade formed by *Canariorchestia gomeri* and *Speziorchestia guancha* (*sensu* Lowry & Myers 2019) from Canary Islands, and *Canariorchestia chevreuxi* from Azores, which share the absence of the lobe on the merus of gnathopod 1, and they have *Orchestia gammarellus* as sister species. They share a common ancestor with the clade formed by *Orchestia mediterranea* and *Orchestia aestuarensis*. Therefore, their putative marine common ancestor probably had the sexually dimorphic pereopods 1 (without the small lobe on the merus), 2, and 7. Our sequence-based tree showed that *S. guancha* is distantly related to *S. stephensi*, indicating that the former is not a member of *Speziorchestia*. Finally, *Orchestia montagui* and *Orchestia xylino* from Crete showed identical mitochondrial and nuclear sequences; they formed a Mediterranean clade with *S. stephensi*. Overall, our study suggested that the Atlantic archipelagos, with a sequence of island emergence and ageing over millions of years, might have been colonized by terrestrial talitrid lineages independently and on different times.

ToxMate: an autonomous online biomonitoring tool of water effluent quality based on the video analysis of the locomotor behaviour of the amphipod *Gammarus fossarum*

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Objectives: A partnership between the Irstea-Lyon ecotoxicology laboratory and the SME ViewPoint has made it possible to develop a device that evaluates in real time the locomotor behaviour of the *Gammarus fossarum* amphipod with a high degree of autonomy (~one month) in order to propose a new online water biomonitoring tool.

Methods: To achieve this goal, a video-tracking tool, the ToxMate Lab, was developed to provide a solution to monitor simultaneously isolated organisms over a long measurement period using a cage system that allows continuous water circulation (temperature and oxygen control). Following a priori hypotheses guided by the *Gammarus* ecophysiology (selection of size, sex, food privation, temperature influence, moulting control), a protocol was optimized notably for the selection and conditioning of test organisms.

Results: A first laboratory study made it possible to characterize the locomotor behaviour of *Gammarus fossarum* over a long period of time (30 days) without the need for external intervention, to develop a mathematical signal sensitive to the presence of micropollutants excluding a set of confounding factors that could be found in an online assessment of the toxic quality of treated waste water (temperature variation, major ion composition, physiological change). A second development phase adapted the ToxMate Lab to field conditions in order to perform robust on site measurements: 1- effluent conditioning module (filtration, oxygenation and temperature), 2- analysis of a representative water flow (500ml/min), 3- a toxicity signal based on a large number of replicates (3x16), and 4- a real-time evaluation system with online data every two minutes by tele-transmission.

Conclusions: During two years, different monthly sessions of online monitoring in two wastewater treatment plants and a rainwater retention and infiltration basin have demonstrated the relevance of this tool to evaluate in real time the temporal variability of toxic quality of treated water from urban wastewater treatment plants before released in the aquatic environment.

Phenotypical and genetic characters of the giant Antarctic *Eusirus* of the *perdentatus* complex, with the presentation of a new species

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The taxonomy of the giant Antarctic *Eusirus* with six crested body segments (crested *Eusirus*) is imperfectly resolved because the species of that group are very similar. So far, three species have been named: *Eusirus perdentatus* Chevreux, 1912, *E. giganteus* Andres, Lörz & Brandt, 2002 and *E. propeperdentatus* Andres, 1979. However, genetic data have demonstrated that the two first taxa are actually species complexes. The first complex has been thoroughly investigated, revealing the existence of two closely related, phenotypically similar (but not cryptic) species: *E. perdentatus* sensu stricto and *Eusirus* sp. nov. in the Atlantic sector of the Southern Ocean. Their highly distinctive colour pattern (marbled vs spotted), their subtle morphological differences and their phylogenetic relationships with the related *Eusirus propeperdentatus* Andres, 1979 and *Eusirus giganteus* Andres, Lörz & Brandt, 2002 (also a complex of similar species) are presented. It also appears that *E. perdentatus* sensu stricto reaches a smaller size than *Eusirus* sp. nov. and has a maximum abundance in shallower waters than its relative.

Insights into the ecology of *Cryptorchestia garbinii* on the shores of the urban Lake Tegel (Berlin)

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Talitrid amphipods are semiterrestrial and terrestrial organisms and find their optimal zonation in humid or water-saturated substrates. Some talitrids live in the supralittoral, where they maintain their zonation by means of an active behaviour. Other talitrid groups, like the genus *Cryptorchestia*, live in moist soil. Environmental constraints in this case might be different than those on a beach. The urban shores of Lake Tegel offer shelter to a resident population of *Cryptorchestia garbinii*: under the stones along the shore can be found numerous individuals. While the stones can offer a stable shelter, the lakeshore undergoes seasonal changes, with frozen or dry substrate, depending on the time of the year. To investigate how *C. garbinii* responds to such changes, we carried out a preliminary study to assess eventual mobility and daily activity of a population along the Tegel shore.

Sets of 6 pitfall traps were placed from the stones immediately adjacent to the shore up to the walking path of the Tegel urban park. Traps were emptied in the morning and in the evening (avoiding sunrise and sunset). Sampling was repeated in two subsequent days per each season: August and November 2016; February and April 2017. A test for survival in water on 14 adults was paired with the August sampling. We found a consistent pattern of activity both in space and in time: only the first traps – the closest to the stones – contained talitrids throughout the whole sampling, except in winter when the soil was frozen, incorporating the stones. Also, the night sample was consistently more numerous than the day sample (in spite of the artificial lighting). Temperature did not appear to be a main driver of activity, with animals found in the traps in November, when the minimum temperature recorded was 0°C. All individuals survived in water for the 96 hours of the test, with a female observed to release live offspring after 72 hours.

The results indicate a steadily nocturnal mobility, yet limited to less than one meter along the perpendicular to the shore, hence the potential to connect populations either alongshore or via water.

Do artificial structures create a functional shift in coastal benthic communities?

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Artificial structures have become to dominate shorelines worldwide. Under this framework, increasing our understanding of the ecological functioning of marine habitats incorporating a more holistic and ecosystem-based approach is crucial for preserving biodiversity. The present study aims to explore and compare for first time the main functional patterns of intertidal sessile and amphipod benthic communities on artificial structures with nearby natural hard substrata in Algeciras Bay (Spain). The main questions addressed were (i) whether artificial structures hold different functional assemblages and which kind of artificial designs represent the most similar compared to nearby natural habitats; and (ii) how substrata, both primary (natural or artificial rocky substrata) and secondary (sessile species), modify the functional structure of associated benthic amphipod assemblages. Four artificial substrata (seawalls, acropods, ripraps and cubes) were selected and the functional structure of associated sessile and amphipod intertidal assemblages was studied and compared with close natural habitats using Biological Trait Analysis (BTA). Three replicates (20x20 cm scrapes) were taken at three sites located at each substrata (n=45). Sessile and amphipod taxa were identified up to the lowest possible taxonomic level and were assigned to a total of 16 functional traits subdivided into 49 trait modalities reflecting properties about morphology, life-history, living, behavior and tolerance to environmental stress. Some abiotic variables as structural characteristics of substrata studied were also measured. Multivariate analyses were used to assess potential differences among substrata in species and functional trait composition (abundance-weighted trait by station data) of benthic communities and constrained ordination analyses were used to analyze interactions between biological trait matrices, taxa abundance arrays and abiotic parameters. Our results concluded that artificial structures studied are not functional surrogates of natural habitats, although some types could preserve functional patterns in amphipod communities. Furthermore, primary substrata-features, as surface roughness, were proved to affect the functional structure of the entire benthic community. Thus, the deployment of artificial structures studied was likely to affect the amphipod assemblages both directly and indirectly, through effects on secondary substrata, which could imply cascade effects of benthic functional patterns which may compromise the functioning at higher ecosystem levels.

Anxiety-like state and fear in gammarids: coupled or dissociative emotions?

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Anxiety and fear are often confused. Both modulates defensive behaviours, but fear is a context dependent emotion while anxiety is an emotional state that does not require an identified threat to be expressed. Anxiety is thereby expressed through a sustained apprehension of the environment. Although both emotional states have been evidenced in many animals including invertebrates, it has not yet been established whether their underlying neurophysiological and behavioral mechanisms overlap. Here, we addressed this question by assessing the intra-individual correlation between anxiety-like state (induced by electric shocks) and fear reaction (induced by fish odour) in the freshwater amphipod *Gammarus fossarum*. We estimated the level of anxiety and fear reaction by recording refuge use. We first assessed whether anxiety-like state and fear response were repeatable within individuals, and then whether they are correlated, on a 24 hours interval. The level of anxiety induced by electric shock was positively correlated to the level of fear expressed the day before at the intra-individual level, but the reciprocal was not significant. We discuss the proximate and ultimate mechanisms possibly involved in this asymmetrical overlap between these two emotional states.

The deep-sea Eusiridae from Papua New Guinea waters (SW Pacific Ocean)

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The Tropical Deep-Sea Benthos (TDSB) program, conducted by the Muséum National d'Histoire Naturelle and the Institut de Recherche pour le Développement, is devoted to fill in the gap in our knowledge of deep-sea biodiversity. In Papua New Guinea (PNG) seas, it has represented the first approach on deep-sea benthic fauna after the little attention dedicated to that area by the pioneering and historical expeditions of *Challenger* and *Siboga* and by the subsequent *Galathea* and *Vityaz* ones.

The PNG amphipod fauna was very poorly known and only 9 species were reported below 100 m depth, all of them from the Bismarck Sea: Maeridae (1 sp.), Stegocephalidae (1 sp.), Synopiidae (1 sp.), Tryphosidae (3 sp.), Uristidae (3 sp.). Since 2010, four deep-sea surveys (BIOPAPUA 2010, PAPUA NIUGINI 2012, MADEEP and KAVIENG 2014) were carried out in the Exclusive Economic Zone of PNG, more specifically in Bismarck and Solomon seas. During these surveys (dredge and trawl samplings), benthic amphipods have been collected between 120 and 1252 m depth (a total of 1872 specimens over 160 sampling stations).

Reported for the first time in deep PNG waters, eusirids represent a small component of their amphipod fauna with only 27 specimens collected in 14 stations. They belong to five species new to science, ascribed to three genera (the first one new to science): *Dorotea* Corbari, Frutos & Sorbe, 2019 (characterized by a telson poorly cleft with apically divergent lobes and a distal spiniform process on uropod 1 peduncle; 1 sp.), *Eusirus* Krøyer, 1845 (1 sp.) and *Rhachotropis* S.I. Smith, 1883 (3 sp.). *Dorotea papuana* (1 mature female; 593 m) was collected in the Solomon Sea; *Rhachotropis* sp.A (5 brooding females; 458–720 m) and *Rhachotropis* sp.B (7 brooding females; 837–1207 m) in the Solomon Sea; *Rhachotropis* sp.C (1 brooding female; 695–899 m) in the Bismarck Sea. The 13 *Eusirus* sp.A were collected in both Bismarck and Solomon seas between 340 and 998 m. Even if small, this dataset strongly suggests that PNG waters are still far from fully known about their biodiversity and more exploration should be dedicated to this area.

What do parasites do when their hosts diverge and meet again? Diversity of microsporidian parasites in central European lineages of the *Gammarus fossarum* species complex

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Gammarus fossarum, widespread across central and southeastern Europe, is apparently one of the most diverse amphipod species complexes. Recently it has been demonstrated that a substantial lineage diversity is found also in relatively high latitudes of the Western Carpathians (apparently thanks to long-term glacial survival in situ), which contrasts with rather uniform genetic structure further westwards. More detailed analyses of a contact zone confirmed that the populations of Carpathian lineages are not only distributed in a mosaic fashion but actually frequently occur in sympatry within the same small streams. These lineages, presumably cryptic species, show considerable genetic divergence at both mitochondrial and nuclear loci. However, little is known about their ecological differentiation and mutual ecological and evolutionary interactions including host-parasite interactions. Preliminary data based on ultrastructural and genetic analyses indicate that different microsporidian taxa parasitizing the *Gammarus fossarum* complex in Czechia show contrasting distribution patterns, from widespread species to some that seem restricted to host populations bound to specific river basins. Interestingly, distribution of at least one of these parasites apparently coincides with the boundary between areas of divergent lineages of the host species complex. At present, we are analysing samples collected from genetically characterized populations of multiple *G. fossarum* lineages. By molecular identification of both hosts and their associated microsporidian parasites, we focus on revealing parasitological aspects of past differentiation and subsequent contact of the hosts. Thus, this study, of which we will present the first results, may contribute not only to our knowledge of gammarids and their parasites, but also to understanding of the dynamics of evolution of host specificity.

Diversity and distribution of freshwater amphipods from Algeria

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Freshwater amphipods are much diversified with more than 2400 known species over the world. This group inhabits in all kind of freshwater environment (running waters, lakes, groundwaters) in which they generally represent the first invertebrate biomass. Freshwater amphipods in Algeria are represented by two families (Gammaridae and Pseudoniphargidae), three genera and reach a total of more than 10 epigeal and 2 groundwater species. To further document our knowledge of the freshwater amphipods from Algeria, we sampled more than 50 sites (streams, springs and wells) widely distributed in Northeastern Algeria. In this study, most of the previously reported species have been found and at least three new species have been discovered. We also highlighted that distribution of amphipods is mainly explain by climate and elevation.

Pacific species of *Epimeria* (Amphipoda: Amphilocheia, Epimeriidae) with a description of a new deep-sea species from SW Mexico

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Deep-water amphipods have been collected during exploratory surveys off western Mexico: the TALUD project. Study of this material has allowed the description so far of three new species in the genera *Epimeria*, *Trischizostoma*, and *Stephonyx*. *Epimeria* represents the most speciose genus of the family Epimeriidae, and includes marine amphipods with the highest morphological variations and colourations among the peracarids. The amphipods of this genus had been mainly documented for deep-water worldwide, predominantly in the Southern Ocean. So far, 13 *Epimeria* species inhabit the Pacific Ocean deep-sea: *E. bruuni*, *E. cora*, *E. emma*, *E. glaucosa*, *E. horsti*, *E. morronei*, *E. norfanzhi*, *E. pacifica*, *E. pelagica*, *E. sophie*, *E. subcarinata*, *E. victoria*, and *E. yaquinae*. Both *E. morronei* and the new species were collected during the TALUD project. The specimen of the new species was collected from off SW Mexico (19°19'N, 105°26'W) by the R/V "El Puma" (UNAM), in depth of 1609-1643 m, in mild hypoxic conditions (1.03 ml O₂/l). Female of *Epimeria* sp. nov., is most similar to females of *E. cora*, *E. pacifica*, and *E. morronei*; however, it differs from those species by diagnostic characteristics in the eyes, head ventral lobes, coxae 3-5, epimera 1-3, gnathopods 1-2, uropods 1-3, telson, and mouth parts. The preliminary description of this new *Epimeria* is presented. It increases the number of *Epimeria* species for the Pacific Ocean to 14, and for the Eastern Pacific to three.

Two new species of the rare, deep-sea genus *Vemana* (Amphipoda: Vemanidae) from the northeast and southeast Atlantic

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During examinations of benthic samples from the *Discovery* cruises, *Vema*-TRANSIT and the *DIVA-2* expedition (Diversity of the Abyssal Atlantic benthos), 7 specimens of the rarely collected amphipod genus *Vemana* were found. Upon detailed morphological examination, the specimens have been determined to belong to two new species of the genus *Vemana* Barnard, 1964. This brings the total number of recorded species for the genus to 6, with the most recently described species being *V. geysereensis* Ledoyer, 1986. The 7 specimens belonging to the two new species now brings the total number of known specimens to 15, but we are also aware of 19 other specimens from the KuramBio I expedition (Kurile-Kamchatka Trench, NW Pacific). Therefore, we know of 34 individuals of this rare genus of amphipod. *Vemana* A sp. nov. (4 specimens) was found in the northeast Atlantic, just north of the Cape Verde Islands, while *Vemana* B sp. nov. (2 + 1 rear fragment) has been found in the northeast Atlantic, just north and south of the Cape Verde Islands and southeast Atlantic (Guinea Basin). *Vemana* B sp. nov. is the deepest recorded species, with specimens collected from 4412-5507 m. This new species can be differentiated from the other 4 species, *Vemana compressa* Barnard, 1964 (type species), *V. geysereensis* Ledoyer, 1986, *V. lemuresa* Barnard, 1967 and *V. lizata* Barnard, 1964 in the possession of a strong posterodistal tooth on peduncular article 2 of antenna 1 and with a broad, non-narrowed telson, which has broadly rounded lobes and a short, widely gaping V-shaped cleft. *Vemana* A sp. nov. differs from the other species in having coxa 4 with a rounded posterodistal lobe, an acutely produced but untoothed epimeron 3 and a relatively elongate telson cleft of about 70%. The pereopod 7 basis is as in *V. lemuresa* but lacks the subchelate gnathopod 1 of that species. Up until very recently, *Vemana* was included in the Vitjazianidae, but Lowry & Myers, 2017 transferred it to a new family, Vemanidae.

Historic Peracarid Crustacea Collections in the Natural History Museum, London

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Marine Invertebrate collections at the Natural History Museum, London include specimens collected in the late eighteenth to early nineteenth century. While, the early Porifera, Mollusc and Decapod collections are much discussed and catalogued in various decades, there is little published information on the smaller Crustacea groups. These historic Peracarids specimens include little known Type species of Amphipods and Isopods and were the material studied by Fabricius and Leach to establish the foundations of higher classification in Carcinology. This project documents the NHM's collection of dry pinned Peracarid Crustaceans, databasing and making available this information to the wide scientific community. Using museum labels, old registers and published catalogues from 1847 to 1912 the project enhances the known history of specimens which are currently accompanied by only partial data. The project improves the records of Amphipods and Isopods across three areas 1) leading nineteenth century UK naturalists Col. George Montagu, Charles Spence-Bate, Alfred Merle Norman and 2) past curators of the Natural History Museum Crustacea collection William Elford Leach, Adam White, John Edward Grey and Edward John Miers. Significantly these workers contributed new species names and distribution records to the Northern Atlantic for their era. Lastly the project will focus on 3) major marine expeditions from the eighteenth to the early nineteenth century including the HMS *Fly*, HMS *Beagle*, HMS *Challenger*, HMS *Triton* and HMSS *Erebus & Terror* which represents some of the earliest collecting of Peracarids from the 'Southern Seas' including the Philippines, Fiji, Java, Van Diemen's Land and New Holland (the latter now recognised as Tasmania and Australia, respectfully). Results of this project highlights: previous unrecognised Type material; material with probable Type provenance (where authors did not explicitly designate a Type series) and provides additional commentary on nomenclature surrounding Amphipod and Isopod manuscript names of William Elford Leach that were later applied by Adam White. This project provides new records of specimens on the NHM data portal for important historic Peracarid specimens. This historical curation study is relevant to nomenclature, taxonomy, biodiversity, invasive species research globally with the data delivered to international museum and biodiversity platforms.

A project's blueprint: drivers of cryptic species coexistence in freshwater gammarid communities of Sicily

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In recent years, DNA based biodiversity assessments have proven that species diversity has been vastly underestimated due to the presence of overlooked or cryptic species. Simultaneously, what was once considered intraspecific variability now has to be re-examined, and the actual distribution and ecological traits of cryptic species have to be re-assessed. A frequently supported scenario is the assumption that cryptic species usually do not co-occur but rather are locally separated and are rarely found in syntopy. This is corroborated by the predicted ecological similarities between cryptic species, as they are phylogenetically close, and thus, not expected to exhibit any niche partitioning patterns increasing competition.

Interestingly, four cryptic lineages of the gammarid amphipod *Echinogammarus sicilianus* are known to co-occur on Sicily – even at a single locality – rendering it a unique case of co-occurring cryptic freshwater species. This particular and highly unexpected finding raises the question whether the observed co-existence is stable or unstable, and how it is facilitated. Hence, the goal of our project is to test different hypotheses based on niche partitioning schemes, microhabitat selection and the potential influence of parasites mediating species coexistence. Thereby, we use this case as a model to study the general question how cryptic/sibling species partitioned resources at the local and temporal scale.

All available microhabitats in the river network, adjacent tributaries and affluents, will be sampled in four successive seasonal campaigns. Amphipod specimens for each microhabitat and site will be DNA barcoded. Their gut contents and microbiomes will be analysed via DNA metabarcoding to get insights into potential food resource specialisation among the cryptic species. Additional data from stable isotope analyses, the local hydrological conditions as well as the presence and diversity of microsporidian and acanthocephalan parasites, will help to identify potential drivers of species coexistence in freshwater gammarid communities of Sicily at the spatial and temporal scale.

New insights on the deep-sea amphipods from the sea of Okhotsk (NW Pacific)

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Amphipoda constitutes abundant and diverse group inhabiting the deep sea at all latitudes. Within the framework of the joint Russian-German scientific project for biodiversity studies of the northwestern Pacific deep-sea benthos, the amphipods from the Sea of Okhotsk were sampled on board RV *Akademik M.A. Lavrentyev* during the SokhoBio expedition (6th July–6th August 2015). Amphipods were collected by means of an epibenthic sledge in 19 stations at 11 sites located in the Kuril Basin, the Bussol Strait and on the western abyssal slope of the Kuril-Kamchatka Trench in a depth range between 1696 and 4798 m.

A total of 4222 individuals belonging to at least 32 taxa were identified. The suborder Amphilochidira was the best represented (73.6% of the total), but Senticaudata (25.7%), Hyperioptera (0.5%) and Hyperiidea (0.2%) occurred as well. The 'Corophiida' group constituted 18% of all amphipods, followed by the families Oedicerotidae (16%), Phoxocephalidae (13%) and Eusiridae (12%). The most frequent families were Oedicerotidae, Pardaliscidae and Phoxocephalidae occurring at 16 stations followed by Eusiridae and Stenothoidae (14 and 12 stations, respectively).

Within the high species richness found, three species of the Eusiridae were identified as new to science, one of them, *Rhachotropis marina* Lörz *et al.*, 2018, already described; and other taxon hardly attributable to any known family (ongoing study).

A multivariate analysis carried on the amphipod family abundance data (3 stations excluded), discriminated 4 different assemblages in the studied area: a Kuril Basin assemblage (group A, 11 stations, 3210–3366 m) characterized by Oedicerotidae and Phoxocephalidae; a Bussol Strait assemblage (group B, 2 stations, 2327–2333 m) dominated by 'Corophiida' group; and two assemblages in the Kuril-Kamchatka Trench area: a single station (group C, 4681 m) dominated by Phoxocephalidae and two grouped stations (group D, 3371–4798 m) characterized by Lysianassoidea.

The species composition of this amphipod fauna and its distribution in the Sea of Okhotsk will reveal if is linked to the adjacent abyssal fauna of open ocean waters of the Kuril-Kamchatka area or is conditioned by the presence of the trench.

Barcoding of deep-sea Northwest Pacific Oedicerotidae

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Despite the fact that deep sea covers great area of our planet and in the recent decades it became subject of various studies it is still mostly unexplored. Amphipoda belong to abundant and diverse groups inhabiting bathyal, abyssal and hadal depths. The representatives of the family Oedicerotidae constitute 10-20% of all amphipods collected in the deep sea. Unfortunately, collection of fragile crustaceans from such depths results often in their damage, which hinders morphological identification. DNA barcoding that uses a fragment of the cytochrome I oxidase (COI) gene gives opportunity to recognize the species and may help in biodiversity studies.

The aim of the present study is to recognize the molecular diversity of the deep-sea Oedicerotide from Northwest Pacific as well as to reveal faunal connectivity between semi-enclosed Sea of Okhotsk and the open ocean.

During three international expeditions (KuramBio I and II, SokhoBio) to the Sea of Okhotsk as well as abyssal and hadal of Kuril-Kamchatka Trench, the amphipods were collected from 47 stations at the depths 4800-9500 m. Oedicerotids were initially divided into 16 morphospecies. DNA extraction, amplification and sequencing of the COI gene followed standard protocols used for Amphipoda.

The molecular analysis revealed almost 20 Molecular Operational Taxonomic Units (MOTUs). The majority of morphospecies coincided with the recognized MOTUs. In one case single morphospecies was divided into three molecular entities. The molecularly identified taxa showed various bathymetric and geographic ranges. The separate hadal and abyssal species groups were recognized. Among the abyssal ones some taxa were shared between the Sea of Okhotsk and the open ocean. Certain MOTUs were restricted only to one side of the Kuril-Kamchatka Trench, while others were recorded on its both sides.

Integrative evidence for hidden species diversity and long-term divergence within *Gammarus balcanicus* Schäferna 1923 morphospecies in the northernmost part of the Carpathian Arc

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Carpathians are one of the key “biodiversity hotspots” in Europe. The mountain chain uplifted during Alpine orogenesis and is characterized by a complicated geological history. Their current biodiversity was highly influenced by Pleistocene glaciations especially in their northernmost part comprising of Western Carpathians and the northern part of Eastern Carpathians. Recent studies have already shown that cold adapted gammarids (crustaceans) probably survived the Ice Age in cryptic refugia of the Western Carpathians and that the *G. balcanicus* Schäferna 1923 morphospecies inhabiting northernmost Carpathians is in fact a complex of phylogenetic lineages.

The goal of our current study was to delimit and describe potential new species belonging to *G. balcanicus* morphospecies as well as to trace their demographic and divergence history using integrative approach. This involves morphological (e.g. Scanning Electron Microscopy - SEM) and molecular tools. Additional goal is preparation of detailed reference library of gammarids from the north of Carpathians in the Barcode of Life Data System (BOLD).

Material for the study was collected from over 50 stations in Poland, Slovakia and Czech Republic. It comprises both new and already published data. Molecular species delimitation revealed existence of 5 Molecular Operational Taxonomical Units (MOTUs) of *G. balcanicus* morphospecies with distribution limited to northern Carpathians. The morphological examination supported existence of two morphological types, previously described as “A” and “B”, the SEM analysis did not unambiguously reveal any features that could help in species delimitation. Molecular diversity showed that divergence of these MOTUs is dating back to Miocene what supports the hypothesis of their survival in local northern refugia. Delimited MOTUs show different patterns of postglacial demography. Four of them exhibit postglacial demographic expansion with two that expanded also geographically. One MOTU, restricted to the northern part of Eastern Carpathians is showing demographic decline and very limited range.

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Active biomonitoring using the freshwater amphipod *Gammarus fossarum*: an operational method to monitor chemical contamination and ecotoxicity in watercourses at the French national scale

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Objectives: According to the recommendations of the Water Framework Directive guidance document for biota monitoring adopted in 2014, active biomonitoring based on caged control organisms is considered as one possible approach to assess the contamination of aquatic ecosystems by micropollutants. Thanks to this regulatory support, biomonitoring methodologies in the freshwater amphipod *Gammarus fossarum* were developed in France notably in the framework of a partnership and a technological transfer between an academic laboratory and a brand new company founded in 2014.

Methods: Allowing the acquisition of *in situ* bioassay data at the national scale in a high throughput way, we built databases gathering fully comparable measurements (same protocol, same source population, same selection and conditioning of test organisms) of contamination (bioaccumulated concentrations) and toxicity (feeding inhibition, reproductive alteration, AChE inhibition) in French waterbodies (~1000 deployments). A standardization of the protocol for *Gammarus in situ* caging was notably defined for France and will soon be proposed at the ISO.

Results: We show here how this integrative and robust tool can be proposed to assess bioavailable contamination and ecotoxicological impacts of complex mixtures of pollutants in watercourses. This brings specifically new possibilities to monitor priority substances of the Water Framework Directive (in particular, priority substances of the Directive 2013/39/EU which introduce Environmental Quality Standards (EQSs) in biota). In addition, reference values and indicators of the gravity of bioavailable contamination and toxicity were defined at the national scale.

Conclusions: Using standardized caging protocols with *Gammarus* and reference values (with associated contamination and toxicity thresholds), it is thus possible to compare with reliability different hydroecosystems at large scale. Active biomonitoring methodologies with *Gammarus* permit to establish indicators of bioavailable contamination and ecotoxicity, which quantify chemical exposure gradients and toxic pressure relying on freshwater ecosystems. This makes such indicators relevant as prioritization tools for managers. It also opens perspectives to decipher the structuring role of chemical contamination on freshwater biological communities.

First insights into the deep-sea scavengers at hydrothermal vent fields along the Southeast Indian Ridge

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Hydrothermal vent areas gained increasing interest since they were discovered in 1977. Due to chemoautotrophic bacteria they possess high abundances of vent endemic species as well as many non-vent species around the fields.

Studying scavenging Amphipoda was part of the INDEX (Indian Ocean Exploration Project) cruise 2018 on the research vessel Pelagia. Therefore, an Amphipod Trap was deployed at three newly discovered hydrothermal vent fields along the Southeast Indian Ridge. It was placed by the Canadian ROV Ropos both at active and inactive vent sites at depths of 2500-2900 m and recovered after 7-29 h.

Six species of amphipods (*Abyssorhomene distinctus*; *Eurythenes magellanicus* and *E. cf. magellanicus*; *Hirondellea* sp. 1; *Paracallisoma* sp. 1 and *P. cf. alberti*) could be clearly delimited morphologically and lately confirmed by genetic barcoding using the fragment of genes COI and 16S. The genus *Paralicella* turned out to be more complex with two identified morphospecies that are four according to the genetics.

A surprising discovery is the species *Eurythenes magellanicus* as this is its first report in the Indian Ocean, up to now it was caught in the Brazil Basin, the area of Cape Horn (South America) and off Taiwan. In addition, we detected the largest specimen (105 mm) reported so far which is still an immature female.

***Gammarus lacustris* (Sars, 1863) sexual behavior in small brackish lakes of West Siberian Plain southwest part**

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Lacustrine scuds *Gammarus lacustris* (Sars, 1863) is a cosmopolitan species with a holarctic areal, which includes significant parts of the circumboreal, West American and Central Asian zoogeographic subregions. *G.lacustris* can be considered an ordinary inhabitant of brackish lakes in the Kurgan region (Russia). This is facilitated by the high tolerance of this species to the temperature (from 0° to 30°C) and to the concentration of oxygen dissolved in water (from 0.2 mgO₂ per liter to maximum possible for the lake). Such conditions are characteristic of lakes of the West Siberian Plain southwest part. Their depth is 2.0-2.5 m and salinity is from 3‰ to 20‰.

The objective our work is to study the sexual behavior characteristics of this crustaceans species under influence the seasonally changing of the temperature and oxygen regimes of the lakes of the West Siberian Plain southwest part. We studied gender, age and behavioral structures of populations in native water ecosystems and as well as spent a factorial laboratory experiment with using of oxythermostatic installation.

In the studied lakes there is a 3-4 year cycle of gammarids populations development and exist two reproduction periods of *G.lacustris* in the lakes of the region (since April until May and since August until September). The preparation for breeding of *G.lacustris* individuals begins on the West Siberian Plain southwest part territory in February-March (the number of coupling but non-copulating individuals is up to 15% of the total number of individuals in population). The movement and feeding of motionless females in a pair during this period is carried out due to the activity of the male. The ineffective acts of copulation are rare at this time (1-2% of the generative individuals number). The process of effective reproductive copulation begins after the lakes deliverance from ice cover and increasing the temperature and concentration of dissolved oxygen. It increases to a maximum to the end of April - the beginning of May and practically ends to the end of May (56-92% and 10-12% of the generative individuals number, respectively). The copulative process is carried out when the female fixes the male in the cross-to-cross position. It continues in the studied lakes of region during three days and occurs both in the water column and on the surface of immersed macrophytes. The female becomes inactive after fertilization, loses in biomass by using organic compounds to maintain the development of eggs in the marsupium. The female exists in a pair with a male, which helping her to eat and move, until hatching of young individuals from eggs and the beginning of their independent life.

Combining artificial substrates, morphology and DNA metabarcoding for investigating marine amphipod communities in NW Iberia

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Amphipods are commonly used in biomonitoring programs since they can be used as bioindicators of environmental quality and ecosystem functioning in marine habitats, and are prime vectors of anthropogenic related dispersal. High-throughput techniques coupled with standardized sampling strategies accurately improve the resolution to monitor marine communities. Artificial substrates deployed in coastal areas may selectively influence and enhance the colonization of macrobenthic species, namely amphipods, providing an alternative to easily and routinely assess biodiversity. Here, we used morphology and DNA metabarcoding approaches to monitor coastal amphipod communities and investigate the short-term and seasonal patterns of colonization in artificial substrates. Three different types of artificial substrates: slate, polyvinyl chloride and granite, were deployed close to the dock of Toralla Island (Vigo, NW Spain). After 3, 7, 10 and 15 months, four replicates of each substrate were randomly removed: 3 replicates for morphology and 1 for DNA metabarcoding. Amphipod fauna was separated from other macroinvertebrates and preserved for subsequent analysis. DNA amplification was performed for COI barcode region and for V4 region from 18S rRNA gene. Compared to morphology, DNA metabarcoding retrieved more amphipod taxa and higher species-level resolution. However, some of the species identified with morphology were not detected using DNA metabarcoding (e.g. *Pariambus typicus* and *Melita palmata*). Compared to the other substrates, slate replicates resulted in a higher colonization of target taxa. While some species were evenly detected in nearly all of the substrates and time combinations (e.g. *Jassa slatteryi*), some taxon were time-specific (e.g. *Stenothoe monoculoides* only detected in first recruitment season) or randomly detected with variations in taxonomic diversity among substrates and seasons (e.g. *Microdeutopus* spp.). In general, artificial substrates promoted amphipod colonization and, coupled with molecular tools, capture more realistically the species composition of the natural community. This highlights the importance of the adopted sampling strategy to be used in biomonitoring programs to capture benthic biodiversity. The results also evidence that the substrate and season influence the recruitment of amphipod species. Furthermore, morphology and DNA metabarcoding are somewhat complementary in their ability to detect amphipod species, and both should be used to capture the amphipod richness.

**First records of two hyperiid amphipods,
Phronima atlantica and *Oxycephalus clausi* from Korea**

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During a survey on pelagic crustacean species, two species of hyperiid amphipods, *Phronima atlantica* Guérin-Méneville, 1836, and *Oxycephalus clausi* Bovallius, 1887, were found in East Sea, Korea. These two species are new to Korean water. We provide descriptions and illustrations for these two hyperiid species herein. In previous studies of 1970s, only a small number of the hyperiid amphipods were mentioned appearing in the coast of Korea, and were recorded as unidentified species with other planktonic organisms by some Japanese scientists. The taxonomic study of the Korean hyperiid amphipods was first conducted by Yoo in 1972. Subsequently, 16 of the hyperiid species were described through a monograph of Korean marine zooplankton written by Yoo in 1975. Consequently, a total of 17 hyperiidean amphipod species have been listed from the Korean fauna. There has not been noticeable taxonomic research on the Korean hyperiids for about 50 years since Yoo's representative studies.

Stable indicators of energy metabolism and non-specific stress response as a strategy of biochemical adaptation in eurybathic Baikal amphipods of the genus *Ommatogammarus*

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Among the extraordinary ancient ecosystems, the fauna of Lake Baikal is especially remarkable as a prospective model system to study the adaptation mechanisms in aquatic animals at different levels of biological organization. Baikal is characterized by distinct ultra-deep zones (up to 1642 m) inhabited by unique deep-water freshwater fauna, which is predominantly represented by amphipods (Amphipoda, Crustacea). However, the biochemical adaptation of Baikal inhabitants of high depth, combined with effects of low temperatures and high oxygen content remains almost unexplored so far.

The aim of this study was to compare biochemical and cellular markers of energy metabolism and stress response in deep-water Baikal endemic amphipods of the genus *Ommatogammarus*. As an object of study, we used two most common species, namely *Ommatogammarus flavus* (Dyb., 1874) and *O. albinus* (Dyb., 1874), which are eurybathic specialized scavengers dwelling at the depths of 50 to 1300 m.

Amphipods were sampled near the Bolshie Koty settlement (Southern Baikal) using deep-water traps at the different depths (50, 100, 150, 200, 300, 500, 750 and 1000 meters) and fixed in liquid nitrogen immediately after collection.

To evaluate the energy status, we measured the contents of adenylates, glucose, glycogen, and lactate. Oxidative membrane damage was estimated based on the content of lipid peroxidation products. Non-specific cellular stress response mechanisms were evaluated based on the activities of antioxidative enzymes and the content of heat shock proteins of HSP70 family.

No direct correlation between the measured parameters and habitat depths was found, which indicates the stable metabolic processes and the absence of cellular stress in individual amphipods taken from different depths.

Probably, the stability of the biochemical stress response and energy metabolism indices is an evolutionary adaptation allowing the studied species to be eurybathic and perform an important function of specialized scavengers in benthic ecosystems of Lake Baikal.

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Temporal variation of the amphipod assemblage on sandy sediments at the Ría de Ferrol (Galicia, NW Iberian Peninsula)

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Concentration of human population on the shoreline results in alteration of coastal natural habitats. Most of this impact is due to urbanisation and construction of coastal defences; this translates in alteration of local hydrodynamics and changes in sediment granulometry and the benthic faunal assemblage. For instance, the construction of the outer harbour jetty in the Ría de Ferrol (NW Spain) 20 years ago is expected to have affected the benthic environment of the ría. Therefore, the Marine Biological Station of A Graña (Univ. de Santiago) started in 2008 a monitoring study of the sandy sediments and fauna near the outer harbour, with special attention to the amphipod assemblage due to their sensitivity to environmental changes. Quantitative sampling was carried out bimonthly in two subtidal (7-10 m) sandy sites that differ in the proportion of sandy fractions: Site 1 (medium-fine sand) and Site 2 (mostly fine sand). Five van Veen grabs were collected at each date (starting in January 2008) per site; samples were sieved through a mesh of 0.5 mm. In this communication, results from the first three years of sampling (2008-2010) are presented. Sediment granulometry and organic matter content remained more or less stable through time; silt/clay content was in general low (<5%). Sampling yielded 9660 amphipod specimens corresponding to 51 species (St.1, 36 spp., St.2, 42 spp.). Both sites shared the same numerically dominant species (i.e. *Urothoe grimaldii*, *Photis longipes*, *Leucothoe incisa*) and a similar assemblage mostly composed by Urothoidae (3 species), Oedicerotidae (4), Bathyporeiidae (4), Ampeliscidae (3) and Tryphosidae (3); however, abundances (total and those of dominant taxa) were much higher in St.1. Temporal variation of abundance and number of species showed a seasonal pattern as expected, i.e. higher values in summer and early autumn. There were no significant interannual changes apart from a decrease in the abundance of *P. longipes* in 2010. In all, the amphipod assemblage was diverse and there were no symptoms of alteration due to the construction of the harbour jetty. However, sensible marine management is recommended in order to prevent further perturbations in the ría.

Spatial patterns of coastal amphipods collected by light traps in South Spain

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Benthic amphipods often show well-defined patterns of spatial distribution on coastal habitats, according to depth (intertidal or subtidal), exposure, presence of macroalgae or seagrasses, etc. Many of these species are part of the so-called demersal zooplankton, i.e. migrating species that seek shelter on the substrate during the day but emerge to the water column at night. Although they play a key role on coastal ecosystems as prey source for zooplanktivorous species, many aspects of these migrations remain unknown. In the present study, we aim to characterize spatial patterns of demersal amphipods by comparing samples collected by light traps deployed both at rocky and nearby sandy areas. Since light is the major stimulus driving this migrating behavior, light traps have been proposed as a suitable sampling method when studying demersal zooplankton. Dispersal abilities of such species will be also explored by considering two spatial scales of separation between rocky and sandy substrates: 1) dozens of ms and 2) >1 km (hereafter short and long beaches, respectively). Four “short beaches” and four “long beaches” were considered and three replicates were collected on both substrates within each site. We hypothesized that, although migrating amphipods hide on specific substrates (rocky/soft bottom), these species would mix once individuals emerge to the water column, but only at “short” beaches. Results showed that numerically dominant species in both habitats were those commonly found on sediment (*Periocolodes longimanus*, *Pontocrates areanarius*, *Bathyporeia* sp., *Guernea coalita* or *Nototropis swammerdamei*). Species associated with rocky bottoms during the day, such as *Dexamine spiniventris*, *Echinogammarus* sp. or *Jassa ocia*, were collected at low abundances in traps over sandy bottoms close to rocky surfaces their dispersal abilities do not allow for reaching distant sandy bottoms. Consequently, sandy areas at “long beaches” showed significant lower number of species than rocky bottoms while no differences were found between substrates at “short beaches”. However, multivariate analyses still detected significant differences between rocky and sandy areas both at “short” and “long” beaches. Thus, we can conclude that amphipod assemblages show a well-defined pattern of distribution in the water column, even at small spatial scale.

Amphipod response to host-complexity along an environmental stress gradient

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By creating extensive habitats and/or ameliorating thermal and desiccation stress, intertidal sessile foundation species (such as macroalgae, mussels or barnacles) play a key positive role in amphipods assemblages. Response of such associated communities is largely dependent of the environmental stressful conditions, as well as host traits related with their ability to reduce abiotic stress (e.g. size, health or architectural complexity). However, the interplay between these two factors modulating the intensity of facilitation interactions have been scarcely tested empirically. With this aim, we conduct a colonization experiment using artificial units with different variations in a functional trait (morphological complexity) deployed at four different shore heights (from a very shallow but permanently submerged level to the higher intertidal limit in the study area). It is hypothesized that the importance of such trait variations (i.e. morphological complexity) would be greater in the harsh physical conditions of the high intertidal, rather than the relatively benign conditions of subtidal environments. An additional experiment was conducted using predator-exclusion cages in order to evaluate the role of predation pressure in each of these heights. After 25 days of deployment Amphipoda accounted more than 80% of all specimens collected, being *Jassa slatteryi*, *Caprella* aff. *penantis*, *Stenothoe* sp. and *Erichthonius pugnax* the dominant species at all heights considered. All of them are successful early colonizers of artificial structures and, thus, common inhabitants of fouling communities associated to aquaculture facilities, boats or floating pontoons. The isolated effects of shore-height and host-complexity was in accordance to expectations: number of species and abundance values decrease as units were less complex and remains less time underwater. However, relevance of complexity (differences between lower and higher complexity treatments) in the development of amphipod assemblages were higher at lower elevations. An increasing predator pressure at lower elevations could explain this pattern but our results from cage experiment ruled out that possibility (predation pressure was almost negligible at all heights). Thus, reasons behind the higher community response to complexity values at subtidal or low intertidal levels remains obscure.

A faunistic description of the Amphipod-fauna of Hjeltefjord, Western-Norway

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The objectives for this project was to investigate what amphipod species are present in a western-Norwegian fjord, and whether the species composition and their abundance changes throughout a year cycle. By doing this, a better understanding can be reached about the seasonal variability for a group of species which are highly diverse in their life histories, and which are an important part of the marine food chain. The results of this study will also have implications for environmental monitoring, and whether this needs to be set to a specific season or time of year. Further, it is discussed whether the potential seasonal changes are due to biological reasons or due to sampling effort and methods. Amphipoda was collected throughout a one-year span from November 2017 to October 2018. A total of 17 samples from 9 points in time (two replicates per sampling) from one location were collected. The sampling in June only had one replicate. The samples were collected using an RP-sled hauled at 1 knot for 10 minutes per haul. Amphipods were identified to species were possible and the numbers of all species were recorded at all stations. A total of 73 different species from 38 families were identified. The family Ampeliscidae was highly dominant in all samples and represented 2267 of the total 6520 individuals recorded. Results showed that species richness varied from 21 to 46 species between the replicates, with the highest being in November and the lowest in April and October. Species evenness ranged from 0.59 to 0.79, showing the highest species evenness in April and lowest in March. Two different indices of biodiversity (Shannon Weaver and Simpson) showed no significant difference in the biodiversity between the sampling stations. Our results shows that there is a small change in abundance and composition between the sampled months, but whether this is due to sampling effort or seasonal variation is uncertain.

Syntopic coexistence of gammarid cryptic lineages: rule or exception?

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Recent molecular studies have revealed an enormous cryptic diversity in many presumably widespread *Gammarus* taxa. In fact, most common *Gammarus* species in European inland waters are actually species complexes, which comprise many narrowly endemic evolutionary lineages, particularly in the southeastern part of the continent. A recent study has revealed a substantial diversity of the *Gammarus fossarum* complex in the Western Carpathians, with multiple lineages apparently distributed in a mosaic fashion. However, the sampling design, where usually one individual per locality has been sequenced, did not allow for evaluation of the detailed distribution patterns of individual lineages. Considering that these gammarids seem ecologically very similar despite their long evolutionary isolation, it is of interest whether they are able to coexist after secondary contact, or whether competitive exclusion takes place. In this contribution, we combine two different datasets from Western Carpathians to test for the potential syntopic presence of distinct gammarid lineages belonging to the same species complexes. First, we have focused on detailed patterns of lineage distribution in a small area in eastern Czechia (ca 30 x 30 km) where over 60 gammarid populations were collected, and usually 5 individuals per site identified by assessing the variation of the mitochondrial 16S rRNA gene. Second, we extracted data on gammarid presence and diversity from a project assessing the diversity of macrozoobenthos by COI metabarcoding at 21 Western Carpathian spring fens (ranging from eastern Czechia across northern Slovakia). In both data sets, coexistence of at least two gammarid lineages was confirmed in approx. half of the localities, and even sympatric presence of three or four lineages per site was not exceptional. Especially in case of the spring fens, it seems unlikely that the amphipods are colonizing the sites from other source localities. We thus conclude that coexistence of gammarid cryptic lineages is frequent, and detailed examination of their ecological and microevolutionary interactions are warranted.

Amphipod inhabiting the invasive macroalgae *Sargassum muticum* in the English Channel

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The invasive species *Sargassum muticum* was originated from northeastern Pacific and was introduced with the oyster *Crassostrea gigas* along the French coast. *S. muticum* flourished from the spring to the end of the summer along the English Channel coast mainly in the intertidal zone where seawater stays at low tide. This macroalgae were known to host high biodiversity of mobile marine fauna, especially amphipods, when compared to non-vegetated habitats. The distribution and abundance patterns of the amphipods associated to *Sargassum muticum* species were studied on a spatial scale along the Normandy coast from the Normand-Breton Gulf to the Bay of Seine, in six sites in April 2017 and 2018. Sampling was made with a WP2 zooplankton net 0.500 µm attached on a metallic structure of 0.3 (height) x 0.6 (width). Three replicates on 5 m length were made at each site on dense *Sargassum* population in pool of the rocky shores, to obtain a sampling surface of 3 m². Twenty amphipod species were collected, among them *Gammarus finmarchicus* Dahl, 1938 and *Apohyale prevostii* (H. Milne Edwards, 1830) dominated. Caprellidae and the tube-dwelling species such as *Erichthonius punctatus* (Spence Bate, 1857), *Ischyrocerus anguipes* Krøyer, 1838, *Jassa falcata* (Montagu, 1808) and the non-native species *Monocorophium sextonae* (Crawford, 1937) were also abundant. The abundances were higher in the sites of the North Cotentin than the others. The species richness increased in the low intertidal zone whereas abundances increased with the density of *Sargassum muticum*. The amphipods and other mobile fauna among them the isopods *Dynamene bidentata* (Adams, 1800) and the shrimp *Hippolyte varians* Leach, 1814 were prey sources of fishes during high tides.

Interaction of species, temperature and parasitism may facilitate replacement of native amphipod by invasive species, impacting vital ecosystem process of detritivory

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Freshwater ecosystems are particularly vulnerable to anthropogenic impacts due to their relatively limited volume, connectivity and proximity to human development. Invasive species are one of the main drivers of biodiversity loss, with introduced Ponto-Caspian amphipods, such as the killer shrimp *Dikerogammarus villosus*, altering freshwater community structures across Europe. Parasites, which are often overlooked, are important community members that can affect host survival as well as host trophic interactions. Furthermore, climate change is increasing the frequency and intensity of extreme weather events, with heatwaves having major consequences for ecosystem structures and productivity. It is important to understand how combined stressors of invasive species, parasitism and climate may interact to affect communities and ecosystem processes.

The main basal resource in temperate freshwater ecosystems is riparian leaf litter, which is broken down by microbial decomposers and invertebrate shredders, providing resources to the rest of the community through shredded leaf mass and biomass growth of consumers. Amphipods are often the dominant shredder species in freshwater communities. We study how this key ecosystem function of shredding is affected by the combined stressors of biological invasion, temperature and parasitism and may thus affect the energy flow and productivity of the ecosystem.

We compared the survival and leaf shredding rate of the UK native amphipod *Gammarus pulex* and the invasive *Dikerogammarus villosus*, exploring the effect of temperature and parasitism. The native amphipod species had a higher shredding rate than the invasive species, but was less tolerant of extreme heatwave temperatures, suffering higher mortality. The invasive amphipod benefitted from predator release from microsporidian infection. In contrast, shredding behaviour and survival of *G. pulex* was negatively impacted by the acanthocephalan parasite *Echinorhynchus truttae*.

The higher tolerance of *D. villosus* to elevated temperatures, as well as its escape from parasites may facilitate their replacement of the native species in the changing climate. Furthermore, the lower detritivory by this invader may negatively impact energy flow and productivity in invaded freshwater ecosystems.

Amphipod diversity assessment of fish-farming environmental impact

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The present study forms part of the Marine Aquaculture project on the Environmental Interactions, carried out at 15 coastal areas of Greece during the years 2017-2018. The aim of the project was to monitor the impact of cage aquaculture on the local environment. Sediment samples were collected using VanVeen grab (0.1 m²) from stations within 0m, 25m and 50m of the farm site. In order to determine the impact of fish farms on the macrobenthic assemblages of the region, Shannon–Wiener diversity index (H'), MDS, BioEnv, SIMPER, AMBI and Bentix indices were used. The environment of the areas sampled, varied from small islands with almost minimum riverine inputs, to gulfs with considerable inland water input. The depth ranged from 20 to 100 meters. This study focuses on the benthic amphipod faunal assemblages composition and distribution. The comparison between the different areas show significant variation in terms of diversity and abundance. More than 1000 individuals were collected, belonging to 57 species and 22 families. The results indicate that the impact of fish-farming on benthic amphipod community in our study, largely depends on the study site.

Reconstructing population histories and biogeography of Antarctic *Charcotia* (Amphipoda, Crustacea)

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Historically, Antarctica underwent many environmental changes throughout time. Glaciation and deglaciation periods forced organisms to adapt to new conditions, undergo extinctions, or migrate. During glaciations, migrations occurred to different refugia such as the deep sea, ice-free regions of the Antarctic continent and sub-polar regions. These refugia created barriers with reduced gene flow and increased diversification and speciation. Now, Antarctica is undergoing new alterations induced by global warming and ocean acidification. The RECTO (Refugia and Ecosystem Tolerance in the Southern Ocean) project investigates the historical dynamics forced by previous glaciation periods and possible responses to future climate change. One part of the project reconstructs the population history of different taxa from various trophic levels. Here, we will specifically focus on the amphipod genus *Charcotia* (formerly known as *Waldeckia* sp.), of which two species are investigated: *C. obesa* and *C. amundseni*. Both species are scavenging amphipods, and are morphologically and genetically distinct. They most likely also have different bathymetrical distributions, with *C. amundseni* being more abundant at larger depth. The population history and biogeography will be reconstructed from different localities in the Southern Ocean with molecular tools, including sequencing the COI DNA barcoding region, to construct haplotype networks and test for cryptic diversity. We will also apply Next-Generation-Sequencing (NGS) techniques to unravel the complete mitochondrial genome of these amphipod species. Sequence data from complete mitochondrial genomes will allow us to design primers for long-range PCRs to obtain mitogenomic data from different populations of both species. This way, phylogenies for reconstructing the evolutionary history will be statistically better supported. Possible differences in mitochondrial genomes between species could also be non-neutral and indicate specific temperature adaptations. The latter will be assessed by comparisons with mitogenomes of closely and more distantly related Crustaceans from Antarctica.

Trophic differentiation of *Niphargus* amphipods

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The amphipod genus *Niphargus* is ecologically diverse, living in virtually all types of subterranean aquatic habitats. On a local scale, different *Niphargus* species regularly co-occur. The co-occurring species often differ in microhabitat preferences and morphology, suggesting that these species evolved different ecological niches. The ecology of individual species, and differences in ecological niches are poorly understood. In the present study, we focused on trophic niche differentiation of species occurring within the same community and compared the trophic position of species from different localities. Previous studies suggested that *Niphargus* can feed on various food sources. Besides that, appendages involved into feeding, i.e. gnathopods, show a substantial between-species variation, suggesting that appendage morphology might correlate with feeding ecology. We sampled five caves, in which 2-3 species of *Niphargus* regularly co-occur. We measured carbon (C) and nitrogen (N) isotope ratios of animals and of the different basal resources including sedimentary biofilm and particulate organic matter, assessed the differences in isotope compositions among species, and estimated the trophic position of individuals and species. The results suggest that i) co-occurring species differ in feeding ecology, where ii) some species apparently occupy different trophic levels, whereas iii) species of the same trophic level apparently exploit different food sources. Additionally, iv) co-occurring species differ in shape and/or size of gnathopods, and v) the size of gnathopods seem to correlate with species' trophic position. Put together, current results show that co-occurring species tend to differ in their trophic niches.

Microsporidian infections in the *Gammarus roeselii* species complex (Amphipoda) over its geographic range

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Microsporidia are obligate endoparasites. Both vertical and horizontal transmission routes are known. While the former may promote co-speciation and host-specificity, the latter may promote shifts between host species. Freshwater amphipods are hosts for many microsporidian species. However, no general pattern of host specificity and co-diversification is known. In South-Eastern Europe, *Gammarus roeselii* composes of 13 cryptic lineages of Miocene-Pleistocene age, but only one lineage has spread postglacially throughout North-Western Europe. Our first objective was to explore the Microsporidia diversity in *G. roeselii* and their phylogenetic relationships, especially relative to parasites infecting other gammarids. Our second objective was to test if host phylogeographic history might have impacted host-parasite associations (*e.g.* co-diversifications or recent host shifts from local fauna). *Gammarus roeselii* individuals were collected at 94 sites in 19 countries covering the area of Western, Central and South-Eastern Europe, covering its entire European range. Microsporidia were screen using PCR amplification and positive individuals were sequenced for part of the small subunit rRNA. Bayesian phylogeny reconstruction of microsporidia was performed using sequences product from this study and literature data. Microsporidian diversity was high in *G. roeselii* with 24 detected haplogroups, clustering into 18 species-level taxa. Ten microsporidia species were rare, infecting few individual hosts in few populations. Most of them are phylogenetically related to parasites from other amphipods or crustaceans. Others were widespread genera with high prevalence: *Nosema*, *Cucumispora* and *Dictyocoela*. Two contrasting host association patterns could be observed. First, two vertically-transmitted species *Nosema granulosis* and *Dictyocoela roeselum* share the pattern of infecting *G. roeselii* over most of its range and are specific to this host. It suggests a co-diversification evolutionary scenario. This pattern contrasted with that of *Dictyocoela muelleri*, the three species of *Cucumispora*, present only in the region recently colonised by the host. These patterns suggest recent acquisitions from local hosts, after the spread of *G. roeselii*. Microsporidia infecting *G. roeselii* therefore revealed two scenarios of host-parasite associations: ancient associations with vertically-transmitted parasites that probably co-diversified with their hosts, and host-shift from local host species, after the host's postglacial spread.

Estimating the actual biodiversity and evolutionary history of the amphipod genus *Eusirus* in the Southern Ocean

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The diversity of the Antarctic marine fauna has been shaped by various evolutionary processes (dispersals, diversifications, extinctions), which were greatly influenced by the geological and climatic history of the region. Some Antarctic lineages are descendants of Gondwanan ancestors and arose by vicariance during the progressive breakup of Gondwana, which ultimately led to the complete geographical isolation of the Antarctic continent. The Plio-Pleistocene glacial cycles have been inferred to act as a “diversity pump” on the Antarctic continental shelf. Allopatric speciation of less dispersive organisms could have resulted from the isolation of populations in ice-free refugia during the glacial advances. These glacial cycles were often suggested to have influenced the diversification of numerous complexes of closely related and morphologically very similar Antarctic species. The continuous discovery of such (pseudo-) cryptic species in the Southern Ocean suggests that its biodiversity is currently greatly underestimated. Such species complexes have been found in the amphipod genus *Eusirus*. In a preliminary phylogeny (COI and 28S) of the whole genus, some Antarctic nominal *Eusirus* species are composed of genetically distant clades, suggesting putative new species. In this study, we will sequence complete mitochondrial genomes, using a combination of skim sequencing and long-range PCRs of different *Eusirus* species, to which sequence data from nuclear (28S, ITS2) will be added. By greatly increasing character sampling as well as taxon sampling (including Antarctic and non-Antarctic species) compared to preliminary studies, we intend to reconstruct a robust phylogeny of the genus. Based on this DNA dataset and the phylogeny, we aim to (1) provide a better estimate of the actual diversity within the genus, using various DNA-based species delimitation methods (GMYC, PTP, 4 theta rule and ABDG) and; (2) provide a better understanding of their evolutionary history: where does the Antarctic clade come from? Did *Eusirus* species disperse in and/or out of the Antarctic shelf at any time of their evolutionary history? Were there periods of increased diversification during their evolution on the shelf and how do these relate to the geological/glacial history of the region?

Sediment: Amphipod relationship in a tropical intertidal habitat, South Andaman Islands, India

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The sediment composition association with the benthic marine infaunal community is a well-known phenomenon, and the relationship is considered to be a core theme in the benthic soft bottom ecology. The faunal community and the sediment characters relationship have been considered as a methodology to predict the distribution, composition and diversity of the community. The purpose of the present study was to assess the relationship between the sediment characters and the intertidal amphipod community across five intertidal regions. The investigation was undertaken between September 2013 and August 2015 covering all the tropical seasons. A total of 540 core samples (15cm diameter) were collected in the location across the tidal gradient (High, Mid and Low water line). All the stations samples showed a higher proportion of sand fraction with coarser sediment and higher MGS in the southern part of the survey. The investigation recorded 76 species under 47 genera and 30 families. The sand fraction and MGS showed a negative relationship with species richness and abundance. The OM, Silt and Clay fraction were greatly influenced by the season, i.e. higher species richness and density during the monsoon period. The diversity indices followed the same trend as that of species richness and abundance. Among the sedimental characteristics, OM showed a highly significant relationship with amphipod community structure. The BIOENV and CCA analysis suggested that the amphipod assemblage ordination is mostly influenced by the variation OM, MGS, SRT and Silt across the location and season. The Physico-chemical parameter showed a weak correlation to explain the biotic ordination. Thus, in the present study, it can be concluded that the heterogeneity of sediment composition plays a significant role in depicting the amphipods distribution in the tropical intertidal region.

First records of amphipod species in the Gulf of Naples (Italy, Mediterranean Sea)

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The structural and functional biodiversity of a given area should be studied through a historical analysis of the spatial distribution of the species over time (chronogeonomy analysis), aiming at evaluating fluctuations in species composition possibly due to environmental changes.

In the Mediterranean Sea, the Gulf of Naples (Italy) has a long-standing tradition of studies on amphipods, therefore this geographic area might represent a good laboratory to map the evolution of assemblages due to extinction or introduction of species.

In the present study, three non-indigenous species, namely *Caprella scaura* Templeton, 1836, *Stenothoe georgiana* Bynum & Fox, 1977 and *Jassa slatteryi* Conlan, 1990, were found off the Island of Ischia. A female of *Caprella scaura* was identified in May 2010 from artificial collectors deployed in the water column at 2m depth; after this first finding, in August 2016 a rich population was found on a buoy rope barrier close to a mooring field for recreational boats. Notwithstanding the wide and rapid spread of *C.scaura* in the Mediterranean Sea, this is among the few records off semi-closed environments. *Stenothoe georgiana* was found in June 2011 in artificial collectors deployed on a rocky reef at 2m depth. After its first finding in 2010-2011 in SE Spain, this would be the second record for the Mediterranean Sea and the first for Italy. However, *S.georgiana* has been reported for the Italian coast from 2013 (Ligurian Sea); and in the Gulf of Naples (Sorrento marina) in 2015. The presence of *Jassa slatteryi* in the Mediterranean Sea seems confirmed although similarities with congeneric species should be studied more in depth, and a review of *Jassa* samples might bring to light a previous presence clarifying the temporal patterns of colonization. Here dense populations were found in May 2010 on artificial collectors. The endemic species *Metaphoxus gruneri* Karaman, 1986 was found in July 2017 on soft bottoms (8 and 25m), in an area west of the city of Naples, characterized by a significant anthropogenic impact. After its description off the Island of Malta it was rarely reported along the Italian coast, as in the Adriatic Sea (1993) and in the Tuscan Archipelago (2007).

First impressions on the Amphipoda of Dronning Maud Land, Antarctica. Results from the Norwegian 2019-cruise

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The Norwegian Polar Institute-lead cruise to the waters off the Dronning Maud Land coast, Antarctica in February to April 2019 will collect information about the ecosystem of an area suggested as part of the proposed Weddell Sea Marine Protected Area.

Amphipods are collected using a series of trawls (macrozooplankton trawl, multPelt, bottom trawl (Campelen), beam trawl), plankton nets (WP2, MultiNet), epibenthic sled (RP-sled) and ROV (suction sampler, sediment-scoops). The material will be deposited at the University Museum of Bergen, Norway.

The poster presents the first impressions of the amphipod-fauna from the Astrid Ridge and the Maud Rise – two seamounts off the Dronning Maud Land. The collections are performed along the ice-edge, where a massive phytoplankton bloom (autumn-bloom) was observed during the cruise.

Amphipods in macrofouling communities of the port area of Livorno (Northern Tyrrhenian Sea)

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Macrozoobenthic fouling assemblages were studied in the port area of Livorno (Northern Tyrrhenian Sea), focusing on the occurrence of amphipods species. Sampling was carried out at ten sites characterised by different anthropic impacts related to their use destination: commercial harbour (two sites), touristic harbour (five sites) and three small touristic marinas located south of the port of Livorno (Molo Nazario Sauro, Ardenza and Antignano). Habitat former classes were identified in each sampling site in order to evaluate their influence on amphipods communities. Among crustaceans, 47 amphipod species, belonging to 17 families, were recorded. The highest abundances were recorded in the sites of touristic harbour, especially in the inner site of the port, while the lowest abundances were recorded in the commercial harbour. The number of species, however, did not show a clear pattern of distribution among sampling sites. Amphipod community compositions showed that Corophiidae was the most abundant family in all sampling site, excluded one site of the commercial harbour, where Hyalidae were the most abundant, and the marinas of Ardenza and Antignano, where amphipod communities were more variable. The main diversity indexes were calculated for each sampling site, showing the highest values in touristic harbour and marinas, while the commercial harbour showed the lowest values. Furthermore, the obtained values of abundances, number of species and diversity indexes showed high variabilities, suggesting a patchy distribution of amphipod species in the port of Livorno. The analysis of similarity percentage showed that *Apocorophium acutum* was the major contributor to the similarity of samples belonging to the same site, and to the dissimilarity between different sites. Moreover, *A. acutum* was the major contributor to the similarity and dissimilarity in and between different habitat formers. The variability based on use destination and habitat formers was tested by the analysis of similarity, resulting all significant. These observations suggest that the use destination of different sites impinged on habitat formers species structuring several microhabitats, which, on their turn, influence the diversity of the amphipod communities.

Distribution patterns of amphipod assemblages along the Iberian Atlantic rocky shores

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The Iberian Atlantic coast is an important marine biogeographic region that exhibits characteristics of a transitional zone between cold and warm waters. It is under the influence of the Mediterranean and African waters, the North Sea and the West Atlantic. The order Amphipoda is a highly diverse crustacean taxon, and one of the most abundant marine invertebrate groups in Iberian Atlantic rocky shores. Food supply and habitat may influence the distribution and diversity patterns of the amphipods in intertidal rocky shores. In this study we aimed to outline the amphipod assemblages of the Atlantic Iberia, testing for latitudinal and habitat partitioning of this taxon. A hierarchical experimental design with four fixed factors and one nested factor was applied, in order to evaluate the natural variability of the Iberian Atlantic rocky shores. Three different regions (North, Centre and South) were at least 100 km apart from each other and the random sites within (3 in each), at least 10 km. The habitat partitioning was divided into the three intertidal levels and in water and sun exposure. The different microhabitats were sampled by scraping 225cm² squares, and the abiotic parameters were measured. After the identification of macroalgae and amphipod species, multivariate analyses were performed and biotic indices calculated. A total of 21472 specimens were collected belonging to 40 species (26 genera and 16 families). Globally, the amphipod assemblages displayed a high γ -diversity, however, the Northern region displayed the highest diversity. The lower tidal level harboured higher diversity, while sun and water exposure were not significant. Turf red macroalgae were correlated with the amphipod distribution in the Northern region, while the prevalence of coralline influenced the South. The abiotic measures clearly discriminated the North and South regions, with the Central region displaying mix characteristics. Our study indicates that latitudinal environmental properties of this region can overcome local microhabitat partitioning in explaining amphipod diversity along the Atlantic Iberia. The present and past high natural variability of this peninsula represent an important marine scenario which can help us to test and answer historical and future predictions on the evolution of the European shore invertebrate fauna.

When one becomes 15: Morphological vs. molecular species delimitation in the “*Niphargus aquilex*” complex

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Niphargus (Amphipoda, Niphargidae) species inhabit mainly groundwater, such as karst aquifers and groundwater flowing or stagnating in the phreatic zone of unconsolidated rocks. More than 400 species have been described so far, mainly based on morphological features.

Niphargus aquilex was first described from Great Britain. Later it was assumed that it is a complex of several morphologically similar species largely distributed across Europe. But their very limited morphological differences have hindered their proper delimitation and description till now.

To fill this gap, we collected “*Niphargus aquilex*” from England (43 specimens), Channel Islands (10), Northern half of France (72), Belgium (29), Luxembourg (64), Germany (1043), the Czech Republic (9). Out of these 1270 specimens, 342 were processed for DNA extraction, among which 314 from 209 sites were successfully sequenced.

We sequenced Folmer’s fragment of the mitochondrial CO1 gene, a fragment of the nuclear 28S ribosomal gene, as well as the ITS region. Automatic barcode gap determination (ABGD) yielded 15 primary species hypotheses among our samples. To refine this analysis, we performed haploweb analyses of the 28S data, yielding our final species delimitation.

Several of our molecularly delimited species show notable morphological differences, while other species seem impossible to distinguish morphologically and can therefore be considered cryptic species. *Niphargus schellenbergi* is nested within “*Niphargus aquilex*”, making the latter species group paraphyletic. *Niphargus aquilex* is rare in England (although its type locality is there), but widespread in the continent. Some of the new species have a large distribution while others seem to be narrow endemics.

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