



ZOOLOGY 2016

23rd Congress of Zoology

Antwerp, Belgium

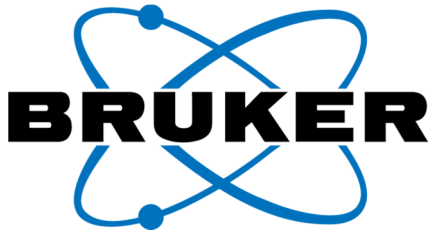
15 – 17 December 2016

Initiated by the:

Royal Dutch Zoological Society (KNDV) – www.kndv.nl

Royal Belgian Zoological Society (RBZS) – rbzs.myspecies.info

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Koninklijke Maatschappij voor Dierkunde van Antwerpen vzw

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Organising & Scientific Committee

Local organising Committee:

Peter Aerts (UAntwerpen, Belgium) – Chair
Herwig Leirs (UAntwerpen, Belgium) – co-Chair

Simon Baeckens (UAntwerpen, Belgium)
Lieven Bervoets (UAntwerpen, Belgium)
Ronny Blust (UAntwerpen, Belgium)
Marcel Eens (UAntwerpen, Belgium)
Jana Goyens (UAntwerpen, Belgium)
Katleen Huyghe (UAntwerpen, Belgium)
Arne Iserbyt (UAntwerpen, Belgium)
Zjef Pereboom (Centre for Research and Conservation and UAntwerpen, Belgium)
Johannes Teuchies (UAntwerpen, Belgium)
Raoul Van Damme (UAntwerpen, Belgium)

Scientific Committee:

Gudrun De Boeck (UAntwerpen, Belgium) – Chair
Peter Galbusera (Centre for Research and Conservation and UAntwerpen, Belgium) – co-Chair

Dominique Adriaens (UGent – RBSZ, Belgium)
Ellen Decaestecker (KULAK – RBSZ, Belgium)
Jana Goyens (UAntwerpen, Belgium)
Katleen Huyghe (UAntwerpen, Belgium)
Arne Iserbyt (UAntwerpen, Belgium)
Jan Kammenga (WUR – RDZS, The Netherlands)
Peter Klaren (RU – RDZS, The Netherlands)
Gilles Lepoint (ULG- RBSZ, Belgium)
Patrick Mardulyn (ULB – RBSZ, Belgium)
Johan Micheaux (ULG – RBSZ, Belgium)
Zjef Pereboom (Centre for Research and Conservation and UAntwerpen, Belgium)
Isa Schön (KBIN – RBSZ, Belgium)
Johannes Teuchies (UAntwerpen, Belgium)
Raoul Van Damme (UAntwerpen, Belgium)

Congress Management:

Peter Aerts (UAntwerpen, Belgium)
Josie Meaney (UAntwerpen, Belgium)

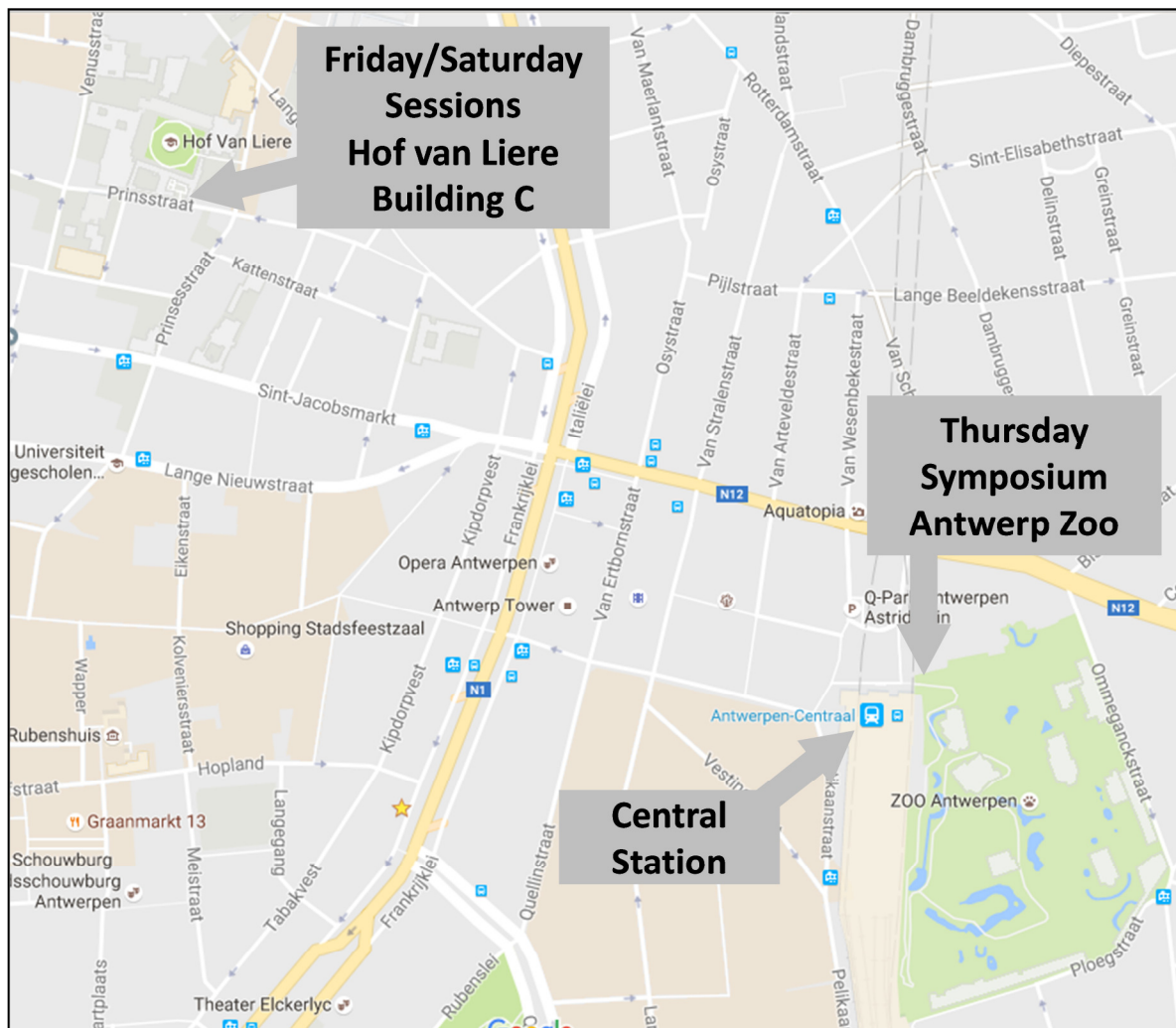
General information

Locations

Thursday 15 December, *CRC ZOO Research Symposium (Satellite Symposium)* in the **Antwerp Zoo** (Darwin Hall, Koningin Astridplein 20-26, 2000 Antwerp, entrance next to Antwerp Central train station).

Thursday 15 December, *Zoology 2016 congress* welcome talks and an icebreaker drink are organised in the Darwin room at the **Antwerp Zoo** (Koningin Astridplein 20-26, 2000 Antwerp, entrance next to Antwerp Central train station).

Friday 16 December and Saturday 17 December, the Zoology 2016 congress takes place at the city campus of the university of Antwerp, **Hof van Liere and Building C** (Prinsstraat 13B, Antwerp, see map below for details).



Venue

Zoology 2016 takes place in the central building of the University of Antwerp's Stadscampus, better known as 'Hof van Liere', which is part of the cultural and historical heritage of Antwerp.

The wonderful 16th-century Hof van Liere and the adjacent historical premises, which were erected by the Society of Jesus in the 17th century, are an oasis of tranquillity in the bustling city centre.

This 'regal residence' was built in 1516 for the then Mayor of Antwerp, Aert van Liere. The city had just entered its golden age, as this exquisite building in the Brabantine Gothic style testifies.



Registration desk

Thursday 15 December at the Antwerp Zoo:

from 8:00 a.m. onwards (CRC satellite symposium and Zoology 2016)

from 3:00 p.m. onwards (Zoology 2016)

Friday 16 December and Saturday 17 December at Hof Van Liere:

from 8:00 a.m. onwards (Zoology 2016)

Contact information

zoology2016@uantwerpen.be

In case of emergency

Ambulance: 112

Police: 101

Wireless internet

Information about wireless internet access in Hof van Liere and on the UA city campus can be obtained at the registration desk.

Awards

The Royal Dutch and Belgian Zoological Societies will jointly offer awards for the best student presentations. Two categories of students are considered: master students (or freshly graduated students presenting results from their master thesis) and PhD students.

During the two days of Zoology 2016, a jury of experts will evaluate talks and posters and select:



- The best master student oral presentation
- The best master student poster
- The best PhD student oral presentation
- The best PhD student poster

Students willing to take part in the contest for these awards could indicate so during registration. Candidates for the best MSc talk and best PhD talk are indicated with respectively one (*) or two asterisks (**). Winners will be announced during the closing session, on 17 December 2016. All contestants are expected to attend this closing session, as awards and certificates will be handed over in person.



Detailed programme

Thursday 15 December at Antwerp Zoo

Participants of Zoology can attend the 9th Annual CRC [ZOO Research Symposium](#) free of charge. See programme [here](#).

08:00 - 09:00	Registration for CRC symposium and Zoology2016
09:00 - 16:00	9th Annual CRC ZOO Research Symposium (Satellite Symposium of Zoology2016)
15:00 - 16:30	Registration for Zoology2016
16:30 - 17:30	Opening of Zoology2016 <u>Darwin Room</u> Gudrun De Boeck - Welcome and Introduction Steven Cooke - Conservation physiology – from mechanisms to policy and practice Jodie Rummer - Today's scientists: diverse leaders, passionate & dynamic communicators
17:30 - 18:30	 Icebreaker drink 

Friday 16 December at Hof van Liere

08:00 - 09:00	Registration for Zoology 2016	
09:00 - 10:00	<u>Tassis Room</u> Jodie Rummer - Coral reef fishes in the Anthropocene Chair: G. De Boeck	
10:00 - 10:30	 coffee 	
	<u>Marine Biodiversity</u> <u>Tassis Room</u> Chair: G. Lepoint, A. Vanreusel	<u>Ecological and Functional Morphology 1</u> <u>Dürer Room</u> Chair: A. Herrel, J. Goyens
10:30 - 10:45	Freija Hauquier et al. - Life in a changing environment: a focus on nematode communities in seafloor sediments near the Antarctic peninsula	Ameline Bardo et al.** - Are humans unique? Are gorillas and/or orangutans unique? What manual specificities exist for each species?
10:45 - 11:00	Brigitte Heylen* - Tracking a marine predator to design flexible boundaries of marine protected areas for an ecosystem approach to fisheries	Marie Vanhoof et al.* - Form-function relationship of the thumb in bonobos (<i>Pan paniscus</i>) and olive baboons (<i>Papio anubis</i>)
11:00 - 11:15	Jon Lapeyra et al. - Edge-effects in <i>Posidonia oceanica</i> seagrass meadows	Charlotte Vanden Hole et al.** - Do the locomotion – development of spatio-temporal gait variables and gait symmetry in newborn piglets
11:15 - 11:30	Dorothee Pête et al.** - Relationships between environmental parameters and the microbenthic loop of <i>Posidonia oceanica</i> meadows at small spatial scale	François Druelle et al.** - The interplay between morphology and locomotion during the development of olive baboons (<i>Papio anubis</i>): Implications for the evolution of primate locomotion

11:30 - 11:45	François Remy et al. - Who would want to live in there? A history of <i>Posidonia oceanica</i> detritus accumulations, the associated invertebrate community, and its food web	Mike Fleuren et al.** - Pregnant as a prey: performance and kinematics of the 3D fast-start escape response of live-bearing fish	
11:45 - 12:00	Tasnim Patel et al.** - JPIOceans: Assessing the ecological impact of deep-sea mining on Crustacea	Allison Luger et al.** - On the jaws of lamniform sharks: explaining function through morphology	
12:00 - 12:15	Jani Sleutel et al.* - Impact of mangrove forest management on birds: field assessment & reflections on ecological functionality	Alessia Huby et al.** - Relationship between jaw morphology, bite performance and diet in Serrasalmidae	
12:15 - 12:30	Anne-Maria Vafeiadou et al.** - Do tropical and temperate meiobenthic communities respond similarly to climate change?	Jens De Meyer et al.** - Head shape related to dietary differences? Dimorphism throughout the European eels' life cycle	
12:30 - 12:45	Nele De Meester et al. - Cryptic diversity matters: implications for ecosystem functioning and management of global change effects		
12:30 - 13:30	 lunch 		
	Behavioural ecology <u>Tassis Room</u> Chair: A. Iserbyt	Population genetics and genomics <u>Dürer Room</u> Chair: P. Galbusera	Ecotoxicology <u>Prenten Cabinet</u> Chair: L. Vergauwen
13:30 - 13:45	Rabia Moussaoui et al. – <i>last minute cancellation</i>	Joost de Jong et al.** - Genome-wide patterns of identity by descent in a bottlenecked and fragmented red deer population	Nathalie Leynen et al. - Nanoparticles: how safe are they? <i>Schmidtea mediterranea</i> as a model organism for toxicity assessment
13:45 - 14:00	Charlotte Van Moorleghem et al.** - Chemical predator detection in the Dalmatian wall lizard (<i>Podarcis melisellensis</i>)	Nienke Beets et al.* - The genetic structure of the European alpine bush cricket genus <i>Anonconotus</i> using phylogeography (Orthoptera: Tettigoniidae)	Charlotte Philippe et al. - A new model species for long-term toxicity testing: Acute and chronic sensitivity of <i>Nothobranchius furzeri</i> to copper and cadmium
14:00 - 14:15	Thomas Raap et al.** - Early life exposure to artificial light at night affects the physiological condition: An experimental study on the ecophysiology of free-living nestling songbirds	Zoë De Corte et al.* - The role of interspecific gene flow in the evolution of a parallel wolf spider radiation from the Galapagos	Ellen D.G. Michiels et al.** - Nano-injection in the zebrafish embryo as an alternative exposure route for environmental risk assessment of endocrine disrupting pharmaceuticals

14:15 - 14:30	Nolwenn Fresneau et al.** - “Tell me what you want, what you really really want”: applying a behavioural reaction norm approach on parent-offspring communication	Tsegazeabe Hadush Haileselasie et al.** - Founder effects determine the genetic structure of the water flea <i>Daphnia</i> in Ethiopian reservoirs	Evelyn Stinckens et al.** - Validation of the AOP network “Thyropoxidase and/or deiodinase inhibition leading to impaired swim bladder inflation”
14:30 - 14:45	Doriane Muller et al. - Impact of learning under sexual selection on the survival of species in a context of climate change	Nathalie Smitz et al. - Resolving the shallow population structure of the African Lion (<i>Panthera leo</i>) in Tanzania through genomics	Luana da Costa Monteiro et al.** - Marine nematodes as bio-indicators of direct oil toxicity: a combination of single-species and community assays
14:45 - 15:00	Dian Zijlmans* - Home not-so-sweet home: social relationships and behaviour change in captive African wild dogs (<i>Lycaon pictus</i>) after pack separation	Manon de Visser et al. - The importance of genomics for the conservation management of the critically endangered pygmy hog (<i>Porcula salvania</i>)	Alice Mouton et al. - Using an RNA-seq approach to investigate the effects of anticoagulants rodenticides in bobcats (<i>Lynx rufus</i>) of the Santa Monica Mountains (CA, USA)
15:00 - 15:15	Christine Webb et al. - Empathic personalities: Chimpanzees consistently vary in the tendency to console others	Sofie Derycke et al. - Speciation genomics of cichlids (<i>Ophthalmotilapia</i>) from Lake Tanganyika	Marika Panagiotou et al.* - (presenting author: Lieven Bervoets) - Environmental distribution and bioaccumulation of POPs and Hg in temperate and Mediterranean river ecosystems
15:15 - 15:30	Astrid Rox et al.** - Female macaques wear the trousers: female fights and female initiated friendships determine immigrant male sexual access	Mirte Bosse et al. - Signatures of natural selection in great tit genomes: Past selection, local adaptation or human imposed change?	An-Sofie Stevens et al. - In vivo prediction and discrimination of carcinogenic compounds using <i>Schmidtea mediterranea</i> 's stem cell proliferation patterns
15:30 - 15:45	Jeroen van Rooijen - Referential gestures or ritualised food sharing in ravens and bankivas?		Annelies Wouters et al.** - Planarians: a (pluri)potent tool to study stem cell responses to carcinogenic stress in vivo
15:45 - 16:15	 coffee 		
16:15 - 17:15	<u>Large Auditorium – Building C, C.003</u> Mike Bruford: Can genomics actually make a difference in conservation? A science to policy perspective		
17:15 - 20:00	 Poster session, scientific/social gathering 		

Saturday 17 December at Building C, City campus

08:00 - 09:00	Registration for Zoology2016		
09:00 - 10:00	Large Auditorium – Building C, C.003 Hans Van Dyck - Behavioural responses to human-induced rapid environmental change: what you see is not what other animals get Chair: R. Van Damme		
10:00 - 10:30	☕ coffee ☕		
	Ecology C.003 Chair: M. Eens	Ecological physiology C.002 Chair: G. De Boeck	Ecological and functional morphology 2 C.103 Chair: D. Adriaens, J. Goyens
10:30 - 10:45	Trevor Dube et al.** - Conservation of aquatic invertebrates in temporary wetlands in a tropical biodiversity hotspot	Laurent Duchatelet et al.** - Ventral skin light perception involved in the bioluminescence control mechanism in the velvet belly lanternshark, <i>Etmopterus spinax</i> ?	Simon Baeckens et al.** - Worm lizards flout the burrow/crush catch
10:45 - 11:00	Susanne van Donk et al.** - Reproductive consequences of dietary specialisations in a generalist seabird	Jyotsna Shrivastava et al.** - Acid-base balance and ion regulation in spotted ratfish (<i>Hydrolagus colliei</i>) during hypercapnia	Sam Van Wassenbergh et al. - How mole-rats dig with their teeth
11:00 - 11:15	Ruben Evens et al. ** - Understanding the foraging behaviour of European nightjars <i>Caprimulgus europaeus</i>	Pascal Hablützel et al. - Anthropogenic environments increase systemic immune activity: evidence from a cohort-matched wild–mesocosm comparison	Anne-Claire Fabre et al. - Geometric morphometric approaches to inferring bite force and diet in extinct strepsirrhines
11:15 - 11:30	Pieterjan Verhelst et al.** - Migration of European silver eel in an anthropogenically impacted wetland area in Belgium	Isabelle Gabriels et al.** - Development of a test method for transgenerational effects of genetically modified crops in food using the zebrafish model	Raf Claes et al. - Pharyngotympanic tube response in domestic chicken and mallard to static pressure fluctuations
11:30 - 11:45	Babtiste Le Bourg et al. - Feeding ecology of southern ocean sea stars inferred from stable isotopes ratios of C, N and S	Jelena Periz Stanačev et al. - Ontogeny of steroid hormone metabolism gene transcription during embryo-larval development of the zebrafish	Geoffrey Mélotte et al.** - Interspecific variation of warning calls in piranhas: a comparative analysis
11:45 - 12:00	Marianna Pinzone et al.** - Exploitation of coastal fish communities by female and juvenile	Ben Colpaert et al.* - Outline based shape analysis of fish scales: a procedure to quantify	Anthony Herrel et al. - Evolution on islands: patterns of phenotypic diversity in two species of <i>Podarcis</i> from the

	harbour porpoises <i>Phocoena phocoena</i> during nursing periods in German Baltic waters	skeletal effects of chronic stress	Adriatic
12:00 - 12:15	Joseph Lushombo et al.** - Distribution and abundance of the Tanganyika introduced killifish, <i>Lamprichthys stanganicanus</i> in Lake Kivu	Soumia Loulida et al.** - Osmotic responses to salinity and dehydration in the Sahara desert's blue-eyed turtle, <i>Mauremys leprosa saharica</i> Firtz, 2006 (Testudines: Geoemydidae) from an isolated brackish pond in the Lower Draa basin, Southern Morocco	Fabrice Teletchea - Domestication level of the most popular aquarium fish species: is the aquarium trade dependent on wild populations?
12:15 - 12:30	Sedat Gündoğdu et al. - Growth of the worldwide genus <i>Diplodus</i>	Safaa Bendami et al.** - Effects of dehydration and salt loading on the osmoregulatory capacities in Moroccan spiny-tailed lizard, <i>Uromastix nigriventris</i> (Reptilia: Agamidae)	
12:30 - 13:30	 lunch 		
	<i>Molecular phylogenetics</i> <u>C.003</u> Chair: T. Backeliau	<i>Conservation and society</i> <u>C.002</u> Chair: Z. Pereboom	<i>Host-parasite relationships</i> <u>C.103</u> Chair: E. Decaestecker
13:30 - 13:45	Michaël Nicolai et al.** - A phylogenetic perspective on the evolution of ecological traits, trans-oceanic dispersal and the diversification of crocodiles	Mohamed Belkacem et al.** - The role of the waste food of the people on the diet composition of the brown-necked raven <i>Corvus ruficollis</i> (Lesson, 1831) during the breeding season inside a hyper-arid region in the Sahara of Algeria	Nikol Kmentová et al.** - Pelagic freshwater fish parasites in Lake Tanganyika: do the monogeneans mirror host origin?
13:45 - 14:00	Sophie Gombeer et al. - Using molecular techniques to identify organisms of policy concern: some examples from the BopCo project	Marianne Desmet et al. - The crop damage compensation scheme as a means of managing conflict between farmers and badger in Wallonia: shortcomings and impact on species protection	Michiel W.P. Jorissen et al.** - A hitchhiker's guide to tilapia: How parasites take a ride on introduced Nile tilapia in the DR Congo

14:00 - 14:15	Kenny Meganck et al. - Constructing a DNA barcode database of Belgian rove beetles (Staphylinidae) and its application in forensic cases	Claver Sibomana - Biodiversity conservation in a political instability: threats, challenges and perspectives	Anne Laudisoit et al. - Monkey see, monkey eat, monkeypox
14:15 - 14:30	Marlies Monnens et al.** - A phylogeny for Schizorhynchia: molecules must guide morphology	Maarten Vanhove et al. - Joining science and policy in capacity development for conservation-relevant biodiversity monitoring in Africa	Mare Geraerts et al.* - Zoonotic pathogens: A study of the diversity and prevalence of the Bartonella bacteria and the Monkeypox virus in different rodent and shrew species in the rainforest of Yangambi (DRC)
14:30 - 14:45	Isa Schön et al. - Phylogeography of <i>Strandesia</i> ostracods from four major Brazilian floodplains	Francisco Benitez-Capistros et al. – <i>Last minute cancellation</i>	Manrico Sebastiano et al.** - Immunity, inflammation, and stress in a long-lived seabird facing a severe herpesvirus disease
14:45 - 15:00			Lucas Terrana et al.** - Parasites and hosts interaction: description of a black coral infestation by a new species of myzostomid, organisms specifically associated with echinoderms
15:10 - 15:25	<u>Large Auditorium – Building C, C.003</u> Maurijn van der Zee - Eco-evo-devo of an evolutionary novelty in insect eggs (Dutch Zoological Society prize) Chair: P. Aerts		
15:25 - 15:40	<u>Large Auditorium – Building C, C.003</u> Klaas-Dauwe Dijkstra - Making dragonflies the new birds: exploring nature in an age of species loss (Pelkewijkstichting prize)		
15:40 - 15:55	<u>Large Auditorium – Building C, C.003</u> Marie-Anne Deprez - The impact of MCT8 deficiency on molecular and cellular mechanisms underlying early development of the chicken optic tectum (Kets prize)		
15:55 - 16:20	☕ coffee ☕		
16:20 - 17:20	<u>Large Auditorium – Building C, C.003</u> John Fa - The role of wild foods for human nutrition and food security Chair: Z. Pereboom		
17:20 - 17:40	<u>Large Auditorium – Building C, C.003</u> Closing ceremony and announcement of Zoology2016 award winners Chair: P. Aerts and G. De Boeck		

Keynote lectures

Keynote – Bruford Michael – genetics and conservation

Cardiff University, United Kingdom

Genetic and genomic tools and concepts are increasingly used in animal conservation efforts. I focus on understanding the determinants of genome diversity and structure over a variety of spatio-temporal scales, from examining the movements of individuals within territories to studying the impacts of social structure on genetic diversity in fragmented ecosystems to studying species throughout their range with continent-wide dispersal patterns.

Presentation: Can genomics actually make a difference in conservation: a science to policy perspective

In these early stages of the application of 'omic tools in conservation, a number of opinions have been expressed about the practical role these technologies may play in conservation prioritisation and policy. While it seems clear that the additional information provided by 'omics can inform decision making, especially in maintaining adaptive variation, a clear framework is still being debated on how these data might be applied in the real world and how realistic it is to expected conservation management organisations to commission, utilise and implement recommendations on the basis of 'omics data. I will discuss these issues in light of ongoing global conservation drivers such as the Aichi conservation targets for 2020 and the current IPBES process on developing biodiversity indicators. I will illustrate potential applications, gains and constraints of using these data in practical conservation decision making from a Eurasian perspective using data from our laboratory on wild and domesticated species.

Contact: brufordmw@cardiff.ac.uk

Keynote – Cooke Steven – physiology and conservation

Carleton University, Canada

Steven Cooke's Fish Ecology and Conservation Physiology Laboratory maintains broad interests in all aspects of aquatic ecology, conservation biology, physiological ecology, animal behaviour and environmental science. Their research efforts primarily focus on freshwater and marine fish. Specific interests include determining the energetic, fitness, and potential evolutionary consequences of a variety of natural (e.g., winter, reproduction) and anthropogenic (e.g., angling, environmental pollution) stressors; and understanding the diversity of energetic, physiological, and behavioural responses of fish to stress at the individual, population, and species level. The fundamental knowledge derived from these basic research activities is applied in the conservation and management of aquatic resources.

Presentation: Conservation physiology – from mechanisms to policy and practice

Conservation scientists are largely concerned with reversing population declines in the face of human-driven environmental change and disturbance. To do so it is necessary to understand the mechanisms behind population declines to help guide policy and management practices to address the specific threats and restore populations. Conservation physiology involves the use of physiological tools, knowledge, and concepts to identify conservation problems and develop effective conservation solutions. I will provide an overview of the current state of conservation physiology with an eye to the future using examples from a variety of animal taxa.

Contact: steven_cooke@carleton.ca

Keynote – Fa John – conservation and society

Manchester Metropolitan University, United Kingdom

My research naturally embraces a broad set of disciplines such as biology, economics, anthropology, and development. Crucially also, I will pursue emerging issues that impinge significantly upon the long-term future of global biodiversity, such as defaunation of tropical rainforests, the impact of loss of wildlife on people dependent on it, climate change or the impact of diseases on wildlife and humans. The fundamental underpinning of my research and career is to advance scientific knowledge but also use it for practical purposes.

Presentation: The role of wild foods for human nutrition and food security

Food production or food acquisition from the natural environment is a key factor for sustainable future especially in the face of rapidly increasing number of humans and a rapidly deterioration of state of biodiversity. This concerns all three pillars of sustainability: cultural, economic and biodiversity. I first review a number of examples of wild plants and animals used as food by humans throughout the world. I then concentrate on the use of wild animals as food in tropical rainforests worldwide. Bushmeat, or the meat from wild animals (primarily the meat of wild mammals), can provide a food security safety net for tropical forest inhabitants. I focus on use of wildlife as food in the rainforest ecoregions of western and central Africa. First, I briefly describe which wildlife species are important as a source of food within these areas. I review the available literature on consumption of wild species to argue that many peoples in African rainforests invariably consume bushmeat, but highlight that although data are available on amounts of bushmeat eaten the importance of bushmeat in people's diets cannot be merely assessed by volume consumed. I then examine how bushmeat consumption and food security may be linked by presenting data on the importance of bushmeat protein to overall protein consumption in central Africa and how the loss of bushmeat consumption may be correlated with the reported incidence of human malnutrition in the same region. Finally, I propose a roadmap towards better governance for a more sustainable formal bushmeat sector that can ensure food security of peoples using wild species for food.

Contact: j.fa@mmu.ac.uk

Keynote – Rummer Jodie – physiology and conservation

ARC Centre of Excellence for Coral Reef Studies, James Cook University, Australia

With over 400 million years of evolution, the fishes represent one of the most successful adaptive radiation events in vertebrate history. Yet, we do not fully understand how fish are responding to environmental and human-induced stress and their capacity to adapt to global climate change, which is my research focus. I have drawn conclusions as to the temporal scale of thermal acclimation and metabolic performance in coral reef fishes and how this relates to temperature preference, a link crucial to developing management strategies for the conservation of marine biodiversity and the sustainable use of marine fisheries, especially in the advent of climate change.

Presentation 1: Coral reef fishes in the Anthropocene

Globally, coral reefs are at risk to human-induced stressors – such as climate change, including ocean warming, acidification, and hypoxia events, and altered water quality due to coastal development – now, more than at any other time in recorded history. Dramatic effects on fish performance, distribution, and overall ecosystem health are predicted. While the success of the fishes over their long evolutionary history is thought to have hinged on key adaptations for maintaining oxygen transport and physiological performance under challenging conditions, whether they possess the necessary plasticity and/or adaptations to keep pace with the large-scale, rapid changes plaguing their habitats today is not known. Moreover, the coral reef fishes – in particular – diversified more recently on the geological time scale, with most species radiating within the last 23 million years, a period characterised by relatively stable environmental conditions. Evolving and existing under stable environmental conditions may heighten the vulnerability of coral reef fishes to the rapidly changing conditions coral reefs are facing today. By harnessing geographic gradients, such as the latitudinal thermal profile along the Great Barrier Reef, and local extreme environments, such as the volcanic CO₂ seeps in the reefs of Papua New Guinea, as analogues for future change and integrating physiological, biochemical, and molecular techniques, the mechanisms that fish use to acclimate and adapt to these stressors can be identified. Such responses may become potential targets of natural selection and will determine which species and populations may be most at risk from climate change and other human-induced stressors.

Presentation 2: Today's scientists: diverse leaders, passionate and dynamic communicators

My research aims to identify and understanding the mechanisms that fish use to acclimate and adapt to environmental stressors, a topic that both fascinates me and is critically important in the face of large-scale global change. Yet my responsibilities as a scientist go far beyond my experiments. I have come to realize the importance of my visibility and leadership as a successful female scientist and communicating my research to the wider scientific community and general public.

1) *If you can see it, you can become it.* Women and other minorities are well represented at postgraduate and post-doctoral levels in science, technology, engineering, and mathematics (STEM) fields, but numbers decline dramatically in academic positions above that. Policy change is needed to fix this problem, and I work to influence that process. I also advocate for women and other minorities in STEM to achieve leadership roles, expand professional networks, and build community locally and internationally. However, efforts toward gender balance and diversity in STEM must start earlier than university. As a visible role model, leader, and science communicator, I can help break down stereotypes and provide a new voice and face for science that encourages long-lasting careers in STEM. Recruiting, supporting, and retaining diversity in STEM leads to happier scientists *and* better science, which benefits everyone.

2) *Science is for everyone.* I describe my research program as “athletes in a changing world” — but my athletes are fish. I publish my findings in high-impact journals and present at conferences, but I also prioritize workshops, outreach, and communicating to the public through media releases, interviews, websites, and social media, so that my voice is heard. Cleverly communicating research findings, reaching large, diverse audiences, and conveying passion when I discuss, for example, how climate change will affect ocean health, has perhaps never been more important than it is today.

Contact: jodie.rummer@jcu.edu.au

Keynote – Van Dyck Hans – behaviour and conservation

Université catholique de Louvain, Belgium

My research naturally embraces a broad set of disciplines such as biology, economics, anthropology, and development. Crucially also, I will pursue emerging issues that impinge significantly upon the long-term future of global biodiversity, such as defaunation of tropical rainforests, the impact of loss of wildlife on people dependent on it, climate change or the impact of diseases on wildlife and humans. The fundamental underpinning of my research and career is to advance scientific knowledge but also use it for practical purposes.

Presentation: Behavioural responses to human-induced rapid environmental change: what you see is not what other animals get

Species are typically adapted to the local environmental conditions in which they evolved. Even seemingly benign anthropogenic influences can profoundly interfere with the sensory ecology of organisms. Nature conservation can be strongly biased by the far too human view on habitat and landscape connectivity, but this point is not yet fully appreciated. Organisms experience different perceptual worlds that result from the evolutionary history of their own sensory filters and abilities. They have their own *Umwelt*. I will discuss the significance of sensory and cognitive ecology for several conservation issues and, more generally, for our fundamental understanding of what actually is a functional habitat of a species. An organism-centered, resource-based habitat approach appears a useful and stimulating concept for both basic and applied ecology. I will illustrate this approach with a series of butterfly studies. Next, I will briefly address the related issue of ecological traps. These traps are scenarios in which rapid environmental change disturbs the environmental cue-fitness relationship in organisms that actively select their habitat in altered environments. We studied in detail the case of an ecologically-trapped, migratory bird, the Red-backed shrike. Independent of the habitat, mismatched environmental cues may also create developmental traps that cause problems with the life-cycle regulation of organisms under altered climatic conditions. I will illustrate the principle by the case of the Wall brown butterfly. Behavioural ecology has much to offer to conservation biology in a changing world.

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Award winners

Award Winner (Pelkwijkstichting prize) – Dijkstra Klaas-Dauwe

Conservation Ecology and Entomology, Stellenbosch University, South Africa
Naturalis Biodiversity Centre, Leiden, The Netherlands

Making dragonflies the new birds: exploring nature in an age of species loss

Much has been said about the state of natural history and taxonomy in science and society. This year, celebrating the 90th birthday of Sir David Attenborough, I added my voice in the comment “Restore our sense of species” in the journal *Nature*, arguing that we study biodiversity to instill a consciousness of all species’ existence and impact in every human being. In an age of biodiversity loss, big data, complex analyses, global interdisciplinary research and citizen science, often only taxonomic specialists have the overview to tie everything together. However, specialists with such a broad reach in both science and society seem rare today. I will discuss how the popularization and application of dragonflies and damselflies (Odonata) was achieved by building from the bottom up: from taxonomy to public interest, conservation, consultancy and high-impact research.

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Award Winner (Dutch Zoological Society prize) – van der Zee Maurijn

Jacobs Chris G.C., Institute of Biology, Leiden University

Rezende Gustavo L., Universidade Estadual do Norte Fluminense

Lamers Gerda E.M., Institute of Biology, Leiden University

Braak Nora, Institute of Biology, Leiden University, Oxford Brookes University

Spaink Herman P., Institute of Biology, Leiden University

van der Zee Maurijn, Institute of Biology, Leiden University

Eco-evo-devo of an evolutionary novelty in insect eggs

Insects are extraordinarily successful in occupying terrestrial habitats, in contrast to the mostly aquatic crustaceans. This success is typically attributed to adult traits, such as wings and trachea, but little attention has been paid to innovations of the egg. We have investigated an evolutionary novelty in insect eggs, the serosa, which is not present in other arthropods. The serosa is an extraembryonic epithelium that folds over the embryo and yolk during early development. Using parental RNAi against *Tc-zerknüllt*, the Hox gene that specifies the serosa, we can test the function of this epithelium in the beetle *Tribolium castaneum*. First, we show that hatching rates decrease dramatically at low humidities in absence of the serosa. We demonstrate that the serosa secretes a chitinous cuticle that protects against desiccation. Furthermore, we find that bacteria propagate twice as fast in serosa-less eggs. Serosa-less eggs do not upregulate antimicrobial peptides, prophenoloxidasases and other immune genes upon infection, in contrast to control eggs. Finally, we demonstrate expression of cuticle genes and immune genes in the serosal epithelium using *in situ* hybridization. In conclusion, the serosa protects the insect egg against desiccation and infection. We propose that the origin of this evolutionary novelty greatly supported the insects to radiate into new habitats.

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Award Winner (Kets prize) – Deprez Marie-Anne

Marie-Anne Deprez, Department Biology, KU Leuven

Pieter Vancamp, Department Biology, KU Leuven

Veerle Darras, Department Biology, KU Leuven

The impact of MCT8 deficiency on molecular and cellular mechanisms underlying early development of the chicken optic tectum

An adequate supply of thyroid hormones (THs) is crucial for vertebrate brain development to regulate cellular processes such as cell proliferation, migration and differentiation. The TH transporter monocarboxylate transporter 8 (MCT8) is an essential component hereby, as it facilitates neuronal TH uptake. Inactivating mutations in the *SLC16A2* gene, coding for human MCT8, give rise to a severe neurological phenotype, known as the Allan-Herndon-Dudley syndrome. To elucidate the exact role of MCT8 in human corticogenesis, we used the layered chicken optic tectum as a model. We silenced *MCT8* expression by electroporating an MCT8-RNAi construct into progenitor cells at the beginning of neurogenesis. We demonstrated reduced mitosis and progenitor cell pool expansion due to MCT8 deficiency, explaining the decelerated growth of the optic tectum. Tracing of the first wave of migratory cells showed no defects. However, a decreased number of cells expressing the TH-responsive gene *reelin* suggests a disruption of later migration waves. Additionally, a reduced number of *Brn3a*-expressing neurons indicated defects in neuronal differentiation. The obtained results help to unveil some of the possible mechanisms by which MCT8 deficiency disrupts corticogenesis, and underline the importance of a correctly balanced TH supply from early developmental stages onwards.

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Abstracts oral presentations

Worm lizards flout the burrow/crush catch

Baeckens Simon, University of Antwerp (presenting author)
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Van Damme Raoul, University of Antwerp

Limbless animals that burrow head-first are often considered to be evolutionary constrained in the development of a large head, due to limitations imposed while penetrating the soil. Whilst animals with a small head experience less resistance when digging, they are believed to have a weak bite, hence restricting their potential dietary spectrum to soft prey. Yet, recent findings established molluscivory in the fossorial worm lizard *Trogonophis wiegmanni* (Amphisbaenia), suggesting a high bite capacity for this burrowing species necessary to crush snail-shells. To tackle this burrow/crush dilemma, we examined the relationship between head morphology, bite force and gastropod diet in *T. wiegmanni* males and females. In vivo bite force analyses and shell hardness measurements were used to assess the potential dietary spectrum of the amphisbaenians. In addition, phylogenetic analyses were performed to put *T. wiegmanni*'s head size and bite force into an interspecific comparative context. Our results show a strong positive relation between head size and bite force, and we found no evidence for sexual dimorphism. In sharp contrast to other durophagous lizards, *T. wiegmanni* combines a relatively small body and a (disproportionally) small head with relatively high biting forces. In fact, *T. wiegmanni* is able to crush a wide array of the most abundant gastropod shells in their environment. However, the head size of the strongest biters imposes a limitation towards a common alternative snail-feeding strategy: entering the opening of the gastropod shell. This study shows that head size, and consequently bite force, increases the number and variety of gastropods that can be consumed by 'shell-crushing', but reduces the number and variety of snails that can be consumed by 'shell-entering', and vice versa. The cranial design of (durophagous) limbless burrowers may therefore not only evolve under constraints for efficient soil penetration, but also through selection for diet.

keywords: Amphisbaenia, bite performance, diet, ecomorphology, feeding strategy, Trogonophis wiegmanni

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Are humans unique? Are gorillas and/or orangutans unique? What manual specificities exist for each species?

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Humans are known to possess more complex manual abilities than non-human primates. Though many other primates need their hands for locomotion, they still show some manual abilities that are comparable to humans. However, the dynamic manipulative skills of primates have not been fully explored, especially during the same task. To fill this gap, we investigated performance indicators (e.g. duration of the task, number of wrist movements use etc.) linked to manipulative abilities of humans in the most terrestrial great apes (gorillas, *Gorilla gorilla*) and arboreal great apes (orangutans, *Pongo* sp.) during the same tool use task. The results clearly show that humans perform better than gorillas and orangutans, with performance linked to in-hand movements and specific grip types. Only humans use bimanual grip type, pad-to-pad precision grip and in hand-movements involving fingertips. Gorillas and orangutans use more power grips and gorillas develop more in-hand manipulation than orangutans showing more mouth manipulation. Finally, orangutans show more intra-species variability in the grip techniques. Human specificities quantified here could be explained by morphological and/or neuromuscular coordination differences relative to gorillas and orangutans. However, humans may have no “unique” manual abilities and non-humans primate species may not need to use these abilities to succeed at the task. Differences between these great apes could be explained by their different lifestyles (the most terrestrial of great apes versus the most arboreal).

keywords: manipulation, grasping, in-hand movements, maze task

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The genetic structure of the European alpine bush cricket genus *Anonconotus* using phylogeography (Orthoptera: Tettigoniidae)

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The European alpine bush cricket genus *Anonconotus* was a so far solely morphologically studied group of which the evolutionary relationships were unclear. Because of the uncertainties about its population genetics, alpine endemism in a glacial oscillation evolutionary scenario and sexual coercive behaviour this is an intriguing group to study. For the conservation of narrow endemics it is important to understand the genetic structure and to understand evolutionary scenarios under such conditions. *Anonconotus* is endemic to the European Alps and Apennines and is currently classified into nine species including two additional subspecies, nearly all described since 1987. While the classification changed rapidly over the past 20 years, the amount of morphological variation is quite limited. Some populations of this flightless bush cricket are currently isolated, while some other proposed taxa occur sympatrically. To clarify the genetic structure within this genus we performed a phylogeographic study using two markers (CO1 and ITS) including 238 individuals from over 30 populations. The molecular results are incongruent with the current classification and show a completely different genetic structure as was expected, having consequences for the taxonomy and the conservation status of these bush crickets. A next step will be to look into the processes that have caused this pattern.

Keywords: Orthoptera, evolution, taxonomy, phylogeography, climate change

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The role of the waste food of the people on the diet composition of the brown-necked raven *Corvus ruficollis* (Lesson, 1831) during the breeding season inside a hyper-arid region in the Sahara of Algeria

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The diet of the brown-necked raven was studied by the analyses of 34 faecal pellets collected for the period of the spring season when the species are found in the open desert. In this period we can't find this species in nearby the cities. The trophic spectrum was made up of 157 items of prey, the main components of the ravens' feeding are invertebrates, vertebrates, plants and inert material. The most preferred food was the food waste of people (pasta and chickens) found in the rubbish dump, with frequency of 58.82% and 38.24% respectively. The sun spider *Galeodes* spp is the most eaten arthropod with 7.76%. Dates are also eaten with presence of 26.47% in all the pellets. The results suggest that the brown-necked raven is an omnivorous species which prefers dump sites and the food rejected by humans, and only infrequently completes its diet with other prey only. Despite leaving the urban region in the breeding period the ravens continue to forage from dumps in this period.

keywords: feeding behaviour, diet, corvid, dump, scavenger.

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Effects of dehydration and salt loading on the osmoregulatory capacities in Moroccan spiny-tailed lizard, *Uromastyx nigriventris* (Reptilia: Agamidae).

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Animals inhabiting arid environments use a variety of behavioural and physiological strategies to balance water and salt budgets. We studied the effects of dehydration and salt loading on osmoregulatory capacities in a large herbivorous desert lizard, the Moroccan Spiny-tailed lizard *Uromastyx nigriventris*. These lizards select plants with a high K to Na ratio of 15 to 20, and like other herbivorous lizards, effectively eliminate the extra electrolyte load, mainly via a pair of active nasal salt glands which exude the extra ions from blood plasma. Here we present results of a series of laboratory experiments which tested a five-week food and water deprivation and the excretory response of nasal salt glands, during a short period of five days, following salt loading by daily injections of KCl, NaCl, potassium acetate and sodium acetate. During food-water deprivation, dehydrated lizards lost 32% of their initial body mass (with a decrease of the Body Condition Index from 1.49 to 1.07 g/cm) and 46% of the tail volume as an index of energy (fat) storage. Plasma osmolality significantly increased by 20%. There were also significantly increased plasma sodium (hypernatraemia), chloride and total protein concentrations shown. On the other hand, there was no significant decrease in the plasma glucose level. Most of the salt loaded lizards secreted far more K^+ than Na^+ via the nasal glands, even after NaCl loading. The K^+/Na^+ ratio decreased only after two to three repetitive NaCl injections but insufficient Na was eliminated. Two successive KCl injections were successfully eliminated but daily natural average K^+ administration induced progressive hyperkalemia. These experimental data agreed with previous observations showing variations of plasma Na^+ and K^+ concentrations in free-living lizards. The nasal gland constitutes the main route of Cl^- excretion but the $Cl^-/(Na^+ + K^+)$ ratio may vary according to observations in other herbivorous species.

keywords: Uromastyx, dehydration, salt loading, nasal gland, osmoregulation

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Emergent conservation conflicts between giant tortoises and farmers in the rural agricultural area of Santa Cruz Island, Galápagos, Ecuador

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In the Galápagos Islands conservation efforts have allowed protecting and recovering 11 species of Galápagos giant tortoises (*Chelonoidis* spp.), that today are successfully maintained over six islands: Española, Santiago, Pinzon, Isabela, San Cristobal and Santa Cruz. Although all the islands are protected by the National Park, the last three islands have permanent human settlements in specific designated areas. In Santa Cruz Island, the development of the rural agricultural areas has encroached on the migratory routes of two species of giant tortoises: *C. donfaustoi* in the southeast, and *C. nigrita* in the southwest. Focusing on the southwest species *C. nigrita*, we investigated the social and ecological inter-linkages that are characterising this emergent conservation conflict. We used two methods framed under a participatory rural appraisal (PRA) approach: semi structured interviews and questionnaires to study farmers' perceptions and attitudinal factors regarding giant tortoises; as well as the associated socio-economic impacts of the conflict. Moreover, we coupled the PRA approach with an ecological assessment of giant tortoises' population density by using the transect method in the two corresponding yearly phases of giant tortoises' migration to the lowlands (January to June) and highlands (July to December). Our results indicate that farmers reporting damage and cultivating crops have higher odds of taking actions (fencing and physical actions) towards giant tortoises; regardless of having (or not) a negative perception towards the species. The economic losses for crops and fences averaged 2.8 USD/m² and 13USD/m², respectively; and provide an initial step to further analyse and characterise the direct and indirect damage costs. Finally, we estimated a density of 75 and 185 individuals of giant tortoises per km² in the rural area the lowland and highland migratory phases, respectively. Our approach provides grounded scientific social and ecological information to effectively inform and aid managers, policy and decision makers in the selection of adequate social and ecological criteria to implement the best available options in the resolution of this emergent conservation conflict.

keywords: Conservation Conflicts, Participatory Rural Appraisal, Social-Ecological System, Agro-Production, Adaptive Co-Management

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Signatures of natural selection in great tit genomes: Past selection, local adaptation or human imposed change?

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We are only beginning to understand how genomes are shaped by natural selection. Selection can leave strong genomic footprints in a population under selection, but the types of signatures are highly dependent on the genetic makeup of the species, the strength and timing of selection and the genetic nature of the trait. Moreover, making the link between genotypes and corresponding phenotypes under natural selection remains challenging. We present a detailed analysis of signatures of selection using a panel of 485,122 SNP markers screened in 2322 individuals from long-term ecological study populations of the great tit (*Parus major*) in the UK and the Netherlands. We find striking differences in the types of selection signatures in these populations; strong and consistent selection in both populations hinting at strong selection since divergence from its sister lineages, but also evidence for more recent differentiation, resulting in smaller and more subtle genomic selection signatures. Genes under differential selection between populations were associated with craniofacial features in humans or with bill morphology in Darwin's finches. Genetic variation at these candidate loci for bill morphology was associated with variation in fitness, suggesting ongoing selection for longer bills in the UK. Indeed, birds in the UK have longer bills than birds from mainland Europe, and a 25-year time series revealed that bill length in the UK has increased. Moreover, we show not only that recent evolution of bill length in great tits has occurred, but also identified a potential driver of this pattern by linking gene variants with the frequency of visits at artificial bird feeders, suggesting that widespread activity of feeding wild birds in the UK has resulted in rapid morphological evolution. Overall, we present an unusually detailed description of the underlying genomics of an evolutionary response to past and contemporary selection in a common wild songbird.

keywords : Genomics, ecology, selection, adaptation, great tits

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Pharyngotympanic tube response in domestic chicken and mallard to static pressure fluctuations

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The middle ear (ME) in birds consist of an eardrum, one muscle and one ossicle (columella). This system is enclosed in a cavity which connects to the contra-lateral cavity via the interaural canal, the latter connecting to the outside world via the single pharyngotympanic (Eustachian) tube. Quasi-static pressure differences may exist between the ME and the outside world, e.g. due to altitude changes, meteorology circumstances etc. Birds occupy a wide range of niches and it is interesting to know how different species are adapted to overcome large and sudden pressure differences (e.g. penguin diving to 50m depth, stoop dives in peregrine falcon ...). To find out how an avian middle ear can cope with these pressure fluctuations (i.e. accommodate by opening the pharyngotympanic tube) and how these fluctuations might influence the transport of sound energy from the eardrum to the inner ear, experiments were conducted on two species which occur in different niches, the terrestrial domestic chicken (*Gallus gallus domesticus*) and the diving mallard (*Anas platyrhynchos*). During these experiments the pressure was increased and decreased within the ME and interaural pathway of the bird using a probe, connected to a pressure generator, traversing one of the tympanic membranes. Pharyngotympanic tube opening could thus be assessed from sudden pressure drops (in case of sub-ambient ME pressure) or increases (in case of sub-ambient ME pressure). In chickens pressure fluctuations between -1000Pa and 1000Pa were used, which lies within the natural range in which chickens live. For the experiments conducted on the mallards a range was chosen with maxima at -4000Pa and 4000Pa, as larger pressure gradients can occur during diving. For both species no behaviour other than the normal random opening of the pharyngotympanic tube was observed in response to these static pressure fluctuations. Also micro-CT scans were made of a chicken head with sup-ambient (+1000Pa), sub-ambient (-1000Pa) and ambient ME-pressure. These static pressure conditions cause the eardrum to deform. It is important to know how these deformations affect the columella-extracolumella complex because the configuration of this complex may influence the transport of sound energy from the eardrum to the inner ear.

keywords: domestic chicken, mallard, pharyngotympanic tube, static pressure, middle ear

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Outline based shape analysis of fish scales: a procedure to quantify skeletal effects of chronic stress.

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In Teleostei, cortisol is the active hormone where it is released via the hypothalamic-pituitary-interrenal (HPI) axis, triggered both by acute and chronic stress conditions. Plasma cortisol is the most commonly used biomarker for acute stress determination. The primary function of cortisol is to restore the homeostasis which enables the organism to deal appropriately with the stressful event. Chronic stress conditions can invoke deleterious effects (e.g. decreased reproduction, decreased growth, immunosuppression, increased mortality). Therefore, chronic stress is to be mitigated in aquaculture as much as possible, making stress research pivotal. Several methods for acute stress have already been validated to effectively measure stress in fish but these are often cumbersome and time-consuming.

In the framework of chronic stress measurements using scale cortisol, we optimized an outline based shape analysis on scales. We compared shape changes in carp (*Cyprinus carpio*) scales as they grow (ontogenetic scales), as well as the impact of scale regeneration on its shape (regenerated scales). Using PCA to explore morphospace and levels of variation, it could be concluded that certain steps (e.g. staining protocol, imaging, ...) can facilitate the semi-automated processing of shape analysis. We also discuss some pitfalls in the methodology, and its potential for chronic stress analysis.

keywords: Stress, Cortisol, Carp, Scales

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Marine nematodes as bio-indicators of direct oil toxicity: a combination of single-species and community assays.

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Human activities have been modifying the environment for decades, but many anthropogenic effects are poorly studied or even unknown. Petroleum and its derivatives are still a major source of fuel to human societies and, while acute impacts, like the Deepwater Horizon drilling rig explosion in 2010, still gets most of the public and environmental agencies attention, sources of chronic oil contamination represent the biggest anthropogenic input of petroleum hydrocarbons in the environment. Moreover, a variety of chemicals are added in the composition of lubricant oils, which are highly soluble compounds, thus posing a high risk for aquatic organisms. We have used marine nematodes to investigate the direct impacts of oil pollution in the sea, by combining single-species with community assays. In the single-species experiments, all marine nematode species had their survival affected by the oils tested, with some exhibiting 100% mortality within 24h (e.g. *Diplollaimeloides oschei*). Nematode abundance in the marine microcosms started to decrease after three weeks on oil-contaminated microcosms, with no apparent recovery on the highest concentration treatments fifteen weeks after the beginning of the assay. Species identification is ongoing but preliminary data suggests a considerable decrease on species diversity on oil treatments compared to control replicates. Our study shows that marine nematodes are excellent organisms to assess direct oil toxicity, either in single-species or in community experiments; representing a more relevant alternative to other traditional test organisms, as the freshwater nematode *Caenorhabditis elegans*, when the focus of the study is on the marine environment.

Keywords: Nematoda, sea, pollution, benthos, bio-indicators

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The role of interspecific gene flow in the evolution of a parallel wolf spider radiation from the Galapagos

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The spatial repetition of environmental gradients within island archipelagos offers an unprecedented opportunity to test the role of stochasticity versus determinism in evolutionary diversification. Indeed, along the repeated ecological gradients on the different islands, phenotypic highly similar species often occupy exactly the same niches.

The evolution of each ecotypic species may either occur once, followed by subsequent colonization and speciation on the different islands, or be the result of repeated and independent evolution on each island separately i.e. parallel evolution. Genomics can help us to trace-back the genomic regions involved in ecotypic differentiation, and as such allow us to reconstruct the evolutionary history of the adaptations involved in ecotypic divergence. Here, we attempt to unravel the evolutionary history of a radiation of wolf spiders of the genus *Hogna* (Lycosidae) at the Galápagos. Within this radiation, dark coloured highland and pale coloured lowland species are found across the archipelago, and co-occur on two different islands.

We show that genome wide genetic differentiation is primarily a function of the island on which the species are found rather than the ecotype to which they belong. Hence, when both ecotypically divergent species co-occur on the same island, their degree of genetic differentiation was surprisingly small. Despite the close genetic relatedness of species from the same island, strong heterogeneity across their genome was observed. By investigating patterns of gene-flow, we show that substantial interspecific gene exchange took place between as well as within islands. Gene flow was primarily observed between ecotypes within islands, as well as between species of the same ecotype residing on different islands. Hence, these findings suggest that the observed phylogenetic patterns are at least partly confounded by different levels of gene flow between the species, rendering the distinction between *in-situ* parallel divergence and ecotype dispersal in the genesis of repeated species assemblages less clear-cut as generally assumed.

Keywords: parallel evolution, island radiations, population genomics

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Genome-wide patterns of identity by descent in a bottlenecked and fragmented red deer population

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Van Hooft Pim, Resource Ecology Group, Wageningen University
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While the loss of genetic diversity in wildlife populations due to habitat fragmentation is well established, the impacts at genomic level have been little studied. We used the Illumina CervusSNP50 assay to analyse genome-wide consequences of drift and inbreeding in the bottlenecked and fragmented red deer (*Cervus elaphus*) population of the Veluwe forest area, The Netherlands. First, we determined the genetic structure and verified the division of the Veluwe red deer population into genetically isolated subpopulations with low heterozygosity. Secondly, we investigated genome-wide identity-by-descent patterns. Red deer of the fragmented populations had elevated levels of haplotype sharing, meaning that genomes of different deer shared a relatively high fraction of long chromosomal segments that originate from the same recent ancestor. At the individual level, we observed many long runs of homozygosity, such that in the most affected populations at least 10 % of the genomes of all deer was built up out of autozygous segments. Our results show how the increase of identity-by-descent in small populations depletes genomic variation, both at the individual and the population level. We emphasize the necessity of ongoing projects to improve connectivity, both within and among populations, and discuss the power and usefulness of high-throughput genotyping technologies to monitor the genetic status of wildlife populations.

keywords : SNPs; Accumulation of IBD segments

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Cryptic diversity matters: implications for ecosystem functioning and management of global change effects

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Cryptic species - species which are genetically distinct, but have been classified as a single species because of their morphological similarity - have been found worldwide and in many different taxa. These cryptic species are so similar in their morphology and physiology that a high degree of ecological similarity is expected. As a consequence, they are usually expected to be functionally redundant and therefore not included in management or conservation plans.

Nevertheless, ecological differences may exist between cryptic species. In the cryptic nematode species complex of *Litoditis marina* (Sudhaus, 2011), at least ten cryptic species have been found. The autecology of four of them has been studied and has revealed that they have different salinity and temperature preferences, different dispersal abilities and differences in food resource utilization. These ecological differences may emphasize the importance of including cryptic species in the assessment of anthropogenic impacts and conservation management. We illustrate this using two different experiments.

In a first experiment, we tested if global change differentially influences cryptic species of *L. marina*. Climate change models predict decreasing amplitudes of daily temperature fluctuations, so we compared population performance of individual cryptic species and the outcome of their interspecific interactions under a temperature regime with daily fluctuations vs a constant temperature regime. Only minor or no effects on the population performance of the individual cryptic species were found, but a substantial effect on the interactions between species was discovered. This shows that there may be consequences of climate change on the interactions between cryptic species and that it may be important to take cryptic species into account in management of global change effects.

In a second experiment, we tested if ecological differences between the cryptic species could potentially translate in functional differences. *Litoditis marina* can substantially impact the decomposition process of algal wrack. We demonstrated that species-specific effects on the decomposition process exist. As a result, each cryptic species may play a different role in ecosystem functioning. This proves that the loss of one cryptic species may cause changes in ecosystem functioning and that it may therefore be important to conserve cryptic species diversity.

keywords: cryptic species, global change, ecosystem functioning, nematodes, marine

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Head shape related to dietary differences? Dimorphism throughout the European eels' life cycle

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An organisms' morphology can be related to its ecology and vice versa. Also in the dimorphic European eel, head shape can be related to differences in feeding ecology, with broad-headed phenotypes consuming harder prey than narrow-headed ones. As such, broad-headed eels are expected to have characteristics that increase their bite force to access harder prey. Using 3D-reconstructions of the cranial musculoskeletal system, we compared the morphology of both phenotypes at two life stages: the sub-adult yellow eel stage and its predecessor, the elver eel stage. With elvers at the onset of their predatory phase, this allowed us to find out whether broad- and narrow-headed phenotypes have similar characteristics in both life stages and whether the dimorphic traits become more pronounced during ontogeny. Additionally, we use a 3D-bite model to test whether broad-heads can generate higher bite forces than narrow-heads. We found that broad-headed phenotypes in both stages are characterized by larger jaw muscles, a broader skull and elongated upper and lower jaws with a higher coronoid, although these features did not become more pronounced during ontogeny. The bite model indicates that the larger jaw muscles of broad-heads allow the generation of higher bite forces to deal more efficiently with hard prey. Additionally, these larger muscles and the elongated lower and upper jaws may improve grip during spinning behaviour, which is applied on hard prey. In conclusion, this study showed that the European eels' head shape can be related to its feeding ecology and that in both life stages, dietary differences can take place.

keywords: anguilla, osteology, myology, bite force

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The importance of genomics for the conservation management of the critically endangered pygmy hog (*Porcula salvania*)

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The existence of a large number of animal species is threatened, often due to human impacts. One of these species is the critically endangered pygmy hog (*Porcula salvania*). The pygmy hog is the world's smallest and rarest wild pig species and it is currently living on the brink of extinction. Only one viable population exists in the wild, consisting of merely a few hundred individuals. The Pygmy Hog Conservation Programme (PHCP) has been managing a captive breeding and reintroduction programme for over four decades to support conservation efforts. However, little is known about the genetic background of the animals involved in the PHCP. Recent development in genome research techniques now makes it possible to sequence multiple individual genomes. The analysis of this type of data provides comprehensive insight into the demography, evolutionary history, degree of inbreeding and overall genetic diversity of the species. We analysed whole genome re-sequence data of six individual pygmy hogs: three from the wild and three from the captive population. To determine the degree of inbreeding we searched their genomes for regions of homozygosity (ROHs), i.e. regions with little genetic variation. We used the length of the ROHs as a predictor for the time frame of inbreeding where relatively long ROHs suggest recent inbreeding. We also determined overall genetic diversity and the proportion of mutations within protein coding genes that are predicted to be damaging. Moreover, pedigree information was studied using the program PMx to investigate the relationship between the sampled individuals. The results of this study are valuable to the conservation management of this and other endangered species.

keywords: pygmy hog, genomics, conservation, regions of homozygosity, inbreeding

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Speciation genomics of cichlids (*Ophthalmotilapia*) from Lake Tanganyika

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Organismal diversification involves the development of ecological and/or behavioural changes restricting gene flow in such a way that the ancestral gene pool drifts apart into separate gene pools that are subsequently maintained by reproductive isolation. Although the processes underlying restricted gene flow – e.g. geographic barriers, adaptive divergence and sexual selection - are well known, the type and number of genomic changes involved in reproductive isolation remain to be discovered. To this end, we investigate the genome-wide distribution of SNP's among 428 specimens of four closely related species of the cichlid genus *Ophthalmotilapia* endemic to Lake Tanganyika. We performed lake-wide sampling including allopatric and sympatric populations within and between the species. SNP's were distributed across the genome and were mainly located in introns and flanking regions of genes. Average F_{st} values increased with increasing geographic distance. In total, 3488 SNP's were shared between all species pair comparisons. Less than 20% of these SNP's had F_{st} values that were consistently higher than 0.5 in all species comparisons. These SNP's may point to genomic regions involved in the speciation process. To link the observed genomic differences to underlying behavioural components of the speciation process, we analysed gene expression patterns in six brain regions of female *O. ventralis* and *O. nasuta* after they had laid their first egg in the presence of a conspecific male or, in the case of *O. ventralis*, in the presence of a heterospecific *O. nasuta* male. Females are mouthbrooders that choose their mates, potentially imposing strong sexual selection. RNAseq data revealed that gene expression was distinct for the six brain regions and that gene expression was different between *O. nasuta* and *O. ventralis* females under conspecific settings suggesting species specific responses. Moreover, gene expression in the brain of female *O. ventralis* was also different in the presence of a conspecific male or an *O. nasuta* male. Functional annotation of differentially expressed genes will allow pinpointing the molecular pathways involved in mating and will, together with the genome wide SNP signatures, contribute to our understanding of how species are formed.

Keywords: Genotype-by-sequencing, population genomics, mate choice, RNA Quantseq

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The crop damage compensation scheme as a means of managing conflict between farmers and badger in Wallonia : shortcomings and impact on species protection

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Conflicts between farmers and wildlife are often dealt with by means of a crop damage compensation scheme. This paper aims to look at such a procedure from a socio-anthropological point of view and focuses on the compensation scheme implemented in Wallonia in the event of crop damage caused by badgers. In Wallonia the species is protected by law. To this protection status is attached a crop damage compensation scheme which is meant to reconcile two definitions of the badger: the “heritage species” and the “harmful species”. In 2012 a significant increase in the amount of damage and the ensuing amount of compensation benefits led to the badger protection status being called into question. The scientists in charge of the monitoring of the species were then able to point out that a large amount of damage had been unduly attributed to badgers. However, in 2016, while the amount of crop damage caused by badgers has greatly been reduced, the protection of the species is yet again about to be undermined. The following question therefore arises: how can such a scheme, which is supposed to foster a peaceful coexistence between farmers and wildlife, generate tension and be a threat to the protection status of the species in question? To answer this question we conducted a qualitative survey with farmers, naturalists, and hunters, all parties involved in the crop damage issue. We have been able to show what the notion of harmfulness implies for farmers and how it is linked to other considerations such as productivity and territoriality. We have also highlighted how the crop damage compensation scheme has become a means of joining the fate of the badger with that of the wild boar, a key actor in the hunting business. In conclusion, the crop damage compensation scheme, originally meant as a pacifying tool, actually makes the damage issue worse and constitutes a – at least temporary – threat to the protection of the badger, a species still on its way to recovery after being on the brink of extinction in Wallonia.

keywords: Conservation In Practice, Crop Damage Management, Badger, Harmful Species

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The interplay between morphology and locomotion during the development of olive baboons (*Papio anubis*): Implications for the evolution of primate locomotion

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The diversity of environments baboons are living in, demands high behavioural flexibility. Their locomotor capacities and the development of these capacities are keys for their survivorship. In order to better understand the locomotor performance of these species we studied an important period of their development: the transition from onset independent foraging to autonomy. We conducted a longitudinal follow-up of six infant olive baboons living in captivity at the Primatology Station of the CNRS in France, where we studied, in parallel, morphology, biomechanics and behaviour. First, our results show that the proportion of quadrupedal walking gradually increased on the expense of grasping behaviours. We demonstrated that this pattern is highly correlated to changes in their morphotype. While limb mass is initially more distally distributed, reflecting important grasping capacities for clinging the mother's fur, the proximal migration of the mass into the limbs at the later stage appears to be adaptive for reducing energy consumption during quadrupedal locomotion. Second, during this transitional period, young baboons are also improving their interlimb coordination during quadrupedal walking. We found that the intrinsic morpho-dynamics of fore- and hindlimbs (at the level of the convergence of the natural pendular period) have a significant and positive impact on this interlimb coordination pattern, thus probably facilitating, very early in development, the control of the coordination as well as the initiation of quadrupedal walking. Interestingly, baboons occasionally also use bipedal walking and this ability goes together with the development of interlimb coordination in quadrupedal walking. Hence, improvement of quadrupedal locomotor capacity does not exclude development of bipedal behaviour. This process, also observed in chimpanzees, questions the emergence of new locomotor modes during the evolution of primates, including man. Indeed, this finding supports the continuum of movements through different locomotor modes. Therefore, a repertoire where the bipedal equilibrium became dominant could have originated from a repertoire where quadrupedal equilibrium was dominant.

keywords: locomotion, ontogeny, body mass distribution, Catarrhini

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Conservation of aquatic invertebrates in temporary wetlands in a tropical biodiversity hotspot

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The Phongolo floodplain in South Africa is the most important floodplain system with high ecological and socio-economic importance, of which part is protected by the Ndumo Game Reserve, known as a hotspot of biodiversity. The Ndumo Game Reserve was declared a RAMSAR site in 1997 due to its unique wetlands that are locally known as pans. Insight in metacommunity structure and a profound understanding of the mechanisms shaping biotic communities are both important in conservation of biodiversity in Ndumo Game Reserve. Partitioning diversity into its different components (alpha, gamma and beta) provides essential information on spatial organization and processes that generate and maintain biodiversity in ecosystems. The temporary pans in Ndumo Game Reserve of South Africa, provide an opportunity to study their importance in invertebrate biodiversity conservation. Based on our findings, we formulate potential conservation strategies that promote invertebrate diversity in temporary pans of the Ndumo Game Reserve.

Keywords: beta diversity, invertebrates, temporary wetlands, conservation, Ndumo Game Reserve

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Ventral skin light perception involved in the bioluminescence control mechanism in the velvet belly lanternshark, *Etmopterus spinax*?

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Etmopterus spinax (Linnaeus 1758), is a bioluminescent deep-sea shark able to emit a blue-green light thanks to thousands of tiny epidermal light organs called photophores spread mainly over the body ventral side. Photophores are composed of photogenic cell clusters (photocytes) enclosed in a pigmented sheath and topped by a shutter-like structure and a lens. Counter-illumination is suspected to be the shark bioluminescence main function. According to recent pharmacological studies, this camouflage function is achieved thanks to a complex photophore control mechanism, which involves hormones (melatonin, prolactin, -MSH) and neural agents (NO, GABA). In addition, new evidences suggest that extraocular photoreception could play a role in the bioluminescence control mechanism.

Here, we investigated, using transcriptomic analyses and immunodetection labelling, (i) the *E. spinax* opsin-based extraocular photoreception; (ii) two hormonal G-protein coupled receptor: melatonin (mel1b) and -MSH receptor (MC4R); and (iii) the different G-protein implicated in the transduction cascade events between photoreception and photoemission. cAMP concentration assays were performed on photogenic tissues stimulated with melatonin (for light induction), with -MSH (for light inhibition) and with blue light (to mimic natural light emission).

Transcriptomic analyses allowed us to identify, in the ventral skin, the expression of an encephalopsin (non visual ciliary opsin), a mel1b receptor, a MC4R receptor, and proteins Gi / Go / Gs / Gt. Immunodetection results allow us to visualized the distribution of all these proteins near or inside the shark photophores. cAMP concentration assay demonstrated that the cAMP levels vary in function of treatments (melatonin, -MSH, blue-green light illumination). These results support the implication of intracellular cAMP in the transduction cascade controlling the light emission within the photogenic cells.

The hypothesis of a deep interaction between light emission and reception is strongly supported. The implication of an extraocular photoreception cascade is suggested in the Etmopteridae bioluminescence control mechanism.

keywords: Bioluminescence, Shark, Extraocular opsin, Hormonal control, Immunohistofluorescence

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Understanding the foraging behaviour of European nightjars *Caprimulgus europaeus*

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European Nightjars *Caprimulgus europaeus* are crepuscular insectivorous birds that breed in semi-natural habitats, closely associated to sandy soils. In Flanders, breeding areas of nightjars are mainly found in heathland habitats. Despite many local conservation programs, current population sizes are still small compared with 19th century estimates after they suffered from severe habitat loss since the late 19th century.

Because foraging habitats, such as extensively grazed farmlands and wet meadows, are not included in current conservation programs and in order to improve the efficacy of conservation measurements, a better understanding of nightjars' foraging ecology is required. To investigate why foraging distances vary between individuals we collected information on foraging behaviour of over 70 nightjars tagged with VHF-tags and another 30 were tracked using nano-GPS-loggers. We 1) identified the influence of habitat configuration and composition on individual's foraging distance, 2) calculated time of absence of adults on their nesting site using temperature loggers and 3) compared food availability between breeding and foraging habitats.

We found that food availability is significantly higher in foraging habitats compared to breeding habitats. Furthermore, a lower percentage of foraging habitat in proximity of a nightjar's nesting site and a clustered landscape (i.e. when different functional habitat types are clustered together) cause foraging distance to increase. Finally, nightjars in our study undertake quick foraging trips at least twice per night: once during dusk and once during dawn. The duration of these foraging trips is related to temperature and time after sundown.

Using remote tracking technologies on a light weight (>100g) bird we collected more detailed information on nightjars' habitat use. We are now able to identify where, why and when individuals forage and how they use the landscape to travel between breeding and foraging sites. This understanding will facilitate the conservation of nightjars because policy makers and conservation managers can implement the protections of foraging habitats in their conservation plans.

keywords : European nightjar, Caprimulgus europaeus, foraging ecology, landscape ecology, connectivity

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Geometric morphometric approaches to inferring bite force and diet in extinct strepsirrhines.

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The cranial system in mammals is highly constrained. Feeding forces, phylogeny, and the need to protect the brain and sensory organs are all important factors driving the evolution of the shape of the skull. Here, we explore relationships between bite force, cranial, and mandibular shape to infer the dietary ecology and bite force in two extinct species of strepsirrhines. We collected data on molar and incisor bite forces and analyzed cranial and mandible shape using 3D geometric morphometric approaches for 18 species of strepsirrhines that differ in feeding ecology. In addition we use data on mandibular shape to infer the diet of two extinct species, *Archaeolemur edwardsi* and *Hadropithecus stenognathus* and use the observed co-variation between bite force and mandible shape in extant taxa to infer bite forces in these taxa. Our results show that bite forces vary across species with dietary specialists differing in bite force, cranial shape, and mandibular shape. The covariation between bite force and mandibular shape was strong and based on these data we inferred molar bite forces of 212 and 237 in *A. edwardsi* and *H. stenognathus* respectively. Finally, mandibular shape data demonstrate that both species were folivores supporting the most recent stable isotope data for these species. [supported by NSF-BCS-1062239 to CEW]

keywords: Functional morphology, lemur, fossil, cranium, mandible, diet

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Pregnant as a prey: performance and kinematics of the 3D fast-start escape response of live-bearing fish

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Unlike most other fish species, females of the live-bearing family Poeciliidae give birth to fully developed precocial young. The internal development of the embryos increases the female's abdominal volume during pregnancy. This may lead to an increased drag and decreased flexibility in the abdominal region, thereby negatively affecting a female's locomotor performance. We studied the negative consequences of internal gestation for the fast-start escape performance of *Poeciliopsis turneri* by repeatedly comparing the locomotor performance of gestating females over the course of their pregnancy to the performance of virgin 'control' females. The body kinematics was studied in three dimensions, using three orthogonally placed high-speed video cameras. The stimulus was applied from the top, resulting in an overall tendency for downwards-oriented escape. The maximum velocity reached was significantly lower in pregnant fish. Moreover, the maximum velocity decreased as the pregnancy progressed. Surprisingly, a similar temporal pattern was found for virgin controls that did not show significant changes in volume over this period. Finally, pregnant females exhibited less curvature at the end of stage 1 (the preparatory stage) and curve slower during both stage 1 and stage 2 (the propulsive stage) of the fast-start escape response. We propose that in live-bearing fish the pregnancy changes how females escape from predators. These results indicate that the decrease in escape performance can be explained by a combination of different changes in the kinematics.

keywords: biomechanics, kinematics, fast-start, viviparity, Poeciliidae

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“Tell me what you want, what you really really want”: applying a behavioural reaction norm approach on parent-offspring communication

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In species with postnatal care as most bird species, offspring signal their need for resources with complex begging behaviours. This triggers parental provisioning, which is essential for offspring growth and survival. However, begging and provisioning behaviour are both costly, yet reciprocally influence each other, and are therefore expected to coevolve. Co-adaptation of offspring begging and parental provisioning has been confirmed by several empirical studies. However, parent-offspring interactions are highly dynamic. Offspring begging changes in function of need as well as parental provisioning and parental provisioning changes in function of begging. Responsiveness to such changes in each other's behaviour will thus likely have a strong impact on parent-offspring co-adaptation. (Co)-variance partitioning techniques are now readily available to distinct earlier observed phenotypic parent-offspring co-adaptation into its (genetic) between-individual and (plastic) within-individual components. In this study we used captive canaries (*Serinus canaria*) in a behavioural reaction norm approach, and measured parental provisioning and offspring begging behaviour at two different hunger levels. This allowed us to study simultaneously the responsiveness of the parents and of the offspring to changes in need. We found that the observed phenotypic co-variation of offspring begging and parental provisioning is driven by within individual co-variance rather than by among individual co-variation. Thus parental and offspring behaviours co-vary due to plastic co-adjustment in response to each other. More specifically, when offspring begging increased with their experimentally enhanced hunger level, both parents responded. This study highlights the importance of taking responsiveness into account when studying parent-offspring communication, and provides important insights for our understanding of co-adaptation between parental provisioning and offspring begging.

Keywords : begging, responsiveness, parent-offspring co-adaptation, Serinus canaria, parental provisioning

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Development of a test method for transgenerational effects of genetically modified crops in food using the zebrafish model

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Ever since genetically modified (GM) crops were introduced, their safety regarding human consumption has been questioned. One of the main concerns is that the current methods for GMO evaluation do not specifically assess effects on embryonic development or reproduction. Therefore, the goal of this study is to develop a new test method, using the zebrafish model, to assess transgenerational effects of GM crops in food.

Since GM maize was selected to develop the test method, the first phase of this study was to determine the maximum percentage of maize tolerable for zebrafish. Fish were fed with 3 controls and 6 experimental feeds ranging from 0% to 25% of non-GM maize. After 4 weeks, growth was slightly decreased when fish were fed with 0% or 25% of maize. The hepatosomatic index (percentage liver weight relative to total body weight) of males was significantly increased when fed with 20% or 25% of maize. Feed digestibility analysis showed a decrease in carbohydrate uptake when fed with an increasing percentage of maize. Based on these outcomes, we selected 15% maize as the maximum tolerable percentage.

Furthermore, it is important that any potential effect of a GM crop is interpreted relative to the natural variation that can be found in response to feeding with non-GM varieties of the same crop species. We therefore fed zebrafish for 12 weeks with 10 different non-GM maize varieties (15%). We observed significant differences for the carbohydrate level in the liver of adult males, for the swimming behaviour of adults and embryos, and for the relative condition factor and length of embryos. These results highlight the importance of defining the natural response variation as even feeding with non-GM varieties can cause significant differences.

Next, a transgenerational experiment was initiated to investigate whether the test system allows us to assess potential transgenerational effects. Fish were fed for 16 weeks with an experimental and a commercial GM maize and their corresponding non-GM controls (15%). No significant differences were observed. We continued by producing the first generation. The next step is to analyse this first generation and produce and analyse a second/third generation.

keywords: food safety, feeding trials, zebrafish

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Zoonotic pathogens: “A study of the diversity and prevalence of the *Bartonella* bacteria and the Monkeypox virus in different rodent and shrew species in the rainforest of Yangambi (DRC)”

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Zoonotic infections are infections which can be transmitted between animals and humans. Many emerging infections in humans are zoonotic in origin. In this study, the Monkeypox virus (MPXV) and *Bartonella* bacteria are chosen as models of pathogens causing zoonotic infections in humans. More than 700 small mammals were trapped at 9 sampling sites over 3 years in the Yangambi Biosphere Reserve (DRC) to investigate the genetic diversity and prevalence of Monkeypox and *Bartonella* infection in these mammals, and environmental and biological features that may have an effect on the chance of infection by these pathogens. Host DNA was extracted from liver samples. For the detection of *Bartonella*, PCR was performed using the primers 1400F and 2300R targeting 852bp of the *Bartonella* RNA polymerase beta subunit (rpoB) gene. For the detection of Monkeypox, nested PCR was performed using the primers FP1 and FP2 (in the first run), and FP3 and FP4 (in the second run), targeting 200bp of the *Orthopox* virus fusion protein gene. A generalized linear model was used to relate the prevalence of the pathogens to family, subfamily, genus, forest type, gender, sexual activity, year of capturing and the presence of ectoparasites. Overall, the prevalence of Monkeypox among small mammals was 13%, the prevalence of *Bartonella* infection was 8.5%. Eight Monkeypox haplotypes were identified: 4 of them clustered with the Congo Basin clade, 4 with the West African clade. For *Bartonella*, 17 haplotypes were identified which were all closely related to *B. elizabethae*. The prevalence of Monkeypox varied with the year of capturing and the presence of ectoparasites. The prevalence of *Bartonella* varied with the family, forest type, year of capturing and the presence of ectoparasites. The fact that both pathogens can cause zoonotic diseases in humans indicates a potential health threat to people living in Central Africa.

keywords: Zoonotic infections, Monkeypox virus, Bartonella bacteria, prevalence, small mammals

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Using molecular techniques to identify organisms of policy concern: Some examples from the BopCo project

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Organisms of policy concern encompass a variety of species which may influence our health and (economic) activities including: invasive alien species, disease causing organisms, CITES protected species, agricultural pests, forensically important insects, organisms of the food chain, etc. Because of the potential harm some of these organisms may cause, rapid and accurate identifications are imperative. The Barcoding of Organisms and tissues of Policy Concern (BopCo) project, therefore, aims at providing access to the knowledge and infrastructure necessary to identify all life stages of organisms of policy concern and their derived products. These identifications may rely on “traditional” morphology-based approaches and/or DNA-based techniques like DNA barcoding.

BopCo considers identification requests from a wide array of stakeholders who deal with biological materials of policy concern and who need a rapid and accurate identification. Examples of past requests include: 1) the identification of bird remains for the Belgian air force in order for them to take appropriate action to prevent crashes, 2) the molecular identification of slugs infected by a parasitic nematode for an epidemiological survey in Germany, 3) the identification of fruit fly pest species on citrus fruits, 4) the identification of a new invasive terrestrial flatworm in Belgium, and 5) the identification of dried lizard remains in imported cereals for a private company. Since a prerequisite to use DNA barcoding is the availability of comprehensive and reliable reference libraries, BopCo also actively generates reference DNA barcodes of organisms of policy concern in order to fill gaps in the barcode databases. Ongoing projects include the construction of a reference library for forensically important rove-beetles (Staphylinidae). Lastly, BopCo seeks to optimise DNA extraction and amplification techniques for samples which have been stored or treated in different manners, e.g. processed food samples.

Identification requests for organisms of policy concern can be made through the BopCo website (www.bopco.myspecies.info), while taxonomic experts who wish to collaborate or lend their expertise can contact us in person or via email (bopco@naturalsciences.be).

Keywords: DNA barcoding, (animal) health, IAS, CITES, forensic insects

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Growth of worldwide genus *Diplodus*

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In this study, the development and use of age and growth studies on genus *Diplodus* are reviewed and analyzed. The scientific papers were scoured for publications reporting von Bertalanffy Growth Parameters (VBGPs) for genus *Diplodus* stocks. The sources used were: Web of Science (apps.webofknowledge.com), Scopus (www.scopus.com), Google Scholar (scholar.google.gr), Researchgate (www.researchgate.com) and Academia (www.academia.edu), conference proceedings (e.g. CIESM Congress Proceedings) and any other document available to the authors, such as technical reports and theses. The search covered the period up to December 2015. Valid names of fish species were checked according to FishBase. The von Bertalanffy growth parameters of species are listed. Growth parameters are compared with ANOVA and Duncan Multiple Comparison Tests according to location, sex, aging method and species. The validity of estimates was based on the maximum observed to asymptotic length ratio (L_{max}/L_{∞}), which in fishes is about 0.96 when excluding all values <0.70 . Thus, VBGP estimates with L_{max}/L_{∞} lower than 0.70 should be used with caution. A summary of 76 data sets on 10 species is given. All growth parameters presented were collected from a total of 48 studies. Two species (*D. vulgaris*, $n=22$; *D. annularis*, $n=17$) were dominated in all studies. The mean \pm std error values of L_{∞} , K and t_0 for all over studies were calculated as 34.48 ± 1.55 , 0.24 ± 0.01 and -0.31 ± 0.12 respectively. A total of 45 growth data sets with age method based on otolith reading were found. Moreover 6 studies were based on length frequency method and 24 studies were based on scale reading method was found. Considering the location in which the studies were performed, significant difference have been found between location for L_{∞} ($p < 0.05$) but not for t_0 and K ($p > 0.05$). Considering L_{max}/L_{∞} ratio, in 3 cases the VBGP estimates led to L_{max}/L_{∞} ratios lower than 0.7. In 73 cases L_{max}/L_{∞} ratios were higher than 0.7.

Collection of VBGPs from published datasets is important for fisheries science. This kind of studies can serve as a reference point for investigating shifting baselines in growth of fishes. Furthermore maximizing available information is important, especially for data-poor areas such as the Mediterranean Sea.

keywords : Diplodus, seabreams, von Bertalanffy Growth Parameters, Fisheries

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Anthropogenic environments increase systemic immune activity: evidence from a cohort-matched wild–mesocosm comparison.

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Domesticated species or species in urbanized areas encounter new environments different from those they evolved to deal with. We know that these environments can impose unprecedented challenges for the immune system of these species. This applies also to humans, who, especially in highly urbanized areas of high income countries, face an increased prevalence of illness from inflammatory diseases caused by malfunction of the immune system.

Despite its importance, few studies have compared the immune function of animals in artificial environments with their co-specifics in nature. Studies on rodents found a more activated immune system in wild animals, which may be the consequence of higher prevalence of infectious diseases in nature. Inbred laboratory rodents maintained under extremely benign and pathogen-free conditions are, however, unrepresentative of the real-world problems. Humans and domesticated animals still encounter many infections, albeit that these are different from those occurring in nature.

We transferred post-larval three-spined sticklebacks (*Gasterosteus aculeatus*), collected in the wild, to an anthropogenic (captive) environment. We then monitored, over eleven months, how the systemic expression of immunity genes changed in comparison to cohort-matched wild individuals in the originator population. We found that a range of innate and adaptive immunity genes were up-regulated in captivity, accompanied by an increase in expression of an anti-oxidant enzyme. For some seasonally expressed genes, seasonality appeared to be reduced in captive fishes. Captive fishes tended to express immunity genes more variably. Furthermore, although gene co-expression patterns shared common structure in wild and captive fishes, there was also significant divergence. For one gene in particular, high expression was associated with adverse health outcomes in captive fishes.

Our observations are consistent with higher anti-oxidant activity that might be directly linked with (or may even control) increased inflammation in captive animals. They also suggest that in anthropogenic environments fish can exhibit levels of immune activation that are not found in nature. Such immune responses have not been refined by selection and may lead to the immunopathology we often observe in anthropogenic environments.

keywords: ecology, evolution, disease, gene-expression, fish

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Founder effects determine the genetic structure of the water flea *Daphnia* in Ethiopian reservoirs

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Founder effects introduce stochasticity in the genetic structure of species at the regional scale. To the extent that founder effects are important that they will result in a reduced signature of space, time and environmental variation in landscape genetic data. We studied the metapopulation genetic structure of recently founded populations of the microcrustacean *Daphnia sinensis* in ten Ethiopian water reservoirs. We used three different methods applied to two independent genetic marker sets to investigate the role of founder effects and to estimate effective size of the founding population. Estimates of founding sizes rarely exceeded eight individuals but were most often limited to less than four individuals. No associations of genetic identities, gene frequencies, measures of genetic diversity or differentiation with environmental and spatial variables were found. Age and size of the reservoirs were not correlated with genetic diversity measures or number of founders in these reservoirs. These findings indicate that neither strong selection, nor dispersal limitation are responsible for the observed pattern of genetic variation. Our results suggest a regional population structure that is strongly impacted by founder events, reflecting colonization by just a few founders per water body, and not noticeably influenced by subsequent dispersal and gene flow. Our results show that rapid colonization of empty habitats and fast population growth by a handful of founders can result in strong founder effects, even in relatively large habitats (estimated populations sizes $\gg 106$) that are likely regularly reached by new immigrants.

Keywords: colonization, Daphnia sinensis, effective population size, founder effects, metapopulation

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Life in a changing environment: a focus on nematode communities in seafloor sediments near the Antarctic Peninsula

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With its low temperatures and pronounced seasonality in primary production and food availability, the marine ecosystem of the Antarctic is unique. Yet parts of it (notably the region of the Antarctic Peninsula) are among the most rapidly warming regions worldwide. Current climate change has resulted in a considerable loss of ice shelves and glaciers as well as declining sea-ice coverage and changes in ocean circulation along the Antarctic Peninsula. Such climate-driven environmental changes have an effect on all levels of the marine ecosystem and are also acting upon seafloor communities through the process of benthic-pelagic coupling. The marine environment around the peninsula is thus a key region for the study of biological processes and the response of biota to environmental change.

We focused on marine free-living nematode communities in seafloor sediments at different locations on the Antarctic Peninsula continental shelf. The aim was to define to what extent local environmental conditions (i.e. oceanographic regime, sedimentary parameters) and climatic drivers (i.e. climate-induced ice-shelf collapse, seasonal sea-ice coverage) have an impact on nematode abundance, diversity, distribution and community composition. Our results pointed towards the importance of environmental conditions in structuring local communities. Short-term alterations in food regime, ice coverage or oceanographic parameters are rapidly translated to the benthic realm. Further warming of Antarctic Peninsula waters and decline in ice-shelf coverage will therefore leave a permanent imprint on seafloor biota. Only by understanding their current distribution patterns and community turnover rate will we be able to formulate clear implementation measures for future protection and conservation. However, long-term responses and consequences for ecosystem functioning remain far from being predictable, at least for the smaller-sized organisms of this study.

Keywords: Antarctica, climate change, Nematoda, community ecology, oceanography

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Evolution on islands: patterns of phenotypic diversity in two species of *Podarcis* from the Adriatic.

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Islands are known to be ideal model systems for testing the drivers of phenotypic variation. Lacertid lizards of the genus *Podarcis* are particularly good organisms for doing so as they occur on islands varying in size and complexity. Moreover, two species of this genus occur in the Adriatic allowing for tests of the predictability of the patterns of phenotypic diversification observed on islands. Here we present recent data from a field trip where we sampled over 20 populations of *Podarcis sicula* and *Podarcis melisellensis* for which we collected data on external morphology, bite force, gut length and diet. Our results show divergent patterns across the two species with *P. melisellensis* showing more variability in gut length. In contrast, variation in cranial morphology and bite force was greater in *P. sicula*. Diet was diverse with most populations consuming mostly insects. However, signals of herbivory were detected in several populations. Yet the phenotypic responses to the inclusion of plant matter in the diet were not the same suggesting that evolutionary responses to changes in diet may not always be predictable.

keywords: lizard, diet, bite force, evolution, phenotype

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Tracking a marine predator to design flexible boundaries of marine protected areas for an ecosystem approach to fisheries

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African penguin *Spheniscus demersus* populations showed a drastic decline during the past decade, and their abundance is substantially linked with the presence of their prey. However, environmental changes and resource competition with purse-seine fisheries disrupt this prey availability. Therefore, conservation efforts should ensure adequate local food availability. In this perspective, marine protected areas (MPAs) have been identified as a valuable tool in an ecosystem approach to fisheries (EAF). Furthermore, when designed with flexible boundaries, MPAs can be beneficial for both penguins and fisheries. In Algoa Bay, South Africa, an EAF has been attempted through experimental purse-seine fisheries closures from 2009 to present. We investigated the effectiveness of these closures and evaluated the conservation value of a newly proposed, zoned MPA. Using GPS loggers, we studied the foraging behaviour of African penguins to assess their spatial overlap with purse-seine fisheries catches. Furthermore, the GPS tags provided a suite of horizontal and vertical foraging measurements, which were modelled with several explanatory variables. Our results showed a decline in purse-seine fisheries catches since 2012, possibly due to limited fish abundance. Nevertheless, the experimental closures showed a marked reduction in the penguins' foraging effort. The presence of prey is probably the main cue to adapt their foraging strategy, and this is likely to be dependent on environmental conditions and fishing pressure. Also, geospatial mapping revealed a strong overlap between the foraging range of African penguin and purse-seine fisheries in Algoa Bay from 2008 until 2015. Conversely, the no-take zones of the proposed MPA cover less than half of that foraging range.

In general, this study indicated that the proposed MPA would provide an improvement to the current situation, but is not sufficient to increase numbers of African penguin populations. Larger no-take zones around the penguins' colonies are necessary when prey biomass is low. As an immediate action, ongoing acoustic surveys could provide information on prey availability to design flexible boundaries and increase the benefits for all stakeholders involved. In the future, more quantitative research is necessary to reconcile conservation goals and the socio-economic needs of the coastal community of Algoa Bay.

Keywords: Spheniscus demersus, GPS tracking, adaptive fisheries management, no-take zones, foraging behaviour

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Relationship between jaw morphology, bite performance and diet in Serrasalminae

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Serrasalminae are mainly known for “piranhas” and their negative reputation of ferocious predatory fishes. A recent study demonstrated that the piranha *Serrasalmus rhombeus* had an extreme bite force that is even proportionally greater than that of the white shark. However, these sharp teeth fishes represent only a minority of Serrasalminae. Other serrasalmid species (pacus and myleus) feed on plants, fruits or seeds and their bite force and feeding capacities are still uninvestigated. In the present research, in vivo bite forces were measured and compared according to jaw morphology in ten species of Serrasalminae including six herbivorous and four carnivorous species. The Bite Force Quotient (BFQ) was calculated for each individual to compare the jaw strength across species. The results of the analysis showed that species feeding on fins and fish flesh have a significant greater bite force than species feeding on plants, fruits or seeds. This difference can be explained by the larger adductor mandibulae muscle in carnivorous species which have comparatively longer and higher skull than herbivorous species. In addition, there is a significant difference in the lower jaw morphology between piranhas and pacus and relatives. The piranha species have longer lower jaws than pacus and myleus species which have shorter and higher lower jaws. This study shows that the Serrasalminae family regroups remarkable biters whose bite performance is mostly related to diet.

keywords: Serrasalminae, functional morphology, bite force, lower jaw, diet

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A hitchhiker's guide to tilapia: How parasites take a ride on introduced Nile tilapia in the DR Congo

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In most tropical regions, the Nile tilapia (*Oreochromis niloticus*, Cichlidae) is introduced for aquaculture, making it one of the major species in culture worldwide. However, it has become invasive in many places with detrimental effects on the local fauna. The literature reports a decline of indigenous cichlid species after the introduction of Nile tilapia in several African regions. Here, Nile tilapia is in direct competition and can hybridize with indigenous cichlids. However, in these studies the effect of parasite co-introduction and thus of introducing additional pest species remains underexplored. Parasite co-introduction can influence the fitness and therefore the competitiveness of both invasive and native species. Also parasite spillover and spillback effects (host-switching) may occur, which can impact competition, fitness, mortality, fecundity, trophic ecology, co-evolution and biodiversity.

We focus on monogenean gill parasites (*Cichlidogyrus*, *Gyrodactylus* and *Scutogyrus*) because they are host-specific, have a high prevalence and a direct lifecycle. Furthermore, we focus predominantly on the Congo Basin because here the monogenean fauna remains largely unstudied. In addition Nile tilapia is introduced multiple times across the Congo Basin, but these introductions received little scientific attention. Studying this through regional case-studies will result in a better understanding of the potential for parasite transfer and the impact of invasive species, which will aid in conserving the native fauna.

We will present a contribution to the biogeographical and host range of these parasites in Haut-Katanga. In total, 13 cichlid and 19 parasite species were collected of which one cichlid and 6 parasite species are new to science and 3 need redescription. For 9 native hosts, this is the first record of their gill monogeneans. On Nile tilapia we found 5 of the 7 *Cichlidogyrus* species known to infect this host. These 5 species also occur on the native *Oreochromis* species in recent and historical samplings, so were already present in the basin before introduction of Nile tilapia. Furthermore, *Cichlidogyrus dossoui* and *C. papernastrema* were found to occur both on mouth-brooding and substrate-brooding cichlids which refutes the hypothesis of a strictly separate gill parasite fauna between mouth-brooders and substrate-brooders.

keywords: Invasive biology, Monogenea, Cichlidae, Parasite transfer, Conservation biology

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Pelagic freshwater fish parasites in Lake Tanganyika: do the monogeneans mirror host origin?

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Parasites have been mainly overlooked for many decades in the Great African Lakes. Lake Tanganyika is a well-known study area attracting scientists for its remarkable species diversity. For some years, its fish parasite fauna, especially monogeneans, received more attention with 24 described species in the lake to date. While most investigations focused on the diverse littoral zone, information about economically important pelagic hosts is still missing. Lake Tanganyika's pelagic zone is dominated by two endemic clupeid species (*Limnothrissa miodon*, *Stolothrissa tanganicae*) and four endemic latids (*Lates angustifrons*, *L. mariae*, *L. microlepis*, *L. stappersii*). All species figure as an important component of the food web and form the main part of local fisheries. Surprisingly, almost nothing is known about their parasite fauna. We examined the abovementioned hosts for the presence of parasites to answer the following questions: which parasites infect clupeids and latids in Lake Tanganyika? Is there any seasonality or geographical variation in infection parameters? And do the parasites mirror host origins?

Samples originated from several localities in Lake Tanganyika and included historical fish specimens deposited in the collection of the Royal Museum for Central Africa and specimens from fieldwork and specimens from recent field works. Parasite species identification and description was based on the sclerotised structures of the copulatory and attachment organs. Molecular characterisation was conducted using markers with different rates of molecular evolution (nuclear 18S, ITS1, 28S rDNA and COI mtDNA).

Morphological as well as molecular identification showed the existence of two different monogenean species of *Ancyrocephalus* infecting clupeids in Lake Tanganyika. This result indicates adaptation of freshwater parasite species to originally marine fishes during their colonisation of African freshwater. Contrary, latids as representatives of an originally marine taxon are infected by a single species of *Diplectanum*, a genus reported mostly from marine and brackish waters, closely related to species reported from *Lates calcalifer* in Asia. Phylogenetic analyses showed the need for revision of both reported parasite genera. Finally, seasonality of parasite prevalence was observed. Further analyses tracking parasite population structure and demographic history linked with host data are planned to reveal the co-evolutionary history of this host-parasite system.

keywords: sardines, Lates, species description, host origin, phylogeny

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Population genomics of the European nightjar *Caprimulgus europaeus*

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European Nightjars *Caprimulgus europaeus* have recently undergone a population and range reduction across Europe. This decline, mostly due to habitat loss, is striking in Belgium, where European Nightjars remain in relict populations. To tackle the potential need for conservation actions, it is important to describe genetic variation and to understand the processes shaping it. We aim to study population genomics of the European nightjar. DNA samples will be collected over a major part of Nightjar's current breeding distribution. We will also focus on the Belgian scale and sample most breeding sites. Several sites have already been sampled: three in Belgium (Limburg province), one in France (Forêt de Fontainebleau) and one in the Netherlands, near the Belgian border. Using this dataset as a starting point, we will detect Single Nucleotide Polymorphisms randomly distributed across the genome by Restriction site-Associated DNA sequencing (RADseq). We intend to characterize genetic variation, determine population structure and reconstruct demographic history. Population genomic analysis will provide valuable insights into the conservation management of the European Nightjar through the identification of populations of conservation concern, the understanding of population connectivity, and the estimation of population size.

Keywords: European nightjar, population structure, demographic history, RADseq

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Edge-effects in *Posidonia oceanica* seagrass meadows

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Structural boundaries in ecosystems play an important role both in the context of seascape architecture, ecological processes and biodiversity. The Mediterranean Seagrass *Posidonia oceanica* (L.) Delile is considered an ecosystem engineer species, forming habitats of great ecological value and providing many ecosystem services. This study aims to (1) determine whether there are differences between seagrass-sand corridors edges and the adjacent continuous meadow, and (2) investigate whether anthropogenic pressures can cause disturbances in the measured parameters along the edges and the meadow. We have developed a multidisciplinary approach combining plant physiology, faunal canopy community studies and seagrass structural parameters characterization. We performed in situ chlorophyll fluorescence measurements using a Pulse Amplitude Modulated (Diving-PAM) fluorometry in order to assess the photosynthetic rate of the shoots. Vagile-macrofauna of the leaf stratum was sampled by a hand-towed net, and the major taxonomic groups were sorted, counted, and identified. Meadow's biometric measurements and the epiphytic biomass were also determined. Regarding edge-meadow matrix, results have shown highest differences on matrix structural parameters such as shoot density and shoot type proportions. Shoot density was found to decrease in edges considerably. We found c.a to 60 % plagiotropic shoots on edges while in continuous meadow orthotropic were predominant (up to 90 %). However vagile-fauna population densities and diversity did not differ significantly among stations studied, neither by sites. Photosynthetic rate and leaf surface values also did not show changes between edges and continuous meadow. However, results did show that plagiotropic shoots had higher photosynthetic rate than orthotropics, and also that epiphyte abundance sorted out to be much higher (up to 54 %) on edges.

Keywords: edge effect, seagrass, vagile fauna, epiphyte, biodiversity

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Monkey see, Monkey eat, Monkeypox

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In the decade preceding the victory of the World Health Organization on Smallpox (1970-80), the prevalence of a symptomatically similar Orthopoxvirus, Monkeypox virus (MPXV), started to increase in the heart of Africa. MPXV had been scientifically described in 1958 during an outbreak in a colony of captive Asian monkeys (hence its name) hosted in Europe and - since no human fatalities occurred - was not considered a threat to man. From the above, nothing could predict that the virus was actually hiding in the wildlife of lowland African rainforests. In 1970, the first human monkeypox (HMPX) case was identified in the Democratic Republic of Congo (DRC). Since then there have been human outbreaks in 10 more African countries. Between 1980 and 1986, active surveillance in the DR Congo revealed i) a 20-fold increase in HMPX with up to 10% mortality, ii) up to 6 consecutive inter-human transmission steps (which has been associated with the existence of two genetic clades and two levels of virulence) and iii) the zoonotic source of several outbreaks with the isolation of a single MPXV strain from a sick squirrel. Yet, a limited number of outbreak responses and ecological studies of candidate reservoirs have so far been dedicated in situ to understanding the factors influencing the disease dynamics in humans, the identity and diversity of the hosts species or the ecological relationships between them. During recent biodiversity field surveys in the DR Congo, we found DNA evidence of Orthopox virus in a series of mammal species, including rodents, bats, primates and small carnivores. Moreover, we found for the first time the MPXV-WA clade (less virulent) and the MPXV-CB clade (virulent) in wildlife originating from a same geographical area. While the MPXV sequences derived from humans and animals were 97-100% identical, the more virulent clade was only detected in humans and a wide array of hosts carried either one or the other clade. In a public health risk context, these findings (co-occurrence and carrier diversity) are critical in understanding and predicting future outbreaks or introduction into our global village.

keywords: One Health, Orthopox virus, Monkeypox, Zoonotic Emerging disease, mammal reservoir species

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Feeding ecology of Southern Ocean sea stars inferred from stable isotopes ratios of C, N and S

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The Southern Ocean undergoes strong and contrasted impacts of climate change. Increasing seawater temperature and sea ice cover reduction in Western Antarctic Peninsula and associated regions will likely impact food web structure and function. Sea stars (Echinoderms: Asteroidea) are an important group of the Southern Ocean benthos. They typically have highly variable feeding habits and are potentially more resistant than other organisms to temperature changes. Consequently, they will likely be impacted by modifications of the food web rather than by direct warming. Investigating their trophic ecology is therefore necessary to infer how climate change will impact them.

In this context, the aim of this study was to use stable isotopes ratios of C, N and S to infer sea stars trophic ecology. During austral summers 2006 and 2009, sea stars were sampled in Subantarctic and Antarctic locations, with most of the samples coming from South Shetland Islands and South Georgia. The isotopic niche (proxy of the trophic niche) associated to each sea star population was explored through SIBER (Stable Isotope Bayesian Ellipses in R) metrics.

Stable isotope ratios of sea stars were clearly different between South Shetland Islands and South Georgia. Sea stars of South Shetland Islands had smaller isotopic niches than sea stars of South Georgia. The overlap between the isotopic niches of sea star species was also important in South Shetland Islands, while isotopic niches of South Georgia were well separated. Difference of niche width and overlap between the two regions may be the result of different environmental conditions. In South Shetland Islands, sea star species may exploit a common benthic community relying on organic matter released during sea ice summer melting. In contrast, South Georgia is an oligotrophic environment with no sea ice. As resources are more limited, a higher trophic segregation between sea stars may appear to limit competition.

Ultimately, this project highlighted the importance of sea ice in the trophic ecology of Antarctic sea stars. Our results suggest that future reduction of sea ice extent in Western Antarctica may have deleterious effect on sea star populations.

keywords : sea stars, Southern Ocean, stable isotopes

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Nanoparticles: how safe are they? *Schmidtea mediterranea* as a model organism for toxicity assessment

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Up to now, the negative impact of the ever-increasing use of manufactured nanoscale materials is unclear. Although considered safe for prolonged internalization in cells, several studies indicate cytotoxic effects of different nanoparticles (NPs). On the subject of genotoxicity, carcinogenicity and stem-cell-related toxicity, conflicting results are reported. More research is needed, as stem cells are an important target in several applications of NPs. Our model organism, *Schmidtea mediterranea*, is a small invertebrate with an easy accessible population of totipotent stem cells. This makes it possible to study underlying mechanisms of nanoparticle toxicity on stem cells *in vivo*. We focus on the toxicity and biocompatibility of silver NPs (AgNPs) and silica NPs (SiNPs) on stem-cell-specific activities. Stem cells are an important target in several applications of AgNPs and SiNPs.

In our *in vivo* model system, we observed the uptake of AgNPs in stem cells via transmission electron microscopy. Stem cells responded by a proliferation decrease, measured via histon H3 immunostaining. We are currently looking into the underlying cause of this decrease, as the genotoxic character of this element is still under debate. Effects on cell cycle progression and differentiation were investigated by looking into the expression of the *smedwi-1* gene and corresponding protein levels, both exclusively present in stem cells and indicative for different phases of the cell cycle. At the phenotypic level, we observed concentration-dependent behavioural effects, including looper movements and curling. Exposure to a range of SiNPs concentrations showed no clear phenotypical or proliferation effects. This is a promising result for the further use of SiNPs, but extra research on the uptake and the effects of coating are needed for both NP types to confirm initial results.

Keywords: nanoparticles, toxicity, stem cells, planarians

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Osmotic responses to salinity and dehydration in the Sahara Desert's Blue-eyed Turtle, *Mauremys leprosa saharica* Firtz, 2006 (Testudines: Geoemydidae) from an isolated brackish pond in the Lower Draa basin, Southern Morocco.

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The peripheral populations of the Blue-eyed Pond Turtle, *Mauremys leprosa saharica*, in the southernmost species distribution range in the Lower Draa, Southern Morocco, are faced with extreme environmental conditions of arid climate and anthropogenic and climate change mediated water and land salinisation. In the present study, we investigated a small and isolated population of the Blue-eyed Pond turtle at Sidi El Mehdaoui oasis in the Lower Draa, in order to assess its osmoregulatory capacities and tolerance to salinity and dehydration. Upon in-situ captures, turtles were weighed and measured for shell morphometric characters and blood and voided urine were taken. Tests of exposure to salt water and maintenance out of water (aestivation simulation) were carried out. Osmolalities and osmolytes (Na^+ , Cl^- , K^+ , urea and glucose concentrations) in plasma and urine were determined. The turtles are not able to survive in brackish waters with salinity over 24‰ seawater; they depend on their water storage in the bladder which allows them to osmoregulate and ionoregulate till the isoosmotic level beyond which osmotic and ionic anhomeostasy (hyperosmolality, hypernatraemia, higher plasma urea and chloride levels) occurs. Osmoregulatory and ionoregulatory capacities in the Saharan Pond turtles are low and limited and do not allow them to survive for long term periods in salt water or out of water because of dehydration indicated by progressive weight loss to a critical threshold. The increased drought and water and land salinisation related to anthropogenic activities and climate change represent great threats to the long term persistence of the vulnerable marginal populations of the Saharan Pond turtle and their habitats. So conservation measures of these populations are particularly urgent.

keywords: Mauremys leprosa, Draa watershed, salinity, dehydration, osmoregulation

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On the jaws of lamniform sharks: explaining function through morphology

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Lamniform sharks vary widely in morphology and feeding niche, however, the functional morphology of their jaws is difficult to study due to the animals' large size, rarity and/or pelagic habit. To determine whether, and how, skeletal structure and performance vary with ecology, we created a custom analysis module for CT data to quantify aspects of structure of the jaw skeleton from all 15 members of the Lamniformes and two outgroup species. The module provides a customizable and slice-wise analysis of jaw structure, outputting several shape-based descriptors relating to skeletal function, such as the second moment of area, mineralized cross-sectional area, cortical wall thickness, and the anatomical orientation of each cross-section's major axis. These parameters help describe the contribution of jaw shape to skeletal bending and torsion resistance, while also localizing regions of reinforcement (e.g. higher wall thickness) and what is likely the predominant orientation of loading (based on the major axis around which material is distributed). Our results suggest diet-specific structural organization in the jaws, but also broad consistencies across the closely related lamniform species. The mineralized tissue of the jaws is arranged in such a way as to resist flexion ~5–20 times better than if it were a solid rod of similar length. The anterior tooth-bearing ends of both upper and lower jaws are rounder in cross-section implying higher torsion resistance, whereas the posterior ends (near the jaw joint and adductor muscle insertions) are extremely narrow, suggesting high, but anisotropic, resistance to flexion and a more uniform loading direction. These data suggest that skeletal geometry in sharks may be organized in predictable ways, as in bone, to resist dominant loading regimes. Furthermore, our CT data provide new anatomical insights, such as previously undescribed gaps in the mineralization layer near the joints at the posterior ends.

keywords: feeding apparatus, elasmobranchs, comparative anatomy

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Distribution and abundance of the Tanganyika introduced killifish, *Lamprichthys tanganicus* in Lake Kivu

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In African lakes, impacts of invasive species represent a serious threat leading to biodiversity loss and environmental change. In this study, some adaptation patterns of *Lamprichthys tanganicus*, an introduced fish species in Lake Kivu were investigated using trimaran lift net and experimental monofilament gillnets. The distribution and abundance of this fish were described.

L. tanganicus was largely frequent in the littoral zone, mainly in rocky substrates than in vegetated areas. This fish was more active in daytime than in night with two peaks: the first peak ranged from 08:00-10:00 hrs while the second was between 14:00-15:00 hrs. These diurnal activities and littoral distribution represent an important strategy for its survival by avoiding food competition with *Limnothrissa miodon* being active during the night and mostly occurring in the pelagic zone. Regarding distribution according to water depth, this species was mostly abundant in the first ten meters of water column and rarely beyond 10 m and absent over 20 m depth. *L. tanganicus* is the second fish abundant in the catch just after *L. miodon*, another introduced fish species, suggesting that *L. tanganicus* is now well established in Lake Kivu ten years after its first scientific record in the Lake. Important catch of the introduced *L. tanganicus* implies that this fish would play a socioeconomic role and food security for riparian in the future.

keywords : *Lamprichthys tanganicus*, introduced species, distribution, abundance, Lake Kivu

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Constructing a DNA barcode database of Belgian rove beetles (Staphylinidae) and its application in forensic cases

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Rove beetles (Coleoptera: Staphylinidae) are early-stage visitors to corpses, feeding on the fauna present in and on the corpse such as the eggs and larvae of flies. The rove beetle eggs are laid on the corpse and the emerging larvae can also be predatory. The duration of the development from the egg to the adult stage is specific for each species of rove beetle and can be used in forensics to estimate the post-mortem interval (PMI), i.e. the elapsed time between death and the moment of discovery. In addition, inferences about the potential displacement of the corpse or the manner and cause of death can also be made. Therefore, correct identification of all life stages is important for forensic investigators, allowing them to make a precise estimation of the PMI. Nevertheless, rearing the early life stages, which are morphologically uniform and indistinguishable, into adults is a risky and time consuming task. Several authors have already demonstrated that the species identification process can be enhanced using DNA barcodes, provided that an elaborate reference library is available. At present, however, forensically important species of Western Europe are not or only sparingly represented in public gene libraries (e.g. Genbank and BOLD). To alleviate this existing knowledge gap, the present project aims at constructing a Belgian reference library based on 134 morphologically identified specimens representing 48 species of rove beetles known to be often found on corpses. We focused on the DNA barcode 5' region of the mitochondrial cytochrome c oxidase subunit I gene (COI), the fragment internationally adopted as universal barcode fragment for animal identifications. Because the extracted DNA was fragmented due to the age of the samples, previously described internal primers were used to amplify smaller overlapping fragments. The sequences were aligned and consensus sequences were generated from these amplicons (388 bp and 403 bp long) for each species. The newly constructed library will be deposited in BOLD and in the forthcoming months its application will be evaluated by examining its capacity to identify unknown samples previously collected by the NICC in forensic cases.

Keywords: Staphylinidae, molecular identification, reference library, post-mortem interval

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Interspecific variation of warning calls in piranhas: a comparative analysis

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Fish sounds are known to be species-specific, possessing unique temporal and spectral features. We have recorded and compared sounds in eight piranha species to evaluate the potential role of acoustic communication as a driving force in clade diversification. All piranha species showed the same kind of sound-producing mechanism: sonic muscles originate on vertebrae and attach to a tendon surrounding the bladder ventrally. Contractions of the sound-producing muscles force swimbladder vibration and dictate the fundamental frequency. It results the calling features of the eight piranha species logically share many common characteristics. In all the species, the calls are harmonic sounds composed of multiple continuous cycles. However, the sounds of *Serrasalmus elongatus* (higher number of cycles and high fundamental frequency) and *S. manuel* (long cycle periods and low fundamental frequency) are clearly distinguishable from the other species. The sonic mechanism being largely conserved throughout piranha evolution, acoustic communication can hardly be considered as the main driving force in the diversification process. However, sounds of some species are clearly distinguishable despite the short space for variations supporting the need for specific communication. Behavioural studies are needed to clearly understand the eventual role of the calls during spawning events.

keywords: Bioacoustics, Morphology, Serrasalminidae

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Nano-injection in the zebrafish embryo as an alternative exposure route for environmental risk assessment of endocrine disrupting pharmaceuticals

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Pharmaceutical companies are required to perform an environmental risk assessment for every drug that is launched on the market. The mandatory tests for potential endocrine disrupting (ED) compounds require a lot of time and laboratory animals, which is not consistent with the 3R principle. Therefore, the goal of this study is to develop a zebrafish embryo test, which is not considered an animal test according to European regulations. However, it is often difficult to expose fish aquatically to ED pharmaceuticals because of their lipophilicity. Nano-injection is therefore proposed as an alternative exposure route because the yolk of zebrafish embryos contains many lipids and it mimics maternal transfer. To use nano-injection as an alternative exposure route it needs to be characterised and compared to the classical exposure route via water. As a case-study 5 ED pharmaceuticals with each a different mode of action (MoA) were chosen (i.e., estrogen receptor (ER) agonism and antagonism, androgen receptor (AR) agonism and antagonism and aromatase inhibition).

Zebrafish embryos were injected with 0.5 nl of one of the pharmaceuticals or with dimethyl sulfoxide (vehicle control). After injection, the embryos were monitored until 120 hours post fertilization. Using a profile based on multiple biological responses both exposure routes were compared.

Transgenic (5xERE-GFP, obtained from the Carnegie Institution of Washington) exposed embryos gave a significantly higher fluorescent signal compared to controls and with a comparable order of magnitude between both routes, indicating that 17 α -ethinylestradiol (ER agonist) was still active 5 days after injection. Nano-injection or aquatic exposure also caused morphological and physiological effects after exposure to 17 α -ethinylestradiol (ER agonist) or to 17 β -trenbolone (AR agonist). This was the case for both routes but the effects were different. After exposure to fulvestrant (ER antagonist) or flutamide (AR antagonist) only mortality or no effects at all were observed. Letrozole (aromatase inhibitor) only caused physiological effects for both routes.

Nano-injection can be used as an alternative exposure route because effects were detectable and pharmaceuticals were still active after 5 days. In general, the effects caused by the pharmaceuticals were comparable between both exposure routes but detailed effects were different.

Keywords: zebrafish embryo, endocrine disruption, pharmaceuticals, nano-injection

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A phylogeny for Schizorhynchia: Molecules must guide morphology

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In recent years, the phylogenetic relationships of Rhabdozoa, the most species rich taxon of free-living flatworms, have been studied rather intensively. Many subtaxa, however, still are underrepresented in these studies, one of them being Schizorhynchia. Schizorhynchia is a morphologically-diverse, monophyletic group belonging to Kalyptorhynchia, rhabdozoans with a true proboscis. The 144 species described typically occur commonly in marine sandy habitats, but hardly anything is known as to phylogenetic relationships and the evolution of morphological traits within this group. Indeed, the most-recently-published phylogenetic analysis of Kalyptorhynchia already showed that the traditional classification of schizorhynchids is no accurate representation of the evolutionary relationships within this taxon.

The aim of this study, therefore, is to analyse the phylogenetic relationships within Schizorhynchia based on molecular markers, which then are used as a backbone to trace the evolutionary history of certain morphological traits, especially those related to proboscis and copulatory organs. Phylogenetic relationships are analysed through a Bayesian and Maximum Likelihood approach, using 18S and 28S rDNA sequences, the same markers which have been used in previous evolutionary studies of rhabdozoans. Based upon these results, the value of several morphological traits as taxonomical markers is assessed. Differential interference contrast microscopy (DIC) and confocal laser fluorescence microscopy are used to study these traits, the ancestral state of which is then reconstructed in BayesTraits. Finally, a revision of the taxonomy of Schizorhynchia is presented and several new species are described and discussed.

Keywords: marine microturbellarians, taxonomy, phylogeny, ancestral state reconstruction

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Female behaviour and mate choice prior to additional sperm receipt in the hermaphroditic snail *Lymnaea stagnalis*

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Reception of seminal fluid affects the reproductive physiology in many animals. For the great pond snail *Lymnaea stagnalis*, we expect that at the behavioural level will become more reluctant to mate as a female after receipt of seminal fluid. Therefore, in this study we aim to provide evidence for the hypothesis that repeated inseminations (i.e. receiving multiple ejaculates) influence sexual behaviour in these simultaneously hermaphroditic snails. To test this, we created two different treatment groups using mature, non-virgin snails. One treatment group was composed of individuals that were all inseminated once (by an 8-days isolated individual) one day before the observation experiment, these are referred to as the inseminated treatment. The other, control group consisted of individuals that were not given a mating partner one day before the actual experiment, these are referred to as the non-inseminated treatment (not under the influence of a previous insemination). On the experimental day, the treatment snails were paired up with a partner that was isolated for 8 days. The female behaviour of the focal individuals was observed continuously for six hours or until both snails mated as male and female. During the experimental observation period we recorded candidate behaviours that were considered to reflect refusal or eagerness to mate in a sexual role by the animal (male or female). Statistical analysis of the data showed no significant difference in sexual role preference between the treatment groups. Nevertheless, we did find significant differences in a number of other behavioural components. Most importantly, we found that the occurrence of active defense behaviours (biting and/or attempting to overthrow the sexual role) and passive defense behaviours (floating, hiding in the shell and crawling out of the water) of the focal individuals were higher in the inseminated treatment group compared to the non-inseminated treatment group. These findings show that individuals of *Lymnaea stagnalis* that are under the influence of previously received seminal fluid try to actively avoid being inseminated again by discouraging partners that mount their shells. These findings are in line with work on other species where remating avoidance is influenced by received seminal fluid products.

Keywords : Lymnaea stagnalis, seminal fluid, sexual conflict, reproductive strategy

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Using an RNA-seq approach to investigate the effects of anticoagulants rodenticides in bobcats (*Lynx rufus*) of the Santa Monica Mountains (CA, USA)

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Anti-coagulant rodenticides (ARs) are the primary chemical control method employed to suppress rodent populations worldwide. AR exposure, however, poses a major conservation threat to wild populations, especially carnivores and raptors for which rodents are a staple food item. While direct mortality from secondary exposure is the most well documented concern for wild populations, chronic, sub-lethal exposure can also negatively impact individuals, with concomitant population level impacts where exposure is pervasive. For example, a demonstrated link between AR exposure and mange susceptibility in bobcats is hypothesized to have resulted from severe immune dysregulation caused by AR exposure, driving a genetic bottleneck in a local population. To determine the molecular mechanisms underlying this observation, we conducted RNA-seq analyses on whole blood samples from free-ranging bobcats captured in the Santa Monica Mountains, for which AR exposure was ($n = 26$) and was not ($n = 26$) detected in whole blood. We used a linear mixed model to assess the effect of exposure on genome-wide expression in whole blood while controlling for technical effects. Additionally, we performed a transcript origin analysis (TOA) to infer the specific cellular mediator of AR effects. Our results show that AR exposure is associated with an overall decrease in transcripts associated with monocytes (particularly immature Ly6c-high/CD16-monocytes) and naive B cells, and increase in transcripts associated with memory B-cell lymphocytes. Our results suggest that chronic AR exposure alters both innate and adaptive immune capabilities, limiting the ability of the animal to mount an appropriate immune response against infections, leading eventually to death. Therefore, ARs may pose a substantial threat to small populations facing additional threats such as disease. We hope that a more thorough understanding of the molecular mechanisms involved in such lethal effects will aid in the reformulation of better methods of rodent control that do not threaten non target wildlife. To our knowledge this RNA-seq study is one of the first that investigate the effect of rodenticides in wild life animals using a non-invasive method and may set an important precedent in future research by demonstrating the utility of RNA-seq to study non-model species.

Keywords: conservation, anticoagulant rodenticides, bobcats, RNA-seq

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Impact of learning under sexual selection on the survival of species in a context of climate change

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The role of learning in mate choice has not yet been assessed in ecologically-relevant environments such as those induced by climate change. Here we test whether learning of mate preference may lead to unsuitable mate choice and risk of population extinction. Mate choice in the tropical butterfly *Bicyclus anynana* was shown to be modified by learning, namely by exposure during sexual maturation to males with distinct (artificial) phenotypic traits. In nature, *B. anynana* displays seasonal polyphenism with alternated wet, intermediate and dry seasonal forms adapted to tropical Africa. *B. anynana* development switches to wet or dry forms depending on late developmental temperature, and female fitness depends on mating with either forms. Here we showed that: 1) increasing unpredictability of climate during seasonal transitions alters the relative proportions of seasonal forms; 2) females learn mate preference based on ecologically relevant, polyphenic male secondary sexual traits; specifically, females show an innate mate preference for dry seasonal males but this preference is suppressed by exposure to either wet or intermediate seasonal forms during female sexual maturation. Our results suggest that, if learning of female mate preference is based on the most abundant male phenotype present in the environment during sexual maturation, learning mate preference could become maladaptive for the species as a response to global warming.

Keywords : learning, climate change, sexual selection, mate choice, non social insect

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A phylogenetic perspective on the evolution of ecological traits, trans-oceanic dispersal and the diversification of crocodiles

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Crocodiles are often portrayed as living fossils from the dinosaur age, but most extant species belong to the so-called true crocodiles (*Crocodylus*), a clade that diversified only in the Oligocene and Miocene. The diversification was associated with a range expansion of the genus, likely from the the Indo-Pacific, giving rise to its current circumtropical distribution. Interestingly, *Crocodylus* diversification occurred during a period of extinction in other crocodylians, resulting in contrasting paucity of the other extant crocodile genera. To investigate how the ancestor of extant *Crocodylus* species dispersed throughout the tropics, we integrated data on the present-day ecology of crocodiles with their evolutionary history and historical biogeography. We first used Bayesian analyses to reconstruct the biogeographic history of crocodiles. Next, we reconstructed multiple ecologically relevant traits that potentially promoted range expansion and correlated them with current large distribution ranges as a proxy for dispersal ability. The combination of these traits was then used to phylogenetically estimate range-expansion abilities on the crocodile evolutionary history. Our results show that the evolution towards an optimal range-expansion phenotype was linked with trans-oceanic dispersal events and that range expansion in turn drove the diversification of *Crocodylus* in the Miocene.

Keywords : crocodiles, historical biogeography, range expansion, dispersal

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Environmental distribution and bioaccumulation of POPs and Hg in temperate and Mediterranean river ecosystems

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The present study aimed to investigate the environmental distribution and the bioaccumulation of several Persistent Organic Pollutants (POPs: (PCBs, PBDEs, DDTs, HCHs, CHLs and HCB) and mercury (Hg) in water, sediment and biota samples from a temperate river system in Belgium and three Mediterranean river systems in Greece. Nitrogen stable isotopes were used to evaluate the bioaccumulation and trophic transfer of the detected contaminants between temperate and Mediterranean food webs and Trophic Magnification Factors (TMFs) were used to investigate the biomagnification of POPs and Hg in the trophic food webs. Finally in order to assess the potential human risk due to the consumption of contaminated fish, Minimal Risk Levels (MRLs), were applied. Overall, Hg concentrations in water and sediment were relatively low compared to high contaminated areas around the world and on the same order of magnitude as global mean values for unpolluted rivers. The highest Hg levels in sediments were detected in Demer (Belgium) (0.29 $\mu\text{g/g dw}$) and in Potami (Greece) (0.27 $\mu\text{g/g dw}$). In regards to biota samples, the highest levels were found in freshwater shrimp *Atyaephyra thyamensis* (0.21 $\mu\text{g/g ww}$), whereas concentrations for other species were almost at the same levels. Hg in fish samples were low compared to other studies with the exception of high levels detected in muscle of *Gobio gobio* (0.24 $\mu\text{g/g ww}$) sampled in Demer. Concerning POPs, almost every analysed compound was detected in samples from Demer, with PCBs, PBDEs, HCHs and DDX dominating in the overall profile, and with the former consisting the most dominant measured compounds in Greece. Trophic transfer of several PCB compounds, chlordanes, DDX and PBDEs were observed in Demer, while only Hg, CB 153, CB 138 and p,p-DDE were transferred in Greek rivers. Moreover, CB 153 and CB 138 were found to undergo higher biomagnification in Demer than in all of the Greek rivers. Finally, the consumption of fish from the studied rivers were found to be safe for most of the measured pollutants but some caution should be taken in regards to PCBs, DDX, Hg and γ -HCH ingestion.

Keywords: Persistent Organic Pollutants, Mercury, Bioaccumulation, Trophic Magnification Factors, Minimal Risk Levels

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JPIOceans: Assessing the ecological impact of deep-sea mining on Crustacea.

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The deep-sea represents the largest ecosystem on the planet, yet our knowledge of deep-sea fauna (<4000m) remains limited. Here, we study and compare the impact of mining of ferro-manganese nodules on deep-sea crustaceans in two oceanic basins; (1) the Clarion-Clipperton Fracture Zone (CCFZ) in the NE Pacific and (2) the Disturbance and Recolonisation (DisCOL) Experimental Area (DEA) in the SE Pacific. More than 60,000 specimens of Amphipoda were collected from the CCFZ and DEA using baited traps and an epibenthic sledge on the RV Sonne in 2015. These have been morphologically sorted and 27 species have been identified thus far, including some undescribed species. *Paralicella caperesca* and *Abyssorchomene gerulicorbis* are two target species which were selected for genetic analysis of connectivity and dispersal potential within and between these two basins. Subsequent to DNA extraction and PCR amplification, the first COI results from 200 sequences are presented, showing evidence of cryptic diversity in *P. caperesca* at a local scale as well as connectivity over vast geographical scales. Our future aims are to use next generation RAD-tag sequencing with a much finer resolution to further contribute to the delimitation of the species within this diverse deep-sea group, and to test for population connectivity at smaller spatial scales.

Keywords: *Amphipoda*, *deep-sea*, *cryptic species*, *connectivity*, *dispersal*

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Ontogeny of steroid hormone metabolism gene transcription during embryonal larval development of the zebrafish

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Zebrafish is widely accepted as an ideal model for studying vertebrate development and impairment of normal development. Early life stages of the zebrafish have been well described morphologically, but little is known about the role of the endocrine system in early development. Although some studies have shown that hormones are involved in various stages of development, available information is still limited.

In this study we described the transcriptional dynamics of key genes involved in the steroid hormone system during normal zebrafish development, which has never been done so far. We isolated RNA at 25 time points between 0 and 32 days of development. We selected genes coding for the key enzymes involved in steroid hormones biosynthesis (*cyp11a1*, *cyp11a2*, *cyp17a1*, *cyp11c1*, *cyp19a1a*, *cyp19a1b*, *hsd17b3*, *hsd11b2* and *hsd17b*), the estrogen and androgen receptors (*esr1*, *esr2a*, *esr2b*, *gper* and *ar*), enzymes involved in cholesterol biosynthesis (*hmgcr α* , *hmgcr β*) and vitellogenin (*vtg1*), a widely used biomarker for toxicological experiments. mRNA levels of these genes were measured using QPCR.

Our results show that some genes, like *hsd17b3*, *esr2a* and *ar*, are maternally transferred. This suggests an important role of steroid hormones in programming the earliest stages of zebrafish development before the embryo's genome is activated around 3hpf. Further, we observed that the nuclear estrogen receptors have very different transcriptional patterns during development. Around the time of embryonic genome activation, *esr1* is abundantly transcribed by the embryo itself and the level of transcription remains high during the entire larval period. After the first day, transcription of *esr2b* gradually increases and peaks during the formation of the immature gonad (around day 10). Interestingly, transcription of the enzyme *hsd17b3*, which is important to both estrogen and androgen synthesis, shows an early peak, suggesting that *hsd17b3* may be essential to steroid synthesis during early development. During the formation of the immature gonad, transcription of brain aromatase *cyp19a1b* and *esr2a* increases, and during gonad differentiation both genes are abundantly transcribed. These results will improve our fundamental understanding of how steroid hormones contribute to the coordination of embryonic and larval development and will be broadly applicable to the zebrafish research community.

keywords: zebrafish early life stages, steroid hormone system, enzymes, receptors, gene transcription

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Relationships between environmental parameters and the microbenthic loop of *Posidonia oceanica* meadows at small spatial scale

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In these times of global change, understanding how carbon flows through ecosystems is of primary importance. In coastal Mediterranean regions, *Posidonia oceanica* meadows produce and store a lot of carbon, but most of it is described as refractory. As a step in the understanding of how organic matter degradation/storage happens in this ecosystem, this study focus on small scale relationships between the microbenthic loop (organic matter, microphytobenthos, bacteria and meiofauna) and environmental parameters (grain size, *P. oceanica* density, vegetal fibre biomass, pore water nutrient content, sediment total carbon (TC), organic carbon (TOC), nitrogen (TN) and phosphorous (TP) contents, phaeopigments and bacterial production (FDC)). Thus, a 1.25 m x 1.25 m frame was put in a pristine *P. oceanica* meadow and twelve points were randomly sampled in May 2008 for all the studied parameters.

At such a small scale, every component of the microbenthic loop presented a heterogeneity, which was the highest for the microphytobenthos biomass and the lowest for total meiofauna abundance (TMA). No relationship was found between the components of the microbenthic loop but the abundances of Turbellaria and Ciliophora were correlated with total organic matter in the sediment (TOM). None of the environmental parameter was linked with the microphytobenthos biomass, suggesting that the high spatial variability observed did not depend on the measured parameters. Relationships were found between TOM and ammonium, total bacteria abundance and biomass (TBA and TBB) and sediment phaeopigments, TMA and TC, TN and TP. TBB variability was however explained by a combination of FDC and nutrient contents in pore water and sediment.

Taking the microbenthic loop as a whole, pore water ammonium and nitrites + nitrates, FDC and phaeopigments were able to explain the observed variability. So, at small scale the variability in the microbenthic loop of a *P. oceanica* meadow is related with parameters linked with degradation processes and bacteria activities (phaeopigments, FDC, ammonium, nitrites + nitrates), except for meiofauna, which is related with the nutrient content of the sediment, especially TC. Those results underline the importance of the relationship between the microbenthic loop and degradation processes, even at a small scale.

Keyword: sediment, microbenthic loop, organic matter, seagrass, degradation

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A new model species for long-term toxicity testing: Acute and chronic sensitivity of *Nothobranchius furzeri* to copper and cadmium.

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Nothobranchius furzeri offers a great potential to perform time- and cost-efficient long-term and multigenerational ecotoxicological studies. With a full life cycle of 10-12 weeks on average, compared to other fish-model species (zebrafish 14-22 weeks, medaka 22-29 weeks, fathead minnow 22-43 weeks) and the production of drought resistant dormant eggs that can be stored, overcoming the need and costs of a continuous culture and allowing for a simultaneous hatching of eggs, it is a promising ecotoxicological model. In this presentation, two short and long-term experiments of metal exposure will be put forward as an initial assessment.

The sensitivity of *N. furzeri* to copper ($\text{Cu}(\text{NO}_3)_2 \cdot 3\text{H}_2\text{O}$) and cadmium (CdCl_2) was assessed in an acute and chronic toxicity test. In these experiments, fish were exposed to a range of metal concentrations, starting from 48h after hatching. In the acute exposure, mortality was scored to quantify LC_{50} values during a period of 14 days. The chronic sensitivity to copper and cadmium was measured using effects on life history traits and bio-accumulation. Additionally, we assessed the effect of temperature (+4°C) on cadmium sensitivity and complemented this test with a CT_{max} measure. To assess transgenerational effects, we tested acute sensitivity to cadmium of the offspring of cadmium exposed fish (F1) by means of an LT_{50} measure.

Results of both acute toxicity tests demonstrate an overlap in sensitivity range with that of current fish models in ecotoxicology. In addition, acute cadmium exposure was more toxic at a higher temperature. Long-term exposure to copper significantly inhibited growth and increased maturation time. However, fish also seemed to conform to the copper environment by altering their bio-accumulation. The chronic exposure to cadmium and increased temperature showed a higher mortality when stressors were combined. Effects on other endpoints mainly revealed patterns of acclimatisation to higher temperatures. However, indicative of transgenerational effects, offspring of cadmium exposed fish were more sensitive to acute exposure than their parents.

Overall, these results show that with its unique trait-set and similar toxicant-sensitivity to conventional fish models, *N. furzeri* could rapidly be developed as a valuable ecotoxicological model for chronic and multigenerational toxicity testing.

Keywords: Ecotoxicology, long-term exposure, multiple stressors, transgenerational effects

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Exploitation of coastal fish communities by female and juvenile harbour porpoises *Phocoena phocoena* during nursing periods in German Baltic waters.

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Baltic sub-populations of harbour porpoises *Phocoena phocoena* meet in in Southwestern waters in Spring when females reach the coastal areas for calving and nursing. In Autumn they separate again for reproduction : the Belt sea populations westwards in the Kattegat/Skarregat region, the Baltic proper population northwards in the central basin. The increased number of juvenile and newborn strandings along the German Baltic coasts give evidence for a possible existence of local calving grounds in this area. Calving and nursing habitats are the most important areas for management purposes.

This project aimed to describe inhabitancy and diet of females and calves along the German Baltic coast, in order to achieve effective conservation measures. Nitrogen, carbon and, for the first time, sulphur stable isotopes ($\delta^{13}\text{C}$, $\delta^{15}\text{N}$ and $\delta^{34}\text{S}$) were analysed in coastal species of fish and invertebrates in spring, autumn and winter 2015/2016 and in four different areas, to assess for seasonal and geographical variation of porpoises habitat use. The structure of ecological niches was inferred within and between communities using the SIBER model, and was compared to results from stomach content analysis.

N, C and S values of fish and invertebrates strongly varied, seasonally and geographically, as a consequence of environmental factors characteristic of each sampling area. Additionally, each species presented large isotopic variability, suggesting possible intraspecific dietary specialisations. Females $\delta^{13}\text{C}$ and $\delta^{34}\text{S}$ signatures integrated both open-waters and coastal feeding, while juveniles presented a more coastal distribution. The absence of difference in $\delta^{15}\text{N}$ values between age classes confirmed persistence of milk assimilation from the mothers. Niches structures and overlaps and stomach content analysis suggested gobies (*Potamoschistus* spp and *Neogobius* spp in particular), crabs and small coastal fish (ex. three-spined stickleback) as the main preys of juveniles. The integration of all three stable isotopes together permitted to well delineate even the highly dynamic food web of the Baltic German waters, confirming the use of sulphur isotopes in marine ecological studies.

keywords : harbour porpoise, Baltic sea, food web, stable isotopes, diet

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Early life exposure to artificial light at night affects the physiological condition: An experimental study on the ecophysiology of free-living nestling songbirds

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Light pollution or artificial light at night (ALAN) is an increasingly important anthropogenic environmental pressure on wildlife, affecting animal behaviour and physiology. Since early life experiences produce effects that can persist throughout life, light exposure during development may have profound effects. Here, we experimentally investigated for the first time the impact of ALAN on body mass, and other important physiological indicators of immunity, health, and physiological condition, using nestlings of a free-living songbird, the great tit (*Parus major*). Body mass, haptoglobin, nitric oxide and multiple metrics of both oxidative damage and antioxidant defences were determined at baseline (13 days after hatching) and again after a two night exposure to ALAN. Light exposed nestlings showed no increase in body mass, in contrast to unexposed individuals. Furthermore, ALAN increased haptoglobin while decreasing nitric oxide. There were no effects on any of the oxidative status parameters. Our study provides rare experimental field evidence that ALAN negatively affects free-living nestlings' development, which could have adverse consequences lasting throughout adulthood.

Keywords : Artificial light at night, Light pollution, Physiology, Development, Early-life

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Who would want to live in there? A history of *Posidonia oceanica* detritus accumulations, the associated invertebrate community, and its food web.

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Most seagrasses are rarely consumed directly by herbivore organisms. The "detrital pathway" thus represents a potentially important way of transfer of the seagrasses production to the coastal food webs. The case of *Posidonia oceanica* is particularly interesting since up to 90% of its foliar primary production may constitute extensive and highly dynamic exported litter accumulations. Preliminary studies concerning these detritus accumulations suggest that an abundant community of vagile macro invertebrates (size > 500µm) lives inside them. We characterized for the first time this community in an exhaustive way (multi-site, seasonal and multi-year study), we linked the observed density and diversity variations to environmental parameters, but also described the trophic web these invertebrates compose.

We sampled an abundant (up to 5000 organisms/m²) community composed of 115 species. We showed that crustaceans were massively dominant, followed by annelids and mollusks, and that one single amphipod species *Gammarella fucicola* represented from 20 to 85% of the whole sampled community. Observed variations appeared to be mostly linked to litter oxygen water concentration in a very species specific way. Most species were linked to no measured environmental parameter at all, but several dominant species were demonstrated (observation and *in situ* experimentation) to be linked positively or negatively to litter oxygen concentration.

The described food web was composed of more than 3 trophic levels, indicating the presence of a trophic web composed of primary consumers/detritivore species, of omnivore species, but also of first and second order predators, each level occupying a distinct isotopic niche. From a specific point of view, we highlighted several different feeding preferences, with SIAR mixing model runs indicating that some species feed mostly on detrital material, other species feed on a mixture of detrital and algal material, other species feed on both animal and vegetal material and finally predator species feed exclusively on animal material. The fact that *P. oceanica* detritus constituted a non-negligible food source for some dominant species confirmed the importance of this macrofauna community as a key transfer link of seagrass organic matter from *P. oceanica* to the coastal food webs.

Keywords: Posidonia oceanica, Stable isotope, Food web, Macrophytodetritus, Macrofauna

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Female macaques wear the trousers: female fights and female initiated friendships determine immigrant male sexual access

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Consistent with the sexual selection theory, dominant males in multi-male multi-female macaque groups have higher sexual access than subordinates. Moreover, males can build friendship with females or use coercion as alternative mating strategies. Females seem to prefer particular males, but do not compete for sexual access. However, female competition over mating partners may be enhanced when a new male enters a group, due to a high female interest in mating with the immigrant male. What determines male sexual access in these socially instable situations remains unclear. Therefore, female and immigrant male mating strategies were studied during the introductions of four adult male rhesus macaques (*Macaca mulatta*) – each into a different social group. All four males were successfully introduced into their respective new group and obtained the alpha position. No evidence was found for male coercion of females, or for a role of the alpha male position in sexual access. Moreover, immigrant male to female grooming was rare and did not result in increased sexual access. In contrast, sexually interested females did fight with other females over sexual access. Additionally, there was a long-term exchange of female to immigrant male grooming and sex, indicating female initiated friendships. To conclude, no evidence was found for the use of any mating strategies by immigrant males. In contrast, females competed with other females and built friendships with males to gain sexual access. These results are the opposite of patterns found in socially stable situations, and show the presence of sexual competition in females. Contrary to the common belief, it is not the immigrant male, but the resident females that determine to whom the male has sexual access. Thus, females macaques wear the trousers and should not be overlooked by solely focussing on the immigrant male during an introduction.

Keywords : Sexual competition, male introduction, female-female competition, friendships, macaques

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Phylogeography of *Strandesia* ostracods from four major Brazilian floodplains

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Besides their generally large size, South American floodplains are special in that they hold a variety of (indigenous) floating aquatic plants, where the root systems can host a complex ecosystem of invertebrate communities (including ostracods) called pleuston. *Eichhornia crassipes* (Mart.) is one of the most common species in these floodplains, and is also one of the most persistent invasive species in (sub-) tropical regions outside of the Neotropics. Studying the distribution of non-marine ostracods within the alluvial valley of the Upper Paraná River has revealed a large potential for dispersal within this floodplain. Here, we study the potential of non-marine ostracods for past and present long-distance dispersal at a (sub-) continental scale of more than 2300 km. Using DNA sequence data from the mitochondrial COI and nuclear Elongation Factor genes, we investigate the genetic connectivity and relationships of four morpho-species and 13 cryptic species in the ostracod genus *Strandesia* Stuhlmann, 1888, forming a species clusters (Higuti et al., 2013) in four large Brazilian floodplains. We also analyse the phylogeographic and evolutionary history of dispersal and vicariance events that might have led to the origin and present-day distribution of these lineages. Applying a universal COI molecular clock in a Bayesian approach, we provide preliminary age estimates of the evolution of this species cluster and try to correlate these to the hydrological history of the studied floodplains.

Keywords: *Ostracods; phylogeography; flood plains; barcoding; phylogeny*

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Immunity, inflammation, and stress in a long-lived seabird facing a severe herpesvirus disease

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An organism's physiological equilibrium is critically reliant on its immune system, which provides protection against parasites and pathogens. There are, however, circumstances under which the immune system is disrupted, making organisms more susceptible to infections. For example, environmental stressors are well known to stimulate the release of corticosteroids, which may reduce immunocompetence. Herpesviruses are one of the most common infectious agents in wild animals. Some clinical studies have suggested that oxidative stress might be one additional physiological mechanism that promotes herpesvirus reactivation from latency. However, the relationship between oxidative stress and herpesvirus infection has never been addressed in wild animals, nor have the effects of herpesvirus outbreaks on the physiology and survival of wild animals been tested so far. The aims of this study are to provide the first data on oxidative stress, inflammation and immunocompetence in a wild animal and to discuss the potential of markers as predictors of the progress of the infection and survival perspectives. To this end, we took advantage of a population of Magnificent frigatebirds *Fregata magnificens*, a large tropical seabird breeding in French Guiana, which experiences annually severe herpesvirus outbreaks that cause up to 80-90% mortality of chicks.

keywords: herpesvirus, oxidative stress, inflammation, immunity, disease

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Acid-base balance and ion regulation in spotted ratfish *Hydrolagus colliei* during hypercapnia

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This study was aimed at investigating the net acid–base flux, nitrogenous waste excretion (ammonia and urea) and ion-regulation in marine water spotted ratfish *Hydrolagus colliei* mediated by hypercapnia. Fish were exposed to 1.5% pCO₂ (~15,000 ppm) for a period of 0 h (control), 4 h, 12h, 24 h and 48 h. Extracellular and intracellular pH, plasma pCO₂, bicarbonate concentration, ion status as well as the net flux of acid (H⁺), ammonia and urea were determined under the experimentation period. Results show that hypercapnia induced a drastic reduction in intracellular pH (RBC) after 4 h of exposure and thereafter values restored to control level. pH of hepatic tissue remained strictly regulated within the control level. On the contrary, respiratory acidosis resulted in blood pH depression. Blood pH subsided relative to the control throughout the hypercapnia exposure, and was momentarily compensated by an increase in plasma [HCO₃⁻]. In addition, these reductions in blood pH were complemented by a parallel increment in plasma TCO₂ level. Ammonia and urea excretion rate remained virtually unchanged during hypercapnia. Likewise, ion-homeostasis was maintained during hypercapnic episodes as no remarkable changes for Na⁺ and Cl⁻ ion levels in plasma were recorded. A slight and temporary increment for net H⁺ flux rate was observed. Overall, the present findings suggest that under hypercapnia spotted rat fish prioritize intracellular blood pH homeostasis over extracellular blood pH, and compensated by bicarbonate taken up from the environmental seawater. Furthermore, since the ammonia excretion rate was not increased during hypercapnia and the plasma electrolyte (Na⁺ and Cl⁻) concentrations remained static, we suggest that these scenarios do not favour the Na⁺/H⁺ ion exchange mechanism. In brief, it can be concluded that the additional bicarbonate gained might be a consequence of active HCO₃⁻/Cl⁻ ion exchange against the electrochemical gradient between the fish and the seawater.

keywords: Acid–base, Hypercapnia, Ammonia, Urea, Ion regulation, Proton flux

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Biodiversity conservation in a political instability: threats, challenges and perspectives

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The Albertine rift is considered as a region with high endemism and high biodiversity. However, the region is one of the most affected by political instability. The political instability in Burundi and neighbouring countries, coupled with high population density has had a negative impact on biodiversity conservation. Studies have shown that in a political crisis, factors such as poor governance, uncontrolled use of natural resources by displaced people, undermining conservation projects by security priorities and inaccessibility to protected areas for managers are linked to threat of biodiversity loss and limiting success of conservation projects. In addition, lack of fund for conservation and poverty combating projects may result in an increase in illegal exploitation of natural resources such as illegal logging and hunting of wildlife for bush meat. Thus, from 1995, Burundi has lost approximately 32,000 ha of its forests including 5000 ha of forests from protected areas whereas the Rusizi National Park, the most affected and sharing border with Democratic Republic of Congo, has lost more than 50% of its savanna mainly converted into crop land. Recently, four hippopotamuses were killed in one month in this park. Increased deforestation may have a devastating impact on the country's wildlife. There is a need for strategies to overcome biodiversity loss in such political instability. Despite the challenges, one can be optimistic as local communities have been involved and understood their role in protected areas management. In case of limited resources for park managers and political instability, community support is critical. Support from donors for conservation mechanisms implementation should continue and partnership with civil society reinforced for efficient conservation and birth control projects.

keywords: Biodiversity conservation, Burundi, DR Congo, Protected areas, Political instability

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Impact of mangrove forest management on birds: field assessment & reflections on ecological functionality

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Matang Mangrove Forest Reserve in Malaysia, is often presented as the ‘most sustainably managed mangrove in the world’. However, the impact of extractive silvicultural practices on biodiversity and ecological functionality is vastly under-researched. In 2015, we conducted a rapid biodiversity assessment and a forest structure characterisation, in undisturbed protective areas and in managed mangrove stands of varying ages following extractive disturbance.

We assessed the diversity and composition of bird assemblages, and we compared the response of individual bird species and dietary guilds to the forest management scheme. Analysis of forest structure in protective mangrove stands show structural development which cannot be found in managed stands. Undisturbed forest are floristically and structurally complex and diverse, and more functional as they provide essential habitat and consequently support more diverse and specialised bird communities, which suggest higher habitat quality. Current silvicultural practices in Matang convert forest to even-aged monospecific stands, disturbed by subsequent thinning activities and eventual clear-felling. Our results show and assess how these practices negatively impact the avifaunal community. Managed stands support bird communities that are drastically reduced in terms of species richness and abundance. Based on these results, we conclude that disturbed monospecific mangrove plantations exhibit a lower ecological functionality for resident forest bird communities due to habitat degradation. Moreover, response to disturbance varied between species and within and between feeding guilds, where adverse effects are especially manifested in functionally specialised species. This has important implications for the functioning of managed forest fragments. Although reduced abundance and richness do not necessarily result in an immediate decline in ecosystem processes, the changes in community composition are likely to disrupt biotic processes, and therefore ecosystem resilience in the long-term. Our findings indicate that bird communities are useful ecological indicators of habitat quality. Furthermore, our findings emphasise the crucial role of habitat and landscape heterogeneity for supporting diverse avian communities and maintaining the ecological functionality of the ecosystem, especially in intensively managed mangrove forests where faunal populations are under continual anthropogenic pressure.

Keywords: mangrove, forest management, birds, ecological functionality, conservation

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Resolving the shallow population structure of the African Lion (*Panthera leo*) in Tanzania through genomics

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The African lion (*Panthera leo*) is listed as “vulnerable” by the IUCN Red List. The species is mainly threatened by indiscriminate killing, primarily as a result of retaliatory or pre-emptive killing to protect human life and livestock, and by prey base depletion. In addition, habitat loss and its conversion into farmland have led to a number of subpopulations becoming small and isolated. As a consequence of the weakened connectivity between the main strongholds, genetic drift and loss of genetic diversity could affect the long-term survival of the species. In the present study, we investigated the evolutionary history of *P. leo* at different temporal and spatial scales. A total of 182 individuals were used, 77 of which came from Tanzanian protected areas. The mitochondrial cytochrome b gene was sequenced and the specimens were genotyped for 11 microsatellites and more than 9,000 SNPs through the Genotyping by Sequencing methodology. Results indicate that the African lion is structured into two lineages at the continental scale (West-Central vs South-Eastern), a pattern observed within many other large savanna species displaying large distribution ranges. Pleistocene climatic oscillations and biogeographical barriers were proposed as the main factors to have driven the lineage sorting. The SNPs in addition, allowed for the identification of 3 lion populations in Tanzania (STRUCTURE), geographically structured between the North, South and West-Southern regions. Overall, the Tanzanian populations displayed good levels of genetic diversity with limited signs of inbreeding, while their effective population sizes were shown to have been decreasing over the last 70 generations. Since the uncovered population structure did not seem to emerge from isolation-by-distance (IBD, spatial autocorrelation) and was shown to be of recent origin (DIYABC), recent land conversion and agricultural activities appear to best explain the genetic population differentiation within the African lion of Tanzania. Using various molecular markers, the present work will further explore the evolutionary history of the species to bring new insights in its conservation requirements.

Keywords: Panthera leo, Genotyping-By-Sequencing, SNPs, inbreeding, conservation implications

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In vivo prediction and discrimination of carcinogenic compounds using *Schmidtea mediterranea*'s stem cell proliferation patterns

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Accurate and reliable carcinogenicity assays are imperative, as cancer risks are directly associated with the type and potency of a compound. A challenge for the development of alternative test methods is the prediction of non-genotoxic carcinogens, which entail different assessments of human cancer risk. The variety of non-genotoxic cancer pathways complicates the search for sensitive and reliable parameters expressing their carcinogenicity.

The presented assay enables a simple, rapid and inexpensive prediction and discrimination of both genotoxic and non-genotoxic carcinogens by means of flatworm stem cell dynamics. Our methodology entails an exposure to carcinogenic compounds during the animal's regeneration process, and the most striking differences between non-genotoxic and genotoxic carcinogen-induced proliferative responses were detected during the initial stages of the regeneration process, i.e. at the moment stem cells proliferate. We present a two-step-approach that combines *in vivo* adult stem cell proliferation patterns and phenotypic appearances. Based on the observed differences in stem cell dynamics we were able to discriminate between genotoxic and non-genotoxic carcinogens in a selected group of compounds (MMS, 4NQO, CsA, S-PB, MPH, CPZ). More specifically, genotoxic carcinogens were characterized by significantly fewer mitotic cells after 3 days exposure in comparison with a 1-day exposure set-up, while, on the contrary, non-genotoxic carcinogens were characterized by significantly more mitotic cells after 3 days exposure in comparison with a 1-day exposure set-up. The ability to discriminate between genotoxic and non-genotoxic compounds makes this approach unique and with significant added value to current research and drug development.

Keywords: Planaria, stem cells, carcinogenicity assay

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Validation of the AOP network “Thyroperoxidase and/or deiodinase inhibition leading to impaired swim bladder inflation”

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The vast number of industrial chemicals has generated a strong focus on alternative test development for ecological risk assessment. Therefore, we are developing a non-animal testing strategy for the prediction of chronic aquatic toxicity, including in vitro tests and in vivo FET (Fish Embryo Acute Toxicity Test, OECD TG 236) assays. Our assay development process has employed the adverse outcome pathway (AOP) framework to identify key events (KEs) that could be used to predict chronic toxicity.

We developed an AOP network, encompassing thyroperoxidase (TPO) and deiodinase (DIO) inhibition, leading to decreased T4 and/or T3 concentrations, impacting swim bladder inflation and ultimately young of year survival. The swim bladder of zebrafish and fathead minnow, the two species used to construct the network, consists of a posterior and an anterior chamber, which inflate during a FET (early development) and Fish Early-life Stage Toxicity Test (FELS, OECD TG 210, late development) timeframe, respectively.

To assess the selected KEs, we first optimized in vitro assays to screen a battery of 50 environmental contaminants for their TPO/DIO inhibitory potential. Results were used to predict the impact on swim bladder inflation in vivo. Predictions were validated using 120/168 hours post fertilization (hpf) FET and 32 days post fertilization (dpf) FELS tests.

Results show that compounds identified as TPO inhibitors do not directly impair posterior chamber inflation at 168 hpf, while DIO inhibitors do. Compounds without TPO/DIO inhibitory capacities did not affect posterior inflation. An inter-lab validation experiment confirmed these findings. In addition, effects on posterior chamber surface area were found at lower concentrations when posterior inflation was impaired at higher concentrations.

Our results increase confidence in our AOP network-based hypothesis demonstrating that embryonic TPO activity is not essential to posterior inflation, but DIO activity is needed to activate maternal T4 into T3. However, both enzymes are needed at later developmental stages and thus anterior chamber inflation. FELS exposures with methimazole and mercaptobenzothiazole indeed resulted in impaired anterior chamber inflation at 21 dpf.

In conclusion, we successfully used an AOP-based approach to select key events, develop assays, and to correctly predict chronic toxicity.

Keywords: Thyroid disruption, Zebrafish embryo, Swim bladder inflation, Adverse outcome pathway

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Domestication level of the most popular aquarium fish species: is the aquarium trade dependent on wild populations?

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Aquarium fish trade has strongly increased in the past decades to become one of the most popular hobbies globally. Historically, all aquarium fish traded were wild-caught. Then, an increasing number of fish species have been produced in captivity. The main goal of the present study is to apply the concept of domestication level to the hundred most popular aquarium fish species in Europe and North America. The levels of domestication of freshwater aquarium fish species (n = 50) ranged from 0 to 5, with 20 species classified at the level 5 (selective breeding programmes are used focusing on specific goals) and only three species at the level 0 (capture fisheries) and 1 (first trials of acclimatization to the culture environment). In contrast, the levels of domestication of marine fish species (n = 50) ranged from 0 to 3, implying that the production of all marine aquarium fish species is based either entirely or partly on the capture of wild-caught specimens. Based on this new classification, the main advantages and drawbacks of fisheries and aquaculture are discussed.

keywords: Aquarium fish, Wild fish, Domestication, Aquarium trade, Conservation

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Parasites and hosts interaction: description of a black coral infestation by a new species of myzostomid, organisms specifically associated with echinoderms

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Myzostomids are minute, soft-bodied, marine “worms” that are associated with echinoderms. They are found in all oceans from subtidal to a depth of over 3,000 m. Most of them are ectocommensals of crinoids but some species are parasites of crinoids, asteroids, or ophiuroids. When they are parasites, they infest the gonads, the coelom, the integument or the digestive system of their hosts. Due to their long history as host-specific symbionts, myzostomids have acquired a unique, highly derived anatomy that has obscured their phylogenetic affinities to other metazoans during decades. Recent advances in molecular phylogeny show that they are undoubtedly close to annelids. The body plan of most myzostomids is singular inasmuch as they are incompletely segmented, parenchymous, acoelomate organisms with chaetae.

We described here for the first time a new species of myzostomid, *Eenymeenymyzostoma nigrocorallium* sp. n. Terrana & Eeckhaut, 2016, associated with black corals. *E. nigrocorallium* were observed on three species of antipatharians from the Great Reef of Toliara. We report on the infestation, describe the species with SEM and histology and present a 3D model of the new species. This model shows the whole external anatomy and detailed views of the internal organs. We made phylogenetic analyses with 18S rDNA, 16S rDNA and COI genes to estimate the positioning of *E. nigrocorallium* and re-estimate the evolutionary history of the myzostomids taking into account this important new species for the evolution of the myzostomid group.

keywords: corals, Madagascar, worm, symbiosis, antipatharia

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Do tropical and temperate meiobenthic communities respond similarly to climate change?

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To date climate change impacts on marine ecosystems have received substantial attention. Among the main consequences are the sea-surface temperature rise and the increasing frequency of temperature extremes. The responses of coastal marine environments to climate change are of particular interest, not only due to their sensitivity and rapid response to changes but also due to their socio-economic and ecological importance. In intertidal areas in particular, exposure to temperature maxima at low tide may exceed the tolerance of some vulnerable species, causing local extinctions. Here we investigate the response of meiobenthos, and nematodes in particular, to thermal stress in a microcosm experiment, comparing structural and functional diversity of two different communities: a tropical (Brazil) and a temperate (the Netherlands) one. A more pronounced negative effect in abundances of the tropical community was observed under thermal stress, in contrast to the temperate community, but species richness and diversity was maintained throughout the experiment period. No general effect in functional diversity was observed in both communities. Nevertheless, shifts in the proportion of functional groups and in the relative abundance of particular nematodes species were observed within functional groups under increased temperature regimes. Overall, both communities were able to maintain their structural and functional integrity, suggesting that meiobenthos develop plasticity towards temperature-induced stress.

Keywords: stress, temperature, meiofauna, tolerance, nematodes

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Reproductive consequences of dietary specialisations in a generalist seabird

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Generalist populations utilise a variety of resources or foraging areas, yet they may consist of individuals that specialise and use only part of the population level niche breadth. Evidence for individual dietary specialisation is available for many species across a broad range of taxonomic groups. However, the implications of specialisation are not well documented yet. Large gulls (*Larus* sp) are a suitable group of species to study consequences of dietary specialisation; while several species of gulls are considered omnivorous, studies have shown that diet differs among or within populations. We studied the consequences of dietary specialisations of individual breeding pairs in the herring gull *Larus argentatus*, an omnivorous seabird, using an extensive dataset which includes breeding and dietary data of 10 successive years. We hypothesised that pairs that focussed on prey of higher energetic value would yield higher fledging rates. An alternative hypothesis is that in a changing world (i.e. natural or human induced changes of the food landscape), the predictability of particular resources could decline and that pairs that relied on more resources simultaneously would reproduce better. The novelty of this study is that we used two continuous measures, rather than discrete categories, to test both hypotheses representing dietary composition and degree of specialisation. By comparing these two continuous measurements for diet with several proxies for reproductive success we show clear consequences of dietary choice and a somewhat counterintuitive dietary composition of several breeding pairs. We discuss how trade-offs between factors such as resource availability, predictability and the time and energy needed to obtain certain prey species may also influence resource selection.

keywords : *Specialisation, seabird, compositional analysis*

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Chemical predator detection in the Dalmatian wall lizard (*Podarcis melisellensis*)

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Today, many ecosystems face pressure due to the introduction of new predator species. This forces local prey populations to adapt and overcome their naivety towards these predators. The first step in overcoming naivety is to develop the ability to recognize the predator as a threat. Therefore, to predict the effect of predator introduction on prey populations, it is important to understand how the sensory systems of local populations are employed in recognizing risky situations, such as predator presence. In this study, we tested the ability of the Dalmatian wall lizard *Podarcis melisellensis* (Braun, 1877) to detect and recognize via the chemical senses both native and introduced predators as a threat. This was investigated by scoring the lizard's behaviour when a predator smell was presented. We also examined whether the response varied towards predators in relation to the level of threat they pose. Populations from the Croatian mainland, as well as from the Adriatic isles, were sampled. The island populations do not have the ability to recognize predators via the chemical modality. These lizards are, therefore, deprived of a sense that enables them to detect a threat when the predator is beyond hearing or viewing distance. This could imply vulnerability towards potential invasive predator species.

Keywords : predator-prey, invasive species, island biology, chemodetection, \$Podarcis melisellensisE

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Referential gestures or ritualised food sharing in ravens and bankivas?

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The aim of this abstract is to discuss the interpretation of animal behaviour. Therefore, the interpretation of raven behaviour in a more recent article (Pika and Bugnyar, 2011) is compared with the interpretation of bankiva behaviour in an older article (Kruijt, 1964). Pika and Bugnyar (2011) described “referential gestures” in raven as showing and/or offering of non-edible items to recipients, leading to frequent orientation of receivers to the object and the signallers and subsequent affiliative interactions. Referential behaviour is considered to be an indication of the presence of a Theory of Mind (the capability to think what the other thinks). The courtship behaviour “tidbitting” in the male bankiva is very similar. This behaviour is also very flexible and its aim is also to attract the attention of another animal. Mostly it is performed with edible items, however when these are absent non-edible items are used (Kruijt, 1964). This last behaviour fits within Pika and Bugnyar's description of “referential behaviour” however it is commonly interpreted as ritualised food sharing. One possible interpretation is that both behaviours are referential, another that both are ritualised food sharing. The principal of parsimony (Morgan's cannon, Ockham's razor) may be helpful in this choice. The interpretation of ritualised food sharing is only based on phylogeny and natural selection and seems therefore more parsimonious than an interpretation based on a theory of mind. This discussion may influence the interpretation of behaviour in the cognitive ethology.

Keywords : raven, bankiva, referential gestures, ritualised food sharing,

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How mole-rats dig with their teeth

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Mole-rats are known to use their protruding, chisel-like incisors to dig underground networks of tunnels, but it remains unknown how these incisors are used to break and displace the soil. To identify the digging mechanism of mole-rats, a kinematical analysis of this behaviour was performed based on high-speed videos of 20 individuals from the African mole-rat species *Fukomys micklei* placed inside transparent tubes in a laboratory setting. Our analysis showed that the ground is penetrated by both the upper and lower incisors at a relatively high gape angle, generally with the head slightly rotated nose-up. Initially, the upper incisors remain approximately stationary to function as an anchor to allow an upward movement of the lower incisors to break the soil. Next, a quick, nose-down rotation of the head further detaches the soil and drops the soil below the head. Consequently, both the jaw adductor muscles and the head depressor muscles power tooth-digging in *F. micklei*. In order to understand why mole-rats use this excavation behaviour, the mechanical advantages of their preferred behaviour will be compared to those of theoretical alternatives.

keywords: rodents, biomechanics, biting, digging, jaws

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Do the locomotion – development of spatio-temporal gait variables and gait symmetry in newborn piglets

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Locomotion is one of the most important ecological functions in animals. It is essential to find food, mates, shelter or to avoid predators. Motor development is important for the acquisition of locomotor skills. Compared to some other species, gait analysis in pigs is still at a relatively early stage. More so, locomotion studies on newborn piglets are, at the moment, nonexistent. Consequently, a baseline of the locomotor development and associated gait characteristics is lacking for piglets. To this end, we made video recordings of piglets walking through a corridor at several time points (<96 hours). After digitization of the footfalls, we analyzed spatio-temporal characteristics (e.g. stride and step lengths, stride frequencies and duty factors) and asymmetry indices of the gait of newborn piglets to study the early development of inter-limb coordination. All spatio-temporal variables reached stable values within 4 hours after birth, with most of them showing little change after the age of 1 hour. Most asymmetry indices showed stable values, hovering around 0%, within 8 hours after birth. These results are suggestive for a rapidly matured locomotion pattern with great contra-lateral symmetry. Often, variables (e.g. stride length, stride frequency and stance duration) had similar values for all legs or showed a clear difference between front and hind (e.g. swing duration and duty factor). Front legs spent a longer time on the ground (higher duty factor), which is due to a shortening of the swing phase. In addition, front legs generally showed greater contra-lateral symmetry than hind legs. This indicates front legs are very important for the stability of the piglet during early locomotion and may be considered the dominant leg pair.

keywords: Locomotor development, piglets, gait symmetry, inter-limb coordination

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Form-function relationship of the thumb in bonobos (*Pan paniscus*) and olive baboons (*Papio anubis*)

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Primates use their thumb both in manipulation and locomotion leading to conflicting mechanical demands. In this study, we investigated how the primate thumb anatomy is adapted to this stability-mobility conflict. We focussed on two highly dexterous catarrhines, bonobos and olive baboons, with a distinct locomotor and prehensile behaviour. We obtained fresh-frozen cadaveric hand and forearm specimens via collaboration with the RZSA, Belgium (5 bonobos; Bonobo Morphology Initiative) and the CNRS, France (3 baboons). A detailed dissection was performed of each specimen with quantification of soft-tissue parameters and every specimen was CT scanned to create 3D surface models for the trapezium and first metacarpal. Bonobos have a saddle-shaped TMC joint allowing a wide range of motion, while the TMC joint of olive baboons is almost cylindrical but opposability is maintained by the relatively long thumb length. Thumb opposability is reflected in the well-developed thumb musculature, and in some aspects of the anatomical configuration of the thumb, bonobos and olive baboons are surprisingly similar.

(1) movements of the thumb and index finger are closely associated; (2) the FDP tendon to the thumb is a well-developed structure in baboons and in bonobos, but in bonobos it is variably present; (3) the wrist flexors are the most important muscles in both species, but those of baboons are more powerful; (4) the thumb muscles of both nonhuman primates are equally well developed. Despite their distinct locomotor behaviour and socio-ecology, and a large variety of thumb movements, their thumb muscles are developed in a similar way; (5) in nonhuman primates the intermetacarpals and flexors separate muscles, while in humans these muscles have fused to form the dorsal interossei. However, in the dissected bonobo and baboon specimens, we observed a continuum between these two configurations.

Finally, what makes the modern human thumb musculature special within extant primates is the presence of two extrinsic thumb muscles not found in other great apes or baboons; the EPB and FPL, which increases the independence of the thumb.

keywords: thumb anatomy, opposability, TMC joint, similarity

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Joining science and policy in capacity development for conservation-relevant biodiversity monitoring in Africa

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To mainstream biodiversity conservation, use and management into sustainable development, it is imperative to optimize transfer of biodiversity-related knowledge and technology from resource-rich countries to developing countries harbouring biodiversity hotspots. An Achilles heel to conservation in the South is lack of adequate monitoring and enough capacities to do so. Monitoring is needed to evaluate the status of biodiversity and anthropogenic impact and to report for follow-up, policy adjustment and eventual remediation. Capacity development on biodiversity monitoring may hence substantially enrich global knowledge on biodiversity and its conservation.

Devising realistic monitoring programs, sufficiently embedded in policy, remains a challenge. We discuss our approaches to increase capacities for following up habitat conservation and anthropogenic impact on biodiversity in (Central) Africa.

(1) CEBioS, the Capacities for Biodiversity and Sustainable Development program funded by the Directorate-General for Development Cooperation and Humanitarian Aid (DGD), developed a capacity building concept linking scientific data to policy. To guarantee shared ownership, academic institutes and organisations with responsibilities in biodiversity policy were invited to jointly submit competitive applications on biodiversity indicators. Projects focus on subjects as diverse as ethnobotany, charcoal, bushmeat and fisheries. A workshop to exchange best practices and lessons learnt revealed that especially ground truthing, economic valuation of biodiversity, and the application of modern technologies in monitoring were missing capacities in the global South. Also, efforts are needed to avoid that indicators remain purely theoretical.

(2) The RBINS is custodian of the Archives of the former National parks of Belgian Congo, providing studies going back to 1924 and photo and library archives, which have been digitalised and are available online as a baseline for sustainable management. Their use has recently increased, for publications and monitoring purposes.

(3) Supported by VLIR-UOS, DGD and Belspo, we contribute to capacity building for collecting policy-relevant biodiversity data. Topics include indicator taxa for aquatic pollution, a decision support system including technical and societal concerns around environmental conflicts, and the use of genetics and parasitology to evaluate fish stock health. Throughout, stakeholder engagement and an international approach are important in an attempt to ensure broad acceptance and wider application of potential management advice.

keywords: aquatic ecology, collection valorisation, development cooperation, indicator, Measuring Reporting and Verification (MRV)

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LIFE+ OZON project defragmentates the Sonian Forest near Brussels

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Despite its great natural structure and high biodiversity, the Sonian forest near the centre of Brussels (Belgium) is divided in several smaller entities which are separated by harsh barriers such as roads and railways. The LIFE+ OZON (Ontsnippering ZONIënwood) project is defragmenting the Sonian forest between 2013 and 2017.

In general, the OZON project will reconnect the natural habitats between the three Belgian regions in the Sonian Forest by constructing several environmental infrastructures. By connecting the habitats of the animals in the forest again, animals will be able to migrate without having to cross the existing roads which will greatly improve road safety. OZON realizes several green infrastructures (e.g. a wildlife crossing and ecotunnels), increases the nature-friendliness of local forest management (e.g. by restoring forest edges) and redirects recreation to less sensitive areas.

In the last years, three new ecotunnels were constructed under the ring road R0. Moreover, 18 existing tunnels and culverts were restored in order to allow a passage for animals. Finally, 15 wildlife cameras have already been installed in the Sonian forest to monitor the passage of animals. This monitoring campaign will be intensified in the next years. In 2016, the construction of a wildlife bridge of 60m wide crossing the highway started. In combination with the construction of an ecofence of 25km, this bridge will allow a safe passage of all animals.

A budget of €10.8 million is available to finance the defragmentation of the Sonian Forest, of which the EU is contributing €3.5 million. In addition to the Agency for Nature and Forest, the Agency for Roads and Traffic and Brussels Environment, also the municipalities Hoeilaart, Tervuren and Overijse and the Department of Environment, Nature and Energy of the Flemish government are financing the project.

Recently, the OZON project received international support of the United Nations Environment Programme (UNEP). Moreover, the entire Sonian Forest was nominated as a finalist for the European Natura 2000 Award in 2014, 2015 and 2016! These nominations were a true reward for the hard work of the last years. For further information you can visit the website <http://www.zonienwoud.be/lifeozon/>

Keywords: Sonian Forest, Wildlife Crossings, Conservation, Reconnection, Inter-Regional Cooperation

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Migration of European silver eel in an anthropogenically impacted wetland area in Belgium

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Despite substantial efforts to restore the European eel (*Anguilla anguilla* L.) population in the last decade, recovery has failed thus far. Migration barriers are believed to play a significant role in this failure, especially in anthropogenically impacted water bodies. In Belgium, for instance, eel has been unable to reach a vast proportion of the highly suitable lowland river habitats for decades. Consequently, insight into eel migration is needed and therefore we analysed eel behaviour by acoustic telemetry in a polder area. This polder used to be an eel hotspot but has now been blocked by several migration barriers. Between July and October 2012 we tagged 99 eel and observed their behaviour until November 2015. Eel behaviour was linked to environmental conditions (water temperature, habitat conditions, flow), biotic conditions (silvering stage) and migration barriers. Several behaviour types were observed: homing, searching, delay and migration. Based on the results, several mitigation options could be compared and water management in the study area could be optimised to facilitate eel migration. These findings are also of interest in other anthropogenically affected lowland areas with similar migration barriers like weirs and pumping stations.

keywords : European eel, migration, anthropogenic impact, telemetry, barriers

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Empathic personalities: Chimpanzees consistently vary in the tendency to console others

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In contrast to a wealth of human studies, little is known about the ontogeny and consistency of empathy-related capacities in other species. Consolation, post-conflict affiliation from uninvolved bystanders to distressed others, is the best-documented marker of empathetic concern in nonhuman animals. Using a longterm dataset of chimpanzee (*Pan troglodytes*) consolation behaviour, we provide evidence for empathetic personalities. Across development, individuals consistently differed from one another in this empathy-driven response, with higher consolatory tendencies predicting better social integration, a sign of social competence. Further, similar to recent results in other ape species, but in contrast to human self-reported empathy findings, older chimpanzees were less likely to console than were younger individuals. Overall, given consolation's reported links to empathy, these findings provide novel insights to the development of individual socio-cognitive and -emotional abilities in one of our closest relatives.

Keywords : Consolation, empathy, individual differences, chimpanzees

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Planarians: a (pluri)potent tool to study stem cell responses to carcinogenic stress *in vivo*.

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Highly regenerative planarians are a unique model to study stem cell responses. Having a large and easily accessible pool of pluripotent stem cell, they offer the possibility to monitor stem cell reactions *in vivo*, while residing in their natural environment. The latter is often a limitation in other model organisms. As high regenerative capacities coincide with a low vulnerability to carcinogenesis, stress coping mechanisms of their particular stem cell system, which underlies regeneration, holds valuable information. Secondly, there is growing interest in the importance of the niche aspect and its function in directing stem cell responses, a line of research that greatly benefits from an *in vivo* approach.

We used the planarian *Schmidtea mediterranea* to compare stem cell's DNA damage responses following genotoxic exposure during two situations with distinct cellular niches, homeostasis and regeneration, the latter creating a developmental environment. DNA damage was observed within the stem cell population, irrespective of regeneration or exposure time; responses, however, differed. While stem cells immediately responded with a proliferation stop in both situations, the outcome after prolonged exposure depended on the cellular environment and stem cell subtype. A stronger activation of repair systems was detected during regeneration, while apoptosis seemed to be an important outcome during homeostasis. As to the stem cell types, a PCA analysis revealed a co-expression of the more potent subtype-associated genes with DNA repair genes, while a more lineage-restricted subtype was linked with the pro-apoptotic *bax* gene. It is probably this repair capacity present in pluripotent stem cells that underlies the capacity to circumvent chemically induced carcinogenesis, which is generally found in regenerative tissues and organisms. Further niche and potency related differences will be elucidated in the future, utilizing the unique planarian stem cell system.

Keywords: Planaria, regeneration, stem cell

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Home not-so-sweet home: social relationships and behaviour change in captive African wild dogs (*Lycaon pictus*) after pack separation

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African wild dogs (*Lycaon pictus*) are endangered carnivores with a population size that is currently estimated at 6.600 adults in the wild. The European Endangered Species Programme (EEP) for African wild dogs aims to maintain a healthy zoo population that is sustainable on the long-term and thereby prevent extinction of the species. Safaripark Beekse Bergen is one of the zoos that participate in the African wild dog EEP and they recently faced some challenges in the captive management of their breeding pack by the death of the alpha-male. It was decided to move nine male littermates to GaiaZOO in an attempt to restore the complex social structure and decrease the risk of inbreeding in the remaining pack. This study evaluated the captive management decision to move these individuals by comparing the social relationships and behaviour in both zoos before and after pack separation. The results indicate that rank reversals took place in both packs after pack separation. The nine male littermates formed a socially stable pack in GaiaZOO, while the changes in social relationships and behaviour imply that the remaining pack members in Safaripark Beekse Bergen formed a socially unstable pack. Based on the results, recommendations are provided for further improving zoo animal management and the welfare of captive African wild dogs.

Keywords: African wild dogs, captive management, zoo transport, social relationships, behaviour

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Abstracts poster presentations

Morphology of the sperm storage organ of the land snail *Helix aperta* (Pulmonata, Gastropoda): toward a conservation perspective

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Currently, emblematic species are the focus of the most animal conservation efforts. Indeed, they are the subject of programs with large devoted budgets receiving much media attention. Many other threatened species, while they play a key role in ecosystem' maintenance and functioning, are completely neglected. Helicid land snails, apart from being of great economic and gastronomic interest, are useful in the ecosystems. In fact, they are involved in multiple food chains and constitute effective indicators of soil and air pollution. However, strong human influences can jeopardize the existence of certain snail species, hence the necessity of their conservation. Heliciculture may constitute an ideal means of conserving this resource. It is increasingly seen as an attractive practice, either in a food security context or as a way of maintaining biodiversity. Establishing sustainable farming of any animal requires a good understanding of many aspects of its biology, especially its reproductive system. *Helix aperta* is a land snail figuring among the recommended species for heliciculture. Unfortunately, it has been studied very little; so many aspects of its biology remain unknown, thus making its farming difficult. Using histology, the present study investigates the morphology of the sperm storage organ, called spermatheca. It is a key structure for the reproductive biology of this species. The associated fertilization pouch was also examined in detail. The combined spermatheca-fertilization pouch complex containing a C-shaped fertilization chamber, where the fertilization takes place; and a spermatheca where the sperm received from different partners is stored and conserved. The latter is a tubular structure with a common entrance, and the number of tubules varies from between individuals but does not exceed 6 tubules. Spermatozoa were found to be stored in the tubules, with heads in tight contact with the epithelium. This pattern was consistent in the four samples (from 4 populations with 8-16 individuals). Interestingly, this organ may be a site for sperm competition in this polyandrous species. These results, when combined with further investigations on this structure, may elucidate many enigmatic aspects of sperm storage and fertilization in this species, and consequently a better understanding of their reproduction.

keywords: Helix aperta, sperm storage organ, spermatheca.

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Diet of the common genet *Genetta genetta* (L., 1758) in the national park of Tlemcen north-western of Algeria

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This study has been done at the Hafir forest in the national park of Tlemcen, it is situated at the extreme north-west of Algeria. The carnivore chosen for this study is the common genetta (*Genetta genetta*), it is the unique representative of the family of "Viverridae" in the north of Africa. The diet is designed by analysing the content of the droppings of *Genetta genetta*. We chose the drying method to decorticate the dropping, which allows recuperating the most important part of prey's fragments. The dropping has been macerated for 10 minutes in dilute ethanol. After that, the content of the dropping was sorted using a pair of pliers with observation under a binocular microscope. The scats contents have been identified by the use of determination keys and reference collections. During the study period, 56 prey species have been identified; they are distributed on 8 food categories. The insects are the dominant food category (the relative abundance R.A.=61,76%), followed by plants (R.A.=15,5%), arachnids (R.A.=9,66%) and mammals (R.A.=7,98%). The use of the frequency of occurrence indexes allow to notice that the wood mouse *Apodemus sylvaticus* (O.F.%= 63,64%) is the most frequent prey species, than the scorpionidae *Buthus occitanus* (O.F.%= 63,64%) and an indeterminate species of Gryllidae (O.F.% = 54,55%). The indexes of diversity of Shannon-Weaver indicate high values which varied from 2,26 to 4,43 bits which can be explained through the high consummation of arthropods.

keywords: Genetta genetta, National park of Tlemcen, diet, relative abundance, occurrence frequency.

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Interpreting long-term trends in bushmeat harvest in southeast Cameroon

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Measuring hunting sustainability across West/Central African forests remains a challenge. Long-term assessment of trends is crucial. Via village-based offtake surveys we collected hunting data from three settlements near the Dja Biosphere Reserve (southeast Cameroon). Over a 13-year period (2003, 2009 and 2016) we collected data on carcasses brought to the three villages during March-June. We calculated the catch per unit effort (CPUE) and the mean body mass indicator (MBMI). We also examined interactions between year, village, month and hunting method. The total number of carcasses hunted decreased between 2003 and 2016, but number of hunters increased. CPUE remained relatively constant for all species pooled, though there was an observed change from traps to firearms during the study period. CPUE for each of the seven most hunted species also remained constant, and a similar shift from traps to firearms was observed. MBMI of all hunted wildlife remained stable for all species pooled, but declined significantly only in the remotest village. MBMI values for this village were higher than for the other two settlements perhaps because wildlife here is still relatively undepleted. Although there are no alarming signs of overhunting in our study area, the increasing reliance on guns could have dramatic consequences on the larger-bodied species, such as monkeys, in the future. Our results suggest that changes in CPUE and MBMI may be the most accurate indicators of actual sustainability. These indices can be monitored with simple village-based offtake surveys and hunter interviews to improve management of bushmeat hunting.

Keywords: Africa; gun hunting; trapping; sustainability; CPUE; MBMI

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Remote observations of foraging herring gulls (*Larus argentatus*)

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Partially due to changing food availability the population size of herring gulls (*Larus argentatus*) has declined over the last twenty years. Recent developments in the government's coastal protection policy resulted in part of the loss of one of the herring gull's primary food source, namely blue mussels (*Mytilus edulis*) found on breakwaters. We measured the time budgets of herring gulls on breakwaters to understand the role of breakwaters for food provisioning of Dutch herring gulls. Time budgets were quantified with tri-axial accelerometer data collected from trackers attached to the backs of the herring gulls. We present the steps necessary to classify accelerometer data and calculate time budgets. The classification model was able to accurately classify 95.7% of the gulls' behaviour at the breakwater into seven categories. These categories included resting, walking, prey searching, prey handling, flapping flight, soaring flight and a category with other behaviours, thus enabling detailed analysis of the birds' foraging behaviour. The model can be used to calculate time budgets and measure intake rates of mussels, increasing our knowledge on the value of breakwaters as a food resource for herring gulls.

keywords: Larus argentatus, foraging ecology, accelerometer, remote behaviour observation

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***Tuta absoluta* (Lepidoptera: Gelechiidae) ability to develop on potato tubers**

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Tuta absoluta (Lepidoptera: Gelechiidae) is a widespread pest that threatens commercial production of solanaceous crops. Larvae feed on the mesophyll of all aerial parts of the plants resulting in significant yield losses and cosmetic damages. It is classically assumed that underground plant parts are not affected but larval development on potato tubers has recently been suspected. However, this assumption is poorly supported in the literature. Potato tubers might represent an unsuspected mean of persistence and dispersal in agricultural environments. Oviposition tests were here conducted using dormant and active (sprouts less than 5 cm) potato tubers in net cages. Oviposition only occurred on the sprouts of active tubers, supporting larval growth until adult emergency. Tuber dissection revealed burrows starting from sprouts inside the flesh. Additional fitness assays were conducted on non-sprouted tubers and revealed that first instar larvae were able to enter the skin and create burrows, living inside and feeding on potato flesh, although none of them survived.

keywords: Insect-host interaction, Scrobipalpuloides absoluta, Solanaceae, Solanum tuberosum, Potato tuber

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Study of some biological parameters of bullet tuna *Auxis rochei*, (Risso 1810), caught from the bay of Mostaganem.

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The bullet tuna (*Auxis rochei*) is one of the most abundant small tuna species in the Mediterranean Sea. In this work, we present the results of some biological parameters of the bullet tuna *Auxis rochei* like the biometrics and growth parameters. The study of biology is based on 110 bullet tuna, fished in the Bay of Mostaganem between October 2015 to January 2016. The biometric study shows mean spine is 38. On the other hand, the study of size-weight relationships indicates a minorant allometry, so is indicating that the weight is growing less than size. The reproduction study showed a sex ratio in favour of females, with a rate of femininity (59.09%). The study of growth by The Von Bertalanffy growth parameters have been determinate by the study of the structure of length and by using the software FISAT II (version 1.2.0) recommended by FAO. The asymptotic length (L_{∞}) of *Auxis* is 47.78 ; the curvature parameter (K) which determines the speed of the fish to get close to the asymptotic length is 0.48.

keywords: Auxis rochei, biological parameters, bay of mostaganem, growth, biometric parameters

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Biosystematics of the spiders in the regions of Biskra and Touggourt.

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A study about spiders is realized in four palm groves of both regions, those of Biskra and Touggourt, who belong to the Saharian bioclimatic stage. It is the first taxonomic inventory of the stand of spiders in these two regions. The environment studied is an agra-ecosystem composed of different varieties of date palms. Spiders were trapped by pitfall and caught by hand. During one year, 1.621 individuals were collected, including 656 males, 513 females and 452 juveniles divided between 22 families and 123 species. The results show the abundance of the family Gnaphosidae with 29 species, the Lyniphiidae and the Salticidae each one with 11 species. The dominant species is *Zodarion* sp. (Zodariidae). The study of various indexes shows that climatic conditions such as temperature are the main factors that influence in the distribution of spiders in the different palm plantations studied. The phenology of species studied showed that each species has a different phenology of others. The abundance of males is higher than that of females, while females are more present than males during the year.

keywords: Palm groves, Biskra, Touggourt, spiders.

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Inventory of Entomofauna around the Lake of Réghaïa (Algeria).

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This study was conducted at the wetland in Reghaia (36 ° 46 'to 36 ° 47' N .; 3 ° 19 '3 ° 20' E) which overlaps between the sea and the land, This area has got an extraordinary environment and diversity composing a mosaic ecosystems (forest, wetland, lake, dunes and marine).

The analysis of the entomological diversity was carried out by using two methods of trapping, the pitfall traps and sweep net technique during the period September 2013 to March 2014. Each month, we installed 10 pitfall traps. 583 individuals were identified. They belong to 8 orders, 57 families and 94 species. The order Hymenoptera dominated with 71.18%, followed by the order Diptera with 8.75%, beetles with 7.89% and Homoptera 5.32%. The other orders were poorly represented (0, 17% ≤AR ≤2,92%). The family Formicidae was the best shown in species with 17 species and 64.84% of all trapped entomofauna.

keywords: Entomofauna, Inventory, Forest, Marsh of Réghaïa.

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Morphological adaptations of vertebrates species to sandy environment

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Sandy deserts and sandy oceanic floors cover a large surface of our planet. Many species have colonized these ecological niches by living on or under the surface of this particular substrate. Many morphological adaptations have appeared to sustain life and locomotion on or under the surface of sandy substrates. Among those species are the Teleosts *Ammodytes tobianus* (Ammodytidae) and *Heteroconger hassi* (Congridae). These two species have been investigated by histological and immunohistochemical techniques. The results show that these two species have developed different morphological strategies according to their life style in the sand. *H. hassi* show epidermal microridges enabling the retention of mucus on the skin. While *H. hassi* exhibit no scales, *A. tobianus* possesses cycloid scales under the epidermis. *H. hassi* exhibit a large number of goblet cells and sacciform cells. *Ammodytes tobianus* possesses a significantly lower number of goblet cells, whereas no sacciform cells were found. The evolutionary involvements of these adaptations are discussed.

keywords: Fish, Histology, Sand, Vertebrates

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A physiological and developmental analysis of metal mixture toxicity in adult and early-life stages of the zebrafish

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A number of metals are key to life while others do not appear to fulfil essential functions and both become toxic at elevated concentrations. Although the effects of metals on biological systems are well documented on the macroscopic scale, our understanding of the molecular, biochemical and physiological mechanisms of metal toxicity is still limited. Especially the effects of metal mixtures remain very poorly documented and understood.

Within this context we are performing experiments with early life stages and adult zebrafish to investigate the effects of single and combined exposures to Cu and Cd. In adults, effects on survival and behavioural responses were followed up to 28 days and the body burdens of both metals and the major cations were analysed. In zebrafish embryo acute toxicity tests survival and a number of sub-lethal endpoints, including swim bladder inflation, heart rate, mobility and malformations were recorded up to 120 hours post fertilization.

In general, both zebrafish embryos and adults were much more sensitive to Cu than to Cd in single metal exposures on the basis of the observed mortalities. Exposure to Cu and Cd together showed interactions pointing to strong synergistic effects. The metal uptake measured in the adult fish showed a clear dose-response relationship, however neither the metal uptake rates nor body burdens in individual or mixture exposures explain the observed effects.

Analysis of the major body cations showed that a loss of cations, in particular sodium has a large impact on the observed mortality in adults. The results obtained so far with early life stages show a high sensitivity of the development of the posterior swim bladder chamber to the exposure to Cu and Cd compared to other endpoints. In addition to the development of the swim bladder, a co-exposure to Cu and Cd greatly impaired hatching.

keywords: zebrafish, metals, mixture toxicity

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Unravelling the eco-evolutionary dynamics of two non-marine ostracods in response to urbanization

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Humans exert a strong pressure on natural environments. By assessing the response of natural populations and communities to urbanization, the international SPEEDY project (SPatial and environmental determinants of Eco-Evolutionary DYnamics: anthropogenic environments as a model) helps to understand the effect of anthropogenic disturbance on biodiversity. The SPEEDY consortium explores the impact of this disturbance using a nested design wherein both the local as regional urbanization levels are sampled across a broad range of different animal and plant taxa. Our team focuses on ostracods.

Cypria ophthalmica and *Cypridopsis vidua* were selected as target species. Together with the sampling of these non-marine ostracods, various abiotic variables of the ponds were measured. A possible correlation with urbanization and ostracod diversity is presently being tested. After dissecting the specimens, valves were used to quantify their outlines in order to estimate morphological diversity while the soft parts were used for genetic analyses. DNA sequencing data from the mitochondrial COI region revealed the presence of at least 2 cryptic species within *C. vidua* but not in *C. ophthalmica*. There is no clear correlation between the degree of urbanization and the presence / absence of (cryptic) species. Microsatellite analyses are currently being performed to obtain fine-scaled information about the population structure along and across urbanization levels. This will also allow us to test for associations between genetic and morphological ostracod diversity.

keywords: urbanization, ostracod, pond, outline, mitochondrial DNA

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Constructing bat houses matching the thermal characteristics of natural roosts in tree cavities

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The availability of suitable roost sites is essential for the survival of bats. Roosts are used for mating, hibernation, and rearing the young; they offer protection from adverse weather and predators. Selection of specific roost sites by breeding female bats has consequences for survival and reproductive success. Tree cavities are scarce in most intensively managed Western European forests. In the past, several attempts were made to provide forest dwelling bats with alternative roosts with variable results. In general, these experiments failed to attract reproduction colonies of typical tree cavity-dwelling bats, which seriously limits the potential of bat houses as a mitigation measure. Previous research yielded that the internal temperature regime of tree cavities, previously used by bats, are seriously buffered compared to external temperature and temperature peaks inside the cavity show a 6 to 8 hours delay compared to the external peaks. Slight differences in wall thickness had significant influence on the internal temperatures. Therefore, the influence of wall thickness, external colour and material (wood or woodcrete) used on the thermal characteristics of bat houses was further investigated. The objective of this project was to investigate the relationships between wall thickness, material used and internal temperature regimes of artificial bat roosts. Based on those relationships, a type of bat house is suggested that approaches the thermal characteristics of natural tree cavities, but combines ease of manufacture, ease of control and relatively low cost.

keywords: Chiroptera, bat roosts, breeding habitat

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Untangling possible relationships between urbanization and the eco-evolutionary dynamics of the land snail *Cepaea nemoralis*

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Species' eco-evolutionary dynamics can be strongly influenced by anthropogenic disturbances. In the SPEEDY project (SPatial and environmental determinants of Eco-Evolutionary DYNAMics: anthropogenic environments as a model) the impact of such a disturbance is explored via a gradient of urbanization across a broad range of different taxa.

Here, we study the relation, if any, between urbanization and phenotypic and/or population genetic variation in the pulmonate land snail *Cepaea nemoralis*. This species is common across Flanders and occurs in three basic colour morphs (brown, pink and yellow) with various degrees of brown shell banding. Firstly, we performed a shell morphometric analysis to explore whether degree of urbanization correlates with the species' phenotypic shell characteristics such as size, shape, shell thickness, shell strength and colour pattern. Secondly, we used mtDNA Sanger sequencing (COI) and Restriction-site Associated DNA sequencing (RAD-seq; a Next Generation Sequencing technique) to obtain genome-wide population genetic information for exploring population structuring, gene flow and possible signatures of selection. In addition, the DNA sequence data will be correlated with the phenotypic data. Overall, these data will be compared at various levels with data for other organisms surveyed by the SPEEDY project. In this way the SPEEDY project aims at uncovering overarching patterns of effects of urbanization upon local biota.

keywords: urbanization gradient, population genetics, phenotypic variation, Cepaea nemoralis

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HIPE: Human impacts on ecosystem health and resources of Lake Edward; exploring a poorly known ichthyofauna

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The East African Great Lakes are known for their exceptional biodiversity. They harbour unique fish faunas that include a unique assemblage of over 2000 endemic cichlids. Although the cichlid faunas of the largest lakes, Tanganyika, Malawi and Victoria have long been in the forefront of evolutionary research, the faunas of some of the other lakes remain virtually unexplored. Lake Edward is the smallest of the East African Great Lakes. It is situated on the boundary between the Democratic Republic of the Congo and Uganda and is unique among the Great Lakes as it is completely surrounded by protected areas. This previously eutrophic lake also supported a regionally important fishery. This industry was mostly focussed on large fish species of high commercial value such as *Oreochromis*, *Clarias*, *Bagrus* and *Protopterus*. However, during the last decades, the lake's productivity has plummeted and catches have dropped by at least 60%. This was especially the case for the main fisheries target species, causing the fishery to shift towards smaller, economically less valuable species.

A series of field campaigns is set up in order to investigate the causes of this decline, and to gain a better understanding of the recent and past functioning of the ecosystem, in the frame of the BELSPO funded Brain project HIPE (<http://www.co2.ulg.ac.be/hipe/>). To achieve this, a multidisciplinary approach will be followed, combining biology, ecology, biogeochemistry, and socio-economics. One of the main outputs of the project will be an appropriate management plan to mitigate present and further impacts.

In addition to supplying a cheap and sustainable source of protein, the lake is also a hot spot of ichthyofaunal diversity. The lake's basin contains about seventy described fish species. Half of these are cichlids, mostly haplochromines. However, this number is a severe underestimation, and estimates suggest that the lake might contain up to ninety endemic species of haplochromine cichlids, most of which still await formal description. As such, Lake Edward harbours the third largest *Haplochromis* assemblage. The study of these species is ongoing and by contrasting the different cichlid species flocks, we aim to better understand the general patterns in cichlid evolution.

keywords: biodiversity, great lakes, Africa, sustainable development, species flock

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Fish community composition in the Demer basin

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Community composition is affected by local interactions and regional processes as suggested by metacommunity theory. Local interactions (among species, between species and their environment) can be linked to regional processes through dispersal. Dispersal is important for connecting local communities as it determines how strongly similarity of local communities decreases with increasing distance. Several studies have tried to explain to which degree spatial effects are important in determining the composition of local fish communities. We investigated the link between environmental and spatial factors and fish community composition in the Demer basin, which is one of eleven basins located in Flanders. Information on environmental variables was collected using the Belgian Public Monitoring Network provided by the Flemish Environmental Agency (Vlaamse Milieumaatschappij, VMM). Fish sampling data was collected using the Fish Information System database (VIS, Vis Informatie Systeem) composed by the Research Institute Nature and Forest (INBO, Instituut voor Natuur- en Bosonderzoek). Spatial variables included watercourse distances among the different sampling locations. Results show that almost 30 % of the total constrained variance of fish community composition in the Demer basin is predicted by nine environmental variables, while 11.2 % could be explained by geographical distances among watercourses. Chemical Oxygen Demand, Biochemical Oxygen Demand and O₂ are three oxygen related variables significantly influencing community structure. Nitrate, total Kjeldahl nitrogen, total nitrogen and total phosphorus, which indicate eutrophication, significantly impacted fish community composition as well. Eutrophication is a severe problem in the Demer basin with 29 % of all sampling locations exceeding the norm set in Flanders. Thus results demonstrate that environment plays an important role in shaping fish communities in the Demer basin while space seems to be less important. The remaining 68.1 % was not explained by the variables included in this model. Other spatial variables (e.g. migration barriers), local biotic interactions or environmental factors not included in this study (e.g. physical habitat, river morphology and substrate) may play an important role in shaping fish communities in the Demer basin.

keywords: fish community composition

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Three-spined stickleback, *Gasterosteus aculeatus*, as a sentinel species for historical mercury pollution in Flemish rivers and streams.

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Although metal pollution in the surface waters encounters decreasing trends, it is far from gone. Amongst others, mercury-pollution originating from metal processing factories from the past, is still traceable in aquatic food webs of the Flemish rivers and streams.

The overall goal of this project is to discover whether there is a significant inheritability of the adaptive traits of populations towards the presence of sub-lethal mercury concentrations. The three-spined stickleback, *Gasterosteus aculeatus*, has been selected as a sentinel species for this research because of its wide dispersion, and tolerance towards polluted environments.

During a first field campaign, three rivers known for their historical mercury pollution and one near-to-pristine stream were sampled at four different levels; water, sediment, invertebrates and fish. The sampled sticklebacks were dissected, and the liver, gill and muscle were stored for further analysis. For each type of sample, a custom-made protocol was ran to prepare the samples for analysis.

In a first place, we wanted to have an estimation of the mercury load which is still present at those four levels of the food web in each river. Secondly, these background mercury levels were correlated to pollution-specific endpoints in stickleback, namely the activity of genes which play an important role in the anti-oxidant stress response. Total RNA was extracted from liver, gill and muscle tissue samples, reverse-transcribed, and consequently used in real-time qPCR for gene-expression analysis. Novel primer pairs were designed for this purpose, and as such tested for their applicability in future studies to come.

keywords: Mercury, Three-spined stickleback, oxidative stress

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Searching for new luciferases? RNA-seq can help.

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Bioluminescence is the oxidation of a luciferin substrate catalysed by a luciferase enzyme. Luciferins and luciferases are generic terms used to describe a large variety of substrates and enzymes. Whereas luciferins can be shared by phylogenetically distant organisms which feed on organisms producing them, luciferases have been thought to be lineage-specific enzymes. Numerous light emission systems then co-emerged independently along the tree of life resulting in non-homologous luciferases. However, recent examples of homologous luciferases expressed in phylogenetically distant species were recently highlighted. Working on different metazoan model species, we are using RNA-seq analyses to search for potential new luciferases and make the point about the evolutionary relationships between all known luciferases. Additionally, we characterized for the first time the luciferase of a luminous echinoderm. Phylogenomic analyses identified this echinoderm luciferase as homologous to the luciferase of the sea pansy *Renilla* (Cnidaria). Those enzymes might then be convergently co-opted into luciferases in distant lineages. Our findings are controversial to the traditional viewpoint, where after luciferases would generally be of convergent origins.

keywords: Bioluminescence, Luciferase, RNA-seq, Marine Biology

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Feeding ecology of metamorphic and paedomorphic palmate newts (*Lissotriton helveticus*) in Larzac

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It is generally suspected that increased phenotypic divergence among conspecifics may reduce competition between them. Heterogeneous environments can favour the evolution of such polymorphisms by allowing differential resource use. Facultative paedomorphosis, a heterochronic polymorphism, is an example of phenotypic variation in which paedomorphs retain larval traits, such as gills and gill slits, whereas metamorphs are fully metamorphosed. The aim of this study was to determine the feeding habits of palmate newt paedomorphs and metamorphs (*Lissotriton helveticus*) coexisting in three small ponds in Larzac, France. To determine the specialisation in terms of prey between the two phenotypes we identified stomach content samples and examined the number of each prey per newt stomach, as well as, the dry mass of each prey per newt stomach, to check on the input that these ingestions have. Our results showed population variation in feeding habits. Food use and energy intake segregation was found among morphs suggesting that the morphological differences between paedomorphic and metamorphic newts cause a variation of foraging efficiency between morphs and can allow differentiation of diets and microhabitat use. Paedomorphs foraged significantly more on benthic organisms than metamorphs, while metamorphs also relied on amphibian eggs for energy. The total dry mass ingestions were higher for metamorphs than paedomorphs and for females than males, as well. This resource partitioning may facilitate the coexistence of the alternative morphs in ponds and food diversity may thus favour the evolutionary maintenance of facultative paedomorphosis.

keywords: resource partitioning, trophic polyphenism, feeding ecology, facultative paedomorphosis, amphibians

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The hoatzin, a bird like no other

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The hoatzin (*Opisthocomus hoazin*) is an amazing bird. Previous research has revealed that it has a specialized leaf-feeding diet associated with an enzymatic pre-stomach digestion, unique among birds. This folivorous diet involves significant morphological changes because the leaves are digested by fermentation in an enlarged crop. This digestive system modification corresponds to an anatomical change of the sternum. The carina is reduced which leaves little space for the insertion of the pectoral muscles. Consequently, it has been suggested that the flying ability of the hoatzin is reduced. Young hoatzins have a unique feature in birds, two claws on their wings that they use to climb. Indeed, hoatzin chicks jump from their nest into water and then climb back to the nest using their clawed wings to avoid predation. Recently obtained data for animals in the field demonstrate that the chicks move their wings with alternating movements when climbing, a locomotion mode never observed in other species of birds. The morphology of the Hoatzin has not been studied since the first descriptions in 19th century. The goal of the present project is to study the anatomical features of the Hoatzin thanks to new biological material that was obtained in the field in Venezuela. An ontogenetic series will allow us to describe the development of the musculoskeletal system in order to understand the evolutionary compromise between feeding and locomotion observed in this unusual bird.

Key words: Opisthocomus hoazin, morphology, ontogeny, wing claws

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Head shape disparity of the cod icefishes Trematominae (Notothenioidei, Teleostei)

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The suborder Notothenioidei (Teleostei) has undergone a remarkable adaptive radiation in the Southern Ocean. Within this suborder, the subfamily Trematominae is endemic to Antarctic waters and represents a dominant component of the shelf fish fauna. After recent advances in molecular phylogenetics, 14 species of *Trematomus* are currently recognized (including *Pagothenia* and *Cryothenia* spp.) comprising both considerable morphological and ecological diversity. Here, we aim to illustrate the main axes of shape variation in *Trematomus* and explore the evolution of their morphology. A dataset of 96 specimens representing 10 species of *Trematomus* from the collection of the Natural History Museum of Paris was assembled, and landmark-based geometric morphometrics was applied to quantify head shape disparity. Regular regression analysis revealed significant interspecific allometry while a low percentage of shape variation was explained by size ($R^2 = 0.11$; $P < 0.001$). Main shape variation across species was explored using a principal component (PC) analysis on shape variables. Two groups diverged along PC1: (1) *T. bernacchii*, *T. hansonii*, *T. pennellii* and *T. tokarevi* have short cephalic profiles with larger cheeks (lowest values along PC1); and (2) *T. lepidorhinus*, *T. eulepidotus* and *T. newnesi* show lengthened cephalic profiles with larger eyes (highest values along PC1). *Trematomus scotti* differed from all other species mainly along PC3 indicating more elongated cheeks. Phenogram based on Procrustes shape distances will be compared to molecular phylogenetic trees and morphometric data will be mapped onto phylogenetic trees in order to illustrate the mode of phenotypic diversification of *Trematomus* during evolution.

keywords: Geometric morphometrics, morphospace, evolutionary morphology, Southern Ocean, diversity

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Long-term changes of the zooplankton community in the Bay of Calvi (Corsica, France)

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Zooplankton plays diverse crucial roles within the marine ecosystem and can also be used as bio-indicator of climate changes since it is very sensitive to environmental changes. Therefore it is essential to consider long-term plankton series. Given the analysis of plankton samples is time-consuming, it requires an effective and rapid analytical method. We have used in this work a supervised learning approach adapted for the semi-automatic classification of digital images of the mesozooplankton of the Bay of Calvi (Corsica, France) by using the Zoo/PhytoImage software. Together with a 11-years long zooplankton time-series, a set of nine environmental variables were monitored in order to identify controlling factors and determine whether the communities were sensitive to global environmental changes. The main components of the mesozooplankton community were characterized by both seasonal and inter-annual variability. Additionally, variation of holoplankton and meroplankton differentiated one from each other. The holoplanktonic community could be split into two subgroups according to its variation in function of the environment: cladocerans and appendicularians, and to a lesser extent, copepods on one hand, and cnidarians, chaetognathes and thaliaceans, on the other hand. Regarding inter-annual variation, one year (2007) showed particularly low production of total zooplankton which was also the case for all the different holoplanktonic taxa. Accounting for that phenomenon were identified some potentially underlying environmental factors. Finally, although water temperature increased significantly over the last years along with the frequency of marine heat wave events, no evident change in the global zooplankton composition was observed yet.

keywords: Zooplankton, Global changes, Mediterranean Sea, Corsica, ZooImage

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Copper toxicity on coral holobiont photosynthetic processes

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Copper (Cu), an essential micronutrient to organisms, may become toxic when present at too high environmental concentrations. This metal remains an aquatic contaminant of concern, notably because of its recent re-use as biocide in metal-based antifouling paints. The aim of this study was to monitor the physiological alterations in a zooxanthellate coral species and its endosymbionts (i.e. the coral holobiont) exposed to increasing Cu concentrations. Nubbins of *Seriatopora hystrix* were exposed for 8 days in 1 L intermittent respirometers to 5 nominal Cu concentrations: 0-2-5-15-50 ppb. Respirometers were maintained at $25.0 \pm 0.2^\circ\text{C}$ with successive open/close cycles of 30 min. A 12/12 hours day-night light regime was applied with constant daylight intensity of $200 \mu\text{mol photons m}^{-2} \text{ s}^{-1}$. Water renewal rate during the 30 min open cycles was $15 \text{ mL} \cdot \text{min}^{-1}$. The photosynthetic performances of coral endosymbionts were assessed daily with a fluorescence imaging system (imaging-PAM). At the end of the 8-days experiment, the maximal photochemical quantum yield (FV/FM) of coral nubbins had decreased by 12% and 38%, respectively, in the 15 ppb and 50 ppb treatments. This decrease was even greater for the effective photochemical quantum yield (ΦPSII) with values dropping by 41% and 54%, respectively. Cu exposure also affected the symbiosis between the coral host and its endosymbionts. Nubbins of the 15 ppb treatment slightly lightened from day 6, whilst nubbins exposed to the 50 ppb treatment lightened from day 3, and started to bleach from day 6. The analysis of nubbins' primary productivity did not coincide with the above observations, the oxygen production within each respirometer remaining relatively constant during the overall experiment for all treatments. This unexpected observation may be the sign of a compensation mechanism. In conclusion, Cu affected the photosynthetic processes of *S. hystrix* within 8 days from relevant environmental concentrations of 15 ppb. The exposure of corals to toxic chemicals thus has to be considered as an additional stressor to, e.g., ocean acidification or elevated temperature, which may disturb their ecophysiology and lead to bleaching.

keywords: Scleractinian coral, Seriatopora hystrix, copper, toxicology, photosynthetic processes

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Notes on the Schizorhynchia (Platyhelminthes, *Rhabdoceola*) from the Iberian Peninsula, with the description of four new species.

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Rhabdoceola Ehrenberg, 1831 is a very species-rich taxon of free-living flatworms. In many regions of the world, including most of southern Europe, their diversity remains poorly investigated. In the Iberian Peninsula most past research has focused on *Rhabdoceola* of freshwater environments. Here we give an overview of the marine rhabdoceols belonging to the taxon Schizorhynchia Meixner, 1928, collected during several sampling campaigns in the Algarve region in Portugal, as well as the regions of Galicia and Andalusia in Spain. Four species new to science are described, including three species belonging to the genus *Proschizorhynchus* Meixner, 1928 and one to *Schizochilus* Boaden, 1963. These new species are distinguished from their congeners primarily by the structure of the hard parts of the genital system. New data are also presented for *Proschizorhynchus pectinatus* l'Hardy, 1965, *P. reniformis* Brunet, 1970, *P. tricingulatus* Ax, 1959, *Thylacorhynchus conglobatus* Meixner, 1928, *Carcharodorhynchus multidentatus* Brunet, 1979 and *Diascorhynchus caligatus* Ax, 1959. All of these species are reported from the Iberian Peninsula for the first time.

keywords: turbellaria, *Rhabdoceola*, *Schizorhynchia*, Iberian Peninsula, taxonomy

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Distribution of perfluorinated alkyl substances (PFAAs) in an aquatic food chain in the Vaal River, South Africa.

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Perfluorinated alkyl substances (PFAAs) are highly persistent chemicals, which have a bioaccumulative potential and can be found in wildlife around the world. Although multiple studies have been performed on PFAAs pollution of the aquatic environment, little is known on PFAAs pollution on the African continent and the possible risks for human health they pose. In the present study we examined the distribution of 15 PFAAs in fish, invertebrates, sediment and water, collected at three sites, representing a gradient, along the Vaal River, South Africa. Furthermore, possible risks for human health through consumption of contaminated fish was examined.

PFOS was the most dominant PFAA measured and was present in the highest levels in all abiotic and biotic samples. PFAAs levels in water ranged from below LOQ to 28 ng/L, decreased along the gradient and were either intermediate or lower compared to other studies in Europe, Asia and America. In sediment only one concentration of 2.36 ± 0.08 ng/g dw showed good recoveries. Concentrations in biota increased along the gradient. PFAAs levels in invertebrates ranged from below LOQ to 34.39 ng/g dw and were low or intermediate compared to studies in Asia and America. PFAAs levels were higher in liver of fish than in muscle tissue and ranged from below LOQ to 340.2 ng/g ww in liver and below LOQ to 12.2 ng/g ww in muscle.

Assessment of the risk for human health through the consumption of PFAA-contaminated fish indicated no risk for humans. Maximum edible amounts of fish per day for a person of 70 kg (220 g/d for *Cyprinus carpio*) did not exceed the average South African fish consumption of approximately 20 g/d.

keywords: perfluorinated compounds, aquatic, South Africa, PFOS, human health

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DNA Barcoding of small mesopelagic fish from the Southern Ocean

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Small mesopelagic fish are an important trophic link in the world's oceans as consumers of zooplankton and prey for large fish, marine mammals, and birds. Myctophidae (lanternfishes) predominate in terms of abundance and diversity, and comprise up to 65 % of the entire pelagic deep-sea fish biomass. Their photophore patterns are particularly useful to distinguish species. However, early life stages with less pronounced patterns and individuals damaged during the hauling process often lead to misidentification. DNA barcoding can resolve specimen identification issues and furthermore pinpoint cryptic species, synonymies, or intraspecific phylogeographic patterns. Here, we present a large-scale cytochrome c oxidase I gene (COI) data set of 299 previously unpublished Antarctic mesopelagic fishes, with circum-Antarctic sampling range. This data is combined with Rhodopsin (Rho) sequences and publicly available DNA barcodes yielding > 1000 sequences, the largest dataset of Myctophidae sequences as yet. Morphological identifications and sequence clusters were compared. Phylogenetic trees were created using a Maximum Likelihood approach and compared to recent myctophid phylogenies. Intraspecific genetic distances between geographical areas were evaluated, thus creating a comprehensive picture on Myctophids occurring throughout the Southern Ocean. DNA Barcoding proved useful for Antarctic myctophid specimen identification in most cases. We found few hints of cryptic speciation and shallow intraspecific divergences. In general, the spatial phylogeographic structure is low within the Southern Ocean, possibly due to the high abundance of Myctophids and few barriers to gene flow in the well-connected mesopelagic realm. The phylogeny shows that adaptations to (sub-)Antarctic conditions must have occurred several times, yet only few species manage to thrive in cold waters permanently. Understanding the evolution of this ecologically important group in the Southern Ocean is highly topical given rapid environmental changes and potential exploitation.

keywords: COI barcoding, Myctophidae, Lanternfish, Rhodopsin, Phylogeny

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Finding the joint constraints of the forelimb joints of the horse

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The evolution of monodactyly occurred independently in four different horse lineages; *Equus* is the only remaining lineage. This preliminary study is part of a larger research project that will test hypotheses on the disappearance of the three extinct lineages by creating forward dynamic models for representatives of each lineage. Species specific joint constraints are needed to define boundary conditions for these models. In this first step, we focussed on finding joint constraints of our model species (*Equus caballus*). We identified the range of motion (ROM) of the forelimb joints at 3 different stages: 1) the ROM in horses moving at trot, 2) ROM of intact fresh cadaver forelimbs and 3) ROM of skeletal forelimbs including ligaments, without the influence of major muscle groups. A literature study provided information for stage 1. A cadaver study was performed by tracking bone-pins with reflective marker triads using an infra-red six camera system (Vicon) to calculate the 3-D ROM for stages 2 and 3. The ROM was determined in each of the three rotational degrees of freedom (flexion-extension, abduction-adduction and internal-external rotation). In three out of the five joints, the ROM of stage 2 was lower than the ROM of stage 1. While manually moving the leg we were unable to generate forces as the horse is able to do. Rigor mortis also played a role in the ROM observed in stage 2. The shoulder displayed a large variation in all of the rotational degrees of freedom; this was mainly due to the method used, which will be improved in future experiments. In the near future, the ROM based on the joints surfaces of the forelimb bones will be determined using the same setup as described above. More experiments for stage 3 will be performed to increase the size of the dataset. The final results, together with fossils of extinct species, will be used to predict the ROM of 'moving' extinct monodactyl horses.

keywords: evolution, monodactyly, locomotion, joints, horse

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Morphological variations in the Elastic Spring Apparatus of mochokid fishes (Siluriformes)

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The Elastic Spring Apparatus (ESA) of catfishes such as Ariidae, Doradidae, and Mochokidae is composed of a pair of protractor muscles, which inserts on the transverse processes (Müllerian ramus) of the fourth vertebra. The transverse processes being intimately related to the swimbladder wall, rapid contractions of the protractor muscles have been shown to produce sounds. Here, we focus on the ESA of mochokid fishes. This African catfish family is divided into nine genera and contains over 200 species. Some of these genera are monotypic while the *Synodontis* genus underwent an impressive radiation and counts more than 130 species. Recently, it has been demonstrated that the “protractor muscle” of some *Synodontis* (Mochokidae) can also produce electric discharges (EODs) with a putative communicative value. Depending on the species, *Synodontis* fish produce swimbladder sounds, EODs or both (though not simultaneously). To date, EODs and sounds production was only investigated in a handful of *Synodontis* species and this aspect of mochokid biology was never studied in species from other genera. Our research project aims to provide insights into the anatomical, physiological, and neural adaptations that underlie function changes in the protractor muscle of mochokids. We observed that some mochokid congeners present at least differences in the size, shape, and insertions of the protractor muscle as well as pronounced differences in the size and shape of the Müllerian ramus. The ESA of *Microsynodontis batesii*, for example, is more similar to the ESA reported for doradids than the ESA described for the *Synodontis* species investigated so far. Further investigations are needed to determine if such differences in gross morphology can be related to changes in the function of the ESA.

keywords: catfishes, electric discharges, morphology, sounds

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Egg parasitoids, processionary moth *Thaumetopoea pityocampa* (Denis & Schiffermuller, 1775) populations' regulation factors in the cedar forest of Chr ea (Blida), Algeria

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The study concerns some bioecological features of the processionary pine moth eggs parasitoids in the Chrea cedar forest (Blida).

Results for egg masses measurements and eggs quantification show that the processionary moth population is reaching its peak. Three species of active parasitoids were observed from the egg masses of the processionary pine moth, they are: *Baryscapus servadeii*, *Ooencyrtus pityocampae* and *Trichogramma embryophagum*. The global egg parasitism rate is of 11%. The longevity of these eggs parasitoids varies from one species to another. *Trichogramma embryophagum* life time is relatively limited.

keywords: processionary, eggs parasitoids, cedar, Chrea

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Population genomics of the European nightjar *Caprimulgus europaeus*

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European nightjars *Caprimulgus europaeus* have recently undergone a population and range reduction across Europe. This decline, mostly due to habitat loss, is striking in Belgium, where European nightjars remain in relict populations. To tackle the potential need for conservation actions, it is important to describe genetic variation and understand the processes shaping it. We aim to study population genomics of the European nightjar. DNA samples will be collected over a major part of nightjar's current breeding distribution. We will also focus on the Belgian scale and sample most breeding sites. Several sites have already been sampled: three in Belgium (Limburg province), one in France (Forêt de Fontainebleau) and one in the Netherlands, near the Belgian border. Using this dataset as a starting point, we will detect Single Nucleotide Polymorphisms randomly distributed across the genome by Restriction site-Associated DNA sequencing (RADseq). We intend to characterize genetic variation, determine population structure and reconstruct demographic history. Population genomic analysis will provide valuable insights into the conservation management of the European nightjar through the identification of populations of conservation concern, the understanding of population connectivity, and the estimation of population size.

keywords: European nightjar, population structure, demographic history, RADseq

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Defining units with high potential for aquaculture (UHPA) within species: towards an integration of intraspecific differentiation in fish domestication programs

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Fostering the sustainable development of aquaculture relies partly on the production diversification through new species domestication. However, domestication programs usually consider species as a unity disregarding intraspecific geographic differentiation. Therefore, they overlook potential individualistic responses of differentiated allopatric populations to the domestication constraints. Indeed, such a differentiation can shape genetic, phenotypic, and ecologic specificities, which affect the domestication predisposition or the potential socio-economic attractiveness of a particular population. In the current project, we aim to compare the domestication and socio-economic potential between differentiated populations. As model species, we focus on the European perch (*Perca fluviatilis*) and the common roach (*Rutilus rutilus*). We develop an integrative approach based on multi-marker phylogeographic analyses along with ecological niche modelling to assess a likely population-specific domestication potential. We ultimately aim to define Units with High Potential for Aquaculture (UHPA) within fish species. This should pave the way to improved domestication programs focusing on the most adapted populations to aquaculture constraints.

keywords: Domestication, Intraspecific differentiation, Fish, Phylogeography

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Aquatic vertebrate biodiversity in the Draa basin, southeastern Morocco: impacts of water use and climate change

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The Draa valley in southeastern Morocco is one of the 10 most arid watersheds on earth. The valley is also an area of rich cultural diversity and home to an estimated 750,000 people who earn a living from this fragile desert oasis. Yet, it is under threat from human encroachment and global climate change. In this area, dry periods frequently eliminate superficial flow, alternating with violent flash floods. In addition, a major dam was constructed upstream in 1972 and river flows are now severely constrained as water is held back for human use. The trend of increasing aridity and anthropogenically-mediated salinisation strongly aggravates the already severe human impact on the aquatic biodiversity. Using ecologically relevant bioindicators allows highly sensitive insight into this rapidly changing ecosystem. In this study, we investigated the distribution, abundance and tolerance capacities of some aquatic vertebrates and their relationship with and salinization in the main river basins draining arid areas of the Draa basin, based on field sampling and experimental tests. We inventoried 13 species including 7 native fish (2 relict cichlids: *Coptodon zillii* and, *Oreochromis aureus*; 4 cyprinids: *Luciobarbus* spp. and 1 salmonid: *Salmo trutta*), 4 anuran amphibians (*Pelophylax saharicus*, *Barbarophryne brongersmai*, *Bufotes boulengeri* and *Amietophrynus mauritanicus*), a water snake (*Natrix maura*), and the Blue-eyed Pond turtle (*Mauremys leprosa saharica*), with a variable salinity tolerance affecting their presence and abundance in the water bodies. During dry periods, most populations are fragmented into widely separated pools of water in an intermittent and increasingly brackish to saline waters. Long periods of high salinity revealed to be likely to adversely affect some taxa, such as turtles, exposed to severe dehydration and/or osmotic stress. Consequently, populations of some species are on the verge of extinction and require that they should be given full protection.

keywords: Draa basin, aquatic vertebrates, osmotic stress, drought, climate change

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A novel method to track changes in perissodactyl locomotion: the scapular fossa ratio

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The scapula represents an important bone in the forelimb which often goes understudied. As the most proximal forelimb bone, the scapula is integral for control and stability of the forelimb, especially in mammals lacking a clavicle (e.g. Perissodactyla). The deep lateral scapular muscles, the supraspinatus and infraspinatus, represent key shoulder extensor and flexor muscles respectively and together provide stability for the proximal forelimb. Examining variation in the attachment areas of these muscles (supraspinous and infraspinous fossae) may provide insights into the adaptation of forelimb osteology to differing habitual needs, e.g. large infraspinatus to provide increased stability for heavy, graviportal taxa; large supraspinatus for impact cushioning in rapid runners. Well known examples of such changes in locomotor style include the fish-tetrapod transition, the back-to-water transition (cetaceans), and the acquisition of monodactyly in equids (horses). Here, we use the scapular morphology of perissodactyls (equids, rhinoceroses, tapirs and their relatives) to examine shifts in relative scapular muscle attachment areas through time, with particular focus on equid locomotor evolution. Scapulae from 48 individuals (16 sp.) were scanned using a 3D laser scanner, supplemented with high-resolution photogrammetry. The scapular fossae were highlighted using Geomagic and imported into MeshLab for area calculation. The area of the supraspinous fossa was divided by the total of the supraspinous and infraspinous fossae to give a value for each individual, here termed the Scapular Fossa Ratio (SFR). Significant differences between species were calculated using ANOVA, and SFRs were mapped onto a composite phylogeny. Two main results came out of the analysis. Firstly, neotropical tapirs recorded a high SFR, with *T. pinchaque* displaying the highest SFR of all perissodactyls in this study. Conversely, modern equids display the lowest SFR, significantly different from tapirs. The most basal members of the Equidae (e.g. *Hyracotherium*) display SFRs with nearly equal supraspinous and infraspinous areas, whereas transitional equids in this study exhibit comparable SFRs to modern equids. Our study suggests that the ratio of deep lateral scapula muscles shifted early in equid evolution; this was not mirrored in other perissodactyls, with only a more recent change in SFR in neotropical tapirs (e.g. *T. pinchaque*).

keywords: scapula, Perissodactyla, equid, tapir, locomotion

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Spatial patterns and abundance of commensal *Mastomys natalensis* in a Lassa fever endemic area in Guinea

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Lassa fever is a severe haemorrhagic disease in West Africa, where up to 300,000 clinical cases are estimated to occur annually. The etiological agent of the disease is called Lassa virus, which has as its main reservoir and vector species the Natal multimammate rat *Mastomys natalensis*. Humans can become infected with Lassa virus by contact with this rodent or its excretions. Because there exists no vaccine for use in humans and therapeutic options are limited to the broad-spectrum antiviral ribavirin, rodent control and behavioural health changes are currently considered the only options for control of Lassa fever. In order to develop efficient rodent control programs, it is necessary to have basic knowledge about spacing behaviour and abundance of this host. We performed two experiments in Lassa fever endemic rural villages in Guinea: (1) capture-mark recapture experiment and (2) a dyed (rhodamine B) bait experiment. Results of these experiment show that animals easily move between the houses of humans and the neighbouring fields, and the population density of the rodents (223 +/- 55 individuals per hectare) is significantly higher than what was initially expected. We suggest that rodent control in rural villages in Guinea should not be restricted to houses of humans alone, but also to the neighbouring fields in order to be efficient.

keywords: Lassa virus, Mastomys natalensis, rodent control, spatial behaviour, Guinea

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Molecular analysis of the *Baikalodrilus* species flock (Clitellata, Naididae), an endemic genus to Lake Baikal (Siberia, Russia)

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Lake Baikal is the deepest and most voluminous lake in the world, with a unique environment (ultra-oligotrophic and well-oxygenated waters at all depths), and is located in a region that is experiencing rapid climate change. It is populated with an endemic genus of oligochaetes (*Baikalodrilus*), which currently comprises 21 morphospecies. However, the validity of many species is questionable; the great similarity in their description and the lack of unequivocal diagnostic characters often lead species identification to an impasse. In order to clarify the systematics of this genus, we analysed one nuclear (ITS) and two mitochondrial (COI and 16S) markers of 33 *Baikalodrilus* specimens and four specimens of the genera *Spirosperma*, *Embolocephalus*, *Rhyacodrilus* and *Haber* as an outgroup. Phylogenetic inferences based on parsimony, maximum likelihood and Bayesian analyses showed an early separation between two groups of species that belong to two distinct size classes and helped to re-evaluate the validity of some morphological characters as specific diagnostic characters. Three species identified prior to molecular analyses were consistent with clustering based on DNA sequences. A fourth morphospecies proved to be actually an assemblage of two distinct species. It was also possible to isolate a group of specimens that could be considered as a new species. Other clusters remained ambiguous, not only in terms of molecular clustering but also of morphological distinctness. These results will be useful for a taxonomical revision of the genus and a better assessment of the oligochaete species diversity in a lake environment facing contemporary climatic changes.

keywords: Phylogeny, COI, ITS, 16S, systematics, taxonomy

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Detection of invasive crayfish populations by environmental DNA in fishponds from the natural park of Brenne

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Environmental DNA (eDNA) is a powerful method for assessing the presence and the distribution of invasive aquatic species. We used this tool in order to detect and monitor several invasive crayfishes *Procambarus clarkii*, *Orconectes limosus* and *Pacifastacus leniusculus* present or likely to invade the fishponds of the Natural Regional Park of Brenne. The park is one of the most important wetlands in France and listed as an International RAMSAR wetland zone since 1991. We designed specific primers for each crayfish species, and set up an experimental aquarium approach to confirm the specificity of the primers and the sampling protocol. We analysed samples taken in the Natural Regional Park of Brenne in 2014 and 2015. The field experiment has proven the reliability of the eDNA detection method. Both experiments confirm that qPCR using SybrGreen protocol with the same primers give better reliable results than with TaqMan protocol. After optimization of the eDNA detection in water samples, it is concluded that sampling must be made during the main period of activity of crayfish, i.e. in summer. This method is a powerful tool for establishing the presence or absence of invasive species in the numerous ponds (more than 2000) in the National Regional Park of Brenne.

keywords: Invasive crayfish, biological invasion, environmental DNA, detection, qPCR

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Is vocal communication in birds affected by cellular oxidative stress?

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Avian song is a renowned acoustic trait that may convey honestly several attributes of individual quality. Although some constraints are known to limit vocal communication, it is still unclear which cellular mechanisms underlie the expression of acoustic traits. Recently, there has been growing interest in the role of oxidative stress as a mediator of avian song. We experimentally inhibited the synthesis of glutathione, a key cellular antioxidant, in male European starlings *Sturnus vulgaris*, by DL-buthionine-(S,R)-sulfoximine treatment, in order to experimentally test for the first time whether an altered oxidative balance results in decreased song rate. We measured the effect of our treatment on total song rate and on its two components, i.e. undirected and nest-box oriented song. Treated males that did not own a nest-box (subordinates) suffered increased oxidative stress, while treated males that owned a nest-box (dominant males) did not. Treated non-owners also reduced their undirected song rate toward the end of the experiment. On the other hand, nest-box owners did not suffer any reduction in song rate. Our results revealed that a change in individual oxidative balance results in decreased vocal communication in a social vertebrate, depending on its social ranking. Our results provide support to the hypothesis that acoustic signals may honestly convey information about the individual oxidative status and capacity to regulate the oxidative balance.

keywords: vocal communication, individual quality, oxidative balance, song rate, Sturnus vulgaris

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Effects of copper, cadmium, zinc and their mixtures on the survival and behaviour of *C. elegans*.

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In the past decades, the number of anthropogenic sources of heavy metals increased, which can cause serious health hazards for diverse animals including humans, hereby remaining a persistent (eco)toxicological concern. While toxic effects of individual metals have already been extensively characterized, very little is known about their interactions and putative additive effects, which occur in the environment. Especially soils, sediments and surface waters can be contaminated with mixtures of metals. The effects of metals in mixtures can be additive, antagonistic or synergistic.

One of the major challenges in ecotoxicology is thus to obtain insights in mixture toxicology to set realistic environmental quality criteria. We therefore aim to investigate whether and how metal toxicities modulate the survival rate and how this is translated to the behavioural level by looking at the locomotion and chemosensory capacities. To do so, we fully exploit the benefits of the free-living soil nematode *Caenorhabditis elegans* as a unique model to investigate the effects of exposure to copper, cadmium and zinc (as single metal and in combination) for different concentrations.

keywords: mixtures, metals, nematodes, behaviour, survival

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A survey of the peri-urban bushmeat markets along the left and right banks of the Congo River in the region of Kisangani (DR Congo)

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Although there are several studies that address the bushmeat market in Kisangani there are only few studies on the bushmeat trade in the peri-urban area around the city.

Most studies are limited to describing the animal diversity sold as bushmeat on these often small suburban markets. The absence of detailed information on the areas from where these small peripheral markets are supplied does not allow to reliably infer the geographic origin of that bushmeat, nor does it allow to obtain reliable information on the relative importance of these different axes between the city of Kisangani and its hinterland, and how these may have different effects on the biodiversity in the region.

To address these issues, we carried out a five month long survey (February to June 2016) during which we surveyed the carcasses of game displayed on the vendor stalls of vendors of bushmeat, as well as the carcasses transported to and from peri-urban markets along the left bank of the Congo River (more specifically in the Isomela market Pk barrier common Lubunga).

We compared the species composition of the bushmeat that was available at the studied markets, we investigated the source of their bushmeat products, and how the transport of these products was realised. In total, we recorded 3043 carcasses and found that even-toed ungulates (Artiodactyla) and rodents (Rodentia) are the most often detected groups on these markets. The two most encountered species were the African brush-tailed porcupine (*Atherurus africanus*) and the bay duiker (*Cephalophus dorsalis*) while the Black-footed mongoose (*Bdeogale nigripens*) and the Sitatunga (*Tragelaphus spekei*) were the rarest species. Bushmeat transport is mainly done by motorcycle, followed by truck, the bicycle being used least often.

Despite of the detected differences between the studied markets, our results suggests that Artiodactyla and Rodents are currently exposed to the highest hunting pressure related to commercial activity in the studied region. We argue that unless measures are taken, this high pressure could lead to the decline of the affected species in the region, and even lead to their extinction.

keywords: bushmeat, hunting pressure, biodiversity, conservation, DR Congo

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Inventory of Ixodidae and Phtiraptera of pigs (*Sus scrofa domesticus*) in a slaughterhouse of Kisangani (Tshopo, DR Congo)

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The infestation of pigs by bloodsucking arthropods is a neglected issue that causes economic losses in the Afrotropical pig farms. These ectoparasites carry vectors of pathogenic agents that can be transmitted from domestic pigs to man. These pathogens include viruses (Nairovirus, Asfivirus,...), bacteria (*Borrelia duttoni*, *Rickettsia rickettsia*,...) and protozoans (*Babesia microti*, *B. divergens*,...). Those vector-borne diseases are rarely diagnosed by health care workers in resource poor countries such as the DR Congo.

We inventoried the hard ticks (or Ixodidae) and biting lice (or Phtiraptera) collected on pigs (*Sus scrofa domesticus*) sold at a slaughterhouse in Kisangani (IAT market). This preliminary survey was carried out from September 2015 to February 2016 and consisted of weekly collection of all ticks and lice from pigs at that slaughterhouse.

We collected 576 ectoparasites (105 Ixodidae and 471 Phtiraptera) on 91 pigs. The ectoparasites were preserved in ethanol 70% and identified to the species or genus level. While only one species of louse was collected (*Haematopinus suis*; 81.77% of all ectoparasites), we counted eleven Ixodidea species. Of all Ixodidea, *Rhipicephalus lunulatus* was the most abundant species (31.4%), followed by an unidentified *Rhipicephalus* species (29.5%). The genus *Ixodes* was the least represented with 1 specimen (<0.01%).

The pigs sold at the IAT market originated from 11 localities from the Tshopo province, Bumba , Isangi , Kisangani , Lokutu , Opala , Opala road , Ubundu, Ubundu road, Yangambi and Yanonge , with a clear bias towards the axis Kisangani-Basoko. Also the tick and lice index were the highest for the pigs of this region. The second step of this study will involve the molecular detection of pathogenic agents harboured in the collected ectoparasites. That approach will allow us to identify the role of these ectoparasites for the spread of undiagnosed zoonotic diseases in man and animal.

keywords: hard ticks, lice, pigs, slaughterhouse, Kisangani, DR Congo

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Unravelling population structure and recent colonization history of an elusive carnivore, the Eurasian otter (*Lutra lutra*), in western France using microsatellites and Single-Nucleotide-Polymorphism markers

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At the dawn of the 20th century, the Eurasian otter (*Lutra lutra*) was widely distributed in France. However, due to intensive trapping and poaching for its meat and fur, the distribution range of the Eurasian otter got highly fragmented. Since the otter received legal protection in the seventies, a recolonization of its former range from relictual refugia has taken place. The present study therefore aims at evaluating the natural recovery of the otter in France through the investigation of the genetic differentiation and diversity of several otter populations originating from Western and Central France, and Northern Spain (Navarra). Assessing the genetic diversity of endangered species is indeed of major concern in the field of conservation biology since low genetic diversity and inbreeding depression may lead to reduced fitness and lower the adaptive potential of individuals to environmental changes. To investigate the genetic variation within and among the otter populations, STRUCTURE analyses were performed on 14 polymorphic microsatellite markers and almost 6,000 SNPs genotypes. These analyses identified five distinct groups, which appear to coincide with the respective suspected refugia. Indeed, some remnant populations were suggested to have survived along the Atlantic coast and in the Massif Central. Inference on population history (DIYABC) allowed to confirm the probable link between ancient human pressures and populations fragmentation, with the progressive fragmentation over time into several distinct clusters. Recent secondary contact and admixture appeared to have occurred between the genetic clusters, enhancing their genetic diversity and potentially increasing their recolonization dynamics. These regions could be considered as the strongholds where the species survived.

keywords: Lutra lutra, refugia, recolonization pattern, Genotyping-by-Sequencing, genetic diversity

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The interaction between environmental temperature and metal toxicity tolerance in zebrafish (*Danio rerio*)

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Zebrafish has become a valuable vertebrate model organism in a wide range of biological research including ecotoxicology. Although there are several studies on metal toxicity in zebrafish, investigations on the interaction between thermal background of the organism and metal uptake and toxicity are really rare.

Changes in environmental temperature can profoundly change species physiological condition. By this study we aim to see if different temperature regimes affect the organism tolerance against metal toxicity. For this purpose, we have defined two scenarios: Acute: in which fish were shocked in 5 different temperatures (17, 22, 25, 32 and 34 °C) and subsequently introduced to metal contaminated water including Cu, Cd or Cu+ Cd for 10 days. Chronic: in which fish were acclimatized to 5 different temperatures for 28 days and then they were challenged by the same metal pollutants. The condition of the fish was monitored during the experiment, including behavioural and physiological metrics and also water quality monitoring. At the end of the exposure period, whole body metal and essential electrolyte concentrations were determined using ICP-OES.

The results showed that Cu was much more toxic than Cd. However, Cu and Cd together showed a large synergistic effect. A low temperature shock appears to be protective while a high temperature shock increases sensitivity. Whereas, acclimation to warm temperatures increase the tolerance against metal toxicity in comparison to acclimation to cold temperatures.

The results of whole body metal analysis showed that the metal burden in heat shocked fish is significantly higher than the cold shocked ones. While, the fish which acclimatized to cold temperature show a higher metal level in comparison to the fish which acclimatized to a warm temperature.

Considering the major role of electrolytes in keeping the body homeostasis constant. We have also investigated electrolyte levels (Na, K, Ca and Mg). We found a consistent and significant drop in sodium levels between the alive and dead fish. Such an effect was not observed for the other major cations.

The results of these experiments show that the thermal prehistory plays an important role in determining the tolerance of zebrafish towards metal exposure and likely also other stressors.

keywords: thermal prehistory, metal toxicity, electrolyte levels, zebrafish

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A survey of the bushmeat trade of the straw-coloured fruit bat species (*Eidolon helvum* Kerr, 1792, Chiroptera) on Maele Island, Kisangani (DR Congo)

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Although bats carry out important beneficial ecological and agricultural functions such as pollination and dispersion of seeds, they often carry dangerous diseases. This is worrying because of the increased dependence of the urban populations in Kisangani on bats as a source for animal proteins. The straw-coloured fruit bat (*Eidolon helvum*) is one of the most notable bat species that is at the same time important as a food source and as a host for zoonotic diseases. It is a widely distributed species that is fairly common throughout its distribution area, yet it was recently classified as Near Threatened on the IUCN Red List due to a decreasing population trend.

To simultaneously evaluate the hunting pressure on this species, and the supply of straw-coloured fruit bat for human consumption, we inventoried the carcasses of this species on one of the main bushmeat markets in the region of Kisangani, situated on the island Maele. Our survey was carried out between January to December 2013 and targeted hunters as well as traders. In total we counted a total 3034 carcasses.

Our preliminary results suggest that the hunting pressure on the straw-coloured fruit bat is rather stable. It is highest during the months October, September and May, and lowest for the months April and December. Interestingly, our results do not show a decline in trade of these bats during the period that hunting is illegal in the DR Congo (August-November). This suggests that hunting activities are not ceased during that period. The fact that the local population consumes these bats on a regular basis throughout the year, creates a very important opportunity for spill-over events that may lead to the outbreaks of zoonotic diseases (1). In combination with results on the prevalence of selected pathogens, our results will be used to inform the local public on the dangers associated with the consumption of bats, and on the consequences of disregarding the hunting season for the survival of these remarkable representatives of the species rich bat fauna in the DR Congo.

(1) See presentation of Anne Laudisoit et al. on Monkeypox

keywords: bats, bushmeat, hunting, Eidolon helvum, DR Congo

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Application of the ethanol extract of *Cistus ladaniferus* and its impact on the reproductive behaviour of *Schistocerca gregaria* (Forskål , 1775) (Acrididae, Cyrtacanthacridinae)

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In many semi-arid and arid regions, agricultural production is severely tested by periodic drought, soil erosion and desertification. It is also heavily damaged long ago by herbivores, namely locusts. Among the locust pest to agriculture, the desert locust *Schistocerca gregaria* (Forskål, 1775) holds a special place in pests. In order to conduct a reasonable fight against it knowing that populations of this pest are at acceptable levels is important. In this context, we are interested to study the chemical enhancement of plant extracts as potential insecticidal against Desert Locust. To achieve this, the extraction is continued for *Cistus ladaniferus*. The fresh plant organs are harvested and dried in the shade at room temperature in the laboratory. Afterwards it was extracted with absolute ethanol (organic solvent) until a crude alcoholic extract. Then we isolated crickets that just made their fledgling. The results showed that *Cistus ladaniferus* causes a delay in the time of laying. Treatment with *Cistus ladaniferus* delays the time of the first oviposition: females make their first egg case after a 15-day delay compared to the control. The presence of monoterpenes in the *Cistus ladaniferus* has probably induced slowing of nesting females emission.

keywords: Schistocerca gregaria, herbivores, insecticidal potential, crude alcoholic extract, monoterpenes

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How to use bioacoustics to study submarine canyons biodiversity?

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The principle of passive acoustics is to position hydrophones in the water to extract information about biotic and abiotic sounds from the ecosystem. This inexpensive technique (in equipment and human resources) allows to investigate places where man does not have access, like seabeds, and over long periods, allowing to refine observations. In this presentation, we present the methodology and the first preliminary results of the study of the submarine canyon macrofauna in the Mediterranean Sea.

keywords: passive acoustics, submarine canyon, Mediterranean Sea, soundscape ecology, bioacoustics

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Bioaccumulation of trace metals in *Mytilus galloprovincialis* from the Algerian west coast

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Algeria has a 1622 km long coastal strip where a large proportion of the population and the main economic and industrial activities of the country are concentrated. Its coastal fringe therefore suffers from various degradations. In particular, the Bay of Oran is housing industrial, commercial, fishing and recreational activities, where 80 % of domestic and industrial wastewaters are not purified before being discharged into the sea.

Thus, the aim of the present work was to evaluate the degree of metallic contamination of coastal waters of western Algeria. Trace metals (Zn, Cu, Ni, Fe and Pb) were measured by atomic absorption spectroscopy in the dry soft tissues (gills and gonads) of the mussel *Mytilus galloprovincialis* Lamarck, 1819 collected during the four seasons of year 2010 in 2 sites: the highly polluted Oran harbor (S1) and Ain Defla (S2), a site distant enough from Oran and presumed little contaminated.

Oran harbor was globally more contaminated than Ain Defla, especially for Fe, Zn and Ni. However, Pb levels were higher at Ain Defla with concentrations up to 3.35 ± 0.25 ppm in the gills. Metal concentrations differed between organs. Fe, Zn and Cu were more accumulated in gills (46.91 ± 1.60 ppm, 25.6 ± 1.07 ppm, 2.68 ± 0.50 ppm, respectively) compared to gonads (29.06 ± 1.07 ppm, 21.76 ± 1.46 ppm, 1.44 ± 0.20 ppm, respectively). Each metal followed a seasonal trend, showing concentration peaks during winter and spring for gills and autumn for gonads.

This study demonstrated the need to biomonitor the metallic contamination of Algerian coasts. But such monitoring surveys, relying on organisms, will require consensual sampling and analytical protocols to avoid hazardous conclusions due to tissue speciation and accumulation seasonality.

keywords: Algerian coast, Mytilus galloprovincialis, biomonitoring, trace metal, tissue speciation, seasonality

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New species of *Baltoplana* Karling, 1949 (Schizorhynchia, Rhabdocoela, Platyhelminthes).

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Microturbellarians are among the least known meiofaunal taxa, and many areas of the world are virtually unsampled. In total only three species of *Baltoplana* Karling, 1949 are described until now. In this contribution we will focus on species new for science, from different marine localities covering the Mediterranean Sea, the South Atlantic Ocean, the Indian Ocean, and the Pacific Ocean. New species were found in Portbou (Spain), Sao Paulo (Brazil), Port Lincoln (South Australia), and Coffs Harbour (East Australia). These species are described and their taxonomical and phylogenetic position is discussed, based both on morphological and molecular data.

keywords: Flatworms, microturbellarians, biodiversity, taxonomy

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Ants-plants relationship in an apple and citrus orchards.

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Ants are insects of the family Formicidae. They belong to the order Hymenoptera. They are social insects, during their evolution they have developed close relationships with plants and thousands of species of animal organisms.

In order to define the relationship Plants - ants in an apple orchard and in an citrus orchard In the Horticultural Station of E.N.S.A (Algiers); two methods of sampling were used; Barber pots and harvesting by hand.

The method of Barber pots has identified in the apple orchard 9 species with *Tetramorium semilaeve* as the most abundant species with a rate equal to 41%.

Furthermore the value of the diversity index is 0.6 pieces and equitability is 0.63. ($H' = 0.6$ and bits $E = 0.63$). In the citrus orchard 11 species are noted, *Tapinoma nigerrimum* is the dominant species with a rate of 29%. The value of diversity is 3.2 bits and equitability is 0.9 ($H' = 3.2$ and $E = 0.9$ bits).

By the method of harvesting by hand, *Tapinomma nigerrimum* is the only species recorded in the trunks and the crowns in the apple orchard. *Crematogaster scutellaris*, *Plagiolepis barbara*, *Camponotus barbaricus xanthomelas*, *Tapinoma nigerrimum* and *Crematogaster laestrygon* are species noted in trunks and crowns in the citrus orchard.

keywords: Barber pots, ant-plant relationship, Formicidae, apple orchard, citrus orchard

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Corticosterone, oxidative status, and inflammation markers as tools to predict the progress of a herpesvirus disease in frigatebird nestlings

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The immune system provides protection against parasites and pathogens. There are, however, circumstances under which the immune system is disrupted, making organisms more susceptible to infections. Herpesviruses are one of the most common infectious viral agents in domestic and wild animals, but little is known about the effects of viral outbreaks on the physiology and survival of wild animals, and studies assessing the role of oxidative stress as promoter of the viral activity are lacking in wild animals. Here, we have assessed for the first time in a wild vertebrate (i) whether individuals with either low levels of oxidative damage or high levels of antioxidant protection are less susceptible to develop symptoms; (ii) the association between inflammation, oxidative damage, cort and nestling's survival; and (iii) the patho-physiological consequences of herpesvirus infection on corticosterone, and inflammation. To address our questions, we took advantage of a unique population of Magnificent frigatebirds whose nestlings have experienced severe disease likely due to an herpesvirus outbreaks. Our work demonstrates that oxidative markers and inflammation are associated with the occurrence of clinical signs and with nestling's mortality, and how the inflammation marker haptoglobin was associated with nestling's probability of survival.

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Personality types vary in the use of personal and social information and their trade-off

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In a changing world, gathering information about the environment such as the location and the quality of food is crucial for an animal's survival. To acquire this information an individual can choose to collect 'personal information' by interacting with the environment itself, or to observe the behaviour of others and collect 'social information'. Which of these options is used, depends on the situation an animal is in. Moreover, it has been suggested that there is individual variation in the extent to use either personal or social information.

Personality comprises the concept of consistent inter-individual differences in behaviour and could be associated with variation in information use. Besides, the extent to which personal information is used might affect the necessity to use social information and vice versa. Therefore, the use of personal and social information might depend on each other and personality might affect this relation.

We tested this by conducting behavioural experiments based on a colour association task in captive great tits (*Parus major*), for which exploratory behaviour is often used as a proxy for personality. We quantified personal information use by measuring to what extent a bird relied on earlier rewarded options instead of novel options. Social information use was determined by recording how often a bird chose according to social information provided by video playbacks of a conspecific.

We here demonstrate that differences in the use of both personal and social information are personality-related. Furthermore, we show that the decision between personal and social information use is personality-dependent. Our findings indicate that there is individual variation in personal information use, social information use and in the decision between relying on these two sources of information. These differences between the personality types could arise as a consequence of different costs and benefits in acquiring and/or applying the two types of information, possibly due to differences in, for example, cognitive ability. In conclusion, we demonstrate that personality types have different strategies to reduce environmental uncertainty. These findings contribute to understanding individual variation in adapting to a changing world.

keywords: personality, social information, personal information, video playbacks, great tits

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Wildlife Conservation: is Domestication a Solution?

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Biodiversity is facing a major crisis, which is most often described as the sixth mass extinction or Anthropocene extinction. Several solutions have been proposed to save threatened animal species, among which ex situ conservation or captive breeding, which is the essential part of a process called domestication. The main goals of the present chapter is to define clearly what domestication is, describe what the possible consequences are and discuss whether it can truly play a significant role to save threatened animal species. Domestication appears as a possible tool to help saving threatened species. Nevertheless, the time in captive conditions has to be minimized in order to modify as less as possible wild individuals. Therefore, zoos and aquariums can play a crucial role in helping to save the most endangered species and then restore their populations in the wild, but only if they are involved in both in situ and ex situ conservation programmes. More importantly, domestication should be considered as part of the solution, but not the only one, to save threatened species. The protection of wild animals in situ, the restoration of habitats and the development of reserves should first be considered.

keywords: wildlife, domestication levels, endangered species, mammals, fish

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Personality traits and behavioural syndromes across seasons and years in Starlings

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Insights into how personality traits and behavioural syndromes vary over time and context are crucial for adequately estimating their developmental, evolutionary and ecological significance. We repeatedly quantified novel environment exploration and different aspects of the behavioural response towards a female conspecific (sociability traits) in captive male starlings (*Sturnus vulgaris*) across seasons and years. (Co-)variance-partitioning revealed moderate repeatabilities for all traits across seasons and years (range: 0.25-0.41), however, no significant among- (or within-) individual correlations between them. Our results indicate that exploration and sociability traits are context-general and relatively stable personality traits, but do not interlink into behavioural syndromes. This strongly suggests the independent evolutionary potential of these traits under selection, hence not constraining each other's evolutionary trajectories. More informed predictions about ecological and evolutionary implications await cross-validation with results from the wild and studies addressing the relation with life-time fitness variation.

keywords: Animal personality, long-term, across-season, social behaviour, (co)variance partitioning

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The effect of diet-induced obesity on serotonergic enteric neurons in zebrafish

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Obesity is a worldwide epidemic and a major risk factor for numerous diseases including cardiac failure, diabetes and cancer. Peripheral serotonin (5HT) seems to be positively correlated with body weight and altered expression of 5HT-receptor subtypes has been reported in obese patients. These factors might contribute to the altered gastrointestinal (GI) motility in obese patients, but the underlying mechanism still needs to be further elaborated.

The aim of the present study was to investigate the effect of diet-induced obesity (DIO) on enteric 5HT-expression and on GI-transit.

Zebrafish were kept in small colonies and fed either a high caloric diet (HCD: 150 cal/day/fish) or a normal diet (ND: 20 cal/day/fish) for 4 weeks. The proportion of 5HT expressing neurons in the GI-tract was analysed using immunofluorescence staining using antibodies for 5HT and the pan-neuronal marker HuC/D. In addition, quantitative PCR (qPCR) was performed on brain and intestine for the expression of tryptophan hydroxylase (TPH) 1a, 1b and 2, the rate limiting enzymes in the serotonin metabolism, and for the serotonin-4 receptor. GI transit was measured after gavaging glass beads into the proximal intestine.

After 4 weeks, the BMI (body mass index= g/cm^2) of HCD fish was significantly increased. Overfeeding increased the proportion of serotonergic enteric neurons in the proximal and first part of the mid intestine. qPCR revealed significant elevated levels for TPH2 in brain and intestine, but not for TPH1a/b. Furthermore, a significant increase in the expression of 5HT-4 receptor was observed in brain, but not in the intestine. The GI transit did not significantly change after 4 weeks overfeeding, though a trend was observed where the transit time for HCD fish decreased in comparison to ND fish. In this study, analysis of the GI tract of DIO-fish revealed an increase of 5HT-expressing enteric neurons, probably due to an increase in TPH2 expression in brain and gut, affecting intestinal transit. More studies are required to assess the exact mode of action.

keywords: obesity, zebrafish, serotonin, gastrointestinal motility, enteric nervous system

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Molecular taxonomy and phylogeography of the endemic Cuban terrestrial gastropod *Emoda sagraiana* (Helicinidae)

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Despite the fact that the Helicinidae represents a significant proportion of the tropical molluscan fauna, this family of operculate land snails has been poorly explored. The family comprises over 500 described species with a distribution range limited to the subtropical and tropical zones of the New World, Australasia and the Pacific. In this tropical belt, the island of Cuba has a particularly rich helicinid fauna, including four endemic genera, one of which is *Emoda* H. & A. Adams, 1856. This genus comprises 14 species that are mainly restricted to mountain areas and that live on the ground under rotting leaves, on branches, as well as on calcareous rocks. Although *Emoda* species can occur on the emblematic Cuban “mogotes” (isolated steep-sided hills composed of limestone), they are not confined to limestone substrates. The highly shell and colour polymorphic *Emoda sagraiana* (Orbigny, 1842) varies from a small brownish form with an acute notch and thin lip to large greenish forms with a red spire and/or callus and a heavy lip, with all kinds of intermediates. In order to better understand the taxonomic differentiation and phylogeography of *E. sagraiana*, a total of 70 specimens were collected across 14 sites in the provinces of Pinar del Río and Guantánamo, Cuba. DNA sequences were generated. Based on a phylogenetic analysis of three mitochondrial (16S rRNA, COI and Cytb) gene fragments of 20 specimens and the nuclear ribosomal ITS2 of 43 specimens, 14 haplotypes were distinguished and used to infer evolutionary relationships. Separate Neighbour-Joining trees (Kimura 2-parameter distances) of the concatenated mtDNA gene fragments and of ITS2 suggest that there is phylogeographic and/or taxonomic structuring in *E. sagraiana*.

keywords: Emoda sagraiana, molecular taxonomy, phylogeography, endemic, Cuba

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A behavioural analysis and differential proteomics approach to study effects of pharmaceuticals in the zebrafish

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Pharmaceuticals are widely used by humans, for food production or for veterinary purposes, but they may also enter the environment. However, many pharmaceuticals (if not all) have unknown mode of actions in the different environmental niches. Especially neuro-active drugs are of particular concern when acting on non-target species as the neural system is essential for the regulation of various physiological processes and behaviours. Studying altered zebrafish behaviour as a consequence of exposure to defined pharmaceuticals and subsequent monitoring of molecular changes, allows obtaining mechanistic and functional insights underlying aversive physiological and behavioural effects of pharmaceuticals. In this respect, the zebrafish is also one of the most valid models in ecotoxicological research to study effects of chemical pollutants in aquatic environments, on different levels of complexity or organization.

Upon exposure to selected pharmaceuticals, like the psychoactive drug mianserin, we are assessing the spatiotemporal dynamics of free swimming behaviour using 3D video tracking. Next, by adopting differential proteomics, we aim to reveal mechanistic information of toxicity at the molecular level, or at least aim to provide a picture of (biochemical) pathways that are affected. Doing so, a tandem mass tag (TMT) labelling method was combined with liquid chromatography and tandem mass spectrometry to analyse effects of mianserin. We ultimately aim to integrate affected behavioural parameters with altered biochemical pathways as to provide improved mechanistic insights on the mode of action of defined pharmaceutical compounds.

keywords: Behaviour, omics, zebrafish.

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Cortisol from hair; an indicator for elevated stress levels in the common marmoset (*Callithrix jacchus*)

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The relatively new technique of hair cortisol determination may have useful applications in husbandry as a measure of stress in captive animals. Cortisol incorporated into hair can be detected even after years of storage and provide a retrospective measure of cortisol levels at the moment of collection. Cortisol levels may differ between the sexes and depend on age. In the breeding colony, we determined whether cortisol levels were affected by sex and life stage and investigated the effect of multiple (>3) husbandry procedures under sedation on the hair cortisol level. Animals experiencing up to three husbandry procedures under sedation were considered to be non-stressed and have basal cortisol levels. Cortisol levels were obtained from 221 samples collected from captive common marmosets (*Callithrix jacchus*) housed in groups or pairs in the breeding colony of the Biomedical Primate Research Centre (BPRC) in Rijswijk, The Netherlands. Samples were collected from the back of the neck during husbandry procedures from 2010 to 2016. Cortisol was assessed using an Enzyme-linked Immunosorbent Assay (ELISA). Hair cortisol levels of breeding females were higher than those of breeding males and female and male offspring. Male offspring had higher cortisol levels than female offspring. Hair cortisol levels were significantly higher in individuals that experienced multiple husbandry procedures compared to non-stressed breeding males, and offspring of either sex. Therefore, frequent interventions in a breeding group may be considered stressful. This demonstrates that hair cortisol level is a useful indicator of stress in captive marmosets. In contrast, no significant difference was found for breeding females. Breeding females had a relatively high cortisol level. Breeding itself may increase cortisol levels. Alternatively, breeding may be stressful for adult females and this may prevent an additional reaction to stressful events.

keywords: Primate, Hair Cortisol, Stress, Breeding, Husbandry

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An analysis of acoustic telemetry data on river lamprey (*Lampetra fluviatilis*) migration in a fragmented lowland river

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Anthropogenic impact on the freshwater environment is most dramatic and has been increasing with a growing population size and industrialization. The disruption of longitudinal and lateral connectivity of rivers has led to ecological catastrophes such as the extinction of several diadromous fish species. River lamprey (*Lampetra fluviatilis*) require several types of habitat to complete their life cycle including the marine environment for the adults, but also freshwater areas for reproduction. Therefore, this is an important indicator species for the integrity of ecosystems and connectivity within and between catchment areas. In the highly fragmented River Scheldt basin first restoration actions are undertaken, such as the building of nature-like bypasses to solve several lock-weir complexes.

In 2012 thirty-one adult river lamprey were followed during their upstream migration in the River Scheldt and its tributaries using acoustic telemetry (Vemco technology: V7 and V8 transmitters; VR2 and VR2W data loggers). The residence time of river lamprey was found to be significantly higher at receivers downstream of a barrier compared to receivers not nearby a barrier, suggesting that the upriver migration of river lamprey is delayed by migration barriers in the River Scheldt. This information is valuable to optimize migration of fish by providing bypasses and shows the importance of monitoring the applied management strategies.

keywords: river lamprey, anadromous, acoustic telemetry, river connectivity

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Does consistent exploration behaviour affect probability of virus infection?

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A growing body of evidence suggests that consistent differences in behaviour between individuals (i.e. animal personality) could influence parasite and pathogen dynamics in wildlife. While most research focused on ectoparasites, the effect on pathogen transmission has been understudied. This study uses Morogoro virus (MORV) and its natural host, the multimammate mice (*Mastomys natalensis*), as a model system to investigate the relationship between exploration and infection status with (MORV). Transmission of MORV can be either direct (e.g. via saliva, blood) or indirect through viral particles shed in their excretions. We hypothesized that consistent highly explorative individuals have an increased probability to come into contact with infected individuals or excretions, leading to higher prevalence of MORV-specific antibodies. Exploration behaviour of 124 wild caught *M. natalensis* was repeatedly quantified using an Open field and novel object test. Our results showed that juveniles are more explorative than adults but less active in the field. Contrary to our expectations, we found no correlation between exploration and MORV antibody presence. This may indicate that exploration does not increase the chance to get infected with MORV and suggests that MORV transmission occurs mainly through direct interactions between rodents instead of virus particles shed in excretions.

keywords: Personality, Mastomys natalensis, disease transmission, arenavirus, exploration

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DNA barcoding of ants from the Galápagos Islands (Ecuador)

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Ecuador has been plagued by numerous invasive species, due to an increase of tourism and trade. Galápagos in particular is suffering serious conservation and socioeconomic problems caused by invasive ant species. However, currently it remains difficult to infer how many of the ant species in the archipelago are introduced/invasive and how many occur on mainland Ecuador. Notwithstanding, regular monitoring is key for the early detection of new invasive species, which first necessitates a comprehensive taxonomical database for the Galápagos islands and mainland Ecuador. A joint FWO project between Belgian and Ecuadorian researchers was started in order to establish such a database. It aims at producing species-specific DNA-barcodes for the ants of Ecuador. This will: (1) facilitate the future identification of species, (2) help to chart the diversity of Ecuadorian ant species and (3) uncover the presence of putative cryptic species. Our DNA-barcode database will provide a reliable and easy tool for the identification, early detection and monitoring of both introduced and native ant species.

At present, 232 specimens from Galápagos (40 ant species) and 91 specimens from mainland Ecuador (56 different ant species) are barcoded. Barcoding increased the estimated number of ant species in Galápagos to 53, with one species being a newly recorded exotic species (*Cardiocondyla obscurior* Wheeler 1929). Increasing worldwide transport to and within the Galápagos allowed new colonization of exotic species, and an increase in their distribution across the archipelago. Indeed, fourteen such introductions to new islands have been recorded in the survey and 8 ant species have spread to new islands in the Galápagos. A clear case is *Tetramorium lanuginosum* Mayr 1870, whose distribution is now recorded from 5 additional islands in the archipelago. Genetically distinguished species, possibly new endemics, were found in the species complexes *Pheidole* HH01 and *Cyphomyrmex* HH04. Our results stress the need for continued monitoring of the diversity of ants as new introductions, will certainly increase over the coming.

keywords: Invasive ants, Ecuador, Galapagos, barcoding, diversity

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Morphological and kinematical analysis of balance in lacertid lizards

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Detection of body motion and orientation by the vestibular system in the inner ear forms one of the basic senses shared by all vertebrates. Because the vestibular system is crucial for maintaining balance, studying its anatomical characteristics could lead to a better understanding of balance control in fast moving animals, such as lizards. Lacertids use a variety of habitats, that may differ greatly in structural complexity (high/ low vegetation, rocky or sandy areas, trees and bushes). In a first approach, we want to examine whether structural habitat complexity selects for changes in the size and shape of the vestibular system. As such, we categorized 28 species in three distinct groups according to their habitat use (densely vegetated areas, areas with vertical elements, open areas). High resolution micro-CT imaging was used in order to visualize the bony labyrinths of the vestibular system of the species under study. Seven additional individuals belonging to a single species were used to estimate the intra-specific variation.

In a second approach, we chased lizards originating from different habitats through an experimental set-up, mimicking a complex habitat (racetrack consisting of 2 consecutive turns, one left- and one right- orientated) in order to test their balance and assess the vestibular system stimulation resulting from the head dynamics used during natural movements. This experimental setup was used on a population introduction project of the species *Podarcis erhardii* (the Greek wall-lizard) in 5 islets (with different substrates) in the Cyclades, Greece. The setup enables us to investigate the running kinematics, focusing on the head rotations, accelerations and body movements of the animals, while facing obstacles (such as the walls and the turns of the racetrack). Performance of the animals was recorded with a high speed camera (500 frames/second) and then information on the body and head kinematics will be acquired from the recordings by frame-by-frame digitization of the body markers. These data, along with a long term observation of the populations' performance through time, could reveal information on whether different sexes and generations cope in a different way with balance challenges and how this is influenced by their local habitat.

keywords: balance, vestibular system, lacertids, habitat

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Hot! Hot! Hot! The hottest fish on earth lives at mammalian metabolic rates.

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The Magadi tilapia, *Alcolapia grahami*, a small cichlid fish of Lake Magadi, Kenya lives in a soda lake, one of the most challenging aquatic environments on earth. Lake Magadi is characterized by high pH (up to 10.0), extreme alkalinity ($> 300 \text{ mmol L}^{-1}$), high temperature ($> 40^\circ\text{C}$), high levels of reactive O_2 species ($> 8 \mu\text{mol L}^{-1}$), unusual water chemistry with salinity close to 60% seawater, and large daily fluctuations in oxygen levels (severe hypoxia to hyperoxia). In contrast to most fishes which live at temperatures substantially lower than the $36 - 40^\circ\text{C}$ of mammals and birds, an isolated population (South West Hot Springs, SWHS) of Magadi tilapia thrives in fast flowing hot springs with daytime highs of 43°C and night-time lows of 32°C . Another population (Fish Springs Lagoon, FSL) lives in a lagoon with fairly stable daily temperatures ($33 - 36^\circ\text{C}$). The upper critical temperatures (Ct_{max}) of both populations are very high; moreover the SWHS tilapia exhibit the highest Ct_{max} (45.6°C) ever recorded for a fish. Routine rates of oxygen consumption (MO_2) measured on site, together with MO_2 and swimming performance at 25, 32, and 39°C in the laboratory, showed that the SWHS tilapia exhibited the greatest metabolic performance ever recorded in a fish. These rates were in the basal range of a small mammal of comparable size, and were all far higher than in the FSL fish. The SWHS tilapia represents a bellwether organism for global warming.

keywords: temperature tolerance, respirometry, critical swimming speed, aerobic scope

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Insects complex associated with the tropical basil, *Ocimum gratissimum* L. (Lamiaceae) in southern Benin.

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Tropical basil is an aromatic leafy vegetable used for its medicinal and therapeutic properties in numerous countries in West Africa (Benin, Nigeria, Togo, etc.). In Benin, it is produced on almost all urban and periurban garden throughout the year for fresh market. Until now there are few or nearly no publications about the arthropod community of this specie, even less in the context of Benin. Thus, to assess this community, basil plots were mowed using a sweep net in three localities (Ouidah, Togba and Sèmè) of southern Benin.

Preliminary results focus on the different insect families that colonized tropical basil in southern Benin environmental conditions. These include: Aphididae (Homoptera), Cercopidae (Homoptera), Chrysomelidae (Coleoptera), Coccinelledidea (Coleoptera), Meloidae (Coleoptera), Braconidae (Hymenoptera), Ichneumonidae (Hymenoptera), Formicidae (Hymenoptera), Vespidae (Hymenoptera), Apoidae (Hymenoptera), Reduviidae (Heteroptera), Pentatomidae (Heteroptera), Pyrgomorphidae (Orthoptera), Acrididae (Orthoptera), Syrphidae (Diptera), Diopsidae (Diptera). Among these families, there are pests: *Aphis gossypii* G. (Homoptera: Aphididae), *Zonocerus variegatus* L. (Orthoptera: Pyrgomorphidae), etc.; predators: *Ischiodon aegyptius* W. (Diptera: Syrphidae), *Cheilomenes* spp. (Coleoptera: Coccinelledidea), *Rhynocoris* spp. (Heteroptera: Reduviidae), etc.; parasitoids and pollinators.

From this study, it appeared that there is a large diversity of families and functional groups (pests, predators, parasitoids and pollinators) associated with tropical basil . Moreover, the presence of natural enemies could be an advantage for farmers in intercropping systems. This would help reduce the use of synthetic insecticides.

This result, which is a first knowledge of the insect fauna associated with tropical basil under the environmental conditions of Southern Benin, will be supplemented by a spatio temporal study to assess the variability and the dynamics of this insect fauna.

keywords: Tropical basil, insect pest, natural enemies, Southern Benin, West Africa.

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Despotism has little effect on relative body weight in captive group-living macaques

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Macaques live in social groups and group living is known to lead to competition over resources such as food. High-ranking individuals may have more access to food than low-ranking ones, which in captivity may lead to overweight for some high-ranking individuals, while low-ranking individuals may be at risk for underweight. This may be especially prevalent in despotic macaques, where the dominance hierarchy is strictly maintained and enforced. This study investigated the relative body weight of female captive group-living long-tailed macaques (*Macaca fascicularis*), that are considered despotic, and rhesus macaques (*Macaca mulatta*), that are even more despotic. Subjects were housed in social groups that had access to relatively large inside and outside enclosures and were fed a nutritionally balanced diet. The dominance status of individuals was categorized as alpha-position, high-ranking, middle-ranking or low-ranking. Furthermore, body weight and height were measured per individual. The weight-for-height index with height to the power of 2.7 (WHI^{2.7}) was used to measure relative body weight, because it was highly correlated with other measures of relative adiposity and independent of height. Rank category had no influence on the relative body weight of female long-tailed macaques, while rank category did affect WHI^{2.7} in female rhesus macaques, but it only explained little of the variation. Overweight occurred in 4% of the population and underweight was rare, while most individuals had a WHI^{2.7} within the normal boundaries. Our study concludes that despotism has little effect on relative body weight and group-feeding typically does not compromise animal welfare in captive group-living macaques.

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