BZS
Royal Belgian Zoological Society

ZOOLOGY 2018
Zoology in the Anthropocene

13-15 DECEMBER 2018 - @ZOO Antwerpen

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To be cited as: Decaestecker Ellen & Lepoint Gilles (Editors). Zoology 2018, The 25th Benelux congress of Zoology, “Zoology in the Anthropocene”, Abstract Book, 137 pages, Antwerpen, Belgium, 13-15th December 2018.

Welcome word

The Royal Zoological Society of Belgium (RBZS) is happy to welcome you to the 25th Benelux Congress of Zoology in the Congress Centre of the Royal Zoo of Antwerp. The RBZS aims to connect researchers in Zoology throughout Belgium and abroad, providing a network for junior and senior members, who benefit through contacts and collaboration. The RBZS publishes the Belgian Journal of Zoology, which is open access (https://www.belgianjournalofzoology.eu/BJZ/index) and distributed in various institutions of more than 50 countries. This journal gives the opportunity to publish high quality studies in a large area of scientific scopes.

Since 25 years, the RBZS and the Royal Zoological Society of the Netherlands (KNDV) organize this Congress together to give especially young, but also senior researchers the floor to present their master, PhD and postdoctoral work. Given its 25th edition, we celebrate it back-to-back with the FWO Kennismakers meeting, celebrating its 90 years anniversary. This is a joint venture of the RBZS, the KNDV and the National Museum of Natural History of Luxembourg (MNHNL).

We especially welcome our keynote speakers: Andreas Wilting, Hilde Eggermont and Eelke Jongejans.

We congratulate the KETS, RBZS public prize and Netherlands Zoological prize winners: Thomas Luypaert, Nathan Vranken and Sjouke Anne Kingma.

We are especially delighted to have an active PhD workshop organized by our RBZS Young Zoologist group.

It’s a great pleasure for us to welcome you for our 25th Benelux congress of Zoology with the theme: “Zoology in the Anthropocene with the subthemes ‘Why Climatologists and Biologists must speak together’ and ‘How animals face global change: plasticity, resilience, adaptation’.

Ellen Decaestecker and Gilles Lepoint, *President and Secretary of the Royal Belgian Zoological Society* *on behalf of the Zoology2018 organizing and scientific committee*

Organisers ZOOLOGY 2018

Prof. Ellen Decaestecker (KU Leuven) - Dr. Gilles Lepoint (ULiège)

Organisers Workshop YOUNG ZOOLOGIST Group

Allison Luger (UGent)
Marielle Kaashoek (UAntwerpen)
Marianna Pinzone (ULiège)

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ZOOLOGY 2018 Venue

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The Flanders Meeting & Convention Center Antwerp is located in the heart of Antwerp, next to Antwerp Central Station. Train is smartest way to reach us. Nevertheless, parking are available around the Flanders meeting and convention centre.

Check accessibility and map here: https://www.fmcca.com/en/accessibility#by-train

Workshop Young zoologist Group (13th December 2018)

Supported by:

1. FNRS doctoral college “Biology, Evolution, Ecology”
2. Doctoral School KU Leuven
3. Doctoral School UGent
4. Doctoral School UAntwerpen

Program: @ZOO – **room Gorilla 2 & 3, registration in Gorilla 2**

Time	
13:30	Welcome with coffee and thee – Registration
14:00	“the starting point of scientific writing – Prof. Reinhart Ceulemans - UAntwerpen
15:00	Question session
15:15	Coffee break
15:30	“How to remain sane during your PhD” –stress Management Workshop by “Make me Fly!
16:30	Coffee break
16:45	“How to remain sane during your PhD” –stress Management Workshop by “Make me Fly! (Part 2)
17:45	Social event (in a bar close to the Zoo, First drink for free!)

Synthetic program ZOOLOGY 2018

Friday 14th December

12:15	Lunch
13:30	General Assembly Royal Belgian Zoological Society **Room: Peacock**
14:35	FWO session: Impact of climate change on ecosytem services
16:00	Key note 1: **Eelke Jongejans** - "Do we understand why insects are in decline?" **Room: Darwin hall**
16:45	Key note 2: **Andreas Wilting** - "From detections to predictions; high-throughput tools for biodiversity assessment and monitoring in changing environments. " **Room: Darwin hall**
17:30	FWO reception

Saturday 15th December

08:00	Registration **room Okapi 2**			
room	**Gorilla 1**			
09:00	**Keynote talk** by Hilde Eggermont (Biodiversity Platform Belgium – RBINS) - “IPBES: strengthening the science -policy interface in the face of global change.”			
09:45	Initiative for biodiversity conservation by Prof. Caroline Nieberding			
10:00	**Parallel session 1**	**Parallel session 2**	**Parallel session 3**	**Parallel session 4**
	GENERAL 1 (Morphology, Ethology, Miscelleanous) Convener: Prof. Dominique Adrieans	**Zoology in Anthropocene** Convener: Prof. Caroline Nieberding	**GENERAL 2** (Genetics, Phylogeny, phylogeography, Miscellaneous) Convener: Dr Marie Verheye	**GENERAL 3** (Ecotoxicology, Physiology , Molecular mechanism) Convener: Dr Jérôme Delroisse
room	**Gorilla 1**	**Gorilla 2**	**Gorilla 3**	**Gorilla 4**
10:00	FLEUREN 1	ZIZZARI 19	*GRESHAM 38	**BEGHIN 57
10:15		MULLER 20	**CHAPELLE 39	BIJNENS 58
10:30	FREDERICH 2	VISSER 21	VAN STEENBERGE 40	DE MEYER 59
10:45	*LOURTIE 3		DA SILVA 41	**THORE 60
11:00	VAN HOUTVEN 4	**DUSSENNE 22	BRUET 42	DELROISSE 61
11:15	**GILLET 5	DE BRUYN 23	GALBUSERA 43	
11:30	**MAC LAREN 6	GUILLAUMOT 24	VERHEYE 44	**DUCHATELET 62
11:45	**LUGER 7	HEMERIK 25		*JANSSEN 63
12:00	**KAASHOEK 8	**BLANCHARD 26	**ZHANG 45	**RAICK 64
12:15	INDEKEU 9	**MWAIJENGO 27	VANHOVE 46	**MORIS 65
12:30	Lunch and poster sessions			
	GENERAL 1 (continued) Convener: Dr Mike Fleuren	**Zoology in Anthropocene (continued)** Conveners: Dr Bertanne Visser Dr Steven Declerck	**GENERAL 2 (Continued) & COST action DNAqua-Net** Convener: Dr Alexander Weigand	**Zoology in Anthropocene (continued)** Convener: Dr Jérôme Delroisse
room	**Gorilla 1**	**Gorilla 2**	**Gorilla 3**	**Gorilla 4**
14:00	*FINET 10	DEKEUKELEIRE 28	**HAMMOUD 53	**SERTEYN 66
14:15	*CARVALHO 11	**RUTTEN 29	KOCHZIUS 47	**VASTRADE 67
14:30	*VERMEYLEN 12	**WEVERS 30	MARDULYN 50	PADILLA 68
14:45	ERNST 13	GAILLY 31	**CUYPERS 51	**LEJEUNE 69
15:00	**OGER 14	MÜLLER 32	FRANTZ 49	*LAMERIS 70
			DNAqua-Net SESSION	
15:15	*VAN MEER 15	**MARTINET 33	WEIGAND A 52	STURARO 71
15:30	*STEEDAM 16	**NOËL 34	MACHER 54	*VAN DEN BERG 72
15:45	**DE MEESTER 17	VAN DER HULST 35	TEIXEIRA 48	**ZHOU 73
16:00	GOLDSBOROUGH 18	HUGé 36	WEIGAND H 56	DECLERCK 74
16:15	*BAAN 75	DE KEYZER 37		
16:30	Poster session (rooms Okapi 2 & 3)			
17:30	Prizes winner presentation + RBZS grants + Zoology 2018 prize			
18:30	ZOOLOGY 2018 end ceremony			

*: master prize **: PhD prize

Detailed program (Oral communications)

Presentation number	Title
FLEUREN 1	The adaptive benefit of superfetation in live-bearing fishes: a slender body leads to improved escape performance
FREDERICH 2	Diversification and functional evolution in reef fishes: The generalist feeding guild is not an evolutionary sink
LOURTIE 3	Evolution of placoid scales in deep-water sharks: from morphology to atomic composition
VAN HOUTVEN 4	Evidence of locomotor and ecological analogy between modern cervids and extinct equids demonstrated by scapula fossa ratios
GILLET 5	Vertebrae are the backbone of cetacean diversity: How morphological innovations sustained dolphin explosive radiation
MAC LAREN 6	Pigs, peccaries and perissodactyls - convergence in scapular spine osteology and muscle arrangement between tapirs (Perissodactyla) and suiformes (Artiodactyla)
LUGER 7	Prehensile tail used linked to myology in chameleons
KAASHOEK 8	Determining the instantaneous axis of rotation of different monodactyl species
INDEKEU 9	Influence of body mass, phylogeny and ecology on morphological variation in the third metacarpal of rhinos (Perissodactyla; Rhinocerotidae)
FINET 10	Are morphological traits explaining swimming performances of several deep-sea sharks from New Zealand?
CARVALHO 11	A comparative study of the nature and variation in body armour morphology in *Hippocampus abdominalis*”
VERMEYLEN 12	Skeletal deformities in gilthead sea bream (*Sparus aurata*): exploring the association between mechanical loading and opercular deformation.
ERNST 13	Non-canonical thyroid hormone effects on skeletal development in zebrafish (*Danio rerio*)
OGER 14	Dietary supplementation of plant extracts on immune responses and bacterial resistance of striped catfish (*Pangasianodon hypophthalmus*) in the Mekong Delta, Viet Nam – *in vitro* and *in vivo* approaches
VAN MEER 15	Food capture, transport and swallowing in white-spotted bamboo sharks (*Chiloscyllium plagiosum*)
STEEDAM 16	Burrowing behavior of the European eel, *Anguilla anguilla*
DE MEESTER 17	Brain size, ecology and sociality: a reptilian perspective.
GOLDSBOROUGH 18	Individual Differences in the Link between Abnormal Behaviour and Stress in Zoo-Housed Chimpanzees (*Pan troglodytes*)
ZIZZARI 19	Sexual chemical signaling under climate warming
MULLER 20	Maladaptive learning of mate preference in a butterfly facing climate change
VISSER 21	Adaptive phenotypic plasticity in lipid synthesis
DUSSENNE 22	Effects of temperature-induced sex-reversal on arginine-vasotocin neurones in the brain of nile tilapia neomales (*Oreochromis niloticus*)
DE BRUYN 23	Changes in overwintering bat numbers, an effect of global warming?
GUILLAUMOT 24	Inferring the responses of Southern Ocean benthic species to environmental changes using Dynamic Energy Budget models
HEMERIK 25	Predicted climate change impacts on agriculturally important pest-parasitoid systems.
BLANCHARD 26	How ants and aphids will face global change? Impact of temperature and CO_2 concentration on a multitrophic system.
MWAIJENGO 27	Where Does Land Use Matter Most? Contrasting Land Use Effects on River Quality at Different Spatial Scales.
DEKEUKELEIRE 28	Forest fragmentation and tree species composition jointly shape breeding performance of two avian insectivores
RUTTEN 29	One small step for man, one giant leap for wild boar? A landscape genetic analyses of wild boar dispersal in a fragmented landscape

WEVERS 30	Spatial use of wild boar in an urban protected area
GAILLY 31	Flexible habitat use of stonechats *Saxicola torquatus* dealing with different anthropogenic novel environments
MÜLLER 32	A life of ease, foraging habits or just notorious places? Studying behavioural strategies with high-resolution GPS tracking in the lesser black-backed gull
MARTINET 33	Ensuring access to high-quality resources reduces impacts of climate change on bees
NOËL 34	Assessment of pollination ecosystem service throughout wild bees biodiversity and associated phytometer experiment – a case study at farmstead Froidefontaine in ecological transition (Havelange, Belgium)
VEN DER HULST 35	Shut-out or sheltered? An evaluation of the feral pigeon (*Columba livia domestica*) in the context of different management approaches
HUGé 36	Understanding the social-ecological dynamics of Human-Crocodile conflicts in communities around Murchison Falls Conservation Area, Uganda
DE KEYSER 37	Population genomics and stakeholder involvement for the sustainable management of Lake Tanganyika clupeid fishery
GRESHAM 38	Modern human evolution in Africa and the Middle East: could allele sharing between populations accelerate adaptation?
CHAPELLE 39	Boldness and aggressiveness individuality in a self-fertilizing fish despite near-identical rearing conditions: a start for epigenetic variability characterization
VAN STEENBERGE 40	Is differential gene expression in the female brain linked to assortative mating in a mouthbrooding cichlid (*Ophthalmotilapia*) from Lake Tanganyika?
DA SILVA 41	A large and wide-spread inversion is probably lethal in homozygous state in the great tit
DRUET 42	On the path to recovery : characterizing inbreeding in the European Bison with a model-based approach
GALBUSERA 43	How genetic research can help the conservation of Golden-headed lion tamarins: preparing for climate change
VERHEYE 44	Genetic diversity and connectivity of the *Eusirus perdentatus* species complex (Amphipoda, Crustacea) on the Antarctic continental shelf
ZHANG 45	Phylogenetic, morphological and ecological divergence in *Brachionus calyciflorus*, a newly described hybridizing species complex
VANHOVE 46	Exploring mitogenomics for the phylogeny of African monogeneans (Gyrodactylidae and Dactylogyridae)
KOCHZIUS 47	Threatened giants: phylogeography of tridacnid clams
TEIXEIRA 48	Incidence and distribution of cryptic species among polychaetes of the NE Atlantic: potential consequences for biomonitoring and assessment of climate change-induced impacts
FRANTZ 49	Resistance modelling infers physical and behavioural gene flow barriers to the red fox (*Vulpes vulpes*) across the Berlin metropolitan area.
MARDULYN 50	RAD-seq markers reveal only limited gene exchange between two species of leaf beetles across a hybrid zone in the Alps
CUYPERS 51	Combining Pool-Seq and high-throughput SNP genotyping to uncover a morphologically cryptic Multimammate mouse hybrid zone
WEIGAND A 52	Glimpsing into sediments – DNA Metabarcoding of freshwater hyporheic meiofauna indicates high taxonomic diversity and high spatial heterogeneity
HAMMOUD 53	Deep amplicon sequencing as a tool to study the impact of human activities on trematode communities in Ugandan crater lakes.
MACHER 54	Comparison of environmental DNA and bulk-sample metabarcoding using highly degenerate cytochrome c oxidase I primers
WEIGAND H 56	Deciphering the origin of mito-nuclear discordance in two sibling caddisfly species
BEGHIN 57	Assessment of the hazard of an environmentally-relevant mixture of pharmaceutical drugs: a multibiomarker approach on juvenile female rainbow trout (*Oncorhynchus mykiss)*
BIJNENS 58	The planarian microbiome in response to external stressors
DE MEYER 59	The impact of head shape on pollutant accumulation in European eel
THORE 60	Turquoise killifish (*Nothobranchius furzeri*) as a new model in behavioural ecotoxicology
DELROISSE 61	Brain-less & Eye-less: evolution of opsins in the unexpected context of echinoderms

DUCHATELET 62	Embryonic encephalopsin detection supports bioluminescence perception in lanternshark.
JANSSEN 63	Implication of skin pigmentation actors in the bioluminescence control of lanternsharks.
RAICK 64	What do the Brazilian piranhas have to tell us?
MORIS 65	How to find genes involved in cuticular hydrocarbon (CHC) biosynthesis in Hymenoptera? Insights from an extraordinary case of intrasexual CHC profile dimorphism in a mason wasp.
SERTEYN 66	Invasion of Brown Marmorated Stink Bugs and how to control them
VASTRADE 67	Distinct biogeographic origins of androgenetic lineages in *Corbicula* clams
PADILLA 68	Organ and muscle specialization linked to dispersal in an invasive population of African clawed frogs (*Xenopus laevis*) in Western France.
LEJEUNE 69	Global food web alteration following goldfish introduction in palmate newt dominated pond ecosystem
LAMERIS 70	Afrotropical mammal communities under pressure: new insights from functional diversity metrics.
STURARO 71	Trophic plasticity of scleractinian corals under contrasted environmental conditions: evidence from stable isotope analysis
VAN DEN BERG 72	Aquatic omnivores shift their trophic position towards increased plant consumption as plant stoichiometry becomes more similar to their body stoichiometry
ZHOU 73	Life on the stoichiometric knife edge: challenges and responses
DECLERCK 74	Rapidly evolving zooplankton in a salinizing world: to what extent does adaptation to one salt increase tolerance to another one?
BAAN 75	Cranial morphology in European eel (*Anguilla anguilla*) along maturation

Detailed program (Posters)

Number	Presenter		Title
3	AMPOFO	**	Improving the understanding of non-specific mechanisms behind non-polar narcotic toxicity in zebrafish
11	BOUSTANI	**	Preliminary results on the wild bee fauna of Lebanon higher altitudes: The race between a checklist and a climatic risk assessment.
10	BRAEM		Habitat selection and ecotype-specific adaptations of the niche-expanding butterfly *Pararge aegeria* in anthropogenic landscapes
37	BULTEEL		Is bigger better? The microbiome and its role in conferring performance towards parasites in *Daphnia magna*
29	CALCAGNO	*	Description of an “unknown organ” in the aquacultivated sea cucumber *Holothuria scabra* (Holothuroidea, Echinodermata) from the South-West of Madagascar
35	COONE		*Daphnia* as a new microbiome model with respect to the development for innovative colorectal cancer (CRC) therapies focusing on EMT and epigenetics.
28	DELAUNOIS	**	Study of a biological harpoon; microstructure and composition of the mantis shrimp raptorial appendage
4	DELROISSE		The skin ulceration syndrome of the aquacultivated sea cucumber *Holothuria scabra (Holothuroidea, Echinodermata)* in the South-West of Madagascar
6	ENGEELS		Ecophysiological responses of *Seriatopora hystrix* (Dana, 1846) to a hypo- and hypersaline stress in short time
15	FLEUREN		Adjust or bust: functional differences in the morphology of an invasive fish species across Europe
31	FREDERICH		Evolution and development of white stripe patterns in clownfishes (Pomacentridae)
43	GOLDSBOROUGH		Quality over Quantity: Analysing Individual Variation in Abnormal Behaviour in Zoo-Housed Chimpanzees (*Pan troglodytes*)
40	GOMBEER		Bushmeat for sale in Brussels
39	GRIFFOEN	**	Handicapping males negatively affects the alternation of provisioning visits in blue tits
12	GUILLAUMOT		Strict extrapolation in modelling Southern Ocean species distribution
34	HOUWENHUYSE		The *Daphnia* microbiome: What is core and what is flexible?
30	HUBY	**	Evolution of the shape of the cephalic region and oral jaw system in relation with trophic specialisation in Serrasalmidae (Teleostei: Characiformes)
32	KEVER		Motoneuron and premotoneuron pools associated with swimbladder sounds and electric organ discharges in mochokid catfish
42	KOLF	*	Bystander jealousy-driven behaviour in zoo-housed chimpanzees (Pan troglodytes)
44	LEEFLANG		Are mother’s cursing their sons? Prevalence of mtDNA induced sex-specific differences in survival and fertility in zoo populations
36	MACKE		Host genotype shapes the assembly of both the gut microbiota and the surrounding bacterioplankton in the freshwater crustacean *Daphnia magna*
16	MEGANCK		Identifying Invasive Alien Species by DNA-barcoding: possibilities, gaps and pitfalls
25	MULLENS	**	Genome skimming and rapid recovery of mitochondrial genomes. A powerful tool to resolve phylogenetic relationships in Syrphidae.
5	NOIRET	**	Intersexual heterogeneity of the metabolic response to stress: are males and females equal in a challenging environment?
41	PAPADAKI		Is personality consistent across social context? The effect of female personality on social behaviour during male introductions in captive long-tailed macaques
27	PATEL	**	The Biodiversity of deep-sea Scavenging Amphipoda in the Pacific Ocean.

2	PERIZ_STANACEV	**	Mixture toxicity effects of estrogen and aryl hydrocarbon receptor agonists during zebrafish embryonic development
33	PINHEIRO_SILVA	**	Species complementarity drives zooplankton top-down control on phytoplankton in a lake dominated by non-toxic cyanobacteria
1	PINZONE		What is APECS Belgium?
23	PLEVOETS	*	Reconstructing population histories and biogeography of Antarctic *Charcotia* (Amphipoda, Crustacea)
9	PRZYBYLA	*	How hyperthermic stress affects the fertility of bumblebee males?
24	SALABAO	**	Ecological diversification, recent evolution and speciation of Amphipoda in the polar regions: the case study of *Eusirus* genus
13	SCHÖN		Refugia and ecosystem tolerance in the Southern Ocean
38	SHAIKH		Host Control on Symbiont Proliferation mediated by Dynamin, a membrane-modelling GTPase
17	SMITZ 1		Identifying mosquitoes (Diptera: Culicidae) from foreign deployment sites of the Belgian armed forces
18	SMITZ 2		DNA-barcoding: an efficient tool for rapid identification of native and exotic mosquito species (Diptera: Culicidae) intercepted in Belgium
20	VAN BOURGONIE		DNA barcoding and identification of terrestrial gastropods of parasitological concern for animals in Greece
22	VAN CASTER		Connectivity of the big blue octopus (*Octopus cyanea,* Gray 1849) between the eastern and western coast of Madagascar
26	VRANKEN		The ichthyofauna of the Lake Edward system
7	WELLENS	**	Temperature-induced changes in the fatty acid profile of the benthic copepod *Platychelipus littoralis* of the Westerschelde estuary
21	WIEGAND		Genetic monitoring of green frogs in Luxembourg using a NGS-based method
14	WILLEMS	*	Effectiveness of management agreements on farmland birds (nesting place, food and breeding success)
8	ZAMBRA	**	Hyperthermic stress resistance of Belgian bumblebee species
19	ZOURE	**	Molecular Analysis of *Anopheles gambiae* complex mosquito from climatic and cotton areas of Burkina Faso

Key notes

Do we understand why insects are in decline?

Eelke Jongejans[1,2*], Caspar A. Hallmann[1], Nick Hofland[1], Hans de Kroon[1], Martin Sorg[2], Henk Siepel[1]

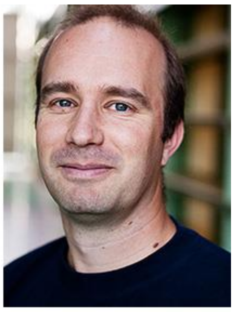
[1] Radboud University, Nijmegen, The Netherlands

[2] Entomological Society Krefeld, Germany

* Corresponding author. E-mail: eelke.jongejans@ru.nl

Global declines in insects have sparked wide interest among scientists, politicians, and the general public. Loss of insect diversity and abundance is expected to provoke cascading effects on food webs and to jeopardize ecosystem services. Our understanding of the extent and underlying causes of this decline is based on the abundance of single species or taxonomic groups only, rather than changes in insect biomass which is more relevant for ecological functioning. Here, we used a standardized protocol to measure total insect biomass using Malaise traps, deployed over 27 years in 63 nature protection areas in Germany (96 unique location-year combinations) to infer on the status and trend of local entomofauna. Our analysis estimates a seasonal decline of 76%, and mid-summer decline of 82% in flying insect biomass over the 27 years of study. We show that this decline is apparent regardless of habitat type, while changes in weather, land use, and habitat characteristics cannot explain this overall decline. This yet unrecognized loss of insect biomass must be taken into account in evaluating declines in abundance of species depending on insects as a food source, and ecosystem functioning in the European landscape.

Personal Summary



Prof. Eelke Jongejans (Radboud University, Nijmegen, The Netherlands)

The main focus of my research is the impact of environmental drivers on spatial population dynamics. I want to understand how ecological and evolutionary processes at the individual level integrate and scale-up to population dynamics. I am interested in ecological frameworks and models that can augment the scientific underpinning of conservation, harvest and control management.

Key note

From detections to predictions; high-throughput tools for biodiversity assessment and monitoring in changing environments.

Wilting, A.[1], Axtner, J.[1], Hörig, L.[1], Mohamed, A.[1], Brozovic, R.[1], Tilker, A.[1], Nguyen, A.[1] & Abrams, J.F.[1]

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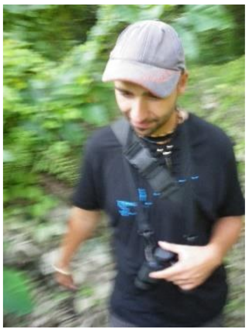
Globally, biodiversity is declining at an alarming rate due to habitat degradation and loss, hunting and climate change. Monitoring threatened populations, particularly in tropical rainforests where the species of interest are often secretive and occur in remote areas, is challenging. Therefore, modern non-invasive high-thoughput approaches are needed to detect the threatened species. I will present advances and challenges of two of these detection methods, remote camera trapping and DNA metabarcoding of environmental (eDNA) or invertebrate-derived (iDNA) samples. In conservation detection of a species is however not very meaningful as it gives little information about the distribution or abundance of species. Therefore, I will give examples how species distribution models can be used to do the transition from detections to predictions. I will present examples from Southeast Asia, where we evaluated the two main drivers of defaunation (forest degradation and hunting) and assessed the impact of climate change on species and species communities.

Personal summary:



Professor Andreas Wilting (Leibniz Institute for Zoo and Wildlife Research)

My research focuses on the ecology, biodiversity and biogeography of Southeast Asian mammals. I am interested in integrating field work in different countries in Southeast Asia with species distribution modelling and genetic approaches using state-of-the-art high throughput sequencing technologies to elucidate the ecological requirements, evolutionary history and past and present distribution patterns of species and species communities. A major focus of my research is to assess the resilience of species to anthropogenic environmental changes in order to contribute to the efficacy of species conservation. Here, the communication of our scientific findings to relevant stakeholders and practitioners is of particular importance to me.

Key note Hilde Eggermont

IPBES: strengthening the science -policy interface in the face of global change.

The Intergovernmental Platform for Biodiversity and Ecosystem Services (IPBES) is an independent intergovernmental body established in 2012. It provides policymakers with objective scientific assessments about the state of knowledge regarding the planet's biodiversity, ecosystems and the benefits they provide to people, as well as the tools and methods to protect and sustainably use these vital natural assets. To some extent IPBES does for biodiversity what the better known Intergovernmental Panel for Climate Change (IPCC) does for climate change: it provides the best available knowledge for decision-making. During this presentation, you will learn about IPBES' mission and the outcomes and impacts its first workplan (2014-2018). You will also learn about IPBES' plans for the next few years, and how it aims to interact with other bodies such as IPCC to adequately tackle topics at the interface between biodiversity, climate change, food security and health. Finally, you will learn how IPBES is structured in Belgium, and how to engage as an expert in the implementation of its work.

Personal summary: Dr. Hilde Eggermont (Biodiversity Platform Belgium – RBINS)

Hilde Eggermont is zoologist by training. Between 2004 - 2011, she was postdoctoral researcher at Ghent University studying aquatic communities and ecosystem function in East African lakes. Since 2012, she has been employed by the Royal Belgian Institute for Natural Sciences as the coordinator of the Belgian Biodiversity Platform, a science-policy interface for biodiversity matters in Belgium. She is acting as the Belgian national focal point for the Intergovernmental Platform for Biodiversity & Ecosystem Services (IPBES), and for the International Union for the Conservation of Nature (IUCN). Hilde is also Vice-Chair for the BiodivERsA Partnership, a pan-european network of organisations funding research on biodiversity and nature-based solutions.

#MeTooForLife Initiative: « 100(0) scientists worry and change »

Caroline M. Nieberding[1], Philippe Marbaix[1], Lucette Flandroy[2], Jean-Pascal van Ypersele[1]

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We are a growing group of Belgian scientists willing to show that many researchers worry for world sustainability and take action in their private life to reduce environmental degradation. We call on you all as scientists in Climatology, Biology, Geography, Bioengineering and Social sciences relevant to environmental degradation (Law, Sociology, Anthropology, Psychology, Economy, Political sciences) to join this initiative. The objective is to show to the public that the alarming signals that we are observing incentivize us to change in our daily lives. An increasing consistency between our professional and private life can encourage other people to act in ways that protects our common environment, in a spirit of social justice.

Vigorous action now and within the next 10 years can still be effective to stop dramatic loss of wildlife and to limit climate change. Every delay makes action more difficult or less effective.

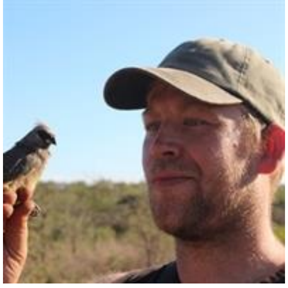
We would like participating researchers to provide:

1. **their first name, surname, title, function, affiliation;**
2. **a recent picture, or a short video (with their response to point 3 below);**
3. **a short text (maximum 100 words) summarizing:**
    - **the main concerns they have in their field of expertise (broadly speaking);**
    - **changes, actions, that they have implemented or plan to implement in their way of life, or contribute to implement in the society (for example: transportation, food, housing, IT, other consumption…);**
    - **difficulties they experienced when seeking to lower their energy consumption or carbon footprint;**
    - **what they regard as key changes in the society or at the political level to facilitate these (r)evolution(s).**

Every person having at least a Msc (including Msc2 students in the course of their last academic year) in Climate sciences, Biology, Bioengineering, Geography, or Social sciences relevant to environmental degradation (Law, Sociology, Anthropology, Psychology, Economy, Political sciences), is eligible to participate. Please send this information to caroline.nieberding@uclouvain.be with the title “MeTooForLife”. Any person with another background but willingness to participate is welcome to contact caroline.nieberding@uclouvain.be.

Before any communication to the public, each participating researcher will have one week to check the information that she or he provided, and ask for corrections if needed. The aim is to communicate the website to the public during the spring of 2019.

Royal Dutch Zoological Society Prize: Sjouke Kingma



Beyond kin selection: direct benefits of helping in cooperatively breeding birds

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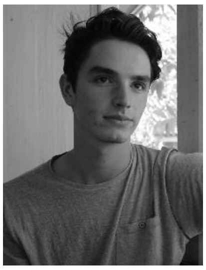
Cooperatively breeding animals live in social groups in which some individuals ('helpers' or 'subordinates') help raising the offspring of others. Such seemingly 'altruistic' helping behaviour contradicts the fundamental predications of selfishness of evolutionary theory, and is an ongoing puzzle for evolutionary biologists. Why do individuals invest time and energy in helping others?

Hamilton's kin-selection theory - predicting that by helping family members, individuals can indirectly promote the transfer of shared genes to next generations - provides one elegant explanation for the evolutionary maintenance of helping in invertebrates and some vertebrates. Nonetheless, in many vertebrate species, cooperation between unrelated individuals is common. This phenomenon is, however, much more difficult to explain. In this presentation I will provide an overview of direct benefits of helping in cooperatively breeding birds, and argue that direct benefits are – as alternative or addition to kin selection – probably much more important than often assumed.

Kets award prize (attributed by the jury): Thomas Luypaert



What poo can tell you: Wildlife response to no-take zone establishment in the tropical forests of New Guinea

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New Guinea is one of the most biologically diverse regions in the world, containing approximately 9% of the global terrestrial diversity in less than 1% of its surface area. Although Papua New Guinea (PNG) still contains part of one of the world's largest tropical forests, much of its biological splendour is under threat by deforestation and forest degradation, compounded by the effects of a burgeoning human population and hunting activities. Thus, there is a growing need for biodiversity conservation in PNG; however, the establishment of protected areas has been a challenging process. The recent gazettal of the YUS Conservation Area, a community-based conservation initiative where no-take zones have been implemented to safeguard wildlife populations from overexploitation, appears promising. Nonetheless, long-term and cost effective biodiversity monitoring is critical to the conservation and management of these community-established and managed areas. In this study, we assessed the relative abundance of four ecologically and culturally significant taxa (macropods, possums/cuscus', cassowaries and monotremes) to investigate whether no-take zones are increasing animal abundance and acting as source areas of wildlife to adjacent hunting grounds. Firstly, Generalized Linear Mixed Models (GLMMs) were used to determine drivers of wildlife abundance, specifically addressing the effects of protection and hunting. Secondly, a pilot study was conducted to assess the feasibility of camera trapping as a potential wildlife monitoring tool in YUS. Results indicate no-take zones can effectively increase wildlife populations and protect populations from hunting in protected areas close to human settlements; however their effectiveness depends on the taxon under investigation. Moreover, camera trapping proves to be an effective monitoring tool in YUS. This study will help optimize the efficacy of the YUS Conservation Area and represents useful background to wildlife managers in establishing, or optimizing existing no-take zones in areas with a similar biological and socio-cultural setting.

Kets awards (Public prize): Nathan Vranken

Exploring the diversity of haplochromines in the Lake Edward system

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Haplochromine cichlids are well known for their extra-ordinary diversity and their ability to form adaptive radiations. In Eastern Africa, they gave rise to the Lake Victoria superflock, which consist of the cichlids from lakes Albert, Edward, George, Kivu, Kyoga, and Victoria, and associated rivers and lakes. Their rapid speciation, numerous ecological adaptations, and distinct colour patterns have intrigued biologists for a long time.

The HIPE-project investigates the human impacts on ecosystem health and resources of Lake Edward. Within the framework of this project, we perform a systematic revision of the largely unexplored *Haplochromis* species assemblage of lakes Edward and George. Hitherto, only 31 of the estimated 100 species that inhabit these lakes have been formally described. As a first step in this revision, specimens are grouped by trophic ecology based on morphological characteristics. For each group, a morphometric study is carried out by taking measurements and counts, which are analysed separately by principal component analyses. Additionally, qualitative characteristics are observed, species are delineated, and stomach content observations are performed to verify their trophic ecology. Newly discovered species are formally described, while valid species are redescribed.

Hitherto, 14 new species were discovered and are being described. These include three species of oral snail shellers that use their teeth to grab the soft bodies of snails and tear them out of their shells; three species of paedophages that attack other mouth-brooding cichlids to steal their eggs from out of their mouths; an insectivore with a very slender snout and lobate lips, well adapted to suck insects out of small crevices between rocks; and at least seven species of piscivores, each with a characteristic colour pattern. Observation of museum collections suggest that lakes Edward and George are inhabited by many more species with peculiar morphologies and interesting ecologies.

Oral Presentations
(Double slots – Session conveners)

Brain-less & Eye-less: evolution of opsins in the unexpected context of echinoderms

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Echinoderms are marine invertebrates characterized by a nervous system decentralization and a pentaradial body plan. Our research aims to better understand how these organisms perceive light via the activation of opsins which are transmembrane proteins generally involved in vision and photoreception in metazoans.

The search for opsin genes has been extended to numerous recent transcriptomes and genomes giving us an extensive glimpse on the echinoderm opsin diversity. Phylogenetic analyses highlight the presence of many opsin groups within each echinoderm lineage. The opsin gene repertoires are very diversified for species that have been largely "sequenced" and include the majority of opsin groups described in bilaterians. Globally, a majority of the ancestral bilaterian-type opsins have been conserved in echinoderms and lost in many other metazoan branches. Our analyses confirm that only xenopsins described in cnidarians, rotifers, brachiopods and molluscs could not be identified in echinoderms. Numerous species/clade-specific gene duplications have also been observed.

We studied opsin gene structure in four model species, for which a genome is available, helping us obtain crucial information on the evolution of opsins by showing, for example, that some echinoderm opsin genes (*e.g.*, chaopsins) do not possess the introns conventionally observed in metazoan opsins. The integration of a DNA copy of an opsin mRNA into echinoderm genomes seems likely to be at the origin of opsin genes characterized by an absence of introns (*i.e.*, retrogene emerging by retrotransposition). These genes potentially lost their "functions" (*i.e*., pseudogene) associated with the perception of light but could also be associated with new derived functions.

The results (*i*) highlight the importance of wide-ranging sampling including non-model species in order to more accurately estimate the diversity of genes involved in light perception in these organisms and (*ii*) emphasize the need to supplement *in silico* data with morpho-functional data.

The adaptive benefit of superfetation in live-bearing fishes: a slender body leads to improved escape performance

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The ability to simultaneously carry multiple litters of different developmental stages in utero, is a complex reproductive adaptation called superfetation. Superfetation increases the frequency of litter production, often in association with a reduction in litter size, and evolved repeatedly in viviparous lineages throughout the animal kingdom. Theory predicts that the evolution of superfetation should reduce the reproductive burden of the mother during pregnancy, leading to a more slender female body shape and an improved locomotor performance.

Here, we apply novel morphological and biomechanical approaches to test these predictions, using three live-bearing fish species with different levels of superfetation. For each species, we created a time-series of three-dimensional body reconstructions during pregnancy for 14 pregnant and 14 (non-pregnant) control females (N_{total} = 84 females). Based on 592 3D body models, we found that superfetation is significantly correlated with a reduction in abdominal distension during pregnancy, suggesting that the evolution of superfetation improves slenderness. We simultaneously studied the fast-start escape performance of the females in 3D, analyzing a total of 1942 high-speed video sequences. We found that an increase in body thickness is significantly correlated with an increase in several key parameters of a fast-start escape response, including abdominal curvature, curvature rate and maximal velocity.

Our results suggest that the increase in body slenderness associated with the evolution of superfetation improves a female's escape swimming performance. Collectively, this suggests that superfetation may have evolved in performance-demanding (e.g. high flow or high predation) environments to reduce the locomotor cost of pregnancy.

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

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

Adaptive phenotypic plasticity in lipid synthesis

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Trait loss is pervasive over long evolutionary timescales, leading to loss of genetic diversity and potentially the extinction of species. Regaining lost traits was long thought impossible, but more cases of reverse phenotypic evolution have accumulated over the years. It has remained unclear, however, how traits lost over extensive evolutionary times can re-evolve. Lipid synthesis is the involuntary conversion of excess energy for storage, which is a highly conserved and essential trait for nearly all organisms. Here, we discovered that lipid synthesis, which was thought to be lost in most, and regained in a few, parasitic wasps, is plastic in the wasp *Leptopilina heterotoma*. Lipid synthesis depended on host lipid content in different field-caught populations: lipid synthesis was completely suppressed when wasps developed on extremely fat hosts, but was induced in adults that developed on lean hosts. Although populations are genetically homogeneous, plasticity in lipid synthesis differed among wasp families, and reaction norms varied in each population. Together, these results show there is genetic variation in, and selection for, plasticity in lipid synthesis in natural populations. We propose that the apparent evolutionary loss and regain of lipid synthesis may in fact be selection on plasticity in a generalist parasitic insect, explaining the maintenance and diversification of the *Leptopilina* lineage over the last 80 million years.

Oral Presentations

Cranial morphology in European eel (*Anguilla anguilla*) along maturation

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The European eel (*Anguilla anguilla*) is a thoroughly studied species. Cranial morphology has already been studied in the glass, elver and yellow eel stages, however, little is known about cranial morphological changes from the yellow to the (artificially matured) silver eel stage. As such, here we investigated the cranial musculoskeletal morphology of eleven male European eels in different stages during the transformation from yellow to silver eel, including artificially matured eels. The heads were µCT-scanned, and 3D-reconstructions were made of the skulls and of the cranial muscle bundles associated with jaw closing and respiration. Eye size was used as a proxy for maturation. Size adjusted jaw muscle volumes were found to not decrease or increase during maturation, meaning that the transformation itself did not decrease jaw muscle volume. Relative bite force did not increase or decrease with maturation, logically, as the closely associated jaw muscle volume also showed no increase or decrease. Size adjusted respiratory muscle volumes, associated with opening and closing of the operculum, increased with maturation, as a preparation for the eel's long migration, which often includes deep and perhaps oxygen poor environments. Interestingly, a difference in skull morphology was found between artificially matured and wild silver eels: artificially matured eels had a wider and taller skull as well as a larger orbit compared to wild silver eels, most likely caused by inducing the transformation process artificially with hormone injections. However, it could perhaps also caused by different environmental conditions and different diets in the yellow eel stages. This emphasizes that the artificial maturing of eels requires more research to determine possible complications with restocking and the effects on offspring.

Assessment of the hazard of an environmentally-relevant mixture of pharmaceutical drugs: a multibiomarker approach on juvenile female rainbow trout (*Oncorhynchus mykiss)*

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Over the last decades an increasing number of studies have reported the occurrence of anthropogenic compounds in aquatic ecosystems. The detection of new compounds known as emerging pollutants has raised concerns as there is little information available on their potential negative impact on aquatic ecosystems. Among them, pharmaceuticals are especially under concerns because of their intrinsic biological activity and ubiquitous environmental occurrence. Current drug regulations focused on the risk caused by individual compounds. However, ecosystems are exposed to cocktails of chemicals, where the interactions between molecules can lead to modifications in their mode of action on non-target organisms, and unknown adverse effects. The evaluation of the toxicological risk of drug mixture is therefore needed. In this context the DIADeM project has been launched. It aims in developing new biological tools to improve de diagnostic of surface water quality. As part of this project, the present study consisted in the exposition of all-female juvenile rainbow trout (*Oncorhynchus mykiss*) to environmentally-realistic concentrations of a mixture of five nonsteroidal pharmaceuticals for 42 days. Paracetamol, carbamazepine, diclofenac, irbesartan and naproxen were selected, as these have been detected in the Meuse River in Belgium. Fish were exposed to three concentrations of the mixture including the environmental concentration, 10- and 100-times the environmental concentration. Effects on plasma levels of sex-steroids and the expression of genes encoding key proteins involved in ovarian development were assessed. Plasma levels of sex-steroid hormones, particularly 11-ketotestosterone, increased in a concentration-dependent way in exposed females. In addition, some key genes involved in ovarian steroidogenesis were significantly overexpressed after 7 days of exposure, such as key genes involved in the maintenance of the ovary. This study highlights that combined occurrence of common pharmaceutical drugs at concentrations present in surface water environments may act as endocrine-disrupting compounds in rainbow trout.

The planarian microbiome in response to external stressors

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Many animals live in close association with complex microbial communities. The so-called microbiomes include bacteria, bacteriophages, fungi and viruses and are believed to have a beneficial effect on the hosts physiology. However, little is known about the invertebrate microbiome and its composition, how it is influenced by external factors and its stability as well as its function for the host physiology and health. In this study, we characterized the microbiome of a freshwater predator, the planarian *Schmidtea mediterranea*. Bacteria were found in the mucus and gut and sequencing results indicate mainly the association of proteobacteria with lab cultivated *Schmidtea mediterranea*. In addition, we investigated how environmental changes influence the planarian microbiome by a combination of ARISA fingerprinting and 16S rRNA sequencing. Of the studied compounds (Cd, MMS and silver nanoparticles) and other external changes (different foods and antibiotics exposure), silver nanoparticles had the highest impact on the planarian microbiome. Future research will reveal if and how an altered microbiome is important for the planarian physiology.

How ants and aphids will face global change? Impact of temperature and CO_2 concentration on a multitrophic system.

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While the impact of climate change on plant or insect communities has received increasing attention during the last decade, plant-insect interactions under a changing environment remain poorly studied. These interactions are of particular importance as regard to the economically dimension of some crop plants and to the pest status of some insect species. In this project, we raise the hypothesis that the predicted changes in climate for the end of the 21th century – i.e. raise of carbon dioxide concentration beyond 700 ppm, with an increase of 2 to 4°C (IPCC 2007) – will impact the semiochemicals interactions and behaviours of multitrophic relationships between herbivorous insect pests, their host plants and their mutualist partners. Studying relations between plants, aphids and ants is an emblematic case of multitrophic relations. Thus, in this study, we are evaluating the impact of an increase in carbon dioxide concentration and temperature, alone or in combination, on a multitrophic interaction model including a plant (*Vicia faba*), an aphid pest (*Aphis fabae*) and an aphid-tending ant (*Lasius niger*). We are having special attention to the plant semiochemicals, the aphid biology, and the behavioural interactions between aphids and ants. Our first results suggest that the aphid-ant mutualism will be impacted through changes in aphid honeydew production, semiochemicals, and bacterial communities and may influence ant behaviour towards aphids. Changes in host plants semiochemicals may also have an influence on aphid attraction and dispersion.

A comparative study of the nature and variation in body armour morphology in *Hippocampus abdominalis*”

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It is currently known which characteristics allow for the extensive mobility of the armoured prehensile tail of the seahorse. However, it is not known which of these characteristics is recurrent or different in the neck and abdomen armoured regions, and how it affects mobility. Due to the pivot feeding mechanism of the seahorse, the neck armour must allow the fast-upwards movement of the head. The abdomen armoured region is responsible for giving support to the body of the seahorse. As we expect this to be reflected in the morphology of the bony plates, the present research focused on identifying which characteristics make the bony armour in the abdomen region less mobile than the neck and tail armoured regions, and how is it linked to the specific functionality required for each region. A specimen of *Hippocampus abdominalis* was µCT scanned and 3D reconstructed in order to look at plate shape variation, and a 3D printed model was constructed in order to better understand the mobility limits of the plated regions. Moreover, a principal component analysis (PCA) was performed on five measurements of the bony plates and showed clear grouping of plates from each body region. PC1 was related to a plate size component and PC2 was related to the antero-posterior overlap. Histological sections of the abdomen region of the specimen showed the presence and organization of connective tissue between plates and between plates and vertebrae. Even though the antero-posterior overlap was the second most significant variable (PC2) explaining plate shape variation throughout the study, the differences in mobility of the neck and abdomen region, compared to the tail, seemed to be more related to an unalignment of the antero-posterior overlap, in the neck region, and due to a potentially larger lateral overlap and substantial connective tissue, in the abdomen region.

Boldness and aggressiveness individuality in a self-fertilizing fish despite near-identical rearing conditions: a start for epigenetic variability characterization

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Our understanding of an organism's capacity to respond to environmental changes has advanced in large part through studies focusing on genotypic variation and manipulating environmental factors. These studies confirm that genotype, environment and their interaction contribute to phenotypic variability, a fundamental prerequisite for evolution by natural selection. Recently, another source of phenotypic variation in ecologically relevant traits has emerged from the molecular and developmental sciences. Epigenetic processes are now known to increase the phenotypic options of a genotype and have been proposed to mediate phenotypic plasticity. Epigenetic variability can either be induced by environmental conditions or can result from spontaneous stochastic modifications (epimutations). Furthermore, epigenetic marks can potentially be inherited through successive generations (Transgenerational Epigenetic Inheritance – TEI) and thus contribute to adaptive evolution of a population. Understanding how epigenetic mechanisms contribute to phenotypic variability is one of the current greatest challenges in evolutionary biology. Studying this question is challenging because natural populations are genetically diverse, which complicates the distinction between genetic and epigenetic effects on phenotype variability. A solution to avoid confounding between genetic and epigenetic effects is to study systems with a very low level of genetic variation. For this purpose, the mangrove rivulus, *Kryptolebias marmoratus*, is a fantastic new model species. Along with its close relative species, *K. hermaphroditus*, they are the only known self-fertilizing hermaphroditic vertebrates. Consistent self-fertilization naturally produces isogenic lineages. Preliminary results (from my Master thesis) showed individuality of boldness and aggressiveness within isogenic lineages and under identical environment. It is totally relevant considering the complex and changing microhabitat of the rivulus and might be considered as a bet-hedging strategy sustained by stochastic epimutations. My PhD thesis general objective is to characterize the sources of epigenetic variability in an isogenic lineage: inherited from the parents or not; induced by an environmental stress or appearing stochastically.

Combining Pool-Seq and high-throughput SNP genotyping to uncover a morphologically cryptic Multimammate mouse hybrid zone

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Mastomys natalensis, the Natal Multimammate mouse, is one of the most widespread mouse species in Sub-Saharan Africa. Across its range, six divergent mitochondrial lineages can be distinguished. They likely diverged from each other around a million years ago, when Africa was more humid and savannah species like *M. natalensis* were restricted to isolated refugia. When the climate changed, and the forest receded, *M. natalensis* carrying these mitochondrial lineages spread, came into contact and formed secondary contact zones. We sampled one of these contact zones in Tanzania, whole-genome sequenced a pool of five individuals for both lineages, mapped the reads to the lab mouse reference genome and found that the mitochondrial lineages correspond to taxa that are distinct genome-wide. We developed SNPs across the genome that can diagnose these morphologically cryptic taxa and genotyped 650 individuals over the contact zone for those markers. This genotyping revealed that the contact zone is a hybrid zone, which some genes can cross, while others cannot (i.e. a semi-permeable species barrier). Allele frequencies of the SNPs change clinally across the hybrid zone. Some SNPs show change over as little as 10 kms, have a strong deficit of heterozygotes and are strongly correlated. These indicate potential barrier regions in the genome. Over all SNPs the pattern of change is asymmetric, indicating preferential introgression of genes of one taxon into the other, or movement of the hybrid zone.

A large and wide-spread inversion is probably lethal in homozygous state in the great tit

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Chromosomal inversions represent an important class of polymorphisms that are of particular interest in evolutionary studies. Inversions are found in various bird species and are associated with traits related to sexual behaviour and sperm morphology/motility. The great tit (*Parus major*) is a songbird that is extensively used as a model in ecology and evolution. Using genotype data from 2,296 Dutch great tits, we identified a pericentric inversion overlapping ≈90% of chromosome 1A (64.2 Mb) and almost 1,000 genes in 5% of the population. Great tits from Belgium and France, analysed with next-generation sequencing data, were also classified as inversion carriers, at a similar frequency. A copy number variation (CNV) complex, located at the downstream inversion breakpoint, supports that the chromosome with the inversion is approximately 3.5 Mb larger than the reference genome. This CNV complex encloses 32 genes related with a wide range of phenotypes, including embryonic lethality. In the offspring of nine heterozygous-heterozygous matings, the rate of heterozygous birds fits what is expected for a lethal variant. Among 56 chicks, 65% are heterozygous, 35% homozygous (no inversion) but none is homozygous for the inversion. It is unclear whether the inversion has phenotypic and fitness effects that justify its spread or whether it is the result of genetic drift.

Changes in overwintering bat numbers, an effect of global warming?

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In temperate regions, many mammal species hibernate to overcome adverse conditions during winter. Hibernation is a physiological and behavioural adaptation to ensure survival through periods of cold weather and low food availability. Climate change causes significant changes including warming of winter periods which might affect hibernating species, especially those that are adapted to low optimal hibernation temperatures. Hibernation under elevated temperatures could lead to premature depletion of energy reserves which can result in lower reproductive success, higher disease susceptibility or even death. Bats, a highly specialised mammalian order characterised by low reproduction rate, are expected to show a strong response to climate change. We analysed population trends in Nietoperek bat reserve (Poland), one of the largest bat hibernation sites in Europe, with annually about 38,000 bats belonging to 10 species. The artificial underground system consists of about 32 km tunnels, 20-30m deep. The hibernating bats were monitored yearly in January since 1999. Bat trends were compared to changes in the local winter temperatures. During the observation period there was a trend that winter temperature increased, especially due to a series of warm winters after 2011. The hibernating population count of three species, *Myotis myotis, M. nattereri* and *M. dasycneme* increased during the monitoring period. These three species are categorised as warm dwelling species. For three species *M. daubentonii*, *Barbastellus barbastellus* and *Plecotus auritus* we observed a declining trend. The latter two are categorised as cold dwelling species.

Population genomics and stakeholder involvement for the sustainable management of Lake Tanganyika clupeid fishery

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Worldwide, fisheries are threatened by the consequences of climate change and overfishing. For people inhabiting a developing region, where the local fisheries is often one of the only protein sources, collapse of the fisheries can be insuperable. The Lake Tanganyika fishery feeds millions of people in one of the poorest regions of the world. Lake Tanganyika is known for its endemic cichlid radiation, a model system for biology of speciation, yet most of its fishery target species are pelagic non-cichlids. About 60% of the catch consists of two endemic clupeid species: *Limnothrissa miodon* and *Stolothrissa tanganicae*. Good management of the lake's resources is necessary for the sustainability of the clupeid fishery. Formulation of a good management plan is hampered because of knowledge gaps concerning stakeholder opinions, and biology and population genomics of the target species. We take a multidisciplinary approach to improve knowledge on fisheries science in a data poor environment, with the help of the local authorities, scientists, and communities. We used a genomic approach for *S. tanganicae* to disentangle their population structure, important for the delineation of management units. 96 specimen from three locations over the entire North-South axis of Lake Tanganyika were analysed, through COI sequencing and RAD sequencing. Results from both methods show weak genetic differentiation between the sampling locations, highlighting the need for integrated management. Interviews with stakeholders and key-informants are ongoing to get insight into preferable policies. The results will be communicated to policy-makers, to allow future integration into management.

Brain size, ecology and sociality: a reptilian perspective.

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Vertebrates show remarkable variation in brain size, both in absolute and relative terms, and why some species have larger brains than others is a question that has fascinated biologists for ages. One common explanation is that larger brains allow to deal with more complex environmental information, by means of enhanced cognition and behavioural flexibility. While an overwhelming amount of research has tried to relate brain size to either habitat or social complexity, mixed results have led to the question whether the same selective factors act on the brain in different vertebrate taxa. Unfortunately, the majority of studies so far focused on either mammals or birds. To tackle this issue, we collected a dataset of brain sizes in 170 squamate species (lizards and snakes) to test the effect of habitat and social complexity on brain size evolution in this taxon. In addition, as larger brains are expected to lead to higher behavioural flexibility, we also tested whether an association existed between relative brain size and habitat generalism. Our study confirmed earlier findings that both the degree of limb reduction and the biogeographical origin of a species affected brain size, and should thus be controlled for. Habitat complexity did not affect relative brain size, and, in contrast to our expectations, solitary species had larger brains than social species. No association was found between brain size and habitat generalism. Our results contribute to a growing literature that the selective forces driving the evolution of larger brains may differ among taxa. Squamata have been neglected in this area of research, and therefore much remains to be learned. We highly encourage comparative studies on brain size in understudied taxa, such as reptiles and amphibians, in order to get a more complete picture of how the vertebrate brain evolved.

The impact of head shape on pollutant accumulation in European eel

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Several aspects of the life cycle of the critically endangered European eel (*Anguilla anguilla*) remain poorly understood. One such aspect is how its head shape dimorphism impacts the overall performance of eels at different stages of their life cycle. At the yellow eel stage, broad-headed eels are known to consume larger prey than narrow-headed eels. Here, we tested whether pollutant accumulation is affected by this disparity. We showed that broad-headed eels have higher concentrations of mercury and several lipophilic organic pollutants compared to narrow-headed ones, irrespective of their lower fat content. This phenotypic disparity is thus linked, through feeding ecology, with effects on pollutant accumulation, and consequently, migratory and reproductive success. Considering that pollution is an important driver of the European eel's decline, our results demonstrate that broad-headed eels are more vulnerable to detrimental pollutant accumulation and are consequently less likely to contribute successfully to reproduction and hence its restoration.

Rapidly evolving zooplankton in a salinizing world: to what extent does adaptation to one salt increase tolerance to another one?

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In many parts of the world, freshwater organisms are increasingly exposed to higher levels of salinization, due to rising sea levels, increased evaporation, intensified irrigation and fertilization, industrial pollution and the use of road salts. Stress due to salinization does not only involve increased osmotic pressure but, depending on salt chemical identity, also toxicity by salt ions. Rapid evolutionary adaptation is a mechanism through which populations of aquatic organisms may be able to cope with these challenges. The objectives of our study were to test (1) the capacity of populations of the freshwater rotifer *Brachionus calyciflorus* to rapidly adapt to increased salinization (i.e. within an ecological time scale), (2) if salts differ in toxicity and (3) if evolutionary adaptation to one type of salt alters the potential to cope with other types of salts? For this we performed a laboratory evolution experiment subjecting replicate populations to low and high NaCl treatments. A subsequent common garden transplant experiment showed that under saline conditions populations with a history of salt exposure had higher exponential population growth rates than populations with a freshwater selection history. In a second common garden, populations from the evolution experiment were exposed not only to NaCl but also to $CaCl_2$ and $NaSO_4$. In each of these treatments, salt levels were gradually increased until populations realized zero net population growth and the corresponding osmolarities were calculated. Comparisons of these osmolarities between salt treatments show that adaptation to NaCl increases the ability of populations to cope with toxicity due to calcium but not to sulphate ions. To conclude, our results suggest that in a metapopulation context evolutionary adaptation to one salt type may facilitate colonization of patches that are salinized by other types of salts, but this outcome will largely depend on salt chemical identity.

Forest fragmentation and tree species composition jointly shape breeding performance of two avian insectivores

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Landscape fragmentation and changing management practices alter the quality of forest patches in cultural landscapes. Apart from increasing forest patch size and connectivity, increasing tree species diversity is expected to result in a higher delivery of ecosystem services and increased biodiversity in managed forests. Yet, how tree species mixing and fragmentation interact to determine resource availability, and how this shapes key demographic processes such as reproductive success of forest-dependent bird species, remains poorly understood. We investigated interacting effects of forest fragmentation and tree species composition and diversity on the breeding performance of Great Tits (*Parus major*) and Blue Tits (*Cyanistes caeruleus*). To assess how resource availability shapes breeding performance across gradients of fragmentation and tree species composition, we also collected data on the abundance of caterpillars, the main food resource for breeding tits. We show that both tree species composition and forest fragmentation impacted the breeding performance of Great and Blue Tit. Tree species composition effects were mainly driven by tree species identity rather than diversity, with highest breeding performance in Pedunculate Oak (*Quercus robur*) monocultures. Fragmentation effects were only present in resource-poor Beech monoculture patches. Structural equation modelling suggests that in Great Tits, tree species composition shapes food availability, which in turn shapes fledging success. In Blue Tits, however, effects of tree species composition on fledging success are mediated through clutch size, rather than food availability, suggesting the presence of seasonal carry over effects. Multiple and species-specific pathways shape the interactions between tree species composition and fragmentation for the breeding performance of insectivorous birds in fragmented landscapes. In smaller forest patches, high breeding success can only be achieved when food resources are abundant.

On the path to recovery : characterizing inbreeding in the European Bison with a model-based approach

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When two alleles from the same individual descend from a single allele in an ancestor, they form an homozygous-by-descent (HBD) or autozygous segment. Increased autozygosity is frequently associated with negative effects on fitness. Population bottlenecks or founder effects can dramatically increase autozygosity levels. We recently developed a model-based approach to identify HBD segments that is particularly valuable when marker information is sparser (e.g., low-fold sequencing experiments, low marker density, marker recruitment bias). This hidden Markov model is also useful when the data is not uniform (variable genotyping errors, marker spacing or recombinations rates). Overall the approach is beneficial in situations encountered in wild organisms. Here, we use our model to characterize individual autozygosity in the restored European Bison. After complete extinction in the wild, restoration programs started as soon as 1929 using only twelve founders kept in European zoos and private breeding centers and leading to the successful restoration of two genetic lines, the lowland and lowland-Caucasian lines. To characterize inbreeding we used a bovine genotyping array encompassing more than 700,000 SNPs. Only 22,602 SNPs were conserved after data filtering. Despite the sparse marker information, we estimated high inbreeding levels (0.30 to 0.40) consistent with pedigree estimates. Many long HBD segments (up to 120 Mb) associated with recent common ancestors, approximately 4 to 32 generations in the past, were identified. Their distribution is compatible with a recent bottleneck. The results obtained with this sparse genotyping data were validated with whole genome sequence data from two individuals. Overall, the presented approach is still efficient when the number of informative markers is reduced compared to traditional high-density genotyping arrays and can also be used with genotyping-by-sequencing data. The same strategy can be applied to wild populations for which the history is not well documented.

Embryonic encephalopsin detection supports bioluminescence perception in lanternshark.

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Camouflage by counterillumination is a widespread defensive strategy across luminescent pelagic organisms which need to be precisely control. *Etmopterus spinax*, a blue-green (486 nm) bioluminescent emitter lanternshark use this function to disappear to the eyes of predators. Recently, researchers highlight the putative extraocular opsin implication within bioluminescence control of several organisms. Encephalopsin is an extraocular opsin shown to be colocalize with the light organ (*i.e.,* photophores) of the *E. spinax* adult shark. According to a recent hypothesis this shark would be able to perceive its own light via this encephalopsin and act as a feedback control mechanism. Thanks to complex transduction pathways involving both hormones (*i.e.,* melatonin, adrenocorticotropic hormone and alpha melanocyte stimulating hormone) and extraocular opsin (*i.e.,* encephalopsin), lanternsharks could regulate their own light emission for a fine-tuned counterillumination strategy. By histological and histochemical analyses, we provide evidences that encephalopsin is expressed in combination with photophore development in order to be ready for the first light emission. According to encephalopsin absorption spectrum, expression within photophores and in utero embryonic luminescence in a fully dark developmental environment, we suggest a deep interaction between photoemission and photoreception.

Effects of temperature-induced sex-reversal on arginine-vasotocin neurones in the brain of nile tilapia neomales (*Oreochromis niloticus*)

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Sex determination in Nile tilapia results from both genetics and environment. During sexual differentiation, genetically XX females can be masculinized by high water temperature, resulting in their differentiation into functional XX neomales. Such individuals have been found in the wild, but the physiological consequences of this sex-reversal are unclear. Arginin-vasotocin (AVT) is a neuropeptide involved in the control of social behaviours. In sex-changing fish, the number and/or size of AVT-expressing neurones vary between sexes. Here we examine the consequences of sex-reversal on AVT-expressing neurons, testis maturation and sex steroid concentrations. Blood, brain and gonads of adult XY males (Mxy), XX neomales (Mxx) and XX females (Fxx) were sampled. AVT neurones were immunostained, counted and their size measured in three subdivisions of the preoptic area (parvocellular (pPOA), magnocellular (mPOA) and gigantocellular (gPOA)). Testes were stained with hematoxylin-eosin and used to perform a morphometric analysis using an intersection grid. Sera were assayed for testosterone, 17β-oestradiol and 11-ketotestosterone with EIA kits (Cayman Chemical). Mxx were heavier than Mxy, but did not present a higher gonadosomatic index (GSI). Mxx present fewer AVT-expressing neurones in the mPOA compared to Fxx. However, they possess bigger AVT neurones in the pPOA compared to the other groups. The analysis of testes did not highlight any difference in maturation between Mxy and Mxx. Circulating concentrations for the three hormones did not differ between males. Estradiol levels were higher in phenotypic females compared to both males, while the opposite relationship could be seen for the 11-KT level. Together these data confirm that temperature-induced sex reversal could affect the growth of XX neomales, even though maturation of testis does not seem to be affected. Our data indicate that the number of AVT neurones in the mPOA and the sex steroid concentrations depend on male's phenotype rather than it's genotype.

Non-canonical thyroid hormone effects on skeletal development in zebrafish (*Danio rerio*)

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A myriad of previous studies have shown the importance of thyroid hormones – primarily T_4 and the active T_3 – in the formation and development of the vertebrate skeleton. Recent research, however, has shown that non-canonical thyroid hormones such as 3,5-T_2 and 3,3',5-triiodothyroacetic acid (Triac) can rescue, amplify, or accelerate the effects of the traditional thyroid hormones T_4 and T_3. The main objective of this study was to determine the effects of non-canonical thyroid hormones on skeletal development in zebrafish (*Danio rerio*). Embryonic developmental-stage characterization was used to show that exposure to different THs during the first 5 dpf had no effect on the progress of larval development. Larval-homogenate luciferase assays of 5 dpf, sp7:luciferase fish showed a significant, 55% increase in osteoblast activity in larvae exposed to Triac. Whole-larva Ca, P, and Mg contents of 5 dpf zebrafish from three different strains – sp7:luciferase, AB, and TLF – revealed both an decrease in the molar Ca content of larvae exposed to T_3 and T_4, and an inter-strain difference between control groups. No significant differences were found in the molar P and Mg contents. Exposures of 5-dpf AB larvae to Triac revealed a significant dose-dependent effect on molar Ca content but not on molar P. An *ex-vivo* scale assay of scales taken from sp7:luciferase fish showed a significant increase in osteoblast activity in scales exposed to Triac for 24 hrs. Alcian blue/Alizarin red staining of 5 dpf AB zebrafish after exposure to Triac expressed dose-dependent, and differential formation of key bone and cartilage structures. Aimed at determining the effects of non-canonical THs on skeletal development in zebrafish, this study demonstrates that TH exposure affects larval bone mineralization – the degree of which is dependent on strain – and that Triac exposure in early development significantly affects larval bone and cartilage formation as well as osteoblast activity.

Are morphological traits explaining swimming performances of several deep-sea sharks from New Zealand?

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Sharks have been present in oceans for more than 400 millions of years and have survived several mass extinctions (Devonian, Permian, Triassic and Cretaceous). Although some morphological features are well preserved between all shark species (cartilaginous skeleton, lack of swim bladder, renewable teeth,...), they show remarkable adaptations to their different lifestyles. Among sharks, data regarding deep-sea species are scares, and especially about their ecology. In this work we focused on deep-sea sharks' swimming performances. Indeed, as active predators, shark swimming capabilities take part in several essential behaviours such as hunting, escaping, home range, migratory behaviours. While the swimming performances are well studied on shallow-water sharks, only limited data about their deep-sea counterparts are available; at most it is suggested they are slow and lazy swimmers. However, recent study shows significant differences of swimming cruise speed between eight deep-sea sharks from New Zealand. Several studies about the shallow-water species show a high importance of morphological traits related with the swimming performances. Here we investigate what are the morphological traits that could take part in deep-sea sharks swimming cruise speed previously observed. We also measure the traits differences between species and correlate it with their phylogeny. Thirty morphological traits from eight deep-sea species and one surface species (control) were measured. These morphological traits include classical measurements of length from the fins or the body but also geomorphological features and ratios for the rostrum and different fins. First results of the statistical analysis seem to show out that variables like area of the pectoral or caudal fins (which play a major role for locomotion of surface sharks), are not the main factors influencing speed of deep-sea sharks. Conversely, rostrum length, distance between the first and the second dorsal fin with the caudal fin, seem to be factors separating the different speed groups.

Resistance modelling infers physical and behavioural gene flow barriers to the red fox (*Vulpes vulpes*) across the Berlin metropolitan area.

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Urbanization affects key aspects of wildlife ecology. Dispersal in urban wildlife species may, for example, be impacted by geographical barriers but also by a species' inherent behavioural variability. There are, however, no functional connectivity analyses resting on continuous individual-based sampling across a rural-urban continuum that would allow a thorough assessment of the relative importance of physical and behavioural dispersal barriers. We used 16 microsatellite loci to genotype 374 red foxes (*Vulpes vulpes*) from the city of Berlin and surrounding rural regions in order to study genetic structure and dispersal behaviour of a mobile carnivore across the urban-rural landscape. We assessed the functional connectivity of our study area applying an individual-based landscape genetic optimization procedure. Three commonly used genetic distance measures yielded different model selection results, with only the results of an eigenvector-based multivariate analysis reasonably explaining genetic differentiation patterns. Genetic clustering methods and landscape resistance modelling supported the presence of an urban population with limited dispersal across the city border. Artificial structures (railways, motorways) served as main dispersal corridors within the cityscape, yet urban foxes avoided densely built-up areas. We show that despite their ubiquitous presence in urban areas, their mobility and behavioural plasticity, foxes were affected in their dispersal by anthropogenic presence. A distinction of man-made structures and sites of actual human activity, rather than natural versus artificial structures, is thus essential to understand urban fox dispersal and perhaps that of other urban wildlife to predict how behaviour can shape population genetic structure beyond physical impacts.

Diversification and functional evolution in reef fishes: The generalist feeding guild is not an evolutionary sink

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Reef fishes have diversified into thousands of species that fill various types of ecological niches, contributing to the tremendous biodiversity of reef ecosystems. Yet, the dynamics of this diversity remain understudied, especially the evolutionary relationships between the different functional traits, which reflect life strategies and ecosystem roles of organisms. Here, we explore how one functional trait, the feeding habit, impacts the dynamics of species diversification and functional evolution. Using comparative phylogenetic methods in conjunction with trophic and functional datasets, we analyse the functional evolution of two major radiations of reef fishes, the wrasses (Labridae) and the damselfishes (Pomacentridae). We demonstrate that feeding habits play a key role in the evolution of the rest of functional diversity. The nature and the diversity of functional roles hosted by fish in reef ecosystems are tightly linked to their feeding attributes. Counter to a simple prediction of ecological opportunism, we found that “generalist” feeding guilds (*i.e.* those composed of species feeding on food sources from the whole bentho-pelagic compartment) do not show higher rates of functional diversification and do not necessarily display higher levels of functional diversity. Furthermore, in contrast to recent macroevolutionary studies on mammals and birds, we argue that these “generalist” guilds of fishes represent the basis of future diversity and cannot be considered as evolutionary sinks or as "dead-ends". These findings clearly re-define our view on the ecological and evolutionary roles played by generalist feeding guilds.

Flexible habitat use of stonechats *Saxicola torquatus* dealing with different anthropogenic novel environments

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Organisms may respond to rapid human induced environmental changes by adapting their habitat requirements through behavioural flexibility. In human-modified landscapes from southern Belgium, recent management activities have generated structurally different and novel land-use types that are now occupied by a number of farmland bird species. However, as birds rely on environmental cues to select their habitat, they can be subject to maladaptive habitat selection if these cues become uncoupled from the underlying habitat quality. We therefore used the European Stonechat *Saxicola torquatus* as a model species to compare the relative attractiveness and breeding quality of the three main land-use types occupied by farmland birds (i.e. intensive grassland, Christmas tree plantations and clear-cut patches in plantation forests) in order to test whether habitat selection is adaptive in a changing landscape. Between 2014 and 2018, we examined the settlement pattern of territorial males to measure habitat preference and we recorded key parameters reflecting reproductive performances and individual survival to assess the quality of the three land-use types for the reproduction of the stonechats. Our results indicate that stonechats preferentially settle in clear-cut patches where they produce lower-quality offspring due to a gradual decrease of nestling body conditions during the breeding season. However, we found that this has no consequence on recruitment rates, because first-year survival was not related to nestling body conditions in our study system. As other parameters of reproductive performances, adult survival and first-year survival were similar between the three land-use types, we concluded that stonechats are capable of flexible habitat use and may find breeding opportunities of similar quality in the three land-use types although these strongly differ in terms of vegetation structure and management. Moreover, our results highlight the importance of measuring multiple fitness components to assess habitat quality in a comprehensive way.

How genetic research can help the conservation of Golden-headed lion tamarins: preparing for climate change

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Understanding how organisms adapt genetically to changing environments is a key topic in evolutionary biology and hugely relevant to biodiversity conservation. Although climate change is the most cited threat to overall ecosystem and species survival, its effects on genetic biodiversity has hardly been studied, which is partly due to the challenges of obtaining suitable samples and generating good quality genomic data. However, recent developments in genomics and remote sensing, and the availability of new analytical tools, allows the identification of genomic regions involved in adaptation. In this project we will assess genetic adaptions in the Golden-headed Lion Tamarin (GHLT) *Leontopithecus chrysomelas,* an endangered small primate endemic to Bahia State (Brazil) for which considerable background knowledge is available, and both *in situ* and *ex situ* conservation efforts are ongoing. Given its occurrence across a natural climate gradient (cline in temperature and precipitation), this species allows us to obtain information on which – likely multiple interacting – genomic regions are involved in adaptation. This will also allow to simulate and predict the effects of climate changes and hence to guide the conservation management of this species. Previous results, using 'traditional' genetic markers (microsatellite DNA), suggest that these populations have a relatively low GD and high population genetic structure, raising questions about actual functional landscape connectivity. Landscape modelling at a finer scale will investigate this issue further and assess the need for management practices such as translocations and/or 'genetic rescue' from captivity. As such, we will verify whether wild adaptive variability is retained in the captive population.

Vertebrae are the backbone of cetacean diversity: How morphological innovations sustained dolphin explosive radiation

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With approximately 90 living species, whales, dolphins and porpoises represent the most diverse clade of extant marine tetrapods. This high level of taxonomic diversity has been often related to ocean restructuring that resulted in an explosive radiation of oceanic dolphins within the past 10 Ma. However, the environmental factor hypothesis can be restrictive as it does not entirely explain how organisms have faced environmental constraints suggesting that other factors could also explain this burst of diversification. In marine taxa such as sharks and ichthyosaurs, morphological variations have been linked to several life-styles which have sustained their diversification in different adaptive zones. The aim of our study is to establish the relationship between the morphology of the axial skeleton of cetaceans, their ecology and their diversification. By combining the most extensive morphological dataset describing the axial skeleton of 73 cetacean species with phylogenetic comparative methods, we demonstrate that extant cetaceans have followed two distinct evolutionary pathways in relation to their ecology. Most oceanic species evolved towards an increased body size leading to gigantism in baleen whales. Interestingly, dolphins have invested another way. While riverine and coastal species exhibit a small body size, lengthened vertebrae and a low vertebral count, small oceanic dolphins show an extremely high number of short vertebrae. We discuss how these modifications have operated as key innovations that contributed to the explosive radiation of dolphins.

Individual Differences in the Link between Abnormal Behaviour and Stress in Zoo-Housed Chimpanzees (*Pan troglodytes*)

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The occurrence of abnormal behaviours in captive animals is both pervasive and ambiguous. By definition, these behaviours are absent or less frequent in a species' wild-living counterparts. However, this lower incidence in the wild does not necessarily mean they are linked to poor welfare, as is often thought. This study hypothesizes individual variation could be one reason why many studies arrive at different conclusions when it comes to the link between abnormal behaviours and stress; if such links vary considerably by individual, this could in turn yield inconclusive results when considering entire groups. To test this, we considered the abnormal behavioural repertoire of a colony of 15 captive chimpanzees (*Pan troglodytes*) housed at Royal Burgers' Zoo in Arnhem, the Netherlands. Firstly, to investigate if there is meaningful individual variation in the link between a given abnormal behaviour and stress, we analysed data from a period of two years on coprophagy. Despite coprophagy being the most well-studied abnormal behaviour in captive chimp groups, results regarding its link to welfare are highly inconsistent. Secondly, to examine if stress is expressed differently by each individual, we focused on eight abnormal behaviours collected over a period of six months. Stress was measured via an individual's rate of self-scratching, considered to be the most reliable behavioural indicator of anxiety in nonhuman primates. Significant individual variation was found in the link between coprophagy and self-scratching, as well as in the link between other abnormal behaviours and stress when considering the entire abnormal behavioural repertoire. Other factors such as age, sex and rank could not account for the reported patterns. These results invite us to speculate that the inconsistencies in the literature on whether abnormal behaviours reflect stress may be partially due to variation between individuals. Whether an abnormal behaviour is harmful or not may be dependent on the individual, and the conditions under which that individual acquired this behaviour. These findings indicate that the individual behavioural repertoire of chimpanzees needs to be taken more seriously when considering their welfare.

Modern human evolution in Africa and the Middle East: could allele sharing between populations accelerate adaptation?

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During their expansion out of Africa and across the globe, modern humans encountered many new evolutionary challenges, including new pathogens, climates and diets, which resulted in selection for populations to adapt to a new local environment. More recent migrations, such as the back-to-Africa migrations from the Middle East 4 kya, have caused significant gene flow between once isolated populations. These admixture events allowed the sharing of locally adapted alleles between populations. A new allele introduced into a population may be more fit or less fit than the local variants already in the population. Selection may then act to increase or decrease the frequency of new alleles in processes known as adaptive introgression or purifying selection respectively. Migration and gene flow between populations has become increasingly common throughout the *Homo sapiens* species range and an accelerated rate of evolution has been observed in humans over the last 40 kya. As adaptive introgression acts on standing genetic variation rather than new mutations, it may have been an important process in speeding up adaptation in humans, although it has been little studied. We used a novel application of the locus specific branch length statistic to identify loci that have undergone recent adaptive introgression and purifying selection in 34 human African and Middle-Eastern populations and find that there has been substantial adaptive introgression and purifying selection of loci across the genome in both regions. Furthermore, the large overlap of selection candidate loci observed between populations and regions strengthens the adaptive introgression hypothesis and suggests that gene variants spread through gene flow are under shared patterns of selection in many populations. These patterns of post-admixture selection have targeted genes involved in the nervous system, metabolism, insulin, and skin UV protection, and include loci not previously identified in previous selection studies.

Inferring the responses of Southern Ocean benthic species to environmental changes using Dynamic Energy Budget models

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The Southern Ocean is facing rapid environmental shifts related to global climate change. This issue is currently the focus of an intense research effort to understand and characterize potential responses of marine benthic species and populations. Our knowledge of the impact of environmental changes on Antarctic species physiology has mostly been studied using short-term experiments constrained by strong financial and technical limitations. The use of dynamic models such as the Dynamic Energy Budget (DEB) models that relate species functional traits to environmental characteristics helps to spatially interpolate this experimental work; DEB models being built using simple observations or experiments from species life cycle that can be extracted from the literature. In this study, we calibrated a DEB model for four common and abundant benthic species of the Southern Ocean (i.e. the sea urchin *Sterechinus neumayeri*, the sea star *Odontaster validus*, the bivalve *Laternula elliptica*, the gastropod *Nacella concinna*). Species sensitivity to environmental changes was simulated and the impact of changes in temperature and food availability on species metabolic performance was assessed (e.g. changes in growth rate, reproductive performance, maximal size and age). The limits and potential of these models developed for Antarctic benthic species are discussed with a special attention devoted to their application to other case studies and the improvement of our understanding of the potential response of Antarctic benthic communities to future environmental changes.

Deep amplicon sequencing as a tool to study the impact of human activities on trematode communities in Ugandan crater lakes.

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Biodiversity loss caused by human activities threatens the capacity of ecosystems worldwide to provide essential ecological services. Hence, ecological research is increasingly directed at understanding the consequences of anthropogenic disturbances on biodiversity. Parasitic organisms have largely been overlooked in these efforts, although parasitism is the most common feeding strategy on Earth. One group of parasites with high societal relevance are trematodes, i.e. flatworms that have snails as intermediate host and generally a vertebrate as final host. Trematodes cause important human diseases such as schistosomiasis, affecting more than 200 million people worldwide. Little is currently known regarding the diversity of trematodes in Africa, the processes shaping their communities or the impact of human activities on these processes. These knowledge gaps somewhat reflect the lack of targeted research, but more importantly the lack of tools to detect and identify these parasites directly in their hosts. To tackle this issue, we developed a tool based on the multiplexing, pooling and next-generation-sequencing of nuclear and mitochondrial genetic markers simultaneously targeting the parasites and snail hosts. This method of genotyping by deep amplicon sequencing will increase the genomic coverage and thus the power to conduct phylogeographic and phylogenetic analyses. Applied to the study of trematodes hosted by populations of snails this tool has the potential to help disentangle the drivers of parasite diversification, community structure, and the ecological context of disease transmission. We then aim to make use of this technique to document patterns of local and regional diversity of trematode communities hosted by planorbid snails in the crater lakes of western Uganda, and to investigate the ecological processes at play. These crater lakes cover wide gradients of habitats and anthropogenic disturbance, therefore representing a natural laboratory to analyse the impact of natural and anthropogenic factors on trematode diversity within and among lakes.

Predicted climate change impacts on agriculturally important pest-parasitoid systems.

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The effects of climatic change can be different for different insect species, because insects are poikilothermic. This will then influence host-parasitoid population dynamics. We investigated the impact of climate change on selected vegetable pests and their natural enemies in Lower Saxony, Germany. The selected pest species are *Brevicoryne brassicae* and *Aleyrodes proletella*. Their respective parasitoids are respectively *Diaeretiella rapae* and *Encarsia tricolor*. Age-structured simulation models were developed in INSIM to estimate changes in population size for each species during the course of a year. Temperature data simulated by the climate model REMO (MPI, Hamburg, Germany) were used to estimate the relative changes in maximum population size and the occurrence of population peaks for two future time periods, from 2021 to 2050 and from 2071 to 2100. We compared these future parameter estimates with those estimated for the reference time period from 1971 to 2000. The relative changes in the considered parameters for each species were calculated for the full Lower Saxony area to investigate regional differences. The interactions between parasitoids and pest are incorporated in the model. The modelling results showed increased populations of the pest and parasitoid species in future periods. In addition alate aphids occur earlier in the year, pointing to a need for adapting pest management protocols.

Understanding the social-ecological dynamics of Human-Crocodile conflicts in communities around Murchison Falls Conservation Area, Uganda

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Human-wildlife conflicts are becoming increasingly common and increasingly serious, as a booming human population encroaches ever more on wildlife habitat. . In Africa, conflicts between people and large herbivores like elephants and between people and mammalian carnivores, particularly lions, have been recognized as serious direct threats to people. However, conflicts with crocodiles are often less noticed and are under-researched, despite their devastating effects. In Uganda, legal protection and conservation efforts have enabled the recovery of the crocodile population after heavy hunting during the 1960s. But as human population is also growing at a rate of 3.3%/year in Uganda, human settlements increasingly overlap with crocodile habitat ranges and human-crocodile conflicts (HCC) ensue. This study aimed at compiling spatial-temporal patterns of HCC, to identify explanatory factors and to identify and prioritize conflict mitigation strategies. This study was conducted using a combination of methods: a literature review (archive search), a questionnaire-based survey to characterize and understand human-crocodile conflicts, and a consensus-building technique to identify and prioritize conflict mitigation strategies, the Nominal Group Technique (NGT). The NGT ranking indicated that the construction of protective barriers -crocodile exclusion barriers- in the lake/river bed was the most preferred mitigation measure, followed by translocation of problem crocodiles. Structures and facilities that reduce the community's dependency on the lake/river would be ultimate mitigation measures. This study has long-term conservation implications both at the local (mapping of HCC, perception studies & tangible mitigation measures prioritization) and at the supra-local level, as understanding and integrating local people's views towards wildlife is critical to inform and guide conservation and protected area management efforts. The ideas generated can be taken into account by the wildlife managers when developing a crocodile management plan.

Influence of body mass, phylogeny and ecology on morphological variation in the third metacarpal of rhinos (Perissodactyla; Rhinocerotidae)

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Rhinoceroses (Perissodactyla: Rhinocerotidae) are a group of well-known and historically widespread large mammals. Rhinos are mesaxonic animals, meaning that the middle (third) digit on their fore- and hindlimbs is the longest, and intuitively bears the greatest proportion of the animal's mass during locomotion. The bones of the third digit are therefore integral for body support, locomotion and substrate interaction. The goal of this research was to test for an effect of body mass or habitat on the shape of the third metacarpal of extinct and modern rhinocerotids. Habitat assignment was reconstructed based on hypsodonty indicies (proxy for feeding behaviour), obtained through a literature study. Body mass was estimated based on linear regression equations. Bone shape was captured by scanning with a laser surface scanner (Faro ScanArm) and quantified with a 3D landmark-based geometric morphometric approach. Landmarks were aligned using a Generalised Procrustes Analysis. A Principle Component Analysis (PCA) isolated the main axes of variance, Ordinary Least Squares (OLS) regressions were performed to test for correlations between shape, size and ecological variables, and one-way PERMANOVAs were performed to test for significant differences between *a priori* phylogenetic groups. Results suggest that metacarpal robustness was correlated with body mass. In general, smaller taxa were more slender and larger taxa more robust. Habitat openness (i.e. high hypsodonty index) also correlated significantly with metacarpal robustness, in addition to correlating with several other changes in metacarpal shape. These included adaptations for weight support and energetically efficient locomotion, which may be expected in open habitats, with adaptations for walking on compliant substrates in closed environments. Phylogenetic relatedness also strongly influenced metacarpal shape in the species studied. Our results demonstrate that metacarpal morphology in rhinocerotids is highly variable, with multiple factors influencing shape in these animals.

Implication of skin pigmentation actors in the bioluminescence control of lanternsharks.

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In the ocean's depths, where light rays are scarce, some organisms have developed a way to chemically produce their own light to fulfil their respective needs. Counterillumination, a method whereby the individual camouflages itself from underlying predators, is a common feature in mesopelagic species.

Recent studies regarding light emission by deep-sea sharks, from Etmopteridae family, show similarities between the bioluminescence control of deep-sea sharks and the skin pigmentation control in epipelagic sharks. Shark photophores (*i.e.,* light-emitting organs) possess strata of cells located between the photocytes (*i.e.*, light-emitting cells) and the lens. This layer of cells, called iris-like structure, is capable of granulation and degranulation of melanin pigment to regulate the total light amount emitted by photophores. Locating major skin pigmentation actors within photophores is essential to further understand deep-sea shark bioluminescence control. Dynein and kinesin are two intracellular motors which enable the mobility of the pigmented granules towards and away from the nucleus. Additionally, it appears that protein kinase A (PKA) is involved in the transduction cascade leading to granular movements.

The present work investigates the implication of skin pigmentation actors (*i.e.,* kinesin, dynein and PKA) in the hormonal bioluminescence control in deep-sea sharks. Transcriptomic analysis were performed in order to retrieve the target protein shark sequences, create phylogeny and select the appropriate commercial antibodies. Detection and localization, within the photogenic tissues, of these actors by immunohistodetection, and by western blotting were carried out, according to different hormonal treatments (stimulation/inhibition of bioluminescence).

Results highlight the *in sili*co presence and affiliation of each protein in the photogenic tissues. Immunodetections confirm the presence and differential location of each protein according to hormonal treatments. All these results add evidences of the implication of these actors in the light emission control of lanternsharks.

Determining the instantaneous axis of rotation of different monodactyl species

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During the Miocene, the Equidea family reduced their number of functional digits to only one, also referred to as a monodactyl manus. Monodactyly evolved independently in four different lineages, the *Equus* genus that includes the asses, donkeys, horses and zebras, is the only remaining lineage. Many hypotheses regarding digit reduction remain untested. Musculoskeletal modelling is a tool that can be used to test hypotheses regarding the evolution of monodactyly by simulating the locomotion of extant as well as fossil species of the Equidea family. An important input variable in an accurate musculoskeletal model is the instantaneous axis of rotation (IAR) of the joint. This axis describes the three-dimensional movements of two adjacent segments with respect to each other. The aim of this study was to determine whether extant monodactyls display similar IAR properties for all forelimb joint over their entire range of motion, given their size by comparing them to horse IAR properties and by contrasting them against multidactyl perissodactyls and more distinct mammals. Cadaver forelimbs with standardized cuts at the midlevel of each segment of different horse breeds, a przewalskii, a zebra and several non-monodactyls were used to determine the IAR over the entire range of motion for all forelimb joints. Bone pins attached with reflective marker triads were drilled into the different forelimb bones. Each forelimb joint was manually moved independently through flexion-extension, abduction-adduction and internal-external rotation. The three-dimensional coordinates of the marker triads were recorded using an infra-red six camera system. IAR properties were calculated with a customized MATLAB script. We found that position properties of the IAR were size-dependent. Similar IAR behaviours over the entire range of motion were found for the different monodactyl species for each of the forelimb joints, suggesting that there are monodactyl specific IAR properties for the different forelimb joints.

Threatened giants: phylogeography of tridacnid clams

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On geological time scales giant clams were able to adapt to global changes, such as the closure of the Tethys Seaway in the Miocene, which separated the Atlantic form the Indo-Pacific Ocean. Even though they became extinct in their Atlantic and Mediterranean centre of biodiversity, they managed to escape into the Indian Ocean. From there, giant clams gradually dispersed throughout most of the Indo-Pacific, establishing their new biodiversity centre in the Southeast Asian Coral Triangle by a radiation in the Pleistocene. Glacial cycles caused sea-level low stands of up to 130 m, exposing shallow shelves in the Coral Triangle that created barriers among populations, fostering allopatric speciation. Signatures of these vicariance events can still be detected in the phylogeographic structure of *Tridacna maxima*, *T. squamosa* and *T. crocea*. In the last decades, giant clams are threatened by global change and other human activities, such as bleaching, ocean acidification and overfishing. Bleaching describes the loss of their symbiotic zooxanthellae, which provide most of the clam's energy budget by photosynthetic products, due to increased seawater temperature. The reduction of pH in seawater due to rising CO_2 concentrations increases the energy demand for the formation of their calcium carbonate shell, which most probably reduces their growth rate. In addition to these negative impacts of global change, overfishing is heavily decreasing population sizes in many regions, which can lead to reduced genetic diversity and even local extinctions. The adaptability to global change depends to a large extend on the genetic diversity of a species and its dispersal potential. These two factors determine the replenishment of populations and colonisation of new regions, which might be necessary due to a poleward shift of suitable habitats caused by global change.

Afrotropical mammal communities under pressure: new insights from functional diversity metrics.

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Tropical rainforests are highly affected by human activities and besides a loss in biodiversity (i.e. species richness and abundances), these pressures also affect ecosystem functioning. Understanding how the diversity in functional roles of species (i.e. functional diversity) is affected by human pressures provides new information about the state of an ecosystem and complements traditional biodiversity metrics. Still, research on functional diversity in tropical ecosystems is lacking. Here we present new insights in how tropical mammal communities in Cameroon respond to human pressures. We analysed how mammal abundance, richness, composition and functional diversity in a village hunting zone changes over time (2002-2016) and how different forms of conservation management affect mammal communities in these forests. Overall, results indicated that by 2009 mammal abundances declined in hunting zones and that species richness and functional diversity declined by 2016. Moreover, we found that sites with less conservation management showed lower mammal abundances and altered community structures, but equal species richness levels and minor changes in functional diversity. Although some of the wildlife decline may be due to behavioural adaptation, loss beyond a certain threshold causes mammal communities to collapse after which functional traits are lost, indicating that ecological decay is likely to begin. The observed lag between the decrease in mammal abundances and reduction in species richness and functional diversity is arguably the result of functional redundancy, due to the presence of functionally similar species, and highlights the ecological resilience of such communities against human activities. This suggests that afrotropical mammal communities are able to remain functionally healthy until certain levels of human pressure. We demonstrate the value of additional functional diversity measures to understand mammal community dynamics and conclude that human-affected forests are still functionally relevant for conservation management, but that actions are needed to prevent future loss of community integrity.

Global food web alteration following goldfish introduction in palmate newt dominated pond ecosystem

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Freshwater ecosystems are central to the development and functioning of human societies and yet they are amongst the most altered worldwide. Alien species introduction is a leading cause of biodiversity loss in fresh waters, with impacts on recipient ecosystems that are recognized as some of the most significant, least controlled, and least reversible. Of particular concern is the replacement of strictly carnivorous apex consumers by omnivorous consumers because they can potentially have important and long-term impacts on biodiversity and ecosystem functioning by re-shaping food web architecture. In Larzac (Southern France), declining trends in palmate newt (*Lissotriton helveticus*) dominating ponds are correlated to goldfish (*Carassius auratus*) introductions. However, the processes leading to local extinction of newts are not fully understood. Additionally, despite being one of the most widespread fish introduced in Europe, goldfish impact on native ecosystems is poorly studied. Because they are omnivorous, goldfish may have a strong impact on the entire pond ecosystem, potentially making it an unsuitable habitat for newts. To assess the impact of goldfish leading to newt extinction, we compared community assemblage and food web structure of consumers in ponds naturally dominated by palmate newts and in ponds where newts have been extirpated following goldfish introduction, using various techniques including Carbon and Nitrogen stable isotope analysis in a Bayesian framework. Our results show that beyond direct interactions with newts, goldfish have profound detrimental impacts on the ecological communities of ponds by operating a global alteration of the food web on multiple trophic levels. Changes were characterized by a reduction in food chain length, trophic diversity and redundancy, and the extirpation of almost all exploitable resources available for newts. In the long-term, these changes likely explain newts' exclusion from invaded ponds and illustrate the complex detrimental effects of omnivorous species introductions for native ecosystems.

Evolution of placoid scales in deep-water sharks: from morphology to atomic composition

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Deep-sea environment represents a wide proportion of the world surface. However, it still remains largely mysterious and poorly studied. Deep-sea ecosystems show a lush and extremely diversified fauna, which sometimes presents surprising characteristics such as bioluminescence! Up to now, scientists consider that only 1% of the entire biotope was sampled. Within this environment, elasmobranches are mainly represented by Etmopteridae, Centrophoridae, Squalidae, or Somniosidae families belonging essentially to the Squaliformes. The present study focused on placoid scales (*i.e.*, scales structurally homologous with vertebrate teeth) of 33 shark species from this order. These scales are associated with the skin and involved in different ecological functions such as the reduction of the drag, the defence against parasitism/predators or abrasion but it is also suggested that they might be functionally related to bioluminescence transmission in luminous species. Based on 33 deep-water shark species, this study makes a comparison of the morphological features and composition of ventral skin placoid scales. Thanks to Scanning Electron Microscopy (SEM) and Energy Dispersive X-ray spectrometry (EDX) analyses, morphometric and atomic composition measurements have been performed. Multivariate statistical analyses (ACP) were performed to determine clade-specific features. According to the known phylogeny of Squaliformes, character-mapping approach was used to predict ancestral character states and assess their conservation along the lineage. Our results clearly highlight a conserved and stereotypical composition of the scales among Squaliformes but, conversely, also demonstrate striking morphological differences between families. Character-mapping reconstruction allow to assess the evolution of various traits within Squaliformes (*e.g.,* shield-like placoid scale morphotype is ancestral), and particularly the link between morphological features and bioluminescence for specific families (*e.g.*, surface occupied by scales reduced in luminous clades). All these results, deriving from an unprecedented sampling, shed light on morphological diversity and composition variation of placoid scales in deep-sea elasmobranches and, more generally, on the adaptations of deep-sea sharks to their mysterious environment.

Prehensile tail used linked to myology in chameleons

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Prehensile appendages represent an adaptation that has evolved in various vertebrate and invertebrate lineages. Prehensility is the ability to hold and grasp firmly onto an object, combining flexibility and strength. Chameleons (Chamaeleonidae) typically have an arboreal lifestyle and use their prehensile tails for anchoring and as a support during feeding. By linking the variation in morphology and musculature to function, we aim to explain what it takes to make a tail prehensile. Previous study focused on the morphological variation in tail vertebrae between prehensile and non-prehensile chameleon species using µCT data, however this data alone does not allow for functional testing without data on the musculature.Our morphological data on the skeleton showed that a lot of shape variation regarding prehensile and non-prehensile species concerns the transversal spine. For this study, we focus on the muscle bundles that attach to the transversal spine, the m. ilio-caudalis, which has an important role in the torsion and ventral flexion of the tail. Both length and angle of the transversal spine differs between prehensile and non-prehensile species, as well as on a regional level within the tail. Prehensile species have a longer transversal spine pointing distally, and the length decreases towards the distal end. Studying prehensile function on a musculo-skeletal level, we used µCT scans of PMA stained specimens and dissections showing exactly where on the spine muscles attach and how many vertebrae they cross before insertion. Simulations using Multi-Body Dynamics allow assessing vertebral kinematics in relation to muscle performance. Using the muscle data as input, together with the virtual 3D reconstructions of the tail vertebrae, we can investigate the functional role of the impact of individual muscles and kinematics on the movement of the tail.

Comparison of environmental DNA and bulk-sample metabarcoding using highly degenerate cytochrome c oxidase I primers

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Freshwater biodiversity provides important ecosystem services and is at the core of water quality monitoring worldwide. To assess freshwater biodiversity, genetic methods such as metabarcoding are increasingly used as they are faster and allow better taxonomic resolution than manual identification methods. Either sampled organisms are used directly for “bulk metabarcoding,” or water is filtered and the extracted environmental DNA serves as a proxy for biodiversity via “eDNA metabarcoding.” Despite the advantages of both methods, questions remain regarding their comparability and applicability for routine biomonitoring and stressor impact assessment. Therefore, we compared metabarcoding results from bulk and eDNA samples taken from 19 streams spanning a wide gradient of farming intensities in New Zealand. We performed PCR with highly degenerate cytochrome *c* oxidase I primers and sequenced libraries on an Illumina MiSeq. The inferred community composition differed strongly between the two methods. More taxa were captured by eDNA than bulk-sample metabarcoding (5,819 vs. 1,483), but more of the commonly used invertebrate bioindicator taxa (mayflies, stoneflies and caddisflies) were found in bulk (47) than eDNA samples (37). Catchment-wide and local land use impacts on communities were detected better by eDNA metabarcoding, especially for non-metazoan taxa. Our findings imply that bulk-sample metabarcoding resembles classical freshwater biomonitoring approaches better, as more indicator macroinvertebrate taxa are captured. However, eDNA metabarcoding might be better suited to infer the impact of stressors on stream ecosystems at larger scales, as many new and potentially more informative taxa are registered. We therefore suggest exploring both methods in future assessments of stream biodiversity.

Pigs, peccaries and perissodactyls - convergence in scapular spine osteology and muscle arrangement between tapirs (Perissodactyla) and suiformes (Artiodactyla)

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The scapula (shoulder blade) of terrestrial quadrupeds is a key component of locomotion. The morphology of this bone is often overlooked in assessing functional differences between species. Recently, the scapular morphology of modern tapirs was quantified, exhibiting interspecific variation. The scapula spine (separating the infraspinous and supraspinous fossae) of the Old World *Tapirus indicus* exhibited a strongly retroverted shape, a feature otherwise observed only in Old World suiformes (pigs). Here, I used a combination of qualitative and quantitative techniques to examine the scapulae of tapirs (Tapiridae) and suiformes (Suidae & Tayassuidae). Dissections of adult and juvenile *T. indicus* were conducted, comparing the arrangement of the supraspinatus and infraspinatus muscles to published muscle information for suids and tapirs. A total of 61 scapulae (36 tapirs; 8 tayassuids; 17 suids) were laser scanned or photogrammed at high-resolution to capture the 3D surface detail. The areas of the supraspinous and infraspinous fossae were calculated to generate scapular fossa ratios (SFRs), and the angle of retroversion of the scapular spine (RA) was calculated from 2D images in ImageJ. Interspecific differences in SFRs and RAs were assessed using ANOVAs. Tapir forelimb dissections categorically confirmed that the infraspinatus of *T. indicus* possesses an accessory head, attaching to the cranial face of the scapular spine, mirroring the muscular arrangement in Old World pigs. However, this is not observed in tapirs or tayassuids from the neotropics. Suids and *T. indicus* show no significant differences to each other in RAs, but are significantly different to the tayassuids and New World tapirs; no significant size effect was observed. These results suggest convergent scapula morphologies and shoulder muscle arrangement evolved in both Old World pigs and tapirs, but not in neotropical members of these clades. The exact function of the accessory infraspinatus in both tapirs and suids remains enigmatic.

RAD-seq markers reveal only limited gene exchange between two species of leaf beetles across a hybrid zone in the Alps

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In a previous multi-locus phylogeographic study, extensive mitochondrial genome introgression was detected in the Alps between *Gonioctena quinquepunctata* and *G. intermedia*, two European sister species of cold-tolerant leaf beetles feeding exclusively on mountain ash (*Sorbus aucuparia*) and bird cherry (*Prunus padus*). Because these cases of introgression involved multiple haplotypes and resulted in the current sharing of identical haplotypes between the two species, we hypothesized that hybridization still occurs today between *G. quinquepunctata* and *G. intermedia* inside their secondary contact zone. To characterize the extent of this gene exchange within the putative alpine hybrid zone, we have sampled nine populations of *G. quinquepunctata*/*G. intermedia* across the western Alps, along a North - South gradient, gradually moving away from the hybrid zone in the North towards the South where only *G. quinquepunctata* is found, and evaluated genomic variation across these populations in a large number of SNPs via a RAD-seq approach. In order to analyse this genomic variation in a wider geographic context, we also included populations from the two species across their entire respective ranges, for comparison. Analysis of genomic variation across the Alps detected a very small number of admixed individuals (from 1 to 3, depending on the method used) associated with a level of admixture below 5%. These results suggest the existence of relatively strong reproductive barriers maintaining the two species apart.

Ensuring access to high-quality resources reduces impacts of climate change on bees

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Pollinators are experiencing declines globally. Well-known drivers of such decline include climatic and nutritional stresses. Understanding potential synergies between these two drivers is needed to improve predictive models on future effects of climate change on pollinators. Here bioassays on bumblebee colonies were used to evaluate the interactive effects of climatic stress, loss of resource quality and colony size. When acting isolated, both nutritional and climatic stress reduced colony development (i.e. lower investment in offspring production). Strikingly, effects of climatic stress were far more accentuated under nutritional stress. In other words, a high-quality diet has the potential to compensate the effects of climatic stress. Small colonies were much more sensitive to climatic and nutritional stresses than large ones, possibly because numerous workers help maintain social homeostasis. Overall, our study suggests that landscape management actions that ensure access to high-quality resources could reduce impacts of climate change on bee decline.

How to find genes involved in cuticular hydrocarbon (CHC) biosynthesis in Hymenoptera? Insights from an extraordinary case of intrasexual CHC profile dimorphism in a mason wasp.

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Cuticular hydrocarbons (CHC) play two essential roles for insects: CHCs act as anti-desiccation agents and they are exploited for intra- and interspecific communication. Yet, although the main steps of CHC biosynthesis are known, only few genes involved in CHC biosynthesis have been identified. By studying an extraordinary case of intrasexual CHC profile dimorphism in the spiny mason wasp*, Odynerus spinipes*, (Hymenoptera: Vespidae), we are able to shed light on the molecular basis of CHC biosynthesis. *O. spinipes* females express two CHC profiles (chemotypes) that differ in more than 70 compounds qualitatively from each other. Females seem to differ exclusively in this specific trait and keep their chemotype during their entire lifespan. We searched for genes that are differentially expressed in females of the two chemotypes. By doing so, we readily identified 16 candidate genes likely involved in CHC biosynthesis (*i.e*., desaturases, fatty acid synthases, elongases,). We currently seek to validate the function of these genes via RNAi-mediated knockdown experiments on *O. spinipes* and on the honey bee, *Apis mellifera*. Tissue-specific expression of the candidate genes was also investigated via whole-mount *in situ* hybridization in the honey bee. We see a phenotypic effect (*i.e.*, a change in the CHC profile) after individual RNAi-mediated knockdown of three candidate genes in the *A. mellifera*. So far, we tested and confirm expression of two of them in oenocytes (*i.e.*, cells in which CHC biosynthesis takes place). We are also able to confirm a significant decrease in the expression level of one gene after RNAi knockdown (via RTqPCR). We are currently perusing the analysis of additional candidate genes for oenocyte-specific expression in order to narrow down the genes subject to future knockdown experiments. In that way, we might be able to identify genes that are currently unknown to play a role in CHC biosynthesis.

A life of ease, foraging habits or just notorious places? Studying behavioural strategies with high-resolution GPS tracking in the lesser black-backed gull

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Many animal species successfully adapted to anthropogenic habitats, and more specifically to human-induced feeding opportunities. Typically, these species are generalists with a wide ecological niche and a high degree of behavioural plasticity. It is therefore assumed that generalists have an edge over specialists when responding to current environmental change. However, populations of many generalist species actually consist of highly specialized individuals. Such a high degree of foraging specialisation may make some individuals within populations of generalist species more prone to environmental change than others. Lesser black backed gulls are a prime example of a generalist species at the population level, while individuals are often highly specialised in their foraging strategies. Intriguingly, as a migratory species, lesser black-backed gulls show pronounced inter-individual variation in migration strategies with some birds wintering as close as Northern France, while others migrate as far as Senegal. Individual gulls then again show only restricted inter-annual variation in migration behaviour. Thus, lesser black-backed gulls are a very interesting model to study the consequences of a changing environment on both the individual and the population level. Using 5 years of GPS tracking data of individual lesser black-backed gulls we determined the extent of foraging niche specialisation within and among our study populations, and explored the spatio-temporal variation in the annual migratory movements. Most gulls appeared to be specialists, but we observed significant variation in the spatio-temporal dynamics of foraging specialisation. When taking the whole annual cycle into account, even highly specialised individuals changed their foraging habits during migration. We also show that on the population level migratory distance has progressively shortened although individuals appear to be highly consistent in their migratory behaviour. Taken together, this study provides important insights in understanding the adaptive significance of specialisation in a changing environment.

Maladaptive learning of mate preference in a butterfly facing climate change

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Climate change is one of the best documented consequences of human activity that threatens biodiversity. So far, organisms were shown to respond to climate warming by changes in distribution ranges, which modify species community structure. While species are assumed to produce adaptive responses to climate change under natural selection, here we document a maladaptive response under sexual selection. For this, we used an ectothermic insect with strong adaptation to historical seasonal changes of climate: the polyphenic tropical butterfly *Bicyclus anynana* alternates generations with "wet" (and warm; "WS") and "dry" (colder; "DS") distinct phenotypes that are adapted to the corresponding sub-Saharan seasons. During the wet-to-dry seasonal transition, wet and dry seasonal phenotypes overlap with a third, intermediate, seasonal phenotype ("IS"). As a first evidence of maladaptation, we found that adults developing under the 2100 climatic scenarios were mostly of the wet seasonal form at the onset of the dry season, compared to the mostly dry seasonal forms produced under the current climate. We next set out to assess the effect of climate change on sexual selection. Our underlying arguments were that, in this butterfly, (i) survival and reproductive fitness differ when mating with either seasonal forms or (ii) early exposure to potential mates is known to modify sexual preferences. While naïve mate preferences were in agreement with the expected fitness increase, females experiencing one of each of the seasonal forms during sexual maturation modified their sexual preferences towards males with intermediate, expectedly maladaptive, phenotypes, which constitutes a second evidence of maladaptation. Altogether, we found that sexual selection can produce immediate maladaptation in living organisms that experience, and respond to, changing abiotic (climate) and biotic (mating partners) factors.

Where Does Land Use Matter Most? Contrasting Land Use Effects on River Quality at Different Spatial Scales.

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Understanding the influence of land use activities on river quality has been a key focus of river monitoring programs worldwide. However, defining which land use spatial scale is relevant remains elusive. In this study we therefore contrasted the influence of land use on river quality using three types of land use estimators namely, circular buffers around a monitoring site, circular buffers upstream of a monitoring site and the entire watershed area upstream of the monitoring site. The land use percentage compositions within the Usa-Kikuletwa River catchment in the Northern Eastern Tanzania were quantified using Landsat-8 satellite images with a maximum mapping resolution of 30m. Redundancy analysis models and generalized linear models were used to evaluate the influence of land use spatial scale on macroinvertebrate assemblages and water quality. Overall water quality variation, macro invertebrate richness and biotic indices were significantly explained by land use of the entire watershed area upstream of the monitoring site. However, macroinvertebrate abundances showed strong links with more local land use patterns within 100m and 2000m radii. Circular buffers upstream the monitoring site were more informative for macroinvertebrate assemblages than circular buffers around the monitoring sites. However, the latter did correlate well with water quality variables. We show that water quality and macro invertebrates respond differently to land uses at different scales, and illustrate that the choice of spatial land use metrics can bias conclusions of environmental impact studies in rivers.

Assessment of pollination ecosystem service throughout wild bees biodiversity and associated phytometer experiment – a case study at farmstead Froidefontaine in ecological transition (Havelange, Belgium)

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Pollination is a key ecosystem service. It contributes to around 87.5% of wild flowering plant reproduction and up to 70% of insect pollinated crops production (i.e. orchards, vegetables…). This service is provided by the pollinators community, including bees (Hymenoptera: Anthophila) which are the most efficient pollen vectors. Therefore, worldwide decline of pollinators could negatively impact human food supply because of pollination service depletion. Organic farming is one alternative strategy to provide solutions against this issue by offering less pesticides use, restoring plant biodiversity (i.e. hedgerows, intercropping, companion weeds …) or reducing tillage impact. The goals of this research study are (i) the analysis of wild bees community structure, (ii) the assessment of pollination service throughout selected phytometer, buckwheat (*Fagopyrum esculentum* Moench 1794), and (iii) the potential relation between wild bees diversity and phytometer seed production amongst four micro-environments (crops, permanent meadow, apple orchard and wetland) located at the Froidefontaine farmstead which is a farm undergoing agro-ecological transition. Alpha diversity measures of wild bees' community show no significant differences between studied micro-environments. On the contrary, bee communities are structured in response to the environment (i.e. beta diversity), explained by distinctive plant communities that offer a diversity of floral resources. Seed production of buckwheat was higher in crops environment than in every other micro-environments. This trend can be explained by concentration and dilution effects of pollinators foraging behaviour at landscape scale. Lastly, our linear models were not able to detect link between wild bee community structure and the range of buckwheat seed production amongst different micro-environments. These new insights point out that more scientific investigations are needed for a better understanding of the management of our agroecosystems in ecological transition.

Dietary supplementation of plant extracts on immune responses and bacterial resistance of striped catfish (*Pangasianodon hypophthalmus*) in the Mekong Delta, Viet Nam – *in vitro* and *in vivo* approaches

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Aquaculture of striped catfish (*Pangasianodon hypophthalmus*) in the Mekong Delta of Viet Nam is one the biggest success stories in Asian aquaculture. However, to prevent disease outbreaks, fish farmers largely spread chemicals and antibiotics in ponds, generating potential negative impacts such as carryover in flesh, antibiotic resistance in bacteria and pollution through waste-water system. To replace antibiotics and chemicals overuse, immunotherapy using plant extracts as dietary supplementation is explored by the project AquaBioActive as a potential solution. The effects of two plant extracts (*Psidium guajava* and *Phyllanthus amarus*) and their combination (1:1) were studied *in vitro* and *in vivo* to determine whether they could boost striped catfish immune system and resistance against bacterial infection with *Edwardsiella ictaluri*. During these experiments, several immunological biomarkers (lysozyme and alternative complement activity, ROS and NOS production) were examined along with hematological biomarkers (hematocrit and red blood cell counts) and growth parameter (feed conversion ratio). *In vitro* experiment showed positive effects from *P. guajava* extracts and from the mixture on lysozyme and complement activities. Also, these extracts tended to be pro-oxidant as shown by the ROS and NOS production assays. In contrast, *P. amarus* extracts and the mixture in low dose inhibited ROS production by two-fold in PBMCs, and dropped NOS production in head kidney leukocytes. *In vivo* experiment showed great antioxidant properties post bacterial challenge from *P. amarus* and the mixture. This might explain their astonishing capacities to diminish post challenge total cumulative mortality when compared with positive control at 48% to as low as 5%. High composition in phenolics was suspected to give these antioxidant properties but it was not investigated within this part of the project. Feed conversion rate did not differ between the different treatments and doses, suggesting that the dietary extracts did not repel the fish, regardless the dose and the plant type. This work introduces the possibilities of using plant based dietary supplementations in aquaculture and the different obstacles that have to be dealt with.

Organ and muscle specialization linked to dispersal in an invasive population of African clawed frogs (*Xenopus laevis*) in Western France.

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Xenopus laevis is a largely aquatic frog native from Sub-Saharan Africa that has become invasive in many areas, including in France. The distribution of the French population currently encompasses more than 207 km² and will likely increase. Previous studies highlighted that populations from the core and from the edge of the dispersal range show differences in term of whole animal performance with individuals from the periphery possessing a higher endurance capacity than ones from the center of the range. In contrast, populations from the core exhibit a higher burst performance capacity. During this study we tested whether populations from the edge invest more in anatomical features linked to dispersal compared frogs from the core of the range. We measured the mass of the internal organs and the mass, length, and physiological cross-sectional area (PCSA) of twenty-eight muscles of the hind limb. Our results show that individuals from the periphery possess heavier, longer, and more forceful muscles than those from the centre. Moreover, females from the periphery possess a notably larger heart compared to those from the centre. The distinct anatomy of each population strengthens the idea of a specialization towards dispersal in frogs at the invasion front.

What do the Brazilian piranhas have to tell us?

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Piranhas (Serrasalmidae, Teleostei) live in fresh water environments of South America. In this taxon, several species from genera *Serrasalmus* and *Pygocentrus* are known to produce sounds, when hand-held, by the contraction of sonic muscles attached on the swimbladder. The piranha clade has however more than 30 species meaning that more samples were needed to realise a deep study dealing with the acoustic abilities and to understand the evolution of the sonic apparatus. To better understand what piranhas have to tell us, a field mission was carried out in Brazil in July 2018. The goal of the field mission was to record sounds of several species of piranhas in different environments. In this presentation, we show preliminary results on the sounds of some Brazilian piranhas. First, we try to understand how the intraspecific variability affects the sounds in a very abundant species of piranha. This step is essential in order to remove the intraspecific variability from the further analyses. We compare a large sample of sounds from individuals of different sizes. Then, we try to understand the differences among the different species of piranhas. This will allow us to better understand the sounds that these species emitted.

One small step for man, one giant leap for wild boar? A landscape genetic analyses of wild boar dispersal in a fragmented landscape

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The wild boar is currently one of the most widespread mammals of the world and in many regions populations keep expanding. In eastern Flanders (Belgium), the wild boar has returned since 2006 after almost half a century of absence and numbers are increasing fast. The Flemish landscape is severely fragmented and is one of the most densely populated areas in the world. Understanding the relationship between landscape structures and species biology is the basis of landscape ecology and leads to the understanding of factors driving wild boar recolonisation and expansion. We conducted a landscape genetics study to gain knowledge on drivers of wild boar expansion in Flanders. A total of 838 DNA-samples collected from wild boar hunting bag between 2007 and 2016 were genotyped for 140 single nucleotide polymorphisms (SNPs). Our results showed that the wild boar population expanded starting from 2 local gene pools while staying relatively genetically distinct with some admixture, and geographically separated. A third gene pool emerged around 2013 in the northwest coming from the Netherlands and Germany. Our analysis revealed that the spatial genetic pattern was mainly driven by isolation by distance and forest cover. The higher the latter, the lower genetic distances seemed to become. To a lesser extent, increasing road density, low nature coverage and habitat patch density resulted in increasing genetic distances while increasing mean habitat patch sizes resulted in decreasing genetic distances. Gaining this knowledge of factors driving expansion and the inhibiting effect of fragmentation during recolonization is essential for the analysis of future dispersal. This analysis can now be conducted and form the basis of a risk assessment of future wild boar expansion which is urgently needed in Flanders as human-wildlife conflicts increase.

Invasion of Brown Marmorated Stink Bugs and how to control them

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Halyomorpha halys Stål, the Brown Marmorated Stink Bug (BMSB), is native of Eastern Asia, where it feeds on a large diversity of host plants. It was first observed outside Asia in the mid-1990's in Pennsylvania (USA). Since, it has widely spread throughout the whole country. BMSB has been accidentally introduced in Switzerland, where first observations occurred in 2007. Europe presents ideal weather conditions for the pest installation and spread, as well as suitable agricultural landscapes and dense human activity. It is probable that the pest will have colonized a large part of Europe within the next decades. BMSB can feed on various plant organs but preferring fruits. It is highly polyphagous in its native region and the most of its host plants are also present in Europe. It already causes huge yield losses in various orchards, crops and vineyards in its invaded areas. Long established integrated pest management strategies have all collapsed when BMSB invaded. In the general goal of pesticide drastic reduction, there is an urgent need for research in biological control of this pest. We propose here a state of the art of such studies, concerning: entomopathogenic fungi, pheromone traps, parasitoids… Our own works on feeding behaviour and salivary proteome aim to fill the gaps in the current knowledge of BMSB biology and on plant-insect interactions. We also call for scientific community and public vigilance, as the pest is already well established in neighbouring countries of Benelux.

Burrowing behaviour of the European eel, *Anguilla anguilla*

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Hiding places are important for Anguillidae, but whether the European eel (*Anguilla Anguilla*) makes and uses burrows has not been studied before. Here, we investigated burrowing behaviour in two life stages, the glass and elver eel stage, during which the eels arrive at the European coast and start migrating up the rivers. Previous research stated that Anguilliformes, except for their long, cylindrical body, have no morphological adaptations that allow or facilitate burrowing. We observed, however, that the eels can burrow very efficiently. During burrowing, the eel performs lateral head shakes, combined with body undulations, indicating that the European eel is a 'head-first burrower'. Using preference experiments, we found that eels generally prefer a fine grain over a coarse grind substrate, with the exception of the smallest glass eels preferring the latter substrate. This can be related to body size, as these individuals are capable to manoeuvre between the interstitial cavities of the grind substrate. Simultaneously, 70% of the tested eels preferred a sandy substrate over the fine grain substrate. Surprisingly, using kinematics, we found that burrowing speed was highest in the fine grain substrate, followed by sand substrate and eventually, coarse grind, indicating that the substrate preference is not related to the potential burrowing speed. The sandy substrate probably best represents the eel's natural habitat and could explain this observation or it might be possible that a sandy substrate is more appropriate to make long-term burrows. Finally, we observed that when eels were given the choice between burrowing or hiding between rock boulders and/or tubes, in most cases burrowing takes place. This suggests that the European eel, at least in its most juvenile life stages, is a spontaneous burrower. Further research is required to find out whether and how burrowing behaviour takes place in the later life stages.

Trophic plasticity of scleractinian corals under contrasted environmental conditions: evidence from stable isotope analysis

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Most scleractinian corals can derive nutrition either autotrophically or heterotrophically, which allows them to use diverse trophic pathways. Therefore, when facing environmental changes, these organisms are expected to demonstrate an intrinsic ability to acclimatise through trophic plasticity. Despite the ecological importance of these corals, our understanding of their trophic plasticity is currently impaired by a lack of rigorous research approaches; a failure to consider the intraspecific variability of coral species and an oversimplification of the proxies of heterotrophic habits (e.g. corallite diameter). In order to understand how trophic plasticity could allow them to acclimatise, this study proposed to assess the trophic plasticity of morphologically contrasted coral species (e.g. *Stylophora pistillata*, *Porites sp*, *Isopora palifera*). We determined the stable isotope ratios of carbon and nitrogen in the coral host tissues and algal symbionts and compared these in corals inhabiting areas around Taiwan characterised by contrasted temperature (from high to low latitudes) and light levels (from shallow to mesophotic waters). For each area, we evaluated the intraspecific trophic variability by estimating and comparing coral isotopic niches as a proxy for trophic niches. Our results on *Stylophora pistillata* revealed no overlap of the isotopic niches for the host and symbiont from different locations, suggesting that these coral colonies are supported by different core resources. Moreover, the isotopic niche of higher latitude coral colonies was larger than those from the lower latitudes, highlighting a certain trophic plasticity that may be related to more variable environmental conditions in the higher latitudes. Analyses of additional species and locations will provide essential insights into the trophic plasticity of scleractinian corals and how these species might adjust their nutrition in response to environmental changes.

Incidence and distribution of cryptic species among polychaetes of the NE Atlantic: potential consequences for biomonitoring and assessment of climate change-induced impacts

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The discovery of cryptic species has grown exponentially over the past decades. Due to their commonality, they can in no way be neglected if we want to correctly assess species diversity and distribution, understand biogeographic patterns, or assess and predict climate change-induced impacts. Occurrence of cryptic species appears to be particularly frequent in polychaetes, one of the most prominent bioindicator groups among the marine benthic invertebrates. To investigate cryptic diversity in this group, we have been conducting a comprehensive morphological and molecular analyses of the polychaete, mainly from the order Phyllodocida in the NE-Atlantic. Attending to the profusion of data available for comparison, and well-known patterns of variation, we used the cytochrome oxidase I barcode region (COI-5P) to screen for intraspecific genetic divergence in suspected cryptic complexes, based on prior evidence. Using three different MOTU clustering algorithms, we detected five additional MOTUs within the *Eulalia viridis/clavigera* complex with 17.3% mean distance (K2P), with one of the them exclusive to the Madeira island, seven MOTUs within *Trypanosyllis zebra* (22.1% mean distance), and an additional MOTU present only in the UK within the large *Eumida sanguinea* complex, comprising 9 different described species (18.8% mean distance). Using data compiled from a previous study we also detected seven MOTUs within *Owenia fusiformis* (22% mean distance). All the above morphospecies occur frequently and are thought to have a very wide geographic distribution. Our findings indicate that these apparently cosmopolitan species may constitute in fact complexes of cryptic species, each of them with much narrower ranges. Hence, failure to recognise this hidden biodiversity may compromise the accuracy and the interpretation of biomonitoring data. Moreover, it is likely that the impact of climate change will be higher in multiple cryptic species with small population sizes, limited geographic distributions and possibly adapted to much more stringent environmental conditions.

Turquoise killifish (*Nothobranchius furzeri*) as a new model in behavioural ecotoxicology

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Pharmaceuticals are essential for human wellbeing. However, due to their increasing and continuous use, sub-lethal concentrations of pharmaceutical compounds have already been detected in the aquatic environment. As these compounds are designed to elicit specific biological effects at low concentrations, standard ecotoxicity tests are unable to correctly assess environmental risks associated with pharmaceutical pollution. Reproducible tests that are based on sensitive behavioural endpoints and that accommodate a high ecological relevance have been promoted to fill this gap. We assessed the impact of a three-week exposure to the antidepressant fluoxetine on behavioural traits in *Nothobranchius furzeri* (Turquoise killifish). Overall, this study shows that fluoxetine can impact life skills, such as feeding behaviour, habitat choice in a novel environment and antipredator response of *N. furzeri* individuals while effects on basic behavioural traits were less clear. *N. furzeri* has recently been introduced as a novel model organism for standard ecotoxicological tests and now its potential for behavioural ecotoxicology is being explored.

Aquatic omnivores shift their trophic position towards increased plant consumption as plant stoichiometry becomes more similar to their body stoichiometry

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Human induced eutrophication has strongly altered aquatic ecosystems. With increasing eutrophication, plant nutrient concentrations increase, making them more attractive for herbivores. However, most aquatic consumers are omnivorous. Ecological stoichiometry theory predicts that animals prefer to consume food which has a similar C:nutrient ratio compared to their own bodies, hence omnivorous animals may prefer to eat animal prey instead of plants. We asked whether aquatic omnivores would shift their diet towards more plant consumption when plants' stoichiometry became more similar to the omnivores'. We hypothesized that: (1) the omnivore increases plant consumption as the plant C:nutrient ratio decreases when there is only plant material available; (2) the omnivore generally prefers animal food over plant material; (3) the omnivore will increase its relative plant consumption as the plant C:nutrient ratio decreases, in the presence of animal food. As a model system we used the pond snail *Lymnaea stagnalis* (omnivorous consumer), the aquatic plant *Potamogeton lucens* (cultured at different nutrient regimes to obtain different plant C:nutrient ratios), and the crustacean *Gammarus pulex* (animal food source, using freshly dead individuals). When there was only plant material available, the consumers increased their relative consumption rate with decreasing plant C:nutrient ratio. When plant material was offered simultaneously with animal food, though the omnivores always preferred animal food over plant material, the omnivores still increased their relative intake of plant material as plant C:nutrient ratio decreased, from virtually nothing at the highest to on average 16% of their diet at the lowest plant C:nutrient ratio, with a maximum of 28%. Therefore, we conclude that as nutrient loading increases in aquatic ecosystems, omnivorous animals may shift their trophic position towards increased plant consumption and alter the food web structure. As a result, we may observe increased top-down control on aquatic plants.

Shut-out or sheltered? An evaluation of the feral pigeon (*Columba livia domestica*) in the context of different management approaches

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Feral pigeons (*Columba livia domestica*) can become very abundant in urban areas, which may lead to human-pigeon conflict. Traditionally, feral pigeons are culled to reduce the population size, yet this practice is regarded as inhumane and an unsustainable management approach. A pigeon shelter, thus a shelter providing suitable nesting sites and regular appropriate feed, is suggested as an animal-friendly alternative. Moreover, shelters provide the possibility for population management by reproductive control through e.g. egg removal. However, monitoring programs or research on the long-term effects of feral pigeon management is scarce. As human populations continue to increase, pigeon populations are expected to increase as well. The emerging conflicts require appropriate and scientifically grounded management. To gain insight into the current situation and management of feral pigeon in the Netherlands, we investigated the density and health of feral pigeons in three Dutch cities (Amsterdam, Rotterdam, and Utrecht). Only in Rotterdam two pigeon shelters are currently installed. Using distance sampling the density of the feral pigeon populations were determined and a health scoring based on external characteristics was applied to obtain an indicator of the general pigeon health. We expected to observe the lowest pigeon density and best pigeon health in Rotterdam, yet the results indicated the lowest density and best pigeon health to be present in Utrecht. The implications of these results on the management and the potential presence of a ‘pigeon problem’ in The Netherlands are discussed. As longitudinal data are missing we cannot confirm or reject the effect of the pigeon shelter. However, interviews with the representatives of the municipalities indicated that the shelter may be beneficial by decreasing the negative perception of the feral pigeon. This study provides reference values for future monitoring- and research purposes, and implicates how perception of a nuisance animal can affect its management.

Evidence of locomotor and ecological analogy between modern cervids and extinct equids demonstrated by scapula fossa ratios

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Throughout their evolution, equids (horses and relatives) underwent ecological shifts, associated with morphological changes in distal limb morphology (including elongation of the phalanges; reduction in the number of toes) and an increase in tooth crown height (hypsodonty). However, changes in the pectoral girdle have not been thoroughly investigated. The scapular fossa ratio (SFR; supraspinous area divided by total fossae area) is a technique recently devised to compare the ratio of origination sites for deep lateral shoulder musculature (infraspinatus and supraspinatus muscles). SFR may be expected to be increase with body size, due to the necessity for increased shoulder stabilisation provided by the infraspinatus muscle with increasing mass. Similar sized animals with comparable locomotor and habitual ecologies intuitively undergo similar mechanical constraints and predation pressures, and may therefore evolve similar SFRs. Here, we investigate the SFR of the scapulae in equids through time, and compare them to potential modern analogues (cervids). 69 scapulae (26 spp.) were obtained from museums and photographed from different angles (photogrammetry). Images were processed using Agisoft PhotoScan to generate 3D models. Three-dimensional fossa areas were then calculated in GeoMagic and MeshLab and statistically compared using ANOVAs and Tukey's pairwise post-hoc tests. Results suggest that cervids exhibit isometric scaling of the SFR, which does not significantly differ with size, aside from *Alces* and *Pudu*. Size, shape and hypsodonty similarities suggest ecological analogy between extinct tridactyl horse *Hippotherium* and modern *Cervus*. Monodactyl equids show an increase in the supraspinatus relative to the infraspinatus compared to both cervids and extinct tridactyl equids. Equids at the phylogenetic root between monodactyl and tridactyl lineages exhibit no significant differences to modern cervids. This similarity between cervid and tridactyl equid SFRs could be due to the absence of a stay-apparatus in these species, and thus a greater dependency on the infraspinatus for shoulder-stabilization.

Food capture, transport and swallowing in white-spotted bamboo sharks (*Chiloscyllium plagiosum*)

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After capturing food, there are at least two equally important steps in feeding: food transport and food swallowing. Previous studies in aquatic vertebrates have found that water currents transport food from the mouth towards the oesophagus (i.e. the hydrodynamic tongue), and that oral cavity expansion through hyoid movement generates this flow. They did not, however, visualize the food position within the animal throughout the entire feeding bout. We used X-ray Reconstruction of Moving Morphology (XROMM) to track the pathway of food in 3D in three white-spotted bamboo sharks, allowing us to measure food and cartilage movement during transport and swallowing. Gape width, ceratohyal and pectoral girdle elevation, and food displacement were analysed for each feeding bout. Our results show that during transport and swallowing, the food moves with a ratchet-like motion once inside the oropharynx. Caudally-directed motion of the food occurs during hyoid elevation, and the food appears to be stationary during ceratohyal depression, perhaps held in place by branchial basket compression. Hyoid elevation compresses the oral cavity, so the shark likely generates water currents through the oropharynx to push food backwards towards the oesophagus. Food is pushed into the oesophagus by hydrodynamics as well. Despite a smaller range of motion of the ceratohyal and pectoral girdle, food velocity is higher, which indicates that branchial basket compression might propel food into the oesophagus. Hence, water currents generated by cranial cartilages and branchial basket compression are key elements in moving food towards and into the oesophagus. These actions are as important as food capture for animal survival.

Exploring mitogenomics for the phylogeny of African monogeneans (Gyrodactylidae and Dactylogyridae)

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Monogenean flatworms are the main fish ectoparasites. The Gyrodactylidae and Dactylogyridae are probably their most species-rich taxa. Their representatives can be harmful fish pathogens, especially in aquaculture or after anthropogenic co-introduction. In Africa, cichlid and clariid fishes are quite well-studied for monogeneans, among which the most important aquaculture fishes on the continent, often widely introduced elsewhere. The small number of available molecular markers for these worms hampers research. Several questions, like the phylogenetic position of *Macrogyrodactylus* and the highly species-rich *Gyrodactylus*, remain unresolved with available markers. The need for more and higher-resolution markers is especially clear when working on a recent timescale, e.g. in phylogeography, population genetics, and barcoding. A small number of established mitochondrial gene fragments are the most variable markers available, and are also used in flatworm systematics on a macro-evolutionary scale. We initiated a mitogenomic approach to African monogenean evolution, starting with species collected in the Upper Congo Basin. Based on Illumina technology, mitochondrial genomes were assembled and annotated for the cichlid parasites *Gyrodactylus nyanzae*, *Cichlidogyrus halli*, *Cichlidogyrus mbirizei* (near-complete mitogenome) and the catfish parasite *Macrogyrodactylus karibae* (near-complete mitogenome). We report a new start codon (TTG) for *Gyrodactylus* and the Dactylogyridae, and a new, incomplete stop codon (TA) for the Dactylogyridae. A mitochondrial phylogeny (alignment of nearly 12,500 bp) confirms the basal position of the Neotropical oviparous *Aglaiogyrodactylus* (and not the African *Macrogyrodactylus*) with respect to other gyrodactylids, and confirms the paraphyly of *Gyrodactylus*. Within dactylogyrids, additional taxon sampling is necessary to increase phylogenetic resolution, but gene order suggests that *Cichlidogyrus* is related to marine ancyrocephalines. Gene order is identical for protein-coding genes and differs between the African representatives of these families in a single tRNA gene transposition. These first mitogenomic data on African monogeneans underscore the potential of mitochondrial genes and gene order in flatworm phylogenetics.

Is differential gene expression in the female brain linked to assortative mating in a mouthbrooding cichlid (*Ophthalmotilapia*) from Lake Tanganyika?

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The East African Great Lakes harbour hundreds of endemic cichlid species with frequently-overlapping ecological niches and distribution ranges. Given their phylogenetic relatedness, and their ability to interbreed, the question remains how such species maintain the integrity of their gene pools. To this end, we studied female mate choice in the endemic Tanganyika cichlid genus *Ophthalmotilapia*. Dissimilarities between mitochondrial and GBS-based phylogenies revealed frequent instances of introgression, especially at locations where distributions of *Ophthalmotilapia* species overlap. However, very few specimens with hybrid morphologies were found, indicating that species boundaries are nevertheless maintained. Two experiments were conducted to investigate the link between gene expression and behaviour in the first (exposure) and last (oviposition) steps of the mating process. We quantified the behaviour of 82 females and, for 36 of them, sequenced the transcriptomes of six brain parts. The first experiment compared females that were briefly exposed to con- or hetero-specific males. Although transcriptomes of all brain parts shared almost 10,000 genes, less than 100 were differentially expressed (5% FDR level) between treatments. Most differences were found in the diencephalon and the optic bulbs and most differentially expressed genes were linked to hormonal activity. The second experiment compared females that mated (performed oviposition) with a con- or hetero-specific male. Here, the transcriptomes shared over 10,000 genes. Although over 1000 genes were differentially expressed between heterospecific females that mated with a conspecific male (5% FDR level), this held for just over 100 genes when comparing conspecific females that mated with heterospecific males. Here as well, differential gene expression was most pronounced in the diencephalon. Whereas in the comparison of heterospecific females differential expression was observed in large set of housekeeping genes, hormonal functions were again important in genes that were differentially expressed between conspecific females that mated with a con- or a hetero-specific male.

Distinct biogeographic origins of androgenetic lineages in *Corbicula* clams

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Corbicula clams are well-known since they have been introduced into America and Europe during the 20th century. They became successful invaders and spread massively. Their ability to reproduce clonally through androgenesis has been determinant in their invasive success with only four invasive clonal lineages being detected in Europe and America, one clone being very abundant and widespread on both continents. Due to their “all-male asexuality” and their egg parasitism between distinct lineages, phylogeographic studies failed to identify the origin of the invasive androgenetic lineages. We therefore analysed the patterns of allele sharing for four different molecular markers in *Corbicula* individuals collected across their worldwide distribution. We identified three distinct genetic pools containing androgenetic lineages. Moreover, while one sexual *Corbicula* species formed a distinct fourth genetic pool, the other sexual lineages clustered with the androgenetic ones. Several androgenetic *Corbicula* lineages therefore appear to have evolved separately in distinct geographic regions. Such multiple biogeographic origins of *Corbicula* androgenetic lineages might suggest that androgenesis could evolve or maintain easily in *Corbicula* but requests further investigations to determine how transition between sexuality and androgenesis occurs.

Skeletal deformities in gilthead sea bream (*Sparus aurata*): exploring the association between mechanical loading and opercular deformation.

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Fish aquaculture is frequently afflicted by morphological abnormalities, mainly at the skeletal level, affecting fish performance, the market value and the image of the sector. In gilthead sea bream (*Sparus aurata*), heavily cultured throughout the Mediterranean, one of the most common types of deformities occurs on the opercula, and has formed the topic of many studies, pointing at a plethora of factors as possible explanation. However, no clear consensus has surfaced yet. Mechanical stressors (due to external forces or muscle contraction) can influence bone remodelling, leading to abnormal skeletogenesis. Such a mechanical loading has not yet been investigated for opercular deformities. In this thesis, we explored the possible association between mechanical loading and opercular deformities, by focusing on altered respiratory rate as a possible cause of altered mechanical loading. A variety of methods, including geometric morphometrics and µCT-scanning were performed on larval seabream from 48 and 55 days post-hatching (DPH), reared under 80, 100 or 200% dissolved oxygen (DO), as this is assumed to trigger altered respiration behaviour. We hypothesized that conditions below 100% DO would result in a higher prevalence of opercular deformities, and that hypoxic conditions can be associated with an increased mechanical loading and opercular deformities. The results showed that 80% DO is not sufficiently low to trigger a significant higher prevalence of opercular deformations, though the opposite holds true under 200% DO. Although no direct link was found, live observations of respiratory behaviour under hypoxic conditions in another species (goldfish), together with opercular shape analysis and 3D reconstructions of CT images of the sea bream larvae, suggest there could be an association between mechanical loading on the operculum, and its deformation. Further analyses are needed, focussing on the relationship of opercular muscle contraction and mechanical loading on the opercular bone.

Glimpsing into sediments – DNA Metabarcoding of freshwater hyporheic meiofauna indicates high taxonomic diversity and high spatial heterogeneity

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The hyporheic zone, i.e. the ecotone between surface water and the groundwater, is a rarely studied freshwater ecosystem. This is certainly also due to the identification of hyporheic meiofaunal organisms (<1mm in size) being a challenging task. No surprise that our current knowledge about those organism groups is far from complete. However, with the ongoing development of DNA barcode reference libraries and the improvement of high-throughput sequencing technologies, the way seems pawed to increase our understanding about the diversity and ecology of even those challenging taxa and relevant ecosystems. This presentation highlights the current potential and challenges of a DNA metabarcoding approach to disentangle the taxonomic diversity and spatial heterogeneity of the freshwater hyporheic meiofauna. Sediments in the River Emscher catchment (Boye tributary, North-Rhine Westphalia, Germany) were collected at five locations, size-sieved to extract their meiofaunal components, and a DNA metabarcoding approach developed using common freshwater primers (BF2/BR2). Three technical site replicates were performed ensuring a robust data interpretation. A total of 180 metazoan taxa were identified after quality filtering, i.e. integrating taxa detected in at least two out of three replicates per site. Of those, 61% were identified to the species level. The two most abundant groups were aquatic oligochaetes (57 taxa with 75% to species-level) and dipterans (38 with 74%). A very high spatial heterogeneity was observed with 70% of the metazoan taxa being present at a single sampling site only. The results highlight the gaps in reference databases for meiofaunal taxa and indicate potential problems of using common freshwater metabarcoding primers by co-amplifying terrestrial environmental DNA and non-metazoan taxa (i.e. bacteria) as well as missing abundant groups such as nematodes and platyhelminthes due to primer bias. Yet, the developed approach provides a robust first glimpse into the diversity and spatial variability of taxa living in freshwater sediments.

Deciphering the origin of mito-nuclear discordance in two sibling caddisfly species

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Macroinvertebrate species are commonly used as bioindicators of water quality. Hence, a correct species-level identification must be seen crucial. Nowadays, they are often identified by sequencing part of their mitochondrial cytochrome c oxidase subunit I gene (COI), so-called DNA barcodes. Even though DNA barcode-based and classical morphology-based species identification usually provide largely congruent results, they sometimes yield contrasting taxonomic assignments. One such case involves the caddisfly sister species *Sericostoma personatum* and *S. flavicorne*. Due to the known discrepancies, we used an integrative-taxonomic approach comprising morphometrics, mitochondrial COI data and nuclear ddRAD data, the latter being a reduced representation based next-generation sequencing method resulting in the parallel generation of over thousand genetic markers. While the nuclear markers were in large agreement with the morphological species identification, we observed a strong pattern of mito-nuclear discordance. This discordance probably originates from historical introgression and ongoing hybridization events. Our study highlights the importance of integrative-taxonomic approaches for meaningful species delimitations.

Spatial use of wild boar in an urban protected area

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Wild boar is native to Belgium, but was driven to virtual extinction in the northern region of the country. In 2006 individual animals were observed again and the population is now increasing rapidly both in numbers and distribution area. The National Park Hoge Kempen (NPHK) was one of the regions were the recolonization process started and is still considered a core area of the current wild boar distribution in Flanders. NPHK is the only national park in Belgium and is a typical urban protected area. Protected areas around the world are crucial for the conservation of endemic species but also provide an opportunity for recreation. For urban protected areas, this dualism is exacerbated by its proximity to urban settlement. Possessing six tourist gates and a variety of hunting regimes but also large patches of protected forest or heathland, NPHK harbours many different forms of land use on a small area. This results in high numbers of human-wild boar interactions which might enhance both the positive and negative effects of human and wildlife behaviour on each other. The spatial use of any animal is influenced by the trade-off between basic needs and safety, and it is shown that humans can mimic or exceed the threat posed by predators. Wild boar however show a highly plastic response towards human disturbance, ranging from complete attraction to complete repulsion of areas used by humans. Therefore, we use occupancy models to study wild boar to determine whether its spatial use is influenced more by habitat or by the strong human presence in NPHK. For this, forty camera traps are rotated monthly to a unique random location within a predetermined grid. The presentation will present preliminary results of the ongoing research.

Phylogenetic, morphological and ecological divergence in *Brachionus calyciflorus*, a newly described hybridizing species complex

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Brachionus calyciflorus is undoubtedly the most studied freshwater monogonont rotifer taxon. Although it has been identified to be a cryptic species complex since more than a decade, its four hitherto known species (*B. calyciflorus*, *B. dorcas*, *B. elevatus* and *B. fernandoi*) have been (re)described only recently, based on a combination of a molecular phylogenetic and morphological analysis. We here present the results of comparative life table and population demographic experiments using genotypes isolated from multiple natural populations in The Netherlands. The life table experiment revealed substantial life history strategy differentiation among species. Traits such as investment in sexual reproduction, juvenile and embryonic development time were found to be species-specific and also translated into divergent population demography structures. In addition, we applied cross-mating experiments between the two sibling species *B. elevatus* and *B. calyciflorus* to test for reproductive isolation. The results of these experiments suggest both pre- and post-zygotic isolation although formation of hybrids seems still possible. The latter is consistent with the occasional observation of hybrid and introgressed genotypes in natural populations. Our results demonstrate that correct identification is essential for the study of ecological dynamics in communities with 'cryptic' species.

Life on the stoichiometric knife edge: challenges and responses

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Anthropogenic activities have strongly reshaped the amount and ratios in which essential elements, such as carbon (C) and phosphorus (P) are available to organisms. Recent studies in the framework of ecological stoichiometry have suggested that organisms may be living on a ‘stoichiometric knife edge’, where either too high or too low food C: P ratios caused performance reductions of consumers. However, the generality of the ‘stoichiometric knife edge’, as well as the physiological and behavioural responses of consumers to different food C: P levels are still poorly understood. Moreover, the benefits and disadvantages of elemental homeostasis are still unclear. Here, we subjected a planktonic rotifer to a broad food C: P gradient and studied its response to different C: P levels. The highest growth rate of animals was observed at an intermediate food C: P level of 180 and any deviations towards higher or lower C: P ratios were associated with reduced performance, confirming the existence of a stoichiometric knife edge. When fed P-limited food, animals showed increased feeding rates and declined P excretion rates as compensatory mechanisms to increase P acquisition, whereas they decreased their ingestion rates and increased P excretion rates in response to food with excess P. Interestingly, the degree of animal homeostatic plasticity was more pronounced in response to high food C: P (>420) compared to low C: P food. Homeostatic deviations at the high C: P end of the gradient were associated with pronounced growth reductions, suggesting that the inability to cope with excess C and limitation of P affect animal performance. In contrast, at the low C:P end performance reductions occurred in the absence of major homeostatic deviations and indicate that, although animals were able to maintain their optimal elemental composition they suffered growth performances as a result of efforts in reducing P-intake and increasing P-excretion, possibly also combined with P-toxicity.

Sexual chemical signalling under climate warming

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Global climate is changing at a rapid pace and the pivotal question arises as to if the rate and extent of species response to stressful events enable them to persist in a changing world. Although the consequences of rapid environmental changes on animal life-history traits are receiving considerable attention, our understanding of how temperature fluctuations influence mating signals in animals is scarce. There is evidence that thermal stress can impair sexual chemical communication, but how organisms are affected by temperature-induced changes at both signaller and receiver levels warrants further investigation. Importantly, male-female interactions often depend on pheromone detectability and changes in environmental conditions are expected to disrupt communication between potential mates. A highly suitable species for studying this largely unknown aspect of the consequences of climate change is the soil arthropod *Orchesella cincta*. *O. cincta* has a unique feature that allows us to disentangle which sensory modality is affected by climate change: it has evolved an indirect way of sperm transfer in which males deposit sperm droplets (spermatophores) in the environment for females to pick up, guided by the spermatophore scent. In this species a choosy female relies solely on the sperm-associated sex pheromone, making olfaction the most important sensory modality involved in reproductive decisions. Our work suggests that thermal stress can indeed affect pheromone communication at different stages of the pheromone journey, from sender to receiver.

Posters

Improving the understanding of non-specific mechanisms behind non-polar narcotic toxicity in zebrafish

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Approximately 70% of the industrial chemicals are believed to act as non-polar narcotics. The toxicity mechanism remains poorly understood, but it is generally assumed that non-polar hydrophobic compounds accumulate in membranes according to the octanol-water partition coefficient (logKow) which results in loss of membrane integrity and function. To date, the accumulation dynamics of non-polar narcotics on the (sub)cellular and whole-organism level are unclear. Moreover, there is large uncertainty on which membrane-related processes are affected and their importance in causing adverse effects. The first part of this project aims to map the tissue- and (sub)cell-specific accumulation patterns of non-polar narcotics using perylene as a non-polar narcotic with fluorescent properties. The time-dependent uptake of perylene will be determined by fluorescence microscopy and this information will provide a basis for the second part of this project, which aims at investigating the toxic effects of non-polar narcotics on membrane-related processes in relevant tissues. As a first step, zebrafish embryos were exposed to perylene up to 120 hours post fertilization (hpf) using a passive dosing method. The first results show a time- and concentration-dependent increase in perylene uptake, and suggest that during the first 48 hpf, perylene mainly accumulated in yolk and yolk extension, whereas in later developmental stages, perylene was mainly detected in the gastrointestinal tract. We also investigated the effect of narcotics on respiration and the dependence of such effects on the LogKow. For this purpose, zebrafish embryos were exposed to compounds with different LogKow using passive dosing: 1,3,5-trichlorobenzene (LogKow = 3.93), phenanthrene (LogKow = 4.46) or pentachlorobenzene (LogKow = 5.22). At 72 hpf, oxygen consumption was measured for 40 minutes using optical oxygen sensors and embryos were sampled for determination of accumulated doses. The results show that oxygen consumption was significantly decreasing after a 14-hour exposure with increasing phenanthrene and pentachlorobenzene concentrations.

Preliminary results on the wild bee fauna of Lebanon higher altitudes: The race between a checklist and a climatic risk assessment.

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The bee fauna of Lebanon is widely unknown are there are very few published papers on the topic. The present study aims to provide data on present species in order to produce the first checklist of Lebanese bee fauna. The focus is on the mountain areas as this region is potentially the most vulnerable facing climatic risks The second aim is to test the heat stress resistance of chosen species. Collections spanned a mountainous area between 900 m and 3000 m where bees in several habitats were sampled. A preliminary list provides an updated list of records for the chosen study area as well as their foraged flowers, of which several are endemic. The most abundant species were sampled for heat resistance testing. A first experimental result on the tested species show different capacities to resist heat stress, with *Bombus niveatus* and *Bombus melanurus* having the lowest margins, rendering them very sensitive to extreme climatic events. In comparison, *Bombus terrestris*, *Xylocopa valga* and *Xylocopa violacea* are much more resistant. Further data processing is required to complete the evaluation of the present bee fauna and it's variation between different habitats and altitudinal levels. Furthermore, heat stress tests performed on additional species will allow a further evaluation of widespread and more localized species in Lebanon.

Habitat selection and ecotype-specific adaptations of the niche-expanding butterfly *Pararge aegeria* in anthropogenic landscapes

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Currently, organisms are confronted with human-induced, rapid and pronounced environmental change (e.g. habitat conversion, climate change, pollution), which causes negative fitness effects for many species leading to severe biodiversity loss. However, there are also species that thrive well in such changing anthropogenic landscapes. They are assumed to adopt different strategies of habitat selection allowing for greater flexibility under rapid environmental change. Within this framework, there is growing interest for the role of behavioural plasticity and how it relates to the divergence of habitat selection strategies. This PhD-project will focus on the developmental plasticity and flexibility of habitat preference for oviposition in the speckled wood butterfly (*Pararge aegeria*). As its ancestral habitat, this butterfly occurs in forests and along forest edges. However, recently it has expanded its ecological niche into anthropogenic environments. Previous experiments have pointed to several adaptive differences between populations of forest landscape and agricultural landscape, here referred to them as ecotypes (e.g. differences in adult morphology, temperature-related fecundity and perceptual performance in the context of habitat detection). To further explore the mechanisms of these ecotypic differentiations, we address in this project (1) whether the adult females of different ecotypes differ in microhabitat selection, and (2) whether larval experience (developmental plasticity) interferes with the innate habitat preference among the ecotypes. During the first year of my PhD, we established a breeding stock with gravid females originating from agricultural and forest populations. Next, we designed an experimental arena in which we released mated females from the F1 offspring, which were raised under standardized conditions in the lab. Individuals were able to choose a host plant for egg laying occurring in an artificial microhabitat simulating either woodland or open grassland conditions. Data on microclimatic-conditions (temperature and humidity) relevant during larval development in different ecotype-related landscapes were also collected in the field.

Is bigger better? The microbiome and its role in conferring performance towards parasites in *Daphnia magna*

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Parasite-host interactions have been the topic of research for many decades. Recently, the contribution of the microbiome in these parasite-host interactions has come under the attention as research indicates that this complex community of microorganisms plays a crucial role in host physiology. It has e.g. been shown that the gut microbiota plays a crucial role in host resistance against invading parasites, a process referred to as colonization resistance. By consuming common limited resources, the indigenous gut microbiota contributes to limit the growth and survival of competing pathogenic bacteria. Additionally, it has been shown that the host genotype shapes the community structure and the functionality of the gut microbiota. In our study, we utilized gut microbiota transplants combined with a metagenetic approach to examine the reciprocal role of the microbiome and parasite in host-parasite interactions. *Daphnia magna* and its parasites is here our model system of choice. Firstly, *Daphnia* individuals (donors) were exposed to one of two different (or no=control) parasite communities, after which the *Daphnia* gut was dissected. We assume that parasite exposure would induce a shift in the gut microbiota in parasite-infected populations and that microbiota beneficial for protection against this parasite community would be selected. Secondly, *Daphnia* individuals (recipients) from three clones were made axenic and received the donor microbiome which were pre-exposed to one or no parasite community. Thirdly, we exposed the recipients of each donor microbiome to one or none of the parasite communities. The same parasite communities utilized to expose the donors, are here utilized to expose the recipients. By doing so, we determine if *Daphnia* exposed to a particular parasite community will obtain a 'protective microbiome', which affects the host's performance (survival and body size) upon re-exposure to this parasite community.

Description of an “unknown organ” in the aquacultivated sea cucumber *Holothuria scabra* (Holothuroidea, Echinodermata) from the South-West of Madagascar

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Echinoderms are morphologically characterized by an unusual 5-fold symmetry not found anywhere else in the tree of life. Recently, our laboratory discovered a mysterious and unidentified “organ” in the aquafarmed sea cucumber *Holothuria scabra* from the South-West of Madagascar (Holothuroidea). The “organ” is directly connected to the ring canal of the ambulacral system. This water-vascular system, operating through hydrostatic pressure, is involved in locomotion, feeding, respiration and sensory perception in these marine invertebrates. The water vascular system is mainly composed of canals connecting numerous tube feet. Despite the occurrence of numerous extensive studies on the echinoderm ambulacral system, we were not able to find any mention of the enigmatic “organ” in the scientific literature. Three hypotheses were elaborated to explain the origin and the nature of this unknown “organ”. Firstly, this could be a pre-existing organ in sea cucumbers that has never been described in *H. scabra* or any other species. Secondly, this could also be a modified parasite (and therefore not an organ) hung on the ambulacral system. Thirdly, this could be a pre-existing organ structurally modified by the presence of potential parasites. *In vivo* observations, histology and electron microscopy analyses have been applied to confirm or refute our hypotheses. Immunohistochemical methods, transmission electron microscopy and metagenomic analyses will be applied in a near future to complete our study. Overall, our results demonstrate a unique histological structure of the unknown organ different, in many ways, from the classical structure observed in other organs from the water-vascular system. The authors thank the company “Indian Ocean Trepang”, based in Toliara, for providing specimens and access to the pens as well as their expertise and advices.

Daphnia as a new microbiome model with respect to the development for innovative colorectal cancer (CRC) therapies focusing on EMT and epigenetics.

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Colorectal cancer (CRC) is the third most common diagnosed cancer in the world and its burden is expected to increase to more than 2.2 million new cases and 1.1 million cancer deaths by 2030. On EU-level, this corresponds with a yearly economical cost of around €13 billion. As the cause of CRC remains unclear, there is an urgent need to identify initial CRC inducers. Recently, the gut microbiome has been identified as a potential risk factor for the development of CRC. However, the role of microbiota in the induction or progression of cancer remains largely elusive. Despite modern breakthroughs in CRC treatments, resistance to therapies and the occurrence of metastasis remains high, with a recurrence degree of 40%-60%. During cancer progression, tumor cells acquire a migratory and invasive phenotype via epithelial-to-mesenchymal transition (EMT), a conserved and reversible process in embryonic development and cancer metastasis. Therefore, focusing on the initial effect op CRC-associated microbial strains on the EMT-process will be important to develop targeted treatments to control recurrence of CRC. The invertebrate hypoxia tolerant model *Daphnia magna* will be used to elucidate these effects on both genetic and epigenetic level. In an unlimited way and without ethical constraints transplant experiments will be performed in which the microbiome of human and mice fecal samples (inclusive recurrent CRC patients upon radiology treatment) will be exposed to the study model, gut (dis)sections will be performed and whole organism and microbial community will be analysed via 16s RNA metagenetics and gene expression via Daphnia transcriptomics (RNA seq.).

Study of a biological harpoon; microstructure and composition of the mantis shrimp raptorial appendage

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Mantis shrimps (Crustacea, Stomatopoda) are among the most surprising crustaceans. Separated from decapods since Cretacean, they display unique features that make them formidable marine benthic predators. These features are a performant 3D vision with the widest visual spectrum ever identified in animals. They use their antennal pallet as a rudder and their transformed telson both as a shield and as a fin. But their most outstanding feature is the development of their second maxilliped in quick predatorial limbs; either smashing hammers to crush shelled preys or harpoons to impale fishes respectively in two taxonomic sister groups. These smashing and spearing limbs are deployed at high speed thanks to locally modified cuticle that quickly release stored elastic energy (in the merus) and are reinforced to endure impacts (front side of the dactyl). The present study will focus on the cuticle of the spearing limbs in the striped mantis shrimp, *Lysiosquillina maculata* (Fabritius,1973). The main goal is to understand how the internal micro-architecture of the the raptorial appendage is arranged to face the mechanical stresses that occurs when harpooning preys. Light and electron microscopy observations combined with X-ray microanalyses allow to define the structure of the cuticle layers and superimpose their elemental composition. First results highlight a complex assembly of at least four layers that can't be directly linked to the classical layer succession in arthropods and decapod crustaceans (e.g. endocuticle, exocuticle and epicuticle). These layers were named lamellar layer, parallel layer, soft helicoidal layer and highly mineralised layer. Each of them differs by fibre orientation, mineralisation rate or mineral composition. They are thought to play precise roles in the mechanical behaviour of the raptorial appendage in stomatopod spearer shrimps.

The skin ulceration syndrome of the aquacultivated sea cucumber *Holothuria scabra (Holothuroidea, Echinodermata)* in the South-West of Madagascar

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The set-up of large-scale marine aquacultures is often associated with the emergence of new diseases and disorders. “Aquafarmed” sea cucumbers from the South-West of Madagascar are no exception to the rule as they suffer from specific disorders called « skin ulceration diseases » (SKUD), more recently described as « skin ulceration syndromes » (SUS) as multicausal origins have been highlighted in other sea cucumber species. Despite an abundant literature on the subject, a strong morphological basis is needed for a better understanding of the symptoms. Our study presents epidemiological data regarding the (i) occurrence of the skin ulceration syndromes within pens from the company Indian Ocean Trepang in Toliara (Madagascar) and (ii) the potential recovery of diseased animals. We also make an update on the symptoms developed in the SUS context and present a precise morphological analysis of the skin ulceration syndrome in *H. scabra*. Finally, transcriptomic analyses of the sea cucumber integument allowed us to highlight differentially expressed genes in the skin ulceration context. The peak of symptom occurrence is observed during the austral winter. The ulcerations are phenotypically characterized by the exposure of the connective tissue that follows the destruction of the cuticle, the epidermis and the upper part of the connective tissue. Our transcriptomic analyses indicate that a large variety of mRNA coding for stress-induced heat shock proteins are expressed in diseased animals while actors of connective tissue restructuration are locally expressed within integument ulcerations. Altogether, our results give new insights on the understanding of the skin ulceration disease as well as the potential causes inducing the symptoms. The authors thank the company “Indian Ocean Trepang”, based in Toliara, for providing specimens and access to the pens as well as their expertise and advices.

Ecophysiological responses of *Seriatopora hystrix* (Dana, 1846) to a hypo- and hypersaline stress in short time

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Coral reefs are considered one of the most biodiverse marine ecosystems on the planet. Coral reefs host a large and various community of organisms such as fishes, echinoderms, plankton, etc. The coral reef is a perfect example of the Darwin Paradox, i.e. it has a high productivity when the available nutrients are low (oligotrophic seawater). Coral reefs are threatened by several stressors. Most of these stressors are directly and indirectly linked to anthropogenic factors such as anthropogenic enrichment, overfishing, climate change, etc. Salinity is another stressor of the coral reef balance. The number of tropical storms and hurricanes has strongly increased over the past decades. These climatic events therefore induce a sharp decrease in salinity a couple of days after their occurrence. Moreover, the desalination industry is a new salinity stressor. Saltwater is desalinised to produce fresh water mainly for crop irrigation. A coral reef mesocosm has been used to study the impact of the hyposaline and hypersaline stress on *Seriatopora hystrix* (Dana 1846), a hermatypic scleractinian species. Three salinity states have been selected: 28 (hyposaline stress), 35 (control) and 42 (hypersaline stress). These states have been kept constant for 7 days. In each condition stress, we have observed a discoloration of corals (not a bleaching), a decline in growth rate, calcification rate and respiration rate. The hypersaline stress reduces more strongly the growth rate that hyposaline stress. The growth comes back to the initial state 3 weeks after the experiment. This experiment could suggest that salinity is an important environmental variable for the coral reef. The variation of salinity, even low and a short duration impacts negatively *S.hystrix*.

Adjust or bust: functional differences in the morphology of an invasive fish species across Europe

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Biological invasions endanger human and animal health, our economy and the ecosystem. We humans are the main cause of this problem, by (un)willingly introducing new species into "naive" ecosystems. The species that become invasive seem to share the ability to first tolerate and then quickly adjust to a range of conditions. However, the role of this rapid adjustment during introduction, establishment and subsequent dispersal is not well known and currently not incorporated in management practices. Therefore, we aim to study the ability of an invasive fish, the round goby (*Neogobius melanostomus*), to adjust to different aquatic ecosystems. We expect that populations of the round goby adjust to local environmental pressures, despite a generalist diet and broad tolerance to (a)biotic factors. Such a broad tolerance is vital when entering a new ecosystem (introduction), but rapid adjustment is expected when conditions are relatively stable (establishment). Knowledge gained on their ability to adjust directly improves management and prevention programmes for invasive gobies and aids those for other invasive species. Here, we present the first data from a continent-wide study on the functional morphology of round goby. Did these fish adjust their head morphology to local dietary sources? We expect that the round goby adjusted its morphology to reflect local optima, e.g. adjustments to processing hard-shelled molluscs where these are highly abundant. We incorporate our morphological results in the Food-Fish Model which provides functional interpretation to the data. We aim to embed our research in a complete mechanistic framework incorporating biomechanics and functional responses in the future. Our findings will eventually provide a mechanistic basis for methods predicting invasiveness currently in use, will directly aid biological invasion management, and will ultimately benefit our understanding of species' ability to adjust to a rapidly changing climate and environments.

Evolution and development of white stripe patterns in clownfishes (Pomacentridae)

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How can we explain the fabulous diversity of color patterns in coral reef fishes? To address this question, we chose to work on the monophyletic group clownfishes. Clownfishes or Amphiprionini tribe comprises 30 species that possess a characteristic colour pattern composed of zero to three vertical white stripes over an orange to black body. Here, we wanted to understand the ultimate and proximate causes at the origin of this diversity of colour patterns by combining eco/evo/devo studies. First, we characterized the cellular nature of the white stripe and showed using drug treatment that those cells correspond to iridophores and that they are indispensable to initiate the formation of the colour pattern. Then, we showed that the common ancestor of clownfishes had three vertical white stripes and, during evolution, we observed a successive caudal to rostral losses of stripes. These results suggested a developmental constrain that we highlighted by studying the development of *Amphiprion ocellaris* (3 white stripes) and *Amphiprion frenatus* (1 white stripe). Interestingly, the white stripes of *A. ocellaris* always appear in a rostral to caudal stereotyped sequence during larval to juvenile transition. Surprisingly, whereas *A. frenatus* has only one stripe at the adult stage, they acquire three white stripes in a same sequential manner as *A. ocellaris* during larval to juvenile transition. Later on, these stripes disappear caudo-rostrally during the juvenile phase leading to the definitive colour pattern. Remarkably, the reduction of stripe number over ontogeny matches the sequences of stripe losses during evolution, showing that colour pattern diversification among clownfish lineages results from changes in developmental processes. Finally, we provided evidence that the diversity of striped patterns plays a role for species recognition.

Quality over Quantity: Analysing Individual Variation in Abnormal Behaviour in Zoo-Housed Chimpanzees (*Pan troglodytes*)

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Animals in captivity are known to display abnormal behaviours, which are either less common or entirely absent under wild conditions. Researchers have attempted to map the abnormal behavioural repertoire of an entire species, especially in order to identify etiological factors that could lead to the development of these behaviours. However, there is still considerable individual variation in the quantity of abnormal behaviours that are exhibited, especially in primates such as chimpanzees, begging the question of whether there is also more qualitative individual variation in such behaviours. In order to test this intriguing possibility, an observational study was conducted on a colony of 15 captive chimpanzees (*Pan troglodytes*) housed at Royal Burgers' Zoo in Arnhem, the Netherlands. Eight abnormal behaviours were assessed using both measures of quantity (for instance, proportion of observations present) and quality (for instance, diversity of behavioural repertoires). Additionally, the composition of the abnormal behavioural repertoire between individuals was compared to obtain a measure of similarity. Substantial quantitative variation was found between individuals in both the proportion of observations in which abnormal behaviour was present and in the size of the abnormal behavioural repertoire. Furthermore, qualitative differences were found in the composition and diversity of the abnormal behavioural repertoire. Other factors that have been suggested to explain the spread of abnormal behaviours, such as age, sex, rank, kinship and affiliation, did not significantly account for the (dis)similarity of individuals' abnormal behavioural repertoires. These findings indicate that there is considerate qualitative as well as quantitative individual variation in the abnormal behavioural repertoire of chimpanzees.

Bushmeat for sale in Brussels

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The European Union prohibits any personal consignment of meat (products) from entering the Union unless specifically authorized and certified as being eligible for import. Notwithstanding these regulations, various recent papers report that large quantities of meat, including bushmeat, are entering Europe via its international airports without such certification. These studies suggest an organized luxury market for African bushmeat in Europe. In response, we explored the following issues: (1) is bushmeat for sale in Brussels, (2) which species are being sold and are these endangered or legally protected (e.g. CITES), and (3) what is the price of bushmeat in Brussels? Between November 2017 and May 2018, African collaborators were able to purchase 15 pieces of meat presented as bushmeat. Species were identified by DNA-barcoding at the Barcoding Facility for Organisms and Tissues of Policy Concern (BopCo) at RBINS and RMCA (http://bopco.myspecies.info/). This revealed that the 15 bushmeat pieces involved nine species, but also that seven of the 15 pieces were sold under a wrong species name. Two pieces were identified as beef instead of bushmeat. None of the nine species are endangered according to the IUCN Red List, but two monkey and two duiker species are CITES listed. The price of bushmeat in Brussels can reach twice the Belgian market price of a piece of premium livestock, but does not seem to be related to the species being sold. The high incidence of erroneously labelled bushmeat might be due to the involvement of several intermediate vendors and the fragmented and heavily smoked nature of the meat, making it extra difficult to identify. This study confirms that various types of bushmeat, including CITES listed species, are available for sale in Brussels. The high prices confirm the luxury status of the product, while DNA-based identifications demonstrated a high mislabelling frequency.

Handicapping males negatively affects the alternation of provisioning visits in blue tits

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Parents of biparental bird species have a conflict about how much each should invest into the current brood. A recent intriguing theory suggests that parents might ameliorate this conflict via alternation of their provisioning visits facilitating equal investment. A handful of studies have shown that some species do actively alternate. However, experimental studies proving whether alternation is actually a stable behavioural strategy, are still lacking. In this study, we handicapped male blue tits (*Cyanistes caeruleus*) by feather clipping and recorded the parental responses of both male and female. In particular, we investigated whether males kept the alternation level stable regardless of their handicap. However, the alternation level was lower when the male was handicapped, indicating that pairs exhibit some degree of flexibility in the level of alternation. Interestingly, females with a handicapped partner had a higher visit rate, whilst males in both groups had similar visit rates. Females might have responded to the handicap of their partner, which likely reduced the male's quality, and therefore compensated by increasing their visit rate. This suggests that the females of the handicapped males distort the alternation pattern. Our study highlights that so-called stable behavioural strategies within pairs can change in response to sudden irreversible asymmetries in individual quality.

Strict extrapolation in modelling Southern Ocean species distribution

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Species Distribution Models (SDM) have been broadly used in Southern Ocean case studies to assess species potential distribution and evaluate environmental preferences of a species. However, when transferring model predictions to other time periods or other areas, a part of the environment may include conditions that are outside of the range of those used to calibrate the model. Therefore, the model makes assumptions, extrapolates and provides uncertain predictions. Considering the lack of presence records, their spatial aggregation and the poor quality of environmental descriptors available in Southern Ocean case studies, we can suppose that the area where strict extrapolation occurs is proportionally large. In this study, we used the Multivariate Environmental Similarity Surface (MESS) index to delineate strict extrapolation areas. The MESS extracts the environmental conditions values contained within the presence records and estimates the areas where the environmental conditions are outside of the calibration area. The method considers that strict extrapolation occurs when at least one environmental descriptor is contained outside of the range of the environment defined during model calibration. Here, the strict extrapolation area of SDM generated for several Antarctic echinoid and asteroid species is compared. Results show that for some species, more than 50% of the area predicted as suitable for species distribution is actually an uncertain prediction, although SDM evaluation indicates accurate and reliable modelling performances. Considering such results for present environmental predictions, we assess the potential relevance of SDM future predictions using future scenarios such as IPCC (Intergovernmental Panel on Climate Change) climatic models (RCP 4.5, 6.0, 8.5). Discussions about the reliability, precision, availability and relevance of climatologic models for studying species distribution are finally provided.

The *Daphnia* microbiome: What is core and what is flexible?

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The gut microbiome represents an important source of metabolic flexibility that may allow the host to rapidly acquire phenotypes that are adapted to changing environmental conditions. Recently, it is suggested that the gut microbiome can be divided in two parts that are the extremes of a continuum to which most bacterial strains belong. The first part is the “core” microbiome, which consists of host-adapted microbes. It is hypothesized that the “core” microbiome is assembled from diverse environments and largely determined by genetic factors. Given the importance of the services that the “core” microbiome provides for the host, one possibility is that the “core” microbiome is vertically transmitted. The second part of the gut microbiome is the “flexible” pool of microbes, which composition varies depending on environmental conditions. These bacteria are mainly acquired through horizontal transmission and exchange with the environment. It is not known in how far genetic factors play a role in this “flexible” microbiome. Knowledge on the microbiome of *Daphnia* is rapidly accumulating. Several bacterial taxa are consistently found in affiliation with *Daphnia*, even in geographically separated populations, indicating a highly specific association between *Daphnia* and its microbiome. Nevertheless, the presence of a “core” microbiome in *Daphnia* is debated, given the inconsistencies found over different experiments. In this study, I will first determine which bacteria belong to the “core” microbiome of *Daphnia magna*. Previous work showed that *Mollicutes* was present in the guts of *Daphnia magna* from ponds in the surrounding of Kortrijk. Based on this work I will isolate and determine the *Mollicutes* strain. Then I will use this sequence to determine if *Mollicutes* is also present in other ponds. Finally I will determine if the *Mollicutes* stays present in the gut if *Daphnia* are kept in laboratory conditions.

Evolution of the shape of the cephalic region and oral jaw system in relation with trophic specialisation in Serrasalmidae (Teleostei: Characiformes)

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Serrasalmidae (about 98 species) is atypical among Neotropical characiforms because the feeding mode of all species is based on biting and diet can be different. Some species prefer to feed on algae, plants, fruits or seeds whereas others eat flesh, fishes, fins, scales or invertebrates. This large trophic diversity provides an excellent opportunity to analyse the evolutionary processes underlying the morphological diversification of this monophyletic taxon. The objectives of this study are to characterise the shape of structures involved in feeding and to explore the influence of the phylogeny on the shape variability of these structures. We examined the shape variations of the cephalic region in 30 serrasalmid species, the oral upper and lower jaws and teeth in 22 species using Procrustes-based geometric morphometrics. We then conducted phylomorphospace analyses to quantify the morphological transformations through evolution in 22 species for which phylogenetic relationships were available. Phylomorphospace plots reveal two main groupings of species that are mainly consistent with diet (carnivorous and herbivorous) and phylogenetic relationships. The shape diversity of the cephalic region and oral jaw system is higher in the herbivorous group compared to the carnivorous group. These different evolutionary trajectories could be related to the feeding constraints and suggest that herbivorous could exploit many more ecological niches than carnivorous species. The present study shows that the trophic specialisation of serrasalmid species occurred via multiple modifications in the skeleton and muscles of the cephalic region and oral jaw system.

Motoneuron and premotoneuron pools associated with swimbladder sounds and electric organ discharges in mochokid catfish

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Depending on the species, synodontid catfish produce swimbladder sounds, electric organ discharges (EODs), or both using the protractor muscle that is connected to the swimbladder via a bony plate. While this muscle has a higher proportion of myofibrils in sound producing than in EOD producing species, possible differences in the neuronal networks underlying these different behaviours remain unknown. Our goal was thus to investigate the protractor motoneuron and premotoneuron pools in mochokid species producing different outputs using dextran biotin or neurobiotin labelling of the protractor nerve(s). We selected three synodontid species: a sound producer (*Synodontis grandiops*), an EOD producer (*S. nigriventris*), and a species that emits both types of signal (*S. eupterus)*. Two species (*Mochokiella paynei* and *Microsynodontis batesii*) from closely-related genera whose ability to produce sounds and/or EODs had never been tested were also investigated. Both species turned out to only be sound producers with a high proportion of myofibrils in the protractor muscle. For the five species studied, the pool of protractor moto- and premotoneurons started 100-200 µm before the caudal end of the fourth ventricle and extended between the medial longitudinal fasciculi and the central canal for approximately 1 to 2 mm. The dorsal part of the protractor nucleus contained mainly premotoneurons, while the ventral part was mostly composed of motoneurons. Considering only dextran-biotin labelling of motoneurons, the protractor nucleus of the EOD producing *S. nigriventris* and of the sound producer *M. batesii* had the shortest lengths and fewest neurons. Based on the neurobiotin tracings (motoneurons and premotoneurons), *S. nigriventris* also had fewer premotoneurons. Research support from US National Science Foundation 1457108 (AHB) and F.R.S-FNRS (LK).

Bystander jealousy-driven behaviour in zoo-housed chimpanzees (*Pan troglodytes*)

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Jealousy is one possible emotion that may not be uniquely human, but rather shared with other social species such as with our highly social complex closest living relative, chimpanzees (*Pan troglodytes*). Jealousy-driven behaviour can be described as a goal-directed behaviour that protects valuable relationships and thereby promotes fitness. In this study, we defined jealousy as a negative reaction from an individual (bystander) towards social closeness between two individuals (recipients), one or both with whom the individual has a close relationship. We studied its occurrence on a group of fifteen chimpanzees housed at Burgers' Zoo, Arnhem. A bystander was more likely to express jealousy when they had a close social bond with one or both recipients compared to neither, showing they did not want to risk the services they received from their valued partners being both or one of the recipients. Thus, bystanders being aware of different social relationships simultaneously in order to keep track of their valued partners and monitor their own relationships in the case of when one is threatened A bystander whom sees that their relationship with a valued partner is threatened, would express jealous-driven behaviour to protect the relationship. This study could further increase the study of secondary emotions such as jealousy in other complex social species.

Are mother's cursing their sons? Prevalence of mtDNA induced sex-specific differences in survival and fertility in zoo populations

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Mitochondria are the powerhouses of the cell and as such influence a great deal of fitness traits, ranging from fertility to the process of aging. Although parents contribute equal amounts of nuclear DNA to their offspring, in general mitochondrial DNA is exclusively transmitted via the mother (maternal inheritance). As a result, mitochondria that negatively affect male fitness will never be selected against. This can lead to an accumulation of male-harming mutations in the mitochondrial DNA, a theory labelled “Mother's Curse”, affecting males and ultimately the entire population. Previously, signs of Mother's Curse have been seen in both humans and livestock (e.g. reduced male fertility and aging). We were particularly interested in whether similar signals can be found in captive breeding programmes. To do this, we analysed a total of sixteen populations through their studbooks, with a focus on the sex-specific difference in aging and fertility. While no significant differences were found for the fertility analysis, our results indicate the survival of males is affected in mitochondrial lineages within several of the sixteen studbooks. Results of our study will be important for the maintenance of healthy populations and safeguarding their genetic diversity.

Host genotype shapes the assembly of both the gut microbiota and the surrounding bacterioplankton in the freshwater crustacean *Daphnia magna*

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The gut microbiota mediates important aspects of its host's biology, as well as tolerance to diverse environmental stressors. Because gut symbionts are mainly acquired from the surrounding environment, it is crucial to understand the interplay between host, gut microbiota and environmental microbial communities. This question is particularly relevant for aquatic organisms and bacterioplankton, which are in close and continuous contact, and are thus expected to have a strong reciprocal influence. Combining metagenetics with microbiota transplants, we here show that in the freshwater crustacean *Daphnia magna*, host genotype and diet interact to shape the structure of both the gut microbiota and the surrounding bacterioplankton. When different *Daphnia* genotypes were exposed to identical microbial communities, both the gut microbiota and the bacterioplankton diverged to reached a genotype- and diet-dependent taxonomic composition. The exposure of germ-free *Daphnia* to different microbial inocula also revealed an effect of the external microbial source on the gut microbiota structure. Our results indicate strong reciprocal interactions between *Daphnia*, their gut microbiota and the bacterioplankton. Importantly, we here provide evidence that *Daphnia* mediate the assembly of their associated microbial communities, both within their gut and in their close environment, depending on their genetic background. This result clearly demonstrates the impact of evolution (i.e. genetics) on ecological processes (i.e. community assembly) and, by illustrating an evo-to-eco link, provides strong support to eco-evolutionary dynamics theory.

Identifying Invasive Alien Species by DNA-barcoding: possibilities, gaps and pitfalls

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Invasive alien species (IAS) have a negative impact on their newly occupied, non-native environments after accidental or deliberate introduction. In order to protect native biodiversity and ecosystems, and mitigate the potential impact on human health and socio-economic activities, the European Commission issued Regulation 1143/2014, detailing 37 IAS impacting EU member states. Since last year's Benelux Congress of Zoology, during which the usefulness of molecular data to identify these species was presented, the number of IAS under EU considerations was expanded to 49 in Regulation 2017/1263. The reliability with which these IAS can be identified, using the online available sequence data, is now described in concise factsheets, one for each species on the Regulation list. These factsheets are publically available on BopCo's webpage (http://bopco.myspecies.info/). The factsheets are divided in two main parts; the first includes an overview of the taxonomic classification and species distribution to inform the second part. In the latter, the DNA reference databases are critically evaluated, specifying the issues encountered and potential actions to improve the usefulness, as well as a conclusion on how well the data covers the identification needs. Additionally, advice is given on which molecular marker(s) to use when identifying a potential IAS sample. An often encountered issue is the lack of sequence data in the online reference databases, especially for closely related species. Examples will be presented, demonstrating the different issues by identifying the gaps in the online reference databases and suggesting potential actions to increase the reliability of invasive alien species identifications.

Genome skimming and rapid recovery of mitochondrial genomes. A powerful tool to resolve phylogenetic relationships in Syrphidae.

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Genome skimming represents a powerful tool allowing to recover in a relatively short time and with a limited budget mitochondrial (mt) gene fragments or whole mitogenomes that can be used to investigate insect phylogenetic relationships. This approach relies on (a) low-coverage whole genome sequencing of individually indexed or pooled specimens, (b) subsequent filtering of mitochondrial reads and de-novo or reference-map assembly of draft mitochondrial genomes and (c) annotation via established bioinformatic pipelines. Recently, the Joint Experimental Molecular Unit of RMCA and RBINS investigated the potential of this approach to resolve the phylogenetic relationships of African hoverflies (Diptera, Syrphidae). Here we present the results of a pilot study aiming at quantifying the strength of phylogenetic signal provided by mitochondrial protein coding genes (PCGs) and ribosomal DNA (rDNA). In this respect we used the HyPhy algorithm (http://phydesign.townsend.yale.edu) on an alignment including five *Eristalinus* mitogenomes and quantified the Phylogenetic Informativeness (PI) of the 13 PCGs and two rDNA. This analysis showed that nad5, nad4 and cox1 were the mt markers with the stronger phylogenetic signal, i.e. the most suitable to resolve phylogenetic relationships within the target genus. Preliminary Bayesian trees including 75 representatives from the genera *Syritta*, *Phytomia*, *Eristalinus* and *Mesembrius*, showed highly resolved nodes with an average boostrap support of 0.985 (SD= 0.053) within the genus *Syritta*, 0.991 (SD= 0.023) within the genus *Phytomia*, 0.996 (SD= 0.020) within the genus *Eristalinus*, and 0.981 (SD=0.063) within the genus *Mesembrius*. These results suggest that mitogenome-based phylogenies represent a suitable and relatively low-cost tool to investigate phylogenetic relationships in Syrphidae.

Intersexual heterogeneity of the metabolic response to stress: are males and females equal in a challenging environment?

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Physiological mechanisms of the responses toward stressors are the core of ecophysiology studies to understand the limits of organism's flexibility and better predict the impact of environmental degradation on natural populations. However, few information is available when we question the inter-individual's variability of these physiological responses, even though they can be particularly important. Some observations of intersexual differences in torpor and hibernation abilities raised the question of an imbalance in energy management between sexes and caused the formulation of a "thrifty female hypothesis", which would confer an advantage to females upon environmental challenges. Here we assess male and female differences in a mouse lemur model (*Microcebus murinus*), a highly seasonal Malagasy primate, studying their physiological flexibility toward caloric restriction, and questioning the impact on their genetic stability and reproductive success. These animals are adapted for naturally changing food availability and climate conditions, and can express deep torpors allowing them to spare their energy expenses over the dry and cold season. We monitored body mass, body temperature and metabolism (basal and mitochondrial) on 12 males and 12 females over winter, applying a chronic 40% caloric restriction to 6 individuals of each group. Our results confirmed the existence of a sex-specific torpor response to food shortage, males showing deeper torpors when submitted to restriction than females, with yet a bigger impact on males' body conditions and mitochondrial capacities. These features suggest that females express more efficient torpors than males and support the thrifty female hypothesis. Still, the results have to be confronted to other parameters used as fitness indicators to confirm the difference in stressor's impact between sexes and show further arguments in considering intraspecific variability to predict the consequences of environmental challenges, especially when the group of study is the one contributing to reproduction and population's renewal.

Is personality consistent across social context? The effect of female personality on social behaviour during male introductions in captive long-tailed macaques

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Individual animals exhibit different behavioural responses that remain consistent across time and context, namely personality. Primates personality is largely based on social behaviour, as they are highly social animals. Their social life includes different kinds of contexts, such as stable and unstable situations. Even though the stability of personality in time is extensively studied, the repeatability in different context is not. The aim of this study was to investigate how female personality defined at a stable context, influences the female's behaviour in unstable context (i.e. male introductions). Observational data from a stable captive group of long-tailed macaques was used to identify each female's personality. Four personality traits were found: Aggressiveness, Sociability, Connectedness and Anxiety. Data from two male introductions in the same group were analysed to explore the effect of female's personality on the females' behaviour in unstable situations. Personality was expected to affect female behaviour similarly during both introductions. Females' that score high in Aggressiveness showed more aggression towards the new male and showed more affiliation and had more sexual interaction with the male during both introductions. Similarly, females that scored high in Sociability were more aggressive towards both males. No consistent effects of Connectedness and Anxiety between the introductions were found. In conclusion, the study provided evidence that female personality from a stable context affects female behaviour in an unstable situation. This implies that personality may indeed be stable across social context. However, not all personality traits may be equally important in all contexts.

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

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The abyssal deep sea (3000 - 6000 m) is one of the largest and most unexplored ecosystems on the planet. As part of the Mining Impact “Ecological aspects of deep-sea mining” JPIO project, we are studying and comparing the long-term ecological impacts of mining of ferro-manganese nodules on deep-sea crustaceans in two basins; (1) the Clarion-Clipperton fracture Zone (CCZ), a manganese nodule province, NE Pacific and (2) the DISturbance and Re-COLonisation (DisCOL) Experimental Area (DEA), a disturbance proxy in the SE Pacific. More than 60,000 specimens of Amphipoda were collected during two cruises. 19 species have been identified thus far, including several undescribed species. At the disturbance proxy site, the scavenging amphipod community shows reduced diversity and is dominated by a single species, *Abyssorchomene gerulicorbis,* indicating that extended time is needed for post-disturbance recovery. Two target species, *Paralicella caperesca* and *Abyssorchomene gerulicorbis,* were selected for molecular analysis of potential genetic connectivity and dispersal. For 200 specimens, we successfully obtained DNA sequences of part of the mitochondrial COI gene. The molecular results provide evidence for cryptic diversity in both species and also demonstrate a previously unknown genetic connectivity between these two basins (3000 km apart). Here, we also present the first nuclear DNA sequence data (Histone 3 (H3) gene) from these species. Although H3 is a very conserved gene, we find genetic variation between these species, confirming the mitochondrial genetic patterns and illustrating that our approximation of deep-sea biodiversity is an underestimation. Developing a suitable protocol of population genomic techniques (ddRAD-seq) for these species with unknown genome sizes is in progress (with the KU Leuven). The CCZ will be revisited in an extended sampling campaign in February 2019, to gather further scavenging amphipod samples with video guided methods (ROV), and also to obtain complimentary abiotic data from these sparsely studied habitats.

Mixture toxicity effects of oestrogen and aryl hydrocarbon receptor agonists during zebrafish embryonic development

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The use of zebrafish for identifying endocrine-disrupting chemicals (EDCs) is receiving increased attention. However, the mechanisms underlying impaired developmental processes are still poorly understood, especially after combined exposure to chemicals that are interacting at the molecular level. First, we provided detailed baseline gene transcription profiles of 20 genes involved in the steroid hormone metabolism during normal zebrafish development until 32 days post fertilization (dpf). Transcript levels were analysed using QPCR. For example, maternally transferred mRNA was detected for all 3 nuclear oestrogen receptors (ER). Interestingly, the development of several organs coincided with an increase of transcript levels of ER which are known to be expressed in these organs during the embryonic period, suggesting a possible role of oestrogens in normal organ development. We used our baseline dataset to investigate the molecular mechanisms of estrogenic endocrine disruption with 17α-ethinylestradiol (EE2). Fish were exposed to EE2 from 2 hours post fertilization until 14 dpf and gene transcription was analysed using QPCR. Mixture effects are complex and still poorly understood and may depend on interactions between chemicals. Aryl hydrocarbon receptor (AhR) agonists are known to interact with the oestrogen pathway. The mechanisms underlying developmental effects of AhR/ER cross-talk in the zebrafish are not yet elucidated. We are investigating potential interactions due to AhR/ER cross-talk in β-naphthoflavone and EE2 single and mixture exposures. Transcript levels are analysed using QPCR. EROD assay is used as an indicator of CYP1 activity induced by BNF. Protein levels of VTG induced by EE2 are studied using ELISA. Morphological parameters such as heart and neuromast development are examined. Our approach of using baseline information on normal development to study disruption of specific processes after exposure will contribute to a more thorough understanding of the mechanisms of endocrine disruption and mixture toxicity.

Species complementarity drives zooplankton top-down control on phytoplankton in a lake dominated by non-toxic cyanobacteria

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Trait-based approaches have the potential to provide stronger predictions of biodiversity–ecosystem functioning (B-EF) relationship than more traditional, taxonomic-based approaches. However, choosing ecologically relevant functional traits that simultaneously respond to environmental change and that influence ecosystem processes is challenging. In aquatic systems, body size is a powerful trait often related to both ecosystem processes and species turnover. Despite its importance, the mechanism by which body size drives ecosystem processes remains poorly known. Two mechanisms are often hypothesized to explain the relationship between body size and the strength of zooplankton top-down control: selection effects (grazing efficiency asymmetry) and complementarity effects (size-based niche partitioning). Here we evaluated the relative importance of zooplankton body size and taxonomic diversity in explaining the strength of top-down control on phytoplankton and aimed at disentangling the mechanism by which this functional trait operates. We found that body size provides strong predictions of top-down control, but taxonomic diversity also plays a role. This reveals that the strength of top-down control on phytoplankton depends on the number of species in the zooplankton community. Surprisingly, though, we observe a negative correlation between functional and taxonomic diversity, showing that size diversity seems to make difference for any two communities with the same number of species. This highlights the limitation in using species richness as a single biodiversity metric to gain new insights into ecosystem functioning. Our results suggest that relatively larger differences in zooplankton body size enhance niche partitioning and top-down control, and that this effect has a strong temporal correlation. Our study demonstrated the importance of accounting for body size to better interpret cascading trophic interactions between phytoplankton and zooplankton, and highlight the importance of considering multiple aspects of biodiversity to allow a more realistic description of the relationship between community and ecosystem ecology.

What is APECS Belgium?

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The Association of Polar Early Career Scientists (APECS) is an international and interdisciplinary organization for undergraduate and graduate students, postdoctoral researchers, early faculty members, educators and other people with interests in Polar Regions and the wider cryosphere. Its main goals are communication, education, outreach, and assistance to early career scientists. The APECS leadership team is comprised of early career researchers that are interested in and committed to furthering the activities and the future directions of the organization. Project initiation and management, web-based or in-person events, are carried out by a number of member-initiated working groups and committees made up of both members and mentors. APECS Belgium, the Belgian National Committee of APECS, was founded in 2011 and has organized and participated in many events and activities since; for example: Conference Symposia, Science fair, school visits, workshops, documentary screenings, outreach events and much more. APECS Belgium encourages polar research at the national level by promoting research projects and institutes in the Belgian territory and sharing the fascination of the Poles with other researchers and the community. Every early career scientist based in Belgium with an interest in the Polar Regions is highly encouraged to join us! We also invite people with links to polar education and research to become part of APECS Belgium. For more information, visit our website: www.apecsbelgium.wordpress.com.

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

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Historically, Antarctica underwent many environmental changes throughout time. Glaciation and deglaciation periods forced organisms to adapt to new conditions, undergo extinctions, or migrate. During glaciations, migrations occurred to different refugia such as the deep sea, ice-free regions of the Antarctic continent and sub-polar regions. These refugia created barriers with reduced gene flow and increased diversification and speciation. Now, Antarctica is undergoing new alterations induced by global warming and ocean acidification. The RECTO (Refugia and Ecosystem Tolerance in the Southern Ocean) project investigates the historical dynamics forced by previous glaciation periods and possible responses to future climate change. WP2. part of the project reconstructs the population history of different taxa from various trophic levels. Here, we will specifically focus on the amphipod genus *Charcotia* (formerly known as *Waldeckia* sp.), of which two species are investigated: *C. obesa* and *C. amundseni*. Both species are scavenging amphipods, and are morphologically and genetically distinct. They most likely also have different bathymetrical distributions, with *C. amundseni* being more abundant at larger depth. The population history and biogeography will be reconstructed from different localities in the Southern Ocean with molecular tools, including sequencing the COI DNA barcoding region, to construct genetic networks and test for cryptic diversity. We will also apply Next-Generation-Sequencing (NGS) techniques to unravel the complete mitochondrial genome of these amphipod species. Sequence data from complete mitochondrial genomes will allow us to design primers for long range PCRs to obtain mitogenomic data from different populations of both species. This way, phylogenies for reconstructing the evolutionary history will be statistically better supported. Possible differences in mitochondrial genomes between species could also be non-neutral and indicate specific temperature adaptations. The latter will be assessed by comparisons with mitogenomes of closely and more distantly related Crustaceans from Antarctica.

How hyperthermic stress affects the fertility of bumblebee males?

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Bumblebees are experiencing a global decline over the world. Among different factors, climate change has been identified as one of the main driver of pollinators decline. Heat waves are known to disturb the physiology and increase the mortality of insects (due to ontogenic development, water balance changes, fertility and immunity decrease). Previously, we showed that hyperthermic stress (up to the heat stupor) induces the mortality of more than 50% of the bumblebee males. We highlighted also that the hyperthermic stress resistance is highly species-specific. However, we have any information on how a hyperthermic stress impacted the fitness of the survivals. Using three model species (one very resistant and ubiquitous, *Bombus terrestris* and two sensitive and geographically restricted species, *Bombus jonellus* and *Bombus magnus*), we aim to test the fertility (sperm viability and Sperm Chromatin Dispersion [SCD]) of males surviving to a hyperthermic stress. Our results show a significant increase of spermatozoid mortality (more than 60%) in all species, particularly for the sensitive species. For the SCD experimentation, no significant difference was observed between control and test group for *B. terrestris*, while difference was very marked in *B. jonellus*. In addition to the direct effect of hyperthermic stress on population (mortality) our results suggest a sublethal effect on the fertility of the surviving bumblebees which could lead to very dramatic consequences for pollinator conservation.

Ecological diversification, recent evolution and speciation of Amphipoda in the polar regions: the case study of *Eusirus* genus

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Because of their long history, the polar regions and especially Antarctica are natural laboratories for evolutionary research. The diverse and specialized polar fauna has evolved during millions of years, and has survived past environmental changes including the glaciations. Given that certain parts of the polar regions are among the fastest warming regions on this planet, knowledge on how these organisms managed to survive climate changes in the past can help us to extrapolate to the future. Here, *Eusirus* amphipods (crustaceans) are chosen as model organisms because they occur on both poles, are very diverse and live in different habitats. Our knowledge on their ecology and biogeography is still very limited although they are an important component of the marine fauna. From the same amphipod specimens, genetic data, morphological data and ecological data (general ecology, trophic ecology) will be acquired. The evolutionary history of *Eusirus* amphipods will be reconstructed through time with phylogenetic and population genetic methods, and the obtained phylogenies will be used to map morphological and ecological diversity. This will ultimately reveal which evolutionary processes led to the current diversity of *Eusirus* amphipods, and if speciation events were constant through time or occurred in bursts. This kind of analyses will also test if there has been convergent evolution of *Eusirus* amphipods in the two polar regions.

Refugia and ecosystem tolerance in the Southern Ocean

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Confronted with fast-paced environmental changes, biota in Antarctic ecosystems are strongly challenged and face three possible outcomes: adaptation, migration or extinction. Past glaciation periods have already forced marine zoobenthos of the Southern Ocean (SO) into refugia, followed by recolonization when the ice retreated. The collaborative Belgian BRAIN project RECTO, "Refugia and ecosystem tolerance in the Southern Ocean", will strive at understanding how such past events have driven diversification and adaptation in different animal groups and how these can be applied as proxies to understand the contemporary situation and predict future scenarios. With molecular approaches, RECTO will reconstruct population histories and spatio-temporal features of Pleistocene refugia. The RECTO target taxa include birds, fish, sea stars, bivalves, amphipods, and ostracods. For all RECTO target taxa, the following molecular data will be obtained: (1) mitochondrial COI barcodes, (2) ddRAD data, and (3) mitochondrial genomes. Mitochondrial genomes will be obtained by genome skimming, and long range PCRs. Mitogenomes can improve the unravelling of phylogeographic relationships and dating of evolutionary events and, through comparisons with non-Antarctic taxa, allow to detect cold adaptations. In fish and amphipods, RECTO will also study in a novel phylogenetic framework how morphological diversification and trophic adaptability (estimated by stable isotope data) are interacting with each other and whether ecotypes of selected species have faster modes of evolution. Geographic models on future species and trait distributions based on physiological and energy limits and present and future climate data will be refined and integrated with individual based models for the SO. Finally, scenarios of future dispersal abilities and possible habitat shifts of the RECTO target groups will be developed to infer how the RECTO target species will respond to future climate change.

Host Control on Symbiont Proliferation mediated by Dynamin, a membrane-modelling GTPase

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The theory of ‘symbiogenesis’ provides an explanation for the evolution of plastids and mitochondria in eukaryotes through engulfment of prokaryotes. The proteins required for the division of these organelles are nuclear-encoded and thus are being controlled by the ‘host’. Studies in *Arabidopsis thaliana* and *Toxoplasma gondii* have suggested an involvement of host-derived GTPase, dynamin, in the regulation of symbiont division. Photosynthetic dinoflagellates in the genus *Symbiodinium* exist as endosymbionts within a series of membranes of both host and symbiont origin in the gastrodermis of various cnidarian taxa. The growth rate of the endosymbionts is higher in culture than within the host (*in hospite*). If not controlled, the symbionts would probably overgrow the host cells. A dynamin-regulated mechanism employed by the host for the control over symbiont proliferation was suggested by us. Dynamin is a membrane-remodelling GTPase employed by the cell in process of membrane fission. This study aimed at examining whether dynamin genes show differential levels of expression in symbiotic versus aposymbiotic anemones (*Exaiptasia pallida*). The documented distribution of this species is around the coast of U.S., throughout Caribbean Sea and the Gulf of Mexico. But it is a known aquarium pest and an upcoming model system for sea anemones. Real-time polymerase chain reaction was used to quantitate dynamin expression. The diel mitotic index was estimated for the endosymbiont (*Symbiodinium minutum* type B_1) in culture and *in hospite* to assess variation in the division patterns. This study is a part of a discovery-study aimed at unravelling the basis of host-control on its symbionts.

Identifying mosquitoes (Diptera: Culicidae) from foreign deployment sites of the Belgian armed forces

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Mosquito-borne diseases impact humans in almost every part of the world since mosquitoes of medical importance are widely distributed. Besides arboviruses, mosquitoes are also vectors of other pathogens of significant public health concern, including protozoans, filarial parasites and to a lesser extent bacteria. Vector control measures help reduce the spread and impact of these diseases. In this framework, the Medical Component of the Belgian Armed Forces has launched a pilot project to investigate the Culicidae biodiversity at foreign sites where the Belgian Army is deployed. Since the project started, adult specimens were collected on military bases in Jordan, Gabon and Mali. A comprehensive list of mosquito species occurring in each of these countries was established based on the available publications and reports, and available DNA-sequences deposited on online reference databases (BOLD and GenBank) were evaluated for their usefulness in identifying mosquito vectors by DNA barcoding. In total, 178 specimens were identified using DNA-based methods. Among these, important disease vectors were identified, including *Aedes aegypti*, *Aedes albopictus*, *Culex quinquefasciatus*, *Culex pipiens*, *Culex perexiguus*, *Anopheles coluzzii* and *Anopheles gambiae*. Some of these species are known to transmit the West Nile and the Rift Valley fever viruses in Africa, while others are important vectors for *Wuchereria bancrofti* (causing lymphatic filariasis) as well as for the yellow and dengue fever viruses in areas where the mosquitoes were collected. Besides providing essential information to set up mosquito control measures (preventive or active), this biodiversity study emphasizes the importance of treating army equipment appropriately when returning to Belgium in order to avoid unintentional introductions of exotic mosquito disease vectors.

DNA-barcoding: an efficient tool for rapid identification of native and exotic mosquito species (Diptera: Culicidae) intercepted in Belgium

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Due to international trade, tourism, and climate/ecological changes, mosquito species are transported, or disperse, get introduced and eventually become established in new territories. Since August 2017, a nationwide three year monitoring project started in Belgium (MEMO: Monitoring of Exotic Mosquitoes). The project is funded by the Belgian federal authorities and the federated entities, and aims at detecting and evaluating the occurrence of exotic mosquito species (EMS) in Belgium. Monitoring activities started at 23 points of entry (PoE) using adult trapping, as well as egg and larval sampling. Whenever potential EMS are suspected based on morphological identifications, samples are identified using DNA-based techniques as molecular confirmation. Additionally, 5% of the overall annual yield (e.g., about 300 specimens out of approximatively 6,000 in 2017) is also identified using DNA-based techniques to verify morphological identifications as a quality control measure. Fifteen native species (or complexes) of five genera were identified and confirmed by DNA-data. Additionally, all intercepted EMS could be distinguished from the native Culicidae. Presently, four EMS were collected once or multiple times at one or multiple PoEs: *Aedes koreicus*; *Aedes japonicus*; *Aedes albopictus;* and *Anopheles pharoensis*. In 2018, *Aedes albopictus* was intercepted at five PoEs, at three of which for the first time. EMS seem to enter Belgium effectively through different introduction pathways: via lucky bamboo and tyre transport, ground traffic, but also possibly by natural dispersal. In this perspective, MEMO will contribute to a better understanding of the introduction process of the different exotic species by providing information on their status (introduction, establishment or spread) and seasonality.

DNA barcoding and identification of terrestrial gastropods of parasitological concern for animals in Greece

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Recently, terrestrial snails and slugs that may act as intermediate hosts of parasites infecting humans and pets, have gained special attention because several of the parasites they transmit are spreading among domestic and wildlife populations throughout Europe. In order to survey the prevalence and expansion of these parasites it is necessary to identify their intermediate snail and slug hosts as accurately as possible. Yet, studying the presence of parasites in their intermediate hosts requires a destructive approach by which a morphological or anatomical identification of the snails and slugs becomes difficult, if not impossible. Moreover, also juvenile gastropods, which often lack their distinctive species-specific characters, must be identified. Hence for such cases, DNA barcoding offers an alternative tool to obtain reliable identifications. Against this background, the Barcoding facility for Organisms and tissues of Policy Concern (BopCo) is applying DNA barcoding to identify snails and slugs in an epidemiological study of nematode parasites in terrestrial gastropod populations in Greece. Snails and slugs were collected in areas were the presence of these nematode parasites was expected. DNA barcoding based on mitochondrial COI (cytochrome c oxidase subunit I) and 16S ribosomal RNA sequences was applied to gastropods that could not be identified on morphological and morphometric characteristics. Using BLAST, the sequences were compared to reference sequences available in Genbank and BOLD. In this way the snails and slugs were identified as *Eobania vermiculata*, *Helix lucorum, Cornu aspersum*, *Ambigolimax valentianus*, *Limax* cf. *conemenosi* and *Tandonia* cf. *sowerbyi*, i.e. all common and widespread species in Greece, except for *Ambigolimax valentianus,* which is probably a recent introduction. All these species are known to be efficient colonizers of new areas and as such have been introduced in several parts of Europe. This could be an important factor underlying the expansion of the nematode parasites they carry.

Connectivity of the big blue octopus (*Octopus cyanea,* Gray 1849) between the eastern and western coast of Madagascar

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Among the coastal communities in Madagascar the fishery for *Octopus cyanea* in coral reefs is one of the three most important activities in term of economic value. In the coastal communities of Madagascar there are few alternatives to marine resource extraction. This economic exploitation of *O. cyanea* has increased the local value of the fishery and transformed a formerly traditional fishery predestined to local consumption into an export-driven fishery. This dramatic increase of fishery raised rates of exploitation and concerns over sustainability. A way to protect this species against overfishing and manage vulnerable marine ecosystems is to introduce marine protected areas (MPAs). An important factor that should be considered when implying MPA networks is gene flow among populations along the coast of Madagascar. *Octopus cyanea* is fished mostly in shallow reefs among the coast, where it is vulnerable and an easy prey for fishers. It is only when female individuals reach maturity that they migrate from shallow reef into deeper subtidal areas for spawning. The planktonic larvae move into the water column for one to two months, and dispersal is thought to be wide ranging. Larvae are thought to travel up to several hundred kilometres with ocean currents. These findings predict a high connectivity among different populations of *O. cyanea.* Connectivity can be determined using genetic markers such as mitochondrial DNA and microsatellites. In this study, the population genetic structure of *O. cyanea* will be studied in order to investigate connectivity among populations, because such information is crucial for the setup of MPAs along the coastal areas of Madagascar. Cytochrome C oxidase subunit-1 (COI) will be used as DNA marker. DNA barcoding will be used to confirm the identification of *O. cyanea* individuals in the samples. Samples from five different sites from the west, north and east coast of Madagascar will be analysed. Samples from the western and eastern coast will be compared with each other and with the samples from the northern coast of the island. In total 88 tissue samples of individuals of *Octopus cyanea* were collected at five different sites. They were preserved in at least 95% ethanol, after collection in field. DNA was extracted using a E.Z.N.A.® Tissue DNA kit. PCR will be conducted using universal primer and COI will be used to analyse the genetic difference between the specimens found on each side of the island. The aim of this study is to provide an answer on the following questions: Is there gene flow between populations on the west and east coast of Madagascar? It is expected that the result of this study will provide baseline data for the conservation and management of *O. cyanea*.

The ichthyofauna of the Lake Edward system

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The Lake Edward system encompasses lakes Edward and George, which are connected through the Kazinga channel, and several inflowing rivers. The fisheries of these lakes are very productive and sustains the livelihoods of the surrounding communities, though a collapse was observed over the last decades. The HIPE project (http://www.co2.ulg.ac.be/hipe/) aims to gain a better understanding of the ecosystem functioning of the catchment. To achieve this, a multidisciplinary approach is followed combining biology, ecology, biogeochemistry, and socio-economics. Within this framework, the entire ichthyofaunal diversity of the system, and the biology of the economically most important fish species are being investigated. We compiled a list of 63 valid species from the Lake Edward system, consisting of 32 non-haplochromine species and 31 haplochromine cichlids. The former includes some introduced species such as *Coptodon zillii* and *Poecilia reticulata*. The latter strongly underestimates the number of *Haplochromis* species as currently 56 presumed species are recognized. Hitherto, 14 of the undescribed *Haplochromis* species were investigated in-depth by morphometric studies. A DNA barcoding study (COI; mtDNA) was executed, covering 27 of the 32 non-haplochromine and 33 of the 56 haplochromine species. Possible cryptic species were revealed in the genera *Labeo, Labeobarbus*, and *Enteromius*. In contrast, all *Haplochromis* species included in the study clustered together, highlighting the young age of the radiation. The diet of the six economically most important fish species is being investigated through stomach contents and stable isotope analyses. Preliminary results provide first insights into their trophic ecologies. All species, regardless of their food preferences, appear to be opportunistic to a certain extent, which is illustrated by many stomachs containing a large variety of prey items in low proportions. So far, no significant influence of seasonality was observed in the diet of these fishes, and an ontogenetic shift was observed for *Labeobarbus altianalis*.

Genetic monitoring of green frogs in Luxembourg using a NGS-based method

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Two species of green frogs are common in the Grand Duchy of Luxembourg, i.e. the pool frog *Pelophylax lessonae* and the edible frog *P.* kl. *esculentus*. Due to their complex mating system, which includes kleptogenesis and polyploidization, most *P.* kl. *esculentus* populations require the presence of *P. lessonae* for successful reproduction, while the reproduction of *P. lessonae* is independent from *P.* kl. *esculentus*. Although both species are difficult to distinguish morphologically and the standard barcoding approach cannot be applied to this species complex because of ongoing hybridisation, both are target species of the EU Habitats Directive (92/43/EEC) and thus have to be individually monitored. Here we apply ddRAD-sequencing, a reduced representation based next-generation sequencing (NGS) method resulting in the parallel generation of hundreds of genetic markers, with the aim to characterise populations of green frogs sampled over complete Luxembourg. Beside of the distribution of each of the two species, the ddRAD-data will help us to get insights into the conservation status of the different populations (e.g. via their genetic diversity and connectivity).

Temperature-induced changes in the fatty acid profile of the benthic copepod *Platychelipus littoralis* of the Westerschelde estuary

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The latest climate change predictions quantify the expected temperature increase in different parts of the world. These temperature changes will have a disproportionally higher impact on coastal ecosystems, such as estuaries. In these estuaries, benthic harpacticoid copepods (Crustacea, Copepoda) play a pivotal role at the base of the food web as they are the main consumers of primary producers such as diatoms and serve as a food source for higher trophic levels like fish. Their high levels of fatty acids (e.g. omega-3, omega-6), are essential for the maintenance of physiological functions in many organisms in this food web. In view of their role in the marine food web, balanced fatty acid profiles in these copepods are indicators for a healthy and stable ecosystem and any changes in these profiles are expected to cascade through the food web. In this study, responses to temperature of the abundant harpacticoid copepod *Platychelipus littoralis* from the Westerschelde estuary (The Netherlands) was studied. Temperatures in this temperate estuary are highly variable throughout the year. We expect that with changing temperatures, the fatty acid content of these copepods will also change to adapt to new environmental parameters. In controlled lab experiments, *P. littoralis* was subjected to different temperature treatments in accordance to the climate change predictions for the North Sea. Our first results indicate that with increased temperatures, concentrations of essential fatty acids such as EPA and DHA decrease in P. *littoralis*. This can induce unfavorable effects on the higher trophic levels as they rely on these primary consumers for the majority of their fatty acid uptake.

Effectiveness of management agreements on farmland birds (nesting place, food and breeding success)

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Population of farmland birds have declined severely during the past decades as a result of habitat loss and fragmentation following the intensification of agriculture. However, the response of different species to various form of habitat degradation is not similar. For example, populations of certain species even show positive trends after the creation of artificial feeding- and breeding areas when they are well placed within the proper environmental context. To protect farmland birds from extinction, the VLM (Flemish Land Agency) attempts to come to agreements with farmers to change their management and to create set-aside areas for farmland birds. Two major types of agreements can be made, the first being the creation of winter crops, such as barley, to supply winter food. The second being the creation of set-aside areas to provide suitable breeding and foraging sites during the breeding season. The goal of our study is to assess whether such agreements are effective in fulfilling farmland birds' needs. To achieve this, we will investigate the spatial and habitat use of four target species: Skylark *Alauda arvensis*, Yellow wagtail *Motacilla flava*, Yellowhammer *Emberiza citronella* and Grey Partridge *Perdix perdix*. In the upcoming years, we will therefore search for nests, assess food availability and track the whereabouts of these species using radio- and GPS-telemetry. Ultimately, we anticipate to provide guidelines to optimize the agri-environmental management that will improve the survival of farmland birds.

Hyperthermic stress resistance of Belgian bumblebee species

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Global warming can result in gradual changes with modifications of main climatic parameters (humidity, temperature, etc.) but also in an increase in the frequency of extreme and localized weather events (e.g. heat waves). These heat waves are hyperthermic stress which have been associated with direct physiological perturbations, which are suspected to dramatically increase insect mortality. Many insect pollinators are experiencing a global decline of their populations. Climate change including heat waves have been pointed out as one of the main drivers of pollinator decline. Here, we assessed the hyperthermic stress resistance through their time before heat stupor (THS) at 40°C of ten Belgian species including sub-boreal species particularly threatened by climate change. We also investigated ethological aspects to define the behavioural time-line to heat stupor. Our results show that heat stress resistance is significantly different among species. Our results highlighted a heat resistance gradient: the heat stress resistance of sub-boreal species is weaker than the hyperthermic resistance of widespread and ubiquitous species.

Molecular Analysis of *Anopheles gambiae* complex mosquito from climatic and cotton areas of Burkina Faso

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Malaria vectors of the *Anopheles gambiae complex* are made up seven species that are stable and are highly efficient vectors. To investigate molecular analayis ,we collected, adult female *An. gambiae complex* from humans residential areas in Burkina Faso, by hand using Prokopack aspirator between August at October 2017. Species were identified by the polymerase chain reaction (PCR) method to the intergenic space (IGS) of ribosomal DNA (rDNA). In our study, *An. gambiae s.s* (more than 90%) and *An. arabiensis*(less than 10%), two subspecies of *Anopheles gambiae complex*, have been found in all climatic zones as well as in cotton and cotton-free zones. Hybrids M/S form of *An. gambiae* and *Arabiensis*/M form as new hybrids, also found. This result have important implications for the control of malaria.

Saturday 15th December

08:00 Registration **room Okapi 2**

09:00 Keynote talk by Hilde Eggermont (Biodiversity Platform Belgium – RIBNS) - “IPBES: strengthening the science - policy interface in the face of global change.” **Room Gorilla 1**

10:00	**Parallel session 1**	**Parallel session 2**	**Parallel session 3**	**Parallel session 4**
	GENERAL 1 (Morphology, Ethology, Miscellaneous)	**Zoology in Anthropocene**	**GENERAL 2 (Genetics, Phylogeny, phylogeography, Miscellaneous)**	**GENERAL 3 (Ecotoxicology, Physiology , Molecular mechanism)**
room	**Gorilla 1**	**Gorilla 2**	**Gorilla 3**	**Gorilla 4**
10:00	FLEUREN 1	ZIZZARI 19	*GRESHAM 38	**BEGHIN 57
10:15		MULLER 20	**CHAPELLE 39	BIJNENS 58
10:30	FREDERICH 2	VISSER 21	VAN STEENBERGE 40	DE MEYER 59
10:45	*LOURTIE 3		DA SILVA 41	**THORE 60
11:00	VAN HOUTVEN 4	**DUSSENNE 22	BRUET 42	DELROISSE 61
11:15	**GILLET 5	DE BRUYN 23	GALBUSERA 43	
11:30	**MAC LAREN 6	GUILLAUMOT 24	VERHEYE 44	**DUCHATELET 62
11:45	**LUGER 7	HEMERIK 25		*JANSSEN 63
12:00	**KAASHOEK 8	**BLANCHARD 26	**ZHANG 45	**RAICK 64
12:15	INDEKEU 9	**MWAIJENGO 27	VANHOVE 46	**MORIS 65
12:30	lunch			

	GENERAL 1 (continued)	**Zoology in Anthropocene (continued)**	**GENERAL 2 (Continued) & COST action DNAqua-Net**	**Zoology in Anthropocene (continued)**
room	**Gorilla 1**	**Gorilla 2**	**Gorilla 3**	**Gorilla 4**
14:00	*FINET 10	DEKEUKELEIRE 28	**HAMMOUD 53	**SERTEYN 66
14:15	*CARVALHO 11	**RUTTEN 29	KOCHZIUS 47	**VASTRADE 67
14:30	*VERMEYLEN 12	**WEVERS 30	MARDULYN 50	PADILLA 68
14:45	ERNST 13	GAILLY 31	**CUYPERS 51	**LEJEUNE 69
15:00	**OGER 14	MÜLLER 32	FRANTZ 49	*LAMERIS 70
			DNAqua-Net SESSION	
15:15	*VAN MEER 15	**MARTINET 33	WEIGAND A 52	STURARO 71
15:30	*STEEDAM 16	**NOËL 34	MACHER 54	*VAN DEN BERG 72
15:45	**DE MEESTER 17	VAN DER HULST 35	TEIXEIRA 48	**ZHOU 73
16:00	GOLDSBOROUGH 18	HUGé 36	WEIGAND H 56	DECLERCK 74
16:15	*BAAN 75	DE KEYSER 37		
16:30	Poster session (rooms Okapi 2 & 3)			
17:30	KETS awards and KDZS prize presentations			
18:30	ZOOLOGY 2018 end ceremony			

*: master prize **: PhD prize