The Benelux Zoology Congress 2024

Celebrating biodiversity between land and sea

Abstract Book

December 12 – 13, 2024

Organised by the University of Mons, Belgium

Palais des congrès de Mons, Avenue Mélina Mercourie 9, 7000 Mons, Belgium

Contact: UMONS.Zoology.2024@gmail.com

Web site: rbzs.be/zoology-2024/

BZS
Royal Belgian Zoological Society

UMONS
University of Mons

fnrs
LA LIBERTÉ DE CHERCHER

The Company of Biologists

biosciences
INSTITUT DE RECHERCHE EN BIOSCIENCES
DE L'UMONS

ZOOLOGY 2024

Celebrating biodiversity between land and sea

Mons - Belgium

12 THU ▶ **13** FRI

December 2024

rbzs.be/zoology-2024/

Plenary speakers

Nicola Nadeau
University of Sheffield
Evolutionary biology of *Heliconius* butterflies

Peter Ladurner
University of Innsbruck
Stem cell biology, reproduction and bioadhesion of flatworms

Scan me!

fnrs LA LIBERTÉ DE CHERCHER
biosciences INSTITUT DE RECHERCHE EN BIOSCIENCES DE L'UMONS
UMONS Université de Mons
RBZS Royal Belgian Zoological Society
The Company of Biologists

Table of Contents

Welcome Words

Dear colleagues, dear friends of zoology,

It is with great pleasure that we welcome you to **Zoology 2024** organized at the University of Mons (UMONS) in collaboration with the Royal Belgian Zoological Society (RBZS). This annual gathering, held this year in Mons, celebrates our shared passion for the study of animal diversity and the scientific advances shaping our understanding of the natural world.

This edition of **Zoology 2024** brings together over 200 attendees from various scientific backgrounds and institutions and promises to be a true celebration of zoological research. We will be delighted to decern like every year two prizes for best oral and poster communications. The rich and varied program features **18 oral sessions**, including **78 oral communications**, addressing highly diverse topics:

- **Animal behavior**
- **Biomechanics & Morphology**
- **Biotic interactions**
- **Conservation biology**
- **Conservation genetics**
- **Distribution & Habitat**
- **Ecology & Evolution**
- **Ecotoxicology**
- **Evolutionary Biology**
- **Adaptative physiology**
- **Global change ecology**
- **Paleobiology**
- **Stress**
- **Taxonomy & Species diversity**
- **Trophic ecology**

We are also delighted to present **73 scientific posters**, showcasing a great variety of topics within our discipline. These contributions highlight the health of the Benelux zoological community and its commitment to fields like conservation, ecology, evolution, and many other fundamental areas.

We extend our heartfelt thanks to our partners and financial supporters (FNRS, UMONS, BioSciences Institute of the UMONS, Company of Biologists), without whom this event would not be possible. We are especially grateful to Extension UMONS and the MUMONS that both contributed to the organization of this conference.

We hope this conference provides each of you with opportunities to share ideas, forge new collaborations, and nourish your scientific curiosity. We wish you fruitful discussions and a memorable experience at **Zoology 2024**.

With our deepest appreciation and best wishes for this event,

Denis Michez & Jérôme Delroisse,

On behalf of the Zoology 2024 Organizing Committee

Organizing and scientific Committees

The organization of such an event is only possible thanks to the dedication of a group of generous colleagues taking their time. Here we would like to acknowledge the people who made this symposium 2024 possible in Mons.

Organisation: Guillaume Caulier, Guillaume Ghisbain, Noé Wambreuse, Kévin Tougeron, Leandro Smacchia, Estelle Bossiroy, Lisa Mussoi, Antoine Flandroit, Patrick Flammang, Gilles Lepoint, Justine Dewaele, Youri Nonclercq, Florian Cosa, Sara Reverté, Paolo Rosa, Christophe Mallet, Natasha De Manincor, Maxence Gerard, Dimitri Evrard, Laetitia Verdy, Clément Tourbez, William Fiordaliso, Simone Flaminio, Wendy Bayaert, Némo Lemaire, Killian Verhoeye. Coordination: Denis Michez, Jérôme Delroisse and Fanny Lallemand.

Reviewers for the abstracts: Ahlam Sentil, Alexandre Barraud, Antoine Gekière, Bruno Frederich, Christophe Mallet, Christophe Rémy, Clément Tourbez, David Gillan, Diego Cejas, Elif Kardas, Elise Hennebert, Frederic Silvestre, Gilles Lepoint, Guillaume Caulier, Guillaume Ghisbain, Igor Eeckhaut, Jérôme Delroisse, Kévin Tougeron, Kimberley Przybyla, Maxence Gerard, Nastasha De Manincor, Paolo Rosa, Patrick Flammang, Sara Reverté, Valentin Fisher. Coordination: Denis Michez.

Evaluation for the pictures: Yvan Barbier, Denis Michez, Kévin Tougeron, Sara Reverté, Patrick Flammang, Jérôme Delroisse, Guillaume Ghisbain, Clément Tourbez, Christophe Mallet, Diego Cejas. Coordination: Paolo Rosa and Alexia Lourtie.

Social event at MUMONS: Noé Wambreuse, Antoine Flandroit, Benjamin Decoux, Jérôme Delroisse, Estelle Bossiroy, Youri Nonclerck, Paolo Rosa, Clément Tourbez, Sébastien Gennaux. Coordination: Lisa Mussoi, Francesco Lobue and Alexia Lourtie.

Conference Schedule

PROGRAM OF THE CONFERENCE ZOOLOGY 2024

	Thursday 12 December 2024			**Friday 13 December 2024**		
08:15 - 08:45	Registration					
	ROOM 1			ROOM 1		
08:45 - 09:00	Welcome: Prof. Ruddy Wattiez, Prof. Denis Michez			Welcome		
09:00 - 10:00	Plenary: Prof. Nicola Nadeau, introduction by Prof. Denis Michez			Plenary: Prof. Peter Ladurner, introduction by Prof. Patrick Flammang		
	ROOM 1	ROOM 2	ROOM 3	ROOM 1	ROOM 2	ROOM 3
10:00 - 11:30	Session 1: CONSERVATION GENETICS (4 presentations)	Session 2: ADAPTIVE PHYSIOLOGY (4 presentations)	Session 3: GLOBAL CHANGE ECOLOGY I (4 presentations)	Session 10: EVOLUTIONARY BIOLOGY (4 presentations)	Session 11: BIOMECHANICS & MORPHOLOGY II (4 presentations)	Session 12: GLOBAL CHANGE ECOLOGY II (3 presentations)
11:00 - 11:30	Coffee break (11h00-11h30)					
	ROOM 1			ROOM 1	ROOM 2	ROOM 3
11:30 - 11:45	RBZS/Kets Prize winner announcement, KNDV Prize winner announcement			Session 13: STRESS BIOLOGY (4 presentations)	Session 14: TAXONOMY & SPECIES DIVERSITY I (4 presentations)	Session 15: PALEOBIOLOGY (3 presentations)
11:45 - 12:00	Kets Jury Prize					
12:00 - 12:15	Clément Tourbez (Ket Public Prize)					
12:15 - 12:30	KNDV Prize					
12:30 - 14:00	Lunch break (12h30-14h)					
	ROOM 1	ROOM 2	ROOM 3	ROOM 1	ROOM 2	ROOM 3
14:00 - 15:15	Session 4: ECOTOXICOLOGY (5 presentations)	Session 5: DISTRIBUTION & HABITAT (5 presentations)	Session 6: ANIMAL BEHAVIOUR (5 presentations)	Session 16: ECOLOGY & EVOLUTION (5 presentations)	Session 17: TAXONOMY & SPECIES DIVERSITY II (5 presentations)	Session 18: TROPHIC ECOLOGY (5 presentations)
15:15 - 15:45	Coffee break (15h15-15h45)					
	ROOM 1	ROOM 2	ROOM 3	Entrance		
15:45 - 17:00	Session 7: BIOTIC INTERACTIONS (5 presentations)	Session 8: CONSERVATION BIOLOGY (5 presentations)	Session 9: BIOMECHANICS & MORPHOLOGY I (4 presentations)	Poster session 2 (ENTRANCE)		
17:00 - 18:30	Poster session 1 (ENTRANCE)					
17:15 - 17:30				Prize + Next conference Announcement + Closure statements (ROOM 1)		
18:30 - 19:30	Social event at MUMONS *(for all registered participants)*					
19:30 - 20:15	Dinner at Warocqué *(for all registered participants)*					

Oral Communications

Program of the 12th of December 2024

Plenary Session 1, Room 1, 9h-10h

Chairperson: Denis MICHEZ

09:00-10:00, Nicola NADEAU: GENETIC AND DEVELOPMENTAL CONTROL OF IRIDESCENT STRUCTURAL COLOUR IN BUTTERFLIES

Session 1, CONSERVATION GENETICS, Room 1, 10h-11h

Chairperson: Diego CEJAS

10:00-10:15, Stephen BERGACKER: THE PHYLOGEOGRAPHY OF PELAGIC EAGLE RAYS (AETOBATIDAE) – GENETIC PATTERNS AND COASTAL ECOSYSTEM DEPENDENCIES.

10:15-10:30, Pascal HABLUTZEL: GENERATING FAIR AND OPEN BIODIVERSITY DATA IN THE FIELD: A CASE STUDY ON BOLIVIAN FISH DIVERSITY

10:30-10:45, Marc KOCHZIUS: CONNECTIVITY OF CORAL REEFS AND MANGROVES IN THE INDIAN OCEAN

10:45-11:00, Michaël MEEUS: GENETIC DIVERSITY ACROSS THE CAT FAMILY (FELIDAE)

Session 2, ADAPTIVE PHYSIOLOGY, Room 2, 10h-11h

Chairperson: Jérôme DELROISSE

10:00-10:15, Wendy-Shirley BAYAERT: CONTROLLING LIGHT IN A LUMINOUS ECHINODERM: FROM ENVIRONMENTAL STIMULI TO LIGHT EMISSION

10:15-10:30, Justine BÉLIK: DEVELOPMENT OF AN EPIGENETIC CLOCK IN A SELF-FERTILIZING VERTEBRATE SPECIES

10:30-10:45, Sarah CORNET: IDENTIFYING TRANSCRIPTOMIC BIAS ACROSS DEVELOPMENTAL SHIFTS IN INSECTS

10:45-11:00, Youri NONCLERCQ: DIVERSITY OF OPSINS AND PHOTOSENSORY STRUCTURES IN SEA CUCUMBERS (HOLOTHUROIDEA, ECHINODERMATA)

Session 3, GLOBAL CHANGE ECOLOGY I, Room 3, 10h-11h

Chairperson: Guillaume GHISBAIN

10:00-10:15, Max DEVIS: VARIED RESPONSES TO URBANISATION IN ABUNDANCE AND BODY SIZE AMONG CLOSELY-RELATED SOCIAL WASPS (VESPINAE) IN BRUSSELS, BELGIUM

10:15-10:30, William FIORDALISO: HIDING INEQUALITIES BEHIND RICHNESS: HOW URBAN LANDSCAPES SHAPE WILD BEE COMMUNITIES

10:30-10:45, Guillaume GHISBAIN: THE NEW EUROPEAN RED LIST OF BEES

10:45-11:00, Mira VAN DEN BROECK: STUCK IN THE SPOTLIGHT: GLOW-WORM LARVAE SLOW DOWN UNDER ARTIFICIAL LIGHT

RBZS and KNDV Award nominee Session, Room 1

Chairperson: Jérôme DELROISSE

12:00-12h15, Clément TOURBEZ: EFFECT OF HEATHER FLAVONOIDS ON THE BUFF-TAILED BUMBLEBEE

12h15-12h30, KNDV Prize nominee: *Awaiting confirmation*

Session 4, ECOTOXICOLOGY, Room 1, 14h-15h15

Chairperson: Justine DEWAELE

14:00-14:15, Mélusine CHEVALIER: ADAPTATION TO ENVIRONMENTAL STRESS IN A SELF-FERTILIZING VERTEBRATE SPECIES (KRYPTOLEBIAS MARMORATUS)

14:15-14:30, Maxime DEBOURCES: EVALUATION OF THE POTENTIAL NEUROPROTECTIVE EFFECTS OF GARDENIN A ON PARKINSONIAN SYMPTOMS IN NOTHOBRANCHIUS FURZERI EXPOSED TO BIFENTHRIN

14:30-14:45, Justine DEWAELE: EFFECTS OF DNBP AND DEHP ON THE SURVIVAL AND IMMUNITY OF BOMBUS TERRESTRIS WORKERS

14:45-15:00, Luca DORIO & Manon Fievet: INTERSPECIFIC VARIATION IN THE EFFECT OF PESTICIDES ON WILD POLLINATORS

15:00-15:15, Imke VAN DINGENEN: THE THYROID HORMONE SYSTEM DISRUPTING POTENTIAL OF RESORCINOL IN FISH

Session 5, DISTRIBUTION & HABITAT, Room 2, 14h-15h15

Chairperson: Maxence GERARD

14:00-14:15, Clément DURET: CLIMATE CHANGE THREATS AND CONSERVATION CHALLENGES FOR THE ENDANGERED JAPANESE GIANT SALAMANDER (ANDRIAS JAPONICUS)

14:15-14:30, Mathilde FOUCTEAU: BREEDING HABITAT SELECTION AND MORPHOLOGY OF THE GREAT CRESTED NEWT (TRITURUS CRISTATUS), THE MARBLED NEWT (TRITURUS MARMORATUS), AND THEIR HYBRIDS AT THE SOUTHERN EDGE OF THEIR CONTACT ZONE

14:30-14:45, Sarah JORISSEN: ENERGIZED AND EFFICIENT: HOW MITOCHONDRIA AND DIGESTIVE EFFICIENCY DRIVE FASTER PACE-OF-LIFE IN A RANGE-EXPANDING SPECIES

14:45-15:00, Gilles LEPOINT: LENS ISOTOPIC COMPOSITIONS AS A TRACER OF CORAL FISH ECOLOGICAL ONTOGENY

15:00-15:15, Helga RAVELOHASINA: HABITAT-USE OF THE RABBITFISH, SIGANUS SUTOR AT THE GREAT REEF OF TOLIARA (SW MADAGASCAR)

Session 6, ANIMAL BEHAVIOUR, Room 3, 14h-15h15

Chairperson: Guillaume CAULIER

14:00-14:15, Tim ANDRIES: FEEDING PERFORMANCE, BEAK KINEMATICS AND SEED HANDLING SKILLS CHANGE WITH AGE IN A GRANIVOROUS SONGBIRD

14:15-14:30, Siebe INDESTEGE: CAMERA TRAP SAMPLING DESIGN MODIFICATIONS IN LONG-TERM ECOLOGICAL MONITORING: IMPLICATIONS ON WILDLIFE ACTIVITY ESTIMATION

14:30-14:45, Wim KUYPERS: THE IMPACT OF DIFFERENT RECREATION TYPES ON SEASONAL SPATIOTEMPORAL BEHAVIOUR OF WILDLIFE – APPLICATION TO A SMALL, HIGHLY VISITED NATIONAL PARK

14:45-15:00, Salomé LABOURY: INDIVIDUAL ACOUSTIC SIGNATURES IN THE DAMSELFISH DASCYLLUS ALBISELLA?

15:00-15:15, Sarah SCHMIDLIN: OYSTERS AS A MODEL ORGANISM FOR SETTLEMENT OF REEF-BUILDING ORGANISMS IN RESPONSE TO COMPLEX SENSORY LANDSCAPES OF CHEMICAL, TACTILE, AND SOUND CUES

Session 7, BIOTIC INTERACTIONS, Room 1, 15h45-17h

Chairperson: Kévin TOUGERON

15:45-16:00, Karen BISSCHOP: THE ROLE OF THE MICROBIOME RELATIVE TO THE GENOME FOR NICHE WIDTH

16:00-16:15, Andrea CHACON-HURTADO: PERFECT CRIME: ENTOMOPATHOGENIC NEMATODES IMPACT ON THE VOLATILE EMISSION PROFILE OF INSECT HOSTS

16:15-16:30, Lisa MUSSOÏ: MIMETIC CRUSTACEANS: PIGMENTATION CHANGES AND CHEMICAL INVESTIGATION OF SCLERACTINIAN ECTOSYMBIONTS

16:30-16:45, Martina TOPIC: SYMBIOTIC INTERACTIONS CHALLENGED BY ENVIRONMENTAL STRESS IN AQUATIC TRANSITIONAL HABITATS

16:45-17:00, Kévin TOUGERON: GLOBAL MODELS OF HERBIVORY VARIABILITY: DATA FROM THE HERBVAR PROJECT

Session 8, CONSERVATION BIOLOGY, Room 2, 15h45-17h

Chairperson: Denis MICHEZ

15:45-16:00, Rémi SANTERRE & Jordan BENREZKALLAH: POPULATION ASSESSMENT AND FORAGING ECOLOGY OF THE RARE SOLITARY BEE MEGACHILE CYPRICOLA ON THE ISLAND OF CYPRUS

16:00-16:15, Denis MICHEZ: EUROPEAN INITIATIVES FOR POLLINATOR MONITORING

16:15-16:30, Ahlam SENTIL: RELATION BETWEEN HONEYBEE ABUNDANCE AND WILD BEES COMMUNITIES IN MOROCCAN AGRO-ECOSYSTEMS

16:30-16:45, Imke TOMSIN: EVALUATING CONSERVATION EFFORTS FOR THE EUROPEAN HAMSTER: INSIGHTS FROM PREDICTIVE MODELLING

16:45-17:00, Marie VERHEYE: INTEGRATING GENETIC CONNECTIVITY AND LOCAL ADAPTATION IN EFFECTIVE MARINE PROTECTED AREA DESIGN: A CASE STUDY ON SOUTHERN OCEAN TREMATOMUS FISHES

Session 9, BIOMECHANICS & MORPHOLOGY I, Room 3, 15h45-16h45

Chairperson: Christophe MALLET

15:45-16:00, Romane FREY: HIT ME (SWIM) BLADDER ONE MORE TIME

16:00-16:15, Arthur VAN DAMME: LINKING FISH ECOLOGY TO OTOLITH DIVERSITY AT A BROAD PHYLOGENETIC SCALE

16:15-16:30, Anastasia SELINI: AN OPPORTUNE MOMENT: INVESTIGATING INERTIAL PROPERTIES OF THE DISTAL LIMB OF HORSES THROUGH AN ICONIC EVOLUTIONARY TRANSITION

16:30-16:45, Christophe MALLET: SHAPE VARIATION IN THE PATELLA OF MODERN PERISSODACTYLS: DECIPHERING THE INFLUENCE OF EVOLUTIONARY LEGACY AND FUNCTIONAL CONSTRAINTS ON SESAMOID BONES

Program of the 13rd of December 2024

Plenary Session 2, Room 1, 9h-10h

Chairperson: Patrick Flammang

09:00-10:00, Peter LADURNER: FLATWORMS AS MODEL SYSTEMS FOR STEM CELL BIOLOGY, REPRODUCTION, AND BIOADHESION

Session 10, EVOLUTIONARY BIOLOGY, Room 1, 10h-11h

Chairperson: Jérôme DELROISSE

10:00-10:15, Jens BOYEN: EVOLUTION OF POLYUNSATURATED FATTY ACID BIOSYNTHESIS IN COPEPODS

10:15-10:30, Michaël NICOLAI: THE FUNCTION AND EVOLUTION OF IRIDESCENT COLOURATION IN BIRDS

10:30-10:45, Maria MADRID-RESTREPO: UNRAVELING CHROMOSOMAL INVERSIONS AND THEIR EVOLUTIONARY DANCE IN A WING POLYMORPHIC BEETLE

10:45-11:00, Jérôme DELROISSE: NEW INSIGHTS INTO THE EVOLUTION OF BIOLUMINESCENCE IN SEA PENS (PENNATULOIDEA, CNIDARIA)

<u>Session 11, BIOMECHANICS & MORPHOLOGY II, Room 2, 10h-11h</u>

Chairperson: Patrick FLAMMANG

10:00-10:15, Gerben DEBRUYN: WHAT, IF ANYTHING, IS A HARD EGG? MECHANICAL PROPERTIES OF REPTILE EGGSHELLS AND THEIR ROLE IN INSPIRING NEW MATERIALS

10:15-10:30, Louise ECHE: STUDY OF THE SOUND-PRODUCING APPARATUS OF TWO CARIBBEAN BOXFISHES, LACTOPHRYS TRIQUETER AND ACANTHOSTRACION POLYGONIUS

10:30-10:45, Danial FOROUHAR: HOW SEAHORSES GOT SACKED: STRUCTURAL AND FUNCTIONAL ANALYSIS OF THE TAIL MUSCLE SAC IN A PREHENSILE TAIL

10:45-11:00, Cas JORISSEN: WHY NOT STRONG AND FAST? THE BIOMECHANICS OF HIGH-FREQUENCY FINGER OSCILLATIONS

<u>Session 12, GLOBAL CHANGE ECOLOGY II, Room 3, 10h-10h45</u>

Chairperson: Clément TOURBEZ

10:00-10:15, Florian COSA: INVASION IN THE ROCKS: HOW BUDDLEJA DAVIDII DISRUPTS PLANT AND POLLINATOR COMMUNITIES IN QUARRY ECOSYSTEMS

10:15-10:30, Jessica ODY: MELAMPUS JAUMEI: THE METABOLOMIC ANALYSIS OF A PULMONATED GASTROPOD TO REVEAL THE MECHANISMS OF ADAPTATION TO ENVIRONMENTAL CHANGES

10:30-10:45, Léa POIRIER: MICROPLASTICS ON THE MENU: EXPLORING INTERACTIONS BETWEEN TWO MOSQUITO SPECIES AND MICROPLASTICS

<u>Session 13, STRESS BIOLOGY, Room 1, 11h30-12h30</u>

Chairperson: Noé WAMBREUSE

11:30-11:45, Benjamin DECOUX: TOO MUCH STRESS? TAKE SOME REST! CHARACTERIZATION OF DORMANCY IN THE SEA SPIDER AMMOTHEA HILGENDORFI, A THRIVING INVASIVE SPECIES IN THE NORTH SEA

11:45-12:00, Martijn HELEVEN: THE REDOX-GUIDED BLUEPRINT OF REGENERATION: LESSONS FROM PLANARIANS

12:00-12:15, Ellen VANDEPUTTE: IMPACT OF ENDOCRINE DISRUPTION ON THE NUMBER OF HAIR CELLS IN NEUROMASTS OF THE LATERAL LINE ORGAN OF ZEBRAFISH LARVAE

12:15-12:30, Noé WAMBREUSE: WHEN ENVIRONMENTAL CHANGES INFLUENCE DISEASE DEVELOPMENT: THE CASE OF THE ENDANGERED SEA CUCUMBER HOLOTHURIA SCABRA

Session 14, TAXONOMY & SPECIES DIVERSITY I, Room 2, 11h30-12h30

Chairperson: Paolo ROSA

11:30-11:45, Christos KAROULIS: STUDYING GENOMES TO SAVE THE SPECIES: HUMAN AND NATURAL EFFECTS ON THE GLOBAL GENETIC DIVERSITY OF MAMMALS

11:45-12:00, Lode OP'T ROODT: EXPLORING THE GENETIC POPULATION STRUCTURE OF INDO-PACIFIC CORAL REEFS: A WHOLE GENOME SEQUENCING APPROACH UTILIZING THE CLOWNFISH AMPHIPRION CLARKII AS A MODEL

12:00-12:15, Iris VAN DE POL: SYNTHESIS OF ANIMAL TRAIT DATA ACROSS THE TREE OF LIFE WITH SHARETRAIT: PROBLEMS, PITFALLS AND POSSIBILITIES

12:15-12:30, Paolo ROSA: ORBIT: THE EUROPEAN TAXONOMIC INITIATIVE FOR POLLINATOR MONITORING

Session 15, PALEOBIOLOGY, Room 3, 11h30-12h15

Chairperson: Denis MICHEZ

11:30-11:45, Stijn GOOLAERTS: TO COLOUR OR NOT TO COLOUR: COLOUR PATTERNS AND PIGMENTS IN INVERTEBRATES FROM THE PALAEOZOIC OF BELGIUM

11:45-12:00, Sophie GRESHAM: THE GREAT PUZZLE OF THE GREAT LAKES: UNCOVERING THE COMPLEX HYBRID ORIGINS OF THE LAKE MALAWI CICHLID RADIATION

12:00-12:15, Mariana VASCONCELLOS: PHYLOGENOMICS OF ENYALIUS LIZARDS REVEALS CRYPTIC DIVERSITY IN THE ATLANTIC FOREST AND MIOCENE RAINFOREST CONNECTIONS WITH THE AMAZON

Session 16, ECOLOGY & EVOLUTION, Room 1, 14h-15h15

Chairperson: Abigaël ANSELMO

14:00-14:15, Julien CAMPISI: THE ICHTHYOLOGICAL SYMPHONY OF MESOPHOTIC CORAL REEFS: HOW LIGHT REDUCTION SHAPES FISH ACOUSTIC COMMUNICATION

14:15-14:30, Hugo GANTE: SOCIAL SELECTION DRIVES THE EVOLUTION OF FACIAL COLOR PATTERNS IN COOPERATIVE BREEDING CICHLIDS

14:30-14:45, Laurent MITTELHEISER: ECOMORPHOLOGICAL DIVERSIFICATION OF GOATFISH HYOID BARBELS

14:45-15:00, Yelle VANDENBOER: ENVIRONMENTAL FACTORS AND UV EXPOSURE AFFECT GENE ACTIVITY IN THE PUTATIVE ANCIENT ASEXUAL OSTRACOD DARWINULA STEVENSONI

15:00-15:15, Abigaël ANSELMO: CHARACTERIZATION AND DETECTION OF FRASS FROM TENEBRIO MOLITOR LARVAE BY NEAR INFRARED SPECTROSCOPY TECHNIQUES

Session 17, TAXONOMY & SPECIES DIVERSITY II, Room 2, 14h-15h15

Chairperson: Sara REVERTE

14:00-14:15, Els DE KEYZER: EXPLORING THE CATALYST ROLE OF HYBRIDISATION: INSIGHTS INTO THE SPECIATION DYNAMICS OF LAKE MATANO’S SAILFIN SILVERSIDES

14:15-14:30, Fernanda HERRERA-MESÍAS: A PICTURE IS WORTH A THOUSAND WORDS: THE ROLE OF MACROPHOTOGRAPHY IN WILD BEE CONSERVATION BIOLOGY IN LUXEMBOURG

14:30-14:45, Ninon LECOQUIERRE: SPECIES DELIMITATION AND GENOME SIZE VARIATION IN TROPICAL MARINE SPONGES

14:45-15:00, Géraldine MERTENS: INFRAFADA: UPGRADING THE TAXONOMIC BACKBONE OF GLOBAL FRESHWATER ANIMAL BIODIVERSITY RESEARCH INFRASTRUCTURES

15:00-15:15, Sara REVERTE: OUTCOMES FROM THE EUROPEAN PROJECT SPRING: CAPACITY BUILDING IN POLLINATOR TAXONOMY

__Session 18, TROPHIC ECOLOGY, Room 3, 14h-15h15__

Chairperson: Natasha DE MANINCOR

14:00-14:15, Martin DOGNIEZ: BENTHIC FOOD WEBS IN ANTARCTICA: WOULD YOU CARE FOR SOME MORE (MICRO)ALGAE?

14:15-14:30, Ulrich MARTIN: SHARKS OF TAIWAN: EXPLORING THEIR TROPHIC ECOLOGY THROUGH THE RESOLUTION OF THREE ISOTOPES

14:30-14:45, Loïc MICHEL: DINING IN THE DEEP: UNRAVELING ENERGY ACQUISITION STRATEGIES IN SYNTOPIC COLD-WATER CORALS

14:45-15:00, Fanny RUHLAND: MULTI-WAY METHODS FOR WIREWORMS’ CONTROL: VOLATILE ORGANIC COMPOUNDS, POTATO VARIETAL PREFERENCES AND ENTOMOPATHOGENIC FUNGI

15:00-15:15, Anthony VOISIN: WHAT DO GRAZERS REALLY GRAZE ON?

Posters Communications

Poster 1. Sezgi Akbal Keskin. PHYLOGEOGRAPHIC PATTERNS OF THE GIANT CLAM TRIDACNA MAXIMA ACROSS THE INDO-PACIFIC.

Poster 2. Ayoub-Lambin Sarah. PHYLOGEOGRAPHIC PATTERNS OF THE GIANT CLAM TRIDACNA MAXIMA ACROSS THE INDO-PACIFIC.

Poster 3. Basten Anne (Van Der Bij Pascal). CROCODYLIA IN THE PALAEONTOLOGICAL FILHOL COLLECTION OF KU LEUVEN.

Poster 4. Azama Shalie Rodoma Théo. EXPLORATION OF THE POTENTIAL LINKS BETWEEN THE GUT MICROBIOTA AND THE BEHAVIOUR OF *KRYPTOLEBIAS MARMORATUS*.

Poster 5. Beaumariage Anaïs. UNLOCKING THE GENETIC DYNAMICS OF THE GREAT CRESTED NEWT (*TRITURUS CRISTATUS*) POPULATIONS: INSIGHTS FOR EFFECTIVE CONSERVATION STRATEGIES.

Poster 6. Beaumariage Anaïs. WILD AT RISK: TRACKING HYBRIDIZATION BETWEEN WILDCAT AND DOMESTIC CAT IN LUXEMBOURG.

Poster 7. Benbachir Mohammed. ORIGIN OF ANDROGENETIC LINEAGES AND SPERM COMPETITION IN THE CLAM GENUS *CORBICULA*.

Poster 8. Boerman Sophie A. C. COMPUTED TOMOGRAPHY (CT) SCANNING IN PALEONTOLOGY: SHEDDING NEW LIGHT ON A 70-MILLION-YEAR-OLD FOSSIL CROCODYLIAN.

Poster 9. Bossiroy Estelle. BREAKING THE RED MYTH: CAROTENOIDS IN HOLOTHUROID COELOMOCYTES.

Poster 10. Brau Thomas. A NEW SPECIES OF *AGAPOSTEMONOIDES* (HYMENOPTERA: HALICTIDAE) FROM MEXICO.

Poster 11. Buratto Noémie. URNING SCIENCE UPSIDE DOWN: WHY THE UPSIDE-DOWN JELLYFISH COULD BE A GAME-CHANGER IN ENVIRONMENTAL RESEARCH.

Poster 12. BÜYÜKGÜNER Tuana. COMPARING MATERNAL CARE IN CAPTIVE PAN: A MULTI-GROUP STUDY.

Poster 13. Callaerts Jonas. UNDERSTANDING THE EFFECTS OF EOCENE WARMING ON MARINE FISH: A DIVE INTO FISH DIVERSITY AND DISTRIBUTION UNDER YPRESIAN WARMING.

Poster 14. Campuzano Curro. RECONSTRUCTING THE DEMOGRAPHIC HISTORY OF THE ADAPTIVE RADIATION OF SILVERSIDES IN THE MALILI LAKES.

Poster 15. Carion Frédéric (Brau Thomas). BEE-ING UNIQUE: UNVEILING A NEW CASE OF GYNANDROMORPHY IN THE PARASITIC BEE GENUS *NOMADA*.

Poster 16. Carnac Enora. EFFECTS OF PHOTOSYMBIOSIS ESTABLISHMENT ON CNIDARIAN REDOX HOMEOSTASIS.

Poster 17. Castiaux Mabel. DECODING SKIN ULCERATION SYNDROME IN THE AQUAFARMED SEA CUCUMBERS: AN INTEGRATIVE TRANSCRIPTOMIC AND METABOLOMIC ANALYSIS.

Poster 18. Chabi Ota Raimi. ASSESSMENT OF THE CONSERVATION STATUS OF THE OLIVE COLOBUS POPULATION (*PROCOLOBUS VERUS*) IN SOUTHERN BENIN.

Poster 19. Cochenille Thomas. INTEGRATIVE CONTROL STRATEGIES FOR CHICORY APHID PESTS.

Poster 20. De Tandt Bastien. ASSESSING THE HABITAT SUITABILITY OF MASON BEES IN EUROPE TO GUIDE CONSERVATION EFFORTS.

Poster 21. DECAESTECKER Ellen. HIERARCHICAL ECO-EVO DYNAMICS MEDIATED BY THE GUT MICROBIOME.

Poster 22. Dimopoulos Alexia. BLACK CORAL SHALLOW-WATER COMMUNITIES OF MADAGASCAR: THE FUNCTIONAL LINK BETWEEN HABITAT AND DIVERSITY.

Poster 23. Donough Nichole. PONDS TO PATTERNS: PARASITE AND KILLIFISH DIVERSITY IN TEMPORARY POOLS.

Poster 24. Dupont Déborah W. E. A SINGLE GENETIC POPULATION OVER 24,000 KM: THE UNUSUAL COHESIVE GENETIC PATTERN IN *ABYSSORCHOMENE DISTINCTUS* (BIRSTEN & VINOGRADOV, 1960).

Poster 25. Eske Annika. UNDERSTANDING THE EFFECTS OF CHANGING ENVIRONMENTAL CONDITIONS AND CLIMATE EVENTS ON PLANKTON COMMUNITIES USING AUTOMATED IMAGE SENSORS.

Poster 26. Flaminio Simone. ITALIAN POLLINATORS: STEPS FORWARD TOWARD THE FUTURE ITALIAN RED LIST.

Poster 27. Flandroit Antoine. AN UNKNOW ALIEN: CHARACTERIZATION OF THE FIRST INVASIVE POPULATION OF SEA SPIDERS.

Poster 28. Gaumez Loic. A PROBABLE NEW SPECIES OF EULIMID (GASTROPODA, MOLLUSCA) INFESTING FARMED *HOLOTHURIA SCABRA* IN MADAGASCAR.

Poster 29. Gennaux Sébastien. COMPARATIVE STUDY OF OCULAR MORPHOLOGY IN FOUR SPECIES OF TROPICAL LIZARDS (SCINCIDAE) LIVING IN DIFFERENT ECOLOGICAL NICHES.

Poster 30. Gérard Maxence. IMPACT OF TEMPERATURE ON BUMBLEBEE COGNITION.

Poster 31. Geslain Enora. THE GENOME SEQUENCE OF THE COMMON SOLE, *SOLEA SOLEA*

Poster 32. Gilbert François. *WOLBACHIA* INVASION: FROM APHID CELLS TO PLANT TISSUE – IT’S EVERYWHERE!

Poster 33. Goede Nicole. EMBRYOS AT RISK: EARLY EMBRYONIC DEVELOPMENT OF AQUATIC ECTOTHERMS IN A WARMING AND POLLUTED WORLD.

Poster 34. Hildebrandt Frida. INCOMPLETE SOCIAL CUES AND NAVIGATIONAL DECISION-MAKING IN SOCIAL AND SEMI-SOCIAL INSECTS.

Poster 35. Hill Alexander. IMPROVING FISH BIODIVERSITY MONITORING IN AFRICA: BUILDING A COMPREHENSIVE EDNA METABARCODING REFERENCE LIBRARY.

Poster 36. Jacquet Maxence. ImPROVING FISH BIODIVERSITY MONITORING IN AFRICA: BUILDING A COMPREHENSIVE EDNA METABARCODING REFERENCE LIBRARY.

Poster 37. Kauffmann Bob. THE ROLE AND REGULATION OF REACTIVE OXYGEN SPECIES (ROS) AND ANTIOXIDANTS (AOX) DURING TISSUE REGENERATION IN *SCHMIDTEA MEDITERRANEA*.

Poster 38. Khan Bilal Saeed. POPULATION DYNAMICS OF PREDATORY SPIDERS OF COTTON FIELDS FROM DISTRICT FAISALABAD, PUNJAB, PAKISTAN.

Poster 39. Kiggen Aaron. UNCOVERING GENE REGULATORY NETWORKS UNDERLYING BEHAVIOURAL PLASTICITY IN DAPHNIA MAGNA THROUGH SINGLE-CELL MULTI-IOMICS .

Poster 40. Kourtidis Alexandros. THE EVOLUTION OF PESTICIDE RESISTANCE IN *DAPHNIA MAGNA* - A POPULATION, COMPARATIVE AND FUNCTIONAL GENOMICS APPROACH.

Poster 41. Leconte Clara. EXPLORING THE INFLUENCE OF INVASIVE PLANT SPECIES ON PLANT-BEE COMMUNITIES, FUNCTIONAL TRAITS, AND INTERACTIONS.

Poster 42. Lescot Sarah. POLLINATOR DIVERSITY ON ROADSIDES AND TRAFFIC-RELATED IMPACTS.

Poster 43. Ma Minglei. THE ADAPTATIONAL AND EVOLUTIONARY HISTORY OF SPECTRAL SENSITIVITY IN ECDYSOZOAN R-OPSINS.

Poster 44. Malice Louise. DOES DIFFERENT KARYOTYPE MAINTAIN CRYPTIC SPECIES BOUNDARIES?

Poster 45. Maniquet Héloïse. DIVERSITY OF THE REEF FISH COMMUNITY WITHIN AND OUTSIDE A FISHING ZONE IN THE BALANDRA BAY MARINE PROTECTED AREA (LA PAZ, MEXICO).

Poster 46. Mattsson Bodil. SOIL AND POLLINATOR CONSERVATION: CAN URBAN SAND BEDS PARTICIPATE TO THE CONSERVATION OF GROUND NESTING BEES?

Poster 47. Mullens Nele. COMPARISON OF THE POLLINATOR MICROBIOME: MANAGEMENT PRACTICES, ALTITUDE AND SEX AS DRIVERS FOR CHANGE.

Poster 48. Nonclercq Youri. OPSIN-MEDIATED PHOTORECEPTION IN THE MOST BASAL ECHINODERM GROUP: THE CRINOIDS (CRINOIDEA, ECHINODERMATA).

Poster 49. Reyes Jhoe. REVISION OF THE GENUS *BALTOPLANA* (RHABDOCOELA: SCHIZORHYNCHIA: CHELIPLANIDAE) WITH THE DESCRIPTION OF TWO NEW SPECIES.

Poster 50. Saha Jaysmita. DE-NOVO GENOME ASSEMBLIES OF HYBRID CICHLID SPECIES GIVE INSIGHTS INTO GENOME DIVERGENCE PATTERNS DUE TO HYBRIDISATION.

Poster 51. Schols Ruben (VANOVERBERGHE Isabel). HOST-BACTERIOME TRANSPLANTS OF THE SCHISTOSOME SNAIL HOST BIOMPHALARIA GLABRATA REFLECT SPECIES-SPECIFIC ASSOCIATIONS.

Poster 52. Sievert Thorbjörn (Lassance Jean-Marc). DEEP LEARNING APPROACHES TO INVESTIGATE OLFACTORY RESPONSES IN BEHAVIORALLY DIVERGENT DEER MICE.

Poster 53. Smacchia Leandro. STUDYING ECHINODERM ADHESIVE PROTEIN EVOLUTIONARY HISTORY.

Poster 54. Steenhuyse-Vandevelde Michael. INTEGRATED TAXONOMIC-TAPHONOMIC INVESTIGATION OF A COMPLEX LATE PLEISTOCENE MOLLUSC FAUNA: A CASE STUDY FROM ZEEBRUGGE.

Poster 55. Tourbez Clément. IMPACT OF INVASIVE PLANT SPECIES ON WILD BEE CONSERVATION.

POSTER 56. Vanbergen Sam. GLOBAL POPULATION GENOMICS OF AN AGRICULTURAL PEST: INSIGHTS INTO HAPLOTYPE VARIATION AND POTENTIAL DRIVERS OF INVASION.

Poster 57. Vandenboer Yelle. JUMPING GENES IN ANCIENT CRUSTACEANS: OSTRACODA.

Poster 58. Vandromme Jérôme. STUDY OF THE IMPACT OF ENVIRONMENTAL CHANGES ON WILD BOAR MICROBIOME INVOLVING HEALTH RISKS.

Poster 59. VanGiessen Sam. GENOMIC APPROACHES TO IMPROVE EX SITU CONSERVATION OF THE TUFTED DEER (*ELAPHODUS CEPHALOPHUS*).

Poster 60. VanGorp Merel. 3D-CALIBRATED MULTI-VIEW HIGH-SPEED VIDEOGRAPHY OF MANOEUVRING BOXFISH.

Poster 61. Vanhussel Margaux. THE WESTERN JACKDAW’S FLIGHT TO THE CITY : A MULTI-DISCIPLINARY APPROACH TO STUDY THE IMPACT OF HUMAN ACTIVITIES ON BIRD POPULATIONS.

Poster 62. VanSteenberge Maarten. THE GREEN HEART OF AFRICA, THE LOMAMI PRIMER.

Poster 63. VanWassembergh Sam. SIMULATIONS OF WATER FLOW THROUGH GEOMETRICALLY SIMPLIFIED MODELS OF FILTER-FEEDING MOUTH CAVITIES.

Poster 64. VANSTEENKISTE Arnaud (Magain Nicolas). ESTIMATING THE IMPACT OF WIND TURBINES MORTALITY ON THE RED KITE (*MILVUS MILVUS*) POPULATION IN WALLONIA.

Poster 65. Verheye Marie. IS ANTARCTICA AN EVOLUTIONARY INCUBATOR? PHYLOGENETIC COMPARATIVE STUDY OF THE AMPHIPOD FAMILY IPHIMEDIIDAE ON THE ANTARCTIC SHELF.

Poster 66. Ver Hoeye Killian. CORAL DWELLING DECAPODS IN THE FACE OF HOST BLEACHING AND HABITAT LOSS.

Poster 67. Vervaecke Hilde. NOSES FOR NATURE: SUPPLY AND DEMAND FOR ECOLOGICAL DETECTION DOGS IN FLANDERS.

Poster 68. Villella-Pacheco Zorimar. UNRAVELING THE GENE REGULATORY NETWORKS OF PREDATOR-INDUCED DEVELOPMENTAL PLASTICITY WITHIN AND ACROSS GENERATIONS IN *DAPHNIA MAGNA*.

Poster 69. Visser Fleur. PRIDE LANDS IN PERIL: FORECASTING LION HABITATS ACROSS CHANGING AFRICAN LANDSCAPES.

Poster 70. Voeten Elke. EVOLUTION IN THE TIDES: UNRAVELLING ADAPTIVE STRATEGIES IN *POGONUS CHALCEUS* BEETLES.

Poster 71. Willam Laura. TRAIT PLASTICITY OF MARINE PHYTOPLANKTON IN *SYNECHOCOCCUS* SP. IN RESPONSE TO LIGHT AND THERMAL VARIATIONS.

Poster 72. Yefimak Kristina. UNRAVELING THE INTERPLAY OF GENETIC AND NONGENETIC TRAIT VARIATION IN RESPONSE TO GEOGRAPHIC MOSAICS OF STRESSORS.

Conference Venue

HOW TO GET TO THE CONGRESS ZOOLOGY 2024

The Venue

The Benelux Zoology Congress 2024 will be held at the Palais des Congrès de Mons, located at **Avenue Mélina Mercouri 9,** 7000 Mons, Belgium.

How to get to the Congress

By plane

The two nearest airports are the national airport, Zaventem Brussel Airport (BRU), and the Brussels South Charleroi Airport (CRL). They are accessible from most locations.

By public transport

The centre of Mons is relatively small, and most sites of interest can be reached on foot. Note that the **conference venue is just in front of the Mons train station**.

- From the Brussels South Charleroi Airport, there is a shuttle bus from Charleroi Airport to Mons, which you can catch outside the arrival area of Terminal 1. This shuttle arrives at Avenue Meline Mercouri in Mons, just in front of the MICX conference center.
- From the Zaventem Brussel Airport, you can take the train to Mons directly from the airport.
- From Amsterdam, take the TGV from Amsterdam-Central to Brussels-South and then take the train to Mons.
- There are trains to Mons from all Belgian train stations. Follow this link to check train timetables in Belgium: https://www.belgiantrain.be
- Follow this link to check shuttle bus timetables from Brussels South Charleroi Airport:

https://www.flibco.com/fr/timing

By car

Mons is easily accessible from the E42 motorway. From the following departure points, take exit 24 – Mons:

- From Brussels: take the E19 towards Paris and then the E42.
- From Liege and Namur: follow the E42 all the way.
- From Antwerp: take the A12 towards Brussels, then the E19 and the E42.
- From Ghent: take the E40 towards Brussels and then follow the E19 and E42.

Code of Conduct

The Benelux Zoology Congress 2024 intends to provide a courteous, professional, free of harassment conference experience for everyone, regardless of gender, gender identity and expression, sexual orientation, disability, physical appearance, ethnicity, or age. Demeaning, abusive, harassing, or threatening behaviour towards other attendees, staff or the public is not permitted in either personal or electronic interactions. Personal and electronic interactions should be professional, rational, and mutually respectful at all conference events, both formal and informal. Intellectual property should be respected by not disseminating photographs, recordings, or other reproductions of presentations or artwork without permission of the author(s).

We invite all conference participants to behave with respect, consideration and dignity towards each other, irrespective of their gender, gender identity and gender expression, sexual orientation, marital or parental status, age, immigration status, disability, neurodiverse status, physical appearance, body size, ethnicity, nationality, religious affiliation, socioeconomic background, educational background, or career stage. Questions and discussions should be both respectful and constructive, focusing on ideas rather than individuals. Comments or behaviour that can reasonably be assumed to have the effect of creating, contributing to or maintaining a hostile or prejudicial environment for an individual or group are prohibited, whether made directly (for example, in person or directly online) or indirectly (for example, via social media).

Unacceptable behaviour includes (but is not limited to):

- Harassment, intimidation, or discrimination in any form.
- Physical or verbal abuse of any meeting attendee.
- Denigrating verbal comments or gestures related to gender, gender identity and expression, sexual orientation, disability, age, physical appearance, body size, ethnicity, religion, national origin.
- Epithets, slurs, or negative stereotyping; threatening, intimidating, or hostile acts; denigrating jokes; display or circulation of written graphic material that denigrates or shows hostility or aversion towards an individual or group. Harassment intended in a joking manner still constitutes unacceptable behaviour.
- Inappropriate use of nudity and/or sexual images in public spaces or in presentations.
- Threatening or stalking any meeting attendee.
- Inappropriate physical contact.
- Unwelcome sexual attention, including sexual advances or propositions; verbal comments or physical actions of a sexual nature; sexually degrading words used to describe an individual; a display of sexually suggestive objects or pictures; sexually explicit jokes.
- Disruption of talks at oral or poster sessions, in the conference hall, or at other events organized during the Zoology 2024 Congress.
- Invasive photography or recording, including no photographs or recordings of minors (under 18 years of age) without explicit permission.
- Recording or photography of talks or posters without express permission from the authors.

Anyone asked to stop unacceptable behaviour is expected to comply immediately. Revenge against anyone who reports harassment or participates in an investigation will not be tolerated and will be subject to further legal action.

If you witness or are the victim of prohibited behaviour, please report it as soon as possible to a member of the congress staff or organizing committee.

Social Event at MUMONS

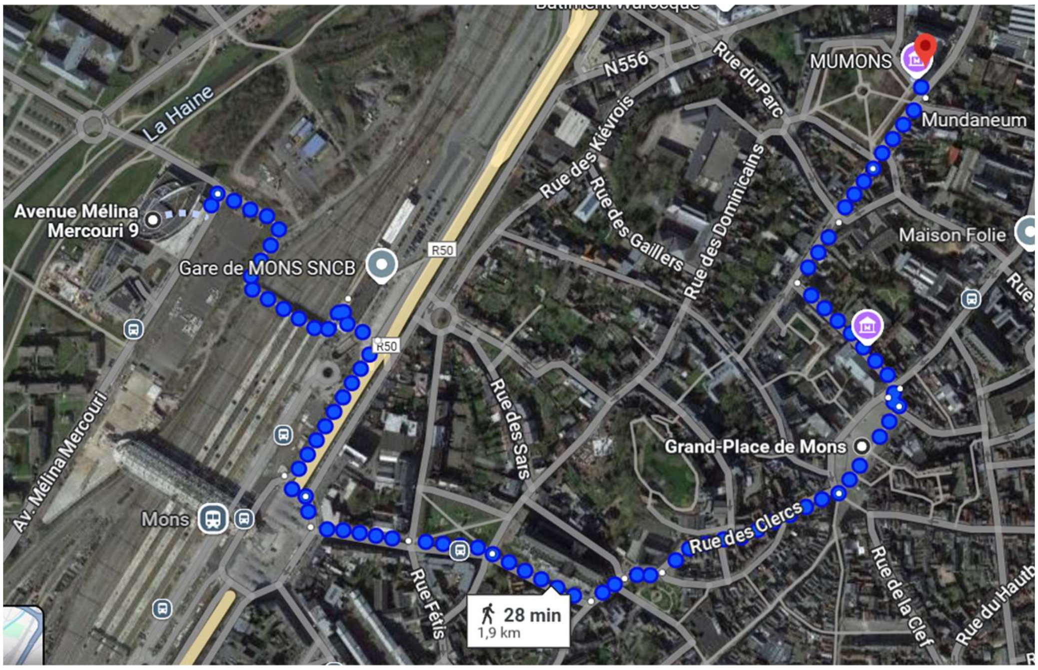
A social event will be organized on the 12th of December at the MUMONS. During the social event, a visit of the exhibition Explorer l'Invisible will be organized.

The exhibition "**Explorer l'Invisible**" recently returned to MUMONS for its third edition, promising a captivating visual experience. Visitors will be greeted by images that reveal surprising worlds, sourced from the laboratories of the University of Mons. This initiative aims to transform scientific photographs into true works of art by showcasing what is usually invisible to the naked eye, whether it be microscopic phenomena or cosmic wonders. Through these images, researchers share the beauty and complexity of their work while exploring significant questions of our time.

The exhibition offers a unique sensory experience where science and art converge. Visitors can look forward to fascinating discoveries, ranging from nebulae and galaxies to microscopic creatures. To enhance this exploration, UMONS guides will share their passion and commitment to science and art, inviting conference attendees to dive into this sensory adventure and appreciate the power of contemporary technologies in revealing the invisible.

Additionally, a **Best Scientific Picture Contest** will be held based on your submitted entries. The award will be presented by the MUMONS team during the Reception Dinner. If the authors consent, the three best pictures will be included in the exhibition. The five best images selected by the jury (members of the Scientific Committee) are visible at the end of this Book of Abstract.

The MUMONS is located in an old church (Chapelle des Visitandines) transformed in a museum and is located on the 24, place du parc, 7000 Mons. There is a 2km walk from the conference place and a possibility to pass though the small but rich and beautiful centre of Mons and its famous Grand-place :



Abstracts of oral Communications

FEEDING PERFORMANCE, BEAK KINEMATICS AND SEED HANDLING SKILLS CHANGE WITH AGE IN A GRANIVOROUS SONGBIRD

Tim ANDRIES[1,2*], Wendt MÜLLER[2], Sam VAN WASSENBERGH[1]

[1] Laboratory of Functional Morphology, Department of Biology, University of Antwerp, 2610 Antwerpen, Belgium.

[2] Behavioural Ecology and Ecophysiology Research Group, Department of Biology, University of Antwerp, 2610 Antwerpen, Belgium.

***Presenting author, tim.andries@uantwerpen.be**

Keywords: Ageing, Feeding performance, Beak kinematics, Songbirds

Granivory in songbirds is a highly specialized feeding strategy that requires well-developed jaw muscles and fast, strongly coordinated movements of beak and tongue. As a result, the performance of feeding on seeds likely changes over the course of a bird's life along with the bird's abilities. It can be expected that abilities generally improve as they mature and decline as they age, given that ageing has profound effects on the physical performance of most animals. We investigated this in the Domestic canary (*Serinus canaria*) by recording individuals during feeding on small canary seeds and larger hemp seeds, using high-speed cameras in a quadroscopic set-up. We filmed both juveniles and adults repeatedly over a span of two years, to capture as much of the canary's total lifespan. From these recordings we extracted metrics of feeding performance, beak kinematics and seed-handling skills, and tested how these change with age. We found parabolic effects of age on the success rate of seed husking and the average frequency of beak opening and closing, where both first increased during the first years and started decreasing again at old age. Additionally, we found that seed handling skills improved linearly, though weakly, with age. This suggests that there is still room for improvement even though canaries are already proficient at seed husking from a very young age. Interestingly, we did not find that birds became faster or slower at handling individual seeds with increasing age. Thus, old individuals might partly compensate for a decrease in physical capabilities due to senescence with improved handling skills.

CHARACTERIZATION AND DETECTION OF FRASS FROM *TENEBRIO MOLITOR* LARVAE BY NEAR INFRARED SPECTROSCOPY TECHNIQUES

Abigaël ANSELMO[1,2*], Audrey PISSARD[1], Pascal VEYS[1], Vincent BAETEN[1], Denis MICHEZ[2]

[1] Quality and Authentication of Products Unit, Knowledge and Valorisation of agricultural products Department, Walloon Agricultural Research Centre, 5030 Gembloux, Belgium.

[2] Laboratory of Zoology, Research Institute for Biosciences, University of Mons, 7000 Mons, Belgium.

***Presenting author, a.anselmo@cra.wallonie.be**

Keywords: Frass, Insect meal, Vibrational spectroscopy

Insects naturally produce frass during their rearing. This residue is defined by the European Commission (2021) as a mixture of insect excrement, food substrate, insect parts, and dead eggs. The inclusion of frass in insect meal produced by companies is prohibited. Nevertheless, with the development of insect meal production, frass could potentially be used to decrease the quality. Consequently, the development of methods to detect the presence of frass in insect meal is needed to comply with legislation.

This study investigates the application of Near Infrared (NIR) Spectroscopy techniques to characterize and detect frass, as they are fast and non-destructive methods that allow the use of untreated samples.

Two samples of *Tenebrio molitor* frass were used for this study, one produced in-house (HFr), and one commercial (CFr). These samples were used to adulterate *T. molitor* larvae meal at 5%, 20% and 50%. First, one adulterated sample, HFr, and the *T. molitor* larvae meal sample were analysed by NIR Spectroscopy (NIRS) to develop models and predict their composition. Results showed a protein content of 63% for the *T. molitor* larvae meal, 16% for the frass sample, and 55% for the adulterated sample. Secondly, adulterated samples were analysed by NIR Microscopy (NIRM) combined with chemometrics to detect the presence of frass (HFr or CFr). Based on a screening method and PLS-DA analysis, the presence of HFr and CFr were detected in the adulterated samples, with good performance of the models supported by sensitivity and specificity values greater than 0.84.

These results are promising and highlight both the fact that frass seems to present a much less interesting chemical composition than insect meal and the possibility of detecting it in samples. Nevertheless, it is essential to complete these results with chemical analyses to improve prediction models.

CONTROLLING LIGHT IN A LUMINOUS ECHINODERM: FROM ENVIRONMENTAL STIMULI TO LIGHT EMISSION

Wendy-Shirley BAYAERT[1*], Laurent DUCHATELET[2], Constance COUBRIS[2], Sam DUPONT[3], Jérôme MALLEFET[2], Martin MAREK[4], Patrick FLAMMANG[1], Jérôme DELROISSE[1,5]

[1] Biology of Marine Organisms and Biomimetics Unit, Research Institute for Biosciences, University of Mons, 7000 Mons, Belgium.

[2] Marine Biology Laboratory, Earth and Life Institute, University of Louvain, 1348 Louvain-La-Neuve, Belgium.

[3] Department of Biological & Environmental Sciences, University of Gothenburg, The Sven Lovén Centre for Marine Sciences, 451 78 Fiskebäckskil, Sweden.

[4] Loschmidt Laboratories, Department of Experimental Biology and RECETOX, Masaryk University, 62500 Brno, Czech Republic.

[5] Laboratory of Cellular and Molecular Biology, GIGA Institute, University of Liège, 4000 Liège, Belgium.

***Presenting author**, wendy-shirley.bayaert@umons.ac.be**

Keywords: Echinoderm, Bioluminescence, Sensory receptors, Pigmented sheath

To avoid predation, echinoderms have evolved a range of defensive strategies, including nocturnal activity and cryptic morphology or behaviors adapted to their habitat. Bioluminescence - the ability to produce light - is another potential defensive strategy that has been observed in over 150 species of luminous echinoderms, half of which are brittle stars.

A well-studied brittle star in the field of bioluminescence is *Amphiura filiformis*, a burrowing species found in European seas. It feeds by extending its arms into the water column to capture organic particles. These arms are equipped with spines that emit blue flashes of light, likely serving as a defense mechanism against predators. Despite over 30 years of intensive research on this species, significant knowledge gaps remain regarding the mechanisms controlling its bioluminescence.

Using luminometric experiments, we demonstrated that *A. filiformis* responds to mechanical stimuli and injuries to nearby conspecifics by emitting light. Electron microscopy analyses revealed that specific ciliated sensory receptors, called *stäbchen*, are anatomically close to the underlying luminous cells, or photocytes, on the spine. The *stäbchen*, thought to be sensitive to both mechanical and chemical stimuli, may therefore serve as the link between environmental stimulus detection and the light response.

It is known that the photocytes are located at the base of the spine, correlating with the spatial expression of the luciferase enzyme, as shown through immunodetection and *in situ* hybridization. However, light emission occurs only at the tips of the spines, presenting a paradox that has remained unresolved. Our histological and ultrastructural analyses support the hypothesis that a pigmented sheath facilitates light transmission along the spine.

These results significantly enhance our understanding of the bioluminescence control in *A. filiformis*, while also highlighting the adaptive importance of bioluminescence in marine environments.

DEVELOPMENT OF AN EPIGENETIC CLOCK IN A SELF-FERTILIZING VERTEBRATE SPECIES

Justine BELIK[1]*, Frédéric SILVESTRE[1]

[1] URBE, University of Namur, 5000 Namur, Belgium.

***Presenting author**, **justine.belik@unamur.be**

Keywords: DNA methylation, Ageing, Self-fertilizing vertebrate

Efficient and accurate estimation of fish age is crucial to understand the demographic structure of populations and consequently population dynamics. Traditional estimation methods, such as counting growth increments in vertebrae or otoliths, require well-trained staff, are time-consuming and lethal. In this context, several biological predictors have been studied, including telomere length, transcriptomic, proteomic or metabolomic predictors and DNA methylation, the latter being the most reliable. DNA methylation, mostly in a cytosine-guanine dinucleotide context (hereafter CpG) is a stable epigenetic mark that plays an important role in regulating genes. Epigenetic clock is based on systematic changes in methylation levels with age. It has already been determined for many vertebrates, including humans, and many teleost species.

The mangrove rivulus, *Kryptolebias marmoratus*, presents a mixed-mating strategy, where hermaphrodite individuals can self-fertilize, producing naturally isogenic lineage, and reproduce with males, thus creating a genetic diversity gradient. This unique mode of reproduction among vertebrates makes the mangrove rivulus a key species to study epigenetics. It shows a distribution covering the entire tropical and subtropical West-Atlantic basin. The studied population originated from Emerson Point Preserve (Florida), with a selfing rate of 97%. Information on the age of natural populations is completely lacking, and no estimator has yet been developed.

Here, we have generated a reduced representation bisulfite sequencing (RRBS) data set of brain tissue from 96 hermaphroditic mangrove rivulus, evenly distributed from 60 to 1300 days post-hatching. Using an elastic net regression, we have determined the most suitable CpG subset, whose methylation levels estimate age with a Mean Absolute Error of 44 days. This study is the first to develop the epigenetic clock in an isogenic vertebrate lineage and shows that the DNA methylation pattern evolves over the lifetime of the rivulus in the absence of genetic variation.

THE PHYLOGEOGRAPHY OF PELAGIC EAGLE RAYS (AETOBATIDAE) – GENETIC PATTERNS AND COASTAL ECOSYSTEM DEPENDENCIES

Stephen BERGACKER[1,2*], Diana PAZMIÑO[3], Kim BASSOS-HULL[4], Julia SPAET[5], Daniel FERNANDO[6], Marc KOCHZIUS[2], Jean-François FLOT[1]

[1] Evolutionary Biology & Ecology, Université libre de Bruxelles (ULB), 1050 Brussels, Belgium.

[2] Marine Biology - Ecology, Evolution & Genetics (bDIV), Vrije Universiteit Brussel (VUB), 1050 Brussels, Belgium.

[3] Galapagos Science Center, Universidad San Francisco de Quito and University of North Carolina at Chapel Hill, San Cristobal, Galapagos, Ecuador.

[4] Sharks and Rays Conservation Research Program, Mote Marine Laboratory, 34236 Sarasota, Florida, United States.

[5] Evolutionary Ecology Group, Department of Zoology, University of Cambridge, CB2 3EJ Cambridge, United Kingdom.

[6] Blue Resources Trust, 00700 Colombo, Sri Lanka.

***Presenting author, stephen.bergacker@ulb.be**

Keywords: Species delineation, Conservation genetics

Spotted eagle rays are large, free-swimming batoids that trophically depend on the benthos. Although commonly occurring on coral reefs and associated habitats, they can undertake long pelagic migrations and are consequently considered semipelagic organisms (*i.e.,* organisms that penetrate oceanic waters but concentrate near continental landmasses). These life history traits, combined with the lack of clear biogeographical barriers to dispersal in marine environments, led to the long-held assumption that spotted eagle rays comprised well-connected populations forming a single circumtropically distributed species. However, molecular data have revealed high levels of genetic structure, possibly due to their apparent dependency on coastal ecosystems. These genetic patterns have resulted in the splitting of spotted eagle rays into several allopatric species.

We herein attempt to link genetic patterns with underlying ecological processes in a phylogeographic study of the pelagic eagle rays (Aetobatidae). We applied molecular species delimitation methods to samples collected throughout the circumtropical distribution of the clade, revealing the presence of several hypothetical species units. These data were then combined with public sequence data to reconstruct a time-calibrated phylogeny of the species complex. Our findings suggest that the evolutionary history of aetobatids is linked to shifts in Indo-Pacific biodiversity hotspots. We conclude that the migratory propensity of these semipelagic organisms is diminished by their dependency on coral reefs and associated coastal ecosystems.

THE ROLE OF THE MICROBIOME RELATIVE TO THE GENOME FOR NICHE WIDTH

Karen BISSCHOP[1*], Tobias ULLER[2], Nathalie FEINER[2,3], Dries BONTE[4+], Ellen DECAESTECKER[1+]

[1] Department of Biology, KU Leuven (KULAK), 8500 Kortrijk, Belgium.

[2] Department of Biology, Lund University, 223 62 Lund, Sweden.

[3] Max Planck Institute for Evolutionary Biology, 24306 Plön, Germany.

[4] Department of Biology, Ghent University, 9000 Ghent, Belgium.

[+]Joint last authorship

***Presenting author, karen.bisschop@kuleuven.be**

Keywords: Niche width, Endosymbionts, *Wolbachia*, Microbiome, Genome, Specialist, Generalist, Host-herbivore interaction Spider mites, *Tetranychus urticae*

Adaptation to global change relies on an organism's ability to survive in shifting environments, traditionally attributed to genetic adaptation and phenotypic plasticity. However, recent insights reveal the significant role microbiomes – complex communities of microorganisms within hosts – play in shaping host resilience. Microbiomes influence critical functions such as nutrient uptake and detoxification, potentially broadening the ecological niches of host organisms and enhancing their adaptive potential. This study examined these dynamics in the two-spotted spider mite (*Tetranychus urticae*), a generalist herbivore known for its rapid adaptability and expansive host range of over 900 plant species, despite narrow individual dietary niches. To investigate the mechanisms behind niche variation, we conducted a combined observational and experimental study, sampling multiple populations from different host plant species in Southern France. Using isofemale lines derived from single females, we assessed offspring performance (fecundity and longevity) across five host plant species, providing a view of individual niche widths. Following these assessments, we applied whole-genome resequencing to identify genetic signatures along the specialist-generalist continuum, linking specific genetic adaptations to host plant specialization and to obtain metagenome-assembled genomes (MAGs). This approach advances our understanding of the environmental, genetic, and microbial contributions to niche width and offers insights into adaptive strategies for species facing fragmentation and habitat loss.

EVOLUTION OF POLYUNSATURATED FATTY ACID BIOSYNTHESIS IN COPEPODS

Jens BOYEN[1*], Naoki KABEYA[2], Óscar MONROIG[3], Patrick FINK[4,5,6], Pascal I. HABLÜTZEL[7,8], Marleen DE TROCH[1]

[1] Marine Biology, Department of Biology, Ghent University, 9000 Gent, Belgium.

[2] Department of Marine Biosciences, Tokyo University of Marine Science and Technology, Minato-ku, 108-8477 Tokyo, Japan.

[3] Instituto de Acuicultura Torre de la Sal (IATS), CSIC, 12595 Ribera de Cabanes, Castellón, Spain.

[4] Department of River Ecology, Helmholtz Centre for Environmental Research - UFZ, 39114 Magdeburg, Germany.

[5] Department of Aquatic Ecosystem Analysis and Management, Helmholtz Centre for Environmental Research - UFZ, 39114 Magdeburg, Germany.

[6] Aquatic Chemical Ecology, Institute for Zoology, University of Cologne, 50674 Köln, Germany.

[7] Flanders Marine Institute (VLIZ), 8400 Oostende, Belgium.

[8] Biology Department, Vrije Universiteit Brussel, 1050 Brussel, Belgium.

***Presenting author, jens.boyen@uantwerpen.be**

Keywords: Copepods, Polyunsaturated fatty acids, Gene evolution, Horizontal gene transfer

Throughout their evolution, copepods (Copepoda, Crustacea) have successfully adapted to a wide range of marine and freshwater habitats each characterized by specific trophic conditions. Copepods are generally known to contain high levels of polyunsaturated fatty acids (PUFAs), notably omega-3 long-chain PUFAs such as eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA). It was long assumed that copepods acquired PUFAs through the food chain, but recent research shows some species can biosynthesize them endogenously. However, the extent to which the copepods' perceived capacity of PUFA biosynthesis coincides with their diversification and niche specialization remains undocumented. Leveraging publicly available copepod transcriptomes and genomes, we demonstrated significant copy number variations within the repertoire of PUFA biosynthesis genes among ecologically diverging copepod orders. Following two presumable horizontal gene transfer (HGT) events from an unknown donor to a common copepod ancestor, methyl-end desaturases and front-end desaturases, key enzymes in PUFA biosynthesis, were retained in Cyclopoida, Harpacticoida and Siphonostomatoida but lost in most Calanoida (except for certain *Calanus* and *Neocalanus* species which still have one front-end desaturase). All orders show strong expansion of the fatty acyl elongase subfamily elovl1/7, and while total elongase copy number did not differ among orders, the expression of these genes was higher than average in Harpacticoida and lower in Calanoida. All desaturase and elongase gene families exhibited non-clustered distribution in the assessed genomes, and positive selection on specific codons following HGT and duplication events. Overall, the unique but varying PUFA biosynthesis capacity of copepods enables maintenance of high PUFA levels even under dietary constraints in certain species and further ensures PUFA provisioning to higher trophic levels. These findings have important implications for nutrient and energy flow in changing environments.

PERFECT CRIME: ENTOMOPATHOGENIC NEMATODES IMPACT ON THE VOLATILE EMISSION PROFILE OF INSECT HOSTS

Andrea CHACON-HURTADO[1*], Fanny RUHLAND[1], Pierre HOTERMANS[1], Clément MARTIN[1], Raquel CAMPOS-HERRERA[2], François J. VERHEGGEN[1]

[1] Chemical and Behavioral Ecology, Gembloux Agro-Bio Tech, University of Liege, 5030 Gembloux, Belgium.

[2] Departamento de Viticultura, Instituto de Ciencias de la Vid y del Vino (CSIC, Universidad de La Rioja, Gobierno de La Rioja), Finca La Grajera, 26007 Logroño, Spain.

***Presenting author, achacon@uliege.be**

Keywords: EPN-bacteria complex, Insect pathogens, Invertebrate pathology, Chemical ecology

Entomopathogenic nematodes (EPNs), from the families Heterorhabditidae and Steinernematidae, are efficient at controlling several crop pests, especially soil-dwelling arthropods. Their free-living juveniles infect and kill the insect host in cooperation with symbiotic enteric bacteria, *Photorhabdus* spp. and *Xenorhabdus* spp respectively. These bacteria secrete toxins that induce rapid insect death, provide a suitable nutrient medium for nematodes growth and reproduction. Whether the infection process modifies the volatile organic compounds (VOCs) released by the insect body during nematode infection is not yet documented, while a VOC modification could be involved in the interactions between the dead body and other organisms, such as other pests or scavengers.

To test this hypothesis, we used the wax moth larva (*Galleria mellonella*) as a model insect host and two EPN species, *Steinernema carpocapsae* and *Heterorhabditis bacteriophora*. Using the Hisorb method, we collected VOCs released by the insect after nematode infection, as well as from larvae killed without nematodes (using liquid nitrogen), at the fourth post-mortem interval (PMI1, PIM3, PMI7, PMI11). The volatile profiles of larvae infected with EPNs differ significantly from those of larvae killed without EPNs. 183 compounds were identified, belonging to 12 chemical classes, including ketones, alkanes, and alcohols, which are the most represented classes. Sulfur compounds, which are generally associated with decomposition, were detected in all VOC profiles. The diversity of odors emitted by larvae infected with EPNs was more significant in PMI1 and PMI2 than in larvae killed with liquid nitrogen. The complexity and diversity of compounds evolve until PMI7 and decrease by PMI11. The observed differences in odor profiles throughout the nematode reproductive cycle are likely influenced by the activity of the symbiotic bacteria. These results provide new insights into the host-parasite relationship, and certain compounds may be of interest for biological control applications.

ADAPTATION TO ENVIRONMENTAL STRESS IN A SELF-FERTILIZING VERTEBRATE SPECIES (*KRYPTOLEBIAS MARMORATUS*)

Mélusine CHEVALIER[1*], Justine BELIK[1], Frédéric SILVESTRE[1]

[1] Department of biology, Université de Namur, Rue de Bruxelles 61, 5000 Namur, Belgium.

***Presenting author**, chevaliermelusine@student.unamur.be**

Keywords: Ecotoxicology, behavior, cypermethrin, *Kryptolebias marmoratus*

Most living organisms are in contact with pesticides, and the mangrove rivulus, *K. marmoratus,* is no exception to this. Cypermethrin is a widely used insecticide belonging to the pyrethroid family, found in mangroves and potentially impacting resident organisms. This insecticide, highly toxic for fish, blocks sodium channels in nerve membranes, preventing the transmission of nerve impulses. *K. marmoratus* shows a unique mixed mating strategy among vertebrates, called androdioecy. Populations consist of hermaphroditic individuals, forming isogenic lines, and males which can cross-fertilize, generating genetic diversity. The aim of this project is to identify the impacts of cypermethrin on behaviour and associated changes in brain gene expression of adult's mangrove rivulus. Fish were exposed for 4 days, starting at 90 dph, to cypermethrin (0,5, 5, 10, 25 and 50 µg/L). Their behavior was assessed using a shelter test after 24 and 96 hours of exposure, measuring both concentration-dependent and time-dependent effects. The total distance moved, the latency time before leaving the shelter and the proportion of time spent at the center and edge of the arena were measured. At the end of the exposure, DNA expression of targeted genes related to detoxification and behaviour (Mecp2, NIPBL, GSS, MAOA, DNMT3a and TOLLIP) were quantified. The qPCR data enables us to determine a concentration-dependent effect of cypermethrin on the expression of these genes. Finally, this study permits to better understand the modes of action of cypermethrin at the gene expression level in the mangrove rivulus and to search for correlation with behavioral patterns.

IDENTIFYING TRANSCRIPTOMIC BIAS ACROSS DEVELOPMENTAL SHIFTS IN INSECTS

Sarah CORNET[1*], Stefanie HARTMANN[2], Alice DENNIS[1]

[1] URBE, Dept Biology, University of Namur, 61 rue de Bruxelles, 5000 Namur, Belgium.

[2] Institute of Biochemistry and Biology, University of Postdam, Karl-Liebknecht-Str. 24-25, 14476 Postdam, Germany.

***Presenting author**, **sarcor236@gmail.com**

Keywords: transcriptomic bias, GC content, development, insects.

Synonymous mutations were thought to be evolutionarily neutral as they do not alter the amino acid sequence of proteins. However, these mutations can alter translation efficiency by affecting mRNA folding and splicing. Thus, the accumulation of these mutations and the selective pressure on them can lead to codon usage bias, a preferred use of one type of codon per amino acid. This bias is related to GC content, a higher or lower GC content in the genome can affect the regulation of gene expression via the methylation mechanism. Since this bias occurred in mRNA in *Lysiphlebus fabarum*, we focused on transcriptomic sequences of insects to see if this phenomenon is shared between taxa. Moreover, GC content shifts during development in this species, so we investigated the GC content shift in differentially expressed genes between larvae and adults in Diptera, Hymenoptera and Lepidoptera species.In seven species, RNA sequences obtained from databases were analyzed and compared between larvae, adult males and females for GC content distribution. First results showed a higher GC content in larval transcripts compared to females. A trend is also observed in males, as they appear to have higher GC content in their transcripts than larvae in most species tested. An analysis of GC content in differentially expressed genes among gene families of orthologs with representatives in almost all species examined showed that these genes tend to have higher GC content in Hymenoptera and Diptera. Searching for an explanation, a model based on whole genome GC content in insects showed an association between parasitic behavior and a reduction in mean GC content in Diptera. This study allows us to identify shifts in GC content within species during development, despite a shared genome. The underlying adaptations behind this bias need to be investigated with the provided candidate genes.

INVASION IN THE ROCKS: HOW *BUDDLEJA DAVIDII* DISRUPTS PLANT AND POLLINATOR COMMUNITIES IN QUARRY ECOSYSTEMS

Florian COSA[1*], Clément TOURBEZ[1], Denis MICHEZ[1]

[1] Laboratory of Zoology, Research Institute for Biosciences, University of Mons, 7000 Mons, Belgium.

***Presenting author**, **florian.cosa@student.umons.ac.be**

Keywords: Quarry ecology, Invasive species, Plant-pollinator networks, Wild pollinators.

Exotic plant species increasingly benefit from anthropogenic activities to colonise new habitats. Highly disturbed environments such as quarries serve as biodiversity hotspots, yet face significant threats from invasive species. One major invader in these areas, the butterfly bush (*Buddleja davidii*), competes with native flora, potentially impacting native plant and pollinator communities. Consequently, *B. davidii* invasion may disrupt plant-pollinator interactions, thereby decreasing network stability, particularly in pioneer habitats. As part of the European Life in Quarries project, this study investigates the impact of *B. davidii* across a gradient of invasion on: (i) plant species richness and floral resource availability, (ii) species richness of three main pollinator groups, *i.e.*, wild bees, syrphid flies, and butterflies, and (iii) robustness of plant-pollinator networks. Plant surveys, floral unit counts, and pollinator samplings were conducted from May to September 2024 across 27 sites in nine Belgian quarries, spanning a gradient of invasion levels. We recorded 168 plant species from 32 families, representing over 150,000 floral units, alongside 88 bee, 44 syrphid, and 25 butterfly species, totalling 3,993 pollinator individuals. Plant-pollinator interaction networks were then constructed based on field-observed interactions of all recorded pollinators. This presentation will provide preliminary results on the impact of *B. davidii* invasion on native quarry flora and its subsequent effects on wild pollinators and plant-pollinator network robustness. In the current context of globalisation, understanding how species invasions compromise mutualistic interactions and habitat resilience is increasingly critical.

EVALUATION OF THE POTENTIAL NEUROPROTECTIVE EFFECTS OF GARDENIN A ON PARKINSONIAN SYMPTOMS IN *NOTHOBRANCHIUS FURZERI* EXPOSED TO BIFENTHRIN

Maxime DEBOURCES[1*], Julie HETRU[1,2], Melissa PAGE[2], Frédéric SILVESTRE[1],

[1] Laboratory of Evolutionary and Adaptative Physiology, University of Namur, 61 Rue de Bruxelles, 5000 Namur, Belgium.

[2] Louvain Institute of Biomolecular Science and Technology, UCLouvain, Croix du Sud, 4-5, L7.07.03, B-1348 Louvain-la-Neuve, Belgium

***Presenting author**, **maxime.debources@student.unamur.be**

Keywords: *Notobranchius furzeri*, Aging, Neurodegenerative disease, Bifenthrin

Aging is an inevitable process in all life forms, resulting in physiological, biochemical, and morphological changes that increase the probability of disease's occurrence and death. Moreover, this process is the main factor in the onset of many known chronic diseases, such as cardiovascular disease, cancer or certain neurodegenerative disorders like Alzheimer's or Parkinson's diseases. The onset of these diseases is not solely due to the genetic predisposition of each individual, since we know that exposure to some environmental substances such as pesticides significantly increases the appearance of several neurodegenerative disorders. Bifenthrin, which is a Type I pyrethroid compound exerts numerous harmful effects on many organisms, especially towards the endocrine and dopaminergic systems, thus inducing adverse effects on behaviour and potentially causing a wide range of neurological disorders. On the other hand, neuroprotectants whose aim are to protect the brain of organisms exposed to these neurotoxins can nowadays be synthesized in laboratory. Gardenin A, a hydroxylated polymethoxyflavonoid has recently shown neuroprotective effects against pesticides-induced neurodegenerative phenotypes in drosophila and rodent models. The aim of our study is to demonstrate and characterize the deleterious effects of sublethal exposure to bifenthrin at the behavioral, biochemical and histological levels in *Notobranchius furzeri.* Additionally, we tested whether the gardenin A can prevail or not the neurotoxic effects of bifenthrin in the turquoise killifish. This fish native to southeastern African freshwater ponds is the vertebrate maintained in a lab with the shortest recorded lifespan, which makes it an extremely interesting model for studying age-related diseases more rapidly than in other animals. The great similarity between this emerging model's brain and our own will enable us to better understand the mechanisms by which environmental chemicals can adversely affect our health.

WHAT, IF ANYTHING, IS A HARD EGG? MECHANICAL PROPERTIES OF REPTILE EGGSHELLS AND THEIR ROLE IN INSPIRING NEW MATERIALS

Gerben DEBRUYN[1*], Yana MAUDENS[2], Eva LOCCUFIER[2], Lode DAELEMANS[2], Matthew D. SHAWKEY[1], Karen DE CLERCK[2], Liliana D'ALBA[1,3]

[1] Department of Biology, Evolution and Optics of Nanostructures Group, University of Ghent, Karel Lodewijk Ledegankstraat 35, 9000 Gent, Belgium

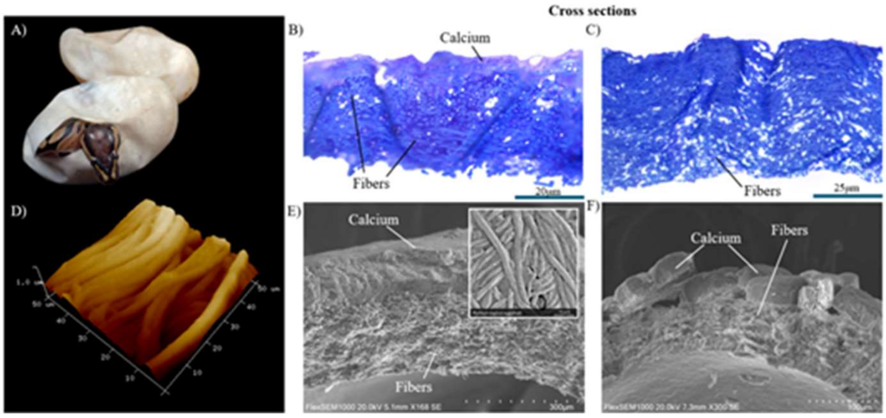
[2] Center for Textile Science and Engineering, Faculty of Engineering and Architecture, Ghent University, Tech Lane Science Park 701, B-9052 Ghent, Belgium

[3] Naturalis Biodiversity Center, Darwinweg 2, 2333 CR Leiden, Netherlands

***Presenting author**, **gerben.debruyn@ugent.be**

Keywords: Reptile eggs, Biomimicking, Comparative analysis, Mechanical testing

Non-avian reptile eggshells show great phenotypical diversity, ranging from thin and paper like to leathery or calcareous and everything in between. This results from adaptations against different selective pressures such as collision damage, abrasion from small particles, or puncture. We currently have a basic understanding of the mechanical properties, mostly focused on highly calcified eggs and one weakly calcified egg, where they are viewed as either rigid or highly flexible, even though recent literature agrees that these eggshells cannot be dichotomized. While the most obvious difference between the eggshell of species is this outermost calcareous layer that forms a thick layer in crocodiles, most turtles, and some squamates, which is generally less thick or sometimes absent in most squamates, and some turtles, there is also a lot of variation in the fibre structure composing these eggshells. Therefore, in this project, we aim to get a more detailed understanding on the mechanical properties and determine how the orientation and proportion of fibres influence this by performing a phylogenetic comparative analysis on 17 species (6 snakes, 10 lizards, and 1 turtle) combining microscopy and tensile strength tests. We found that not only can these eggshells be viewed as bio-composites, consisting of interwoven fibres with various amounts of minerals embedded. They also behave as such. More specifically, we found that the eggshells' stiffness, strength, and toughness vary gradually depending on both the proportion and orientation of the fibres as well as the amount of calcium within the eggshell. These findings highlight that the mechanical properties of non-avian reptile eggshells consist of a gradient rather than two groups and they are not solely determined by the presence of a thick calcified outer layer. They can also serve as inspirations for innovative, sustainable biomimetic designs for producing bio-composites across different fields.



TOO MUCH STRESS? TAKE SOME REST! CHARACTERIZATION OF DORMANCY IN THE SEA SPIDER *AMMOTHEA HILGENDORFI*, A THRIVING INVASIVE SPECIES IN THE NORTH SEA

Benjamin DECOUX[1*], Antoine FLANDROIT[1], Naomie GEERINCKX[1], Raphael CONOTTE[2], Vanessa TAGLIATTI[2], Igor EECKHAUT[1], Guillaume CAULIER[1]

[1] Biology of Marine Organisms and Biomimetics Unit, Research Institute for Biosciences, University of Mons (UMONS), 6 Avenue du Champ de Mars, 7000 Mons, Belgium.

[2] Human Biology and Toxicology, Research Institute for Biosciences, University of Mons (UMONS), 6 Avenue du Champ de Mars, 7000 Mons, Belgium.

***Presenting author, Benjamin.DECOUX@student.umons.ac.be**

Keywords: Dormancy, Metabonomic, Stress-resistance, Pycnogonid

Pycnogonids, most commonly known as sea spiders, are ubiquitous basal chelicerates counting approximately 1,400 species. Despite their unique morphology and ecology, they remain understudied. One of them, called *Ammothea hilgendorfi* (Böhm, 1879), is native to the intertidal zones of the Pacific coasts of the USA and Japan. This species has recently been introduced in Europe and is now highly abundant in Belgium, where it is currently considered invasive. In order to explain the success of this first invasive sea spider species, the present study was carried out on their capacity to withstand different stresses and adapt to new environmental conditions. The organisms were subjected to a vast range of temperatures and salinities for different periods of time. Results revealed that *A. hilgendorfi* exhibits great stress resistance and was even found to be able of entering dormancy. Dormancy has long been a source of fascination for scientists, particularly in the case of invertebrates such as tardigrades and rotifers. Organisms that display dormancy are rare and generally associated with extreme and rapidly changing environments, which require high levels of stress resistance. This phenomenon is frequently accompanied by a reduction in metabolic activity, which can be detected and characterized. To this end, several metabolites of dormant and non-dormant *A. hilgendorfi* were identified and compared using metabonomics (^{1}H-RMN). The findings may lead to a better understanding of pycnogonids dormancy and provide new insights into their ecology. Such discoveries raise questions for future investigations regarding the exact physiological changes that occur in dormant *A. hilgendorfi* and the potential role they might play in their invasion.

EXPLORTING THE CATALYST ROLE OF HYBRIDISATION: INSIGHTS INTO THE SPECIATION DYNAMICS OF LAKE MATANO'S SAILFIN SILVERSIDES

Els L. R. DE KEYZER[1*], Astrid BÖHNE[2], Fabian HERDER[3], Hannes SVARDAL[1,4]

[1] Evolutionary ecology group (EVECO), Department of Biology, University of Antwerp, 2020 Antwerp, Belgium.

[2] Centre for Molecular Biodiversity, Leibniz-Institute for the Analysis of Biodiversity Change (LIB), Museum Koenig Bonn, 53113 Bonn, Germany.

[3] Centre for Taxonomy and Morphology, Leibniz-Institute for the Analysis of Biodiversity Change (LIB), Museum Koenig Bonn, 53113 Bonn, Germany.

[4] Naturalis Biodiversity Center, 2333 Leiden, The Netherlands.

***Presenting author, els.dekeyzer@uantwerpen.be**

Keywords: Speciation, Phylogenomics, Introgression, Fish

While adaptive radiations significantly contribute to global biodiversity, much remains unknown about the genetic and ecological factors driving these rapid speciation events. It has been suggested that hybridisation may facilitate speciation by generating genetic diversity on which diversifying selection can act. We generated whole genome sequences of all species of sailfin silverside fish (*Telmatherinidae*) in Lake Matano, South Sulawesi, Indonesia, one of the world's oldest and deepest lakes. We reconstructed the phylogenetic relationships within this adaptive radiation and inferred past and ongoing introgression patterns. Although genome wide tests confirmed two monophyletic clades, sharpfins and roundfins, we identified discrepancies between morphology-based taxonomic assignments and genome-wide genetic relationships. Evidence for introgression between river-dwelling *Telmatherina bonti* and the lacustrine sharpfin group was indicated by elevated D-statistic, f4-ratios, and f-branch statistics. Notably, signatures of introgression (elevated levels of excess allele sharing) between riverine species and the three most common lacustrine species declined with increasing distance from the river inlet, indicating ongoing introgression at the lake-river interface. An interplay of past and ongoing hybridisation within a radiating species flock positions the *Telmatherina* of Lake Matano a particularly valuable system for investigating fundamental mechanisms driving rapid speciation under genomic exchange. The phylogenomic framework developed in this study lays the groundwork for more in-depth investigations into the processes shaping this charismatic radiation.

NEW INSIGHTS INTO THE EVOLUTION OF BIOLUMINESCENCE IN SEA PENS (PENNATULOIDEA, CNIDARIA)

Jérôme DELROISSE[1,2*], Laurent DUCHATELET[3], Gabriela A. GALEAZZO[4], Constance COUBRIS[3], Laure BRIDOUX[5], Sam DUPONT[6], Marcelo R.S. MELO[7], René REZSOHAZY[5], Anderson G. OLIVEIRA[9], Martin MAREK[10], Patrick FLAMMANG[1], Jérôme MALLEFET[4]

[1] Biology of Marine Organisms and Biomimetics Unit, Research Institute for Biosciences, UMons, 7000 Mons, Belgium.

[2] Laboratory of Cellular and Molecular Biology, GIGA Institute, ULiège, 4000 Liège, Belgium.

[3] Marine Biology Laboratory, Earth and Life Institute, UCLouvain, 1348 Louvain-La-Neuve, Belgium.

[4] Departamento de Oceanografia Física, Química e Geológica, Instituto Oceanográfico, Universidade de São Paulo, 05508-070 São Paulo, Brazil

[5] Animal Molecular and Cellular Biology, Louvain Institute of Biomolecular Science and Technology, UCLouvain,1348 Louvain-La-Neuve, Belgium

[6] Department of Biological & Environmental Sciences, University of Gothenburg, The Sven Lovén Centre for Marine Sciences, Fiskebäckskil, 566 Kristineberg, Sweden.

[7] Departamento de Oceanografia Biológica, Instituto Oceanográfico, Universidade de São Paulo,05508-070 São Paulo, Brazil

[8] Centre for Natural and Human Sciences, Federal University of ABC, 09040-902 Santo André, Brazil.

[9] Department of Chemistry and Biochemistry, Yeshiva University, 10033 New York, USA.

[10] Loschmidt Laboratories, Department of Experimental Biology and RECETOX, Masaryk University,60200 Brno, Czech Republic.

***Presenting author, Jerome.Delroisse@umons.ac.be**

Keywords: Cnidaria, Bioluminescence, Fjord ecology, Molecular evolution

Bioluminescence is the production of visible light by living organisms. It occurs biochemically through the oxidation of specific luciferin substrates, catalysed by enzymes known as luciferases. The bioluminescent reaction also involves auxiliary proteins, such as fluorescent proteins and coelenterazine-binding proteins. These auxiliary proteins may serve various roles, such as altering the wavelength of the emitted light or stabilising the highly reactive luciferin, respectively. Despite the wide variety of bioluminescent species, only a few systems have been fully characterised at the molecular level. In anthozoans, the bioluminescence system of the *Renilla* genus stands out as the sole extensively characterised system, involving a coelenterazine-dependent luciferase, a coelenterazine-binding protein, and a green fluorescent protein.Using a multidisciplinary approach, we investigated the bioluminescent system in three sea pen species: *Pennatula phosphorea, Funiculina quadrangularis*, and *Anthoptilum murrayi* (Pennatuloidea, Anthozoa, Cnidaria). We characterised the emission spectra of the studied species, observing green emission in *P. phosphorea* and *A. murrayi* and blue emission in *F. quadrangularis*. We confirmed the involvement of a coelenterazine-based reaction across all three species. Additionally, we generated reference transcriptomes for *P. phosphorea* and *A. murrayi*, which revealed transcripts encoding luciferases, fluorescent proteins, and coelenterazine-binding proteins, along with insights into their expression profiles. Immunodetections confirmed luciferase expression in *P. phosphorea* and *F. quadrangularis*, while autofluorescence patterns linked to green fluorescent protein and coelenterazine were identified in *P. phosphorea*. Furthermore, the *in vitro* characterisation of recombinantly expressed luciferase from *A. murrayi* validated its bioactivity and blue emission in the isolated luciferase enzyme. Our results indicate a conserved molecular system involved in bioluminescence across these organisms, with an optional involvement of GFPs. This study paves the way for deeper functional and ecological research on these luminous benthic organisms.

VARIED RESPONSES TO URBANISATION IN ABUNDANCE AND BODY SIZE AMONG CLOSELY RELATED SOCIAL WASPS (VESPINAE) IN BRUSSELS, BELGIUM

Max DEVIS[1]*, Thomas MERCKX[1]

[1] WILD, Biology Department, Vrije Universiteit Brussel, Pleinlaan 2, 1050 Brussels, Belgium.

***Presenting author**, **Max.Wim.J.Devis@vub.be**

Keywords: Urban ecology, Body size, Species composition, Vespine wasps

Urbanisation combines several human-induced rapid environmental changes, often resulting in drastic impacts on species diversity, morphology, phenology, and behaviour of various taxa. A trait often investigated in this context is body size, because it is relevant to many aspects of an organism's fitness and life history. Body size is expected to decrease in urban areas due to the urban-heat-island effect and reduced food availability, but urban habitat fragmentation may instead select for larger body size in taxa with positive size-dispersal links. Here, we investigate urbanisation-related changes in diversity and body size of social wasps (subfamily Vespinae) by beer trapping along an urbanisation gradient in Brussels, Belgium. Vespine wasps play important roles in urban ecosystems as pest control agents, pollinators, and decomposers, but are nevertheless understudied and undervalued due to their negative public image. We show that different species of social wasps respond differently to urbanisation, both in terms of their abundances and functional traits. Our findings suggest that native social wasps experience challenges in cities, affecting their species composition, abundance, body size, and phenology, whereas the invasive hornet *Vespa velutina* is less impacted by the urban environment. These changes may negatively affect their ecosystem services capacity, which should be investigated in future studies. To mitigate negative effects of urbanisation on vespines, we suggest implementing various types of urban green space at multiple spatial scales, and working to improve the public perception of this important insect taxon.

EFFECTS OF DNBP AND DEHP ON THE SURVIVAL AND IMMUNITY OF *BOMBUS TERRESTRIS* WORKERS

Justine DEWAELE[1,2]*, Charlotte TERZO[1], Sebastien DUTERNE[1], Audrey PINCHON[1], Anne-Catherine HOLL[2], Yves PIQUOT[2], Nina HAUTEKÈETE[2], Denis MICHEZ[1], Virginie CUVILLIER[2]

[1] Laboratory of Zoology, Research Institute for Biosciences, University of Mons, 20 Place du Parc, 7000 Mons, Belgium

[2] Lab. Evo-Eco-Paleo UMR CNRS 8198, University of Lille, 42 Rue Paul Duez
59000 Lille, France

***Presenting author**, justine.dewaele@umons.ac.be**

Keywords: Phthalates, Lipid metabolism, Environmental exposure, Bombus

Phthalates are volatile molecules used in the petrochemical industry to increase the flexibility of plastic matrices or as solvents for certain detergents, pesticides, etc. Identified as endocrine disruptors in vertebrates, they show effects on the fertility, immunity, and development of aquatic invertebrates. Moreover, their lipophilic nature indicates that terrestrial invertebrates with a lipid cuticle are also exposed to them. In the context of pollinator decline, the effects of phthalates have been little studied in these groups. In urban and agricultural areas, these insects, whose immunity is already weakened by multiple anthropogenic pressures, are exposed to these molecules in varying quantities and profiles. These molecules could therefore act at different levels and disrupt their olfaction, development, and immune system. To investigate these potential impacts, two types of contact exposure experiments were conducted. First, isolated *Bombus terrestris* workers were acutely exposed to the phthalates DnBP and DEHP, and data on mortality, olfaction, metabolism, and immunity was measured. Then, similar exposure was carried out on workers in microcolonies and repeatedly (1x/week) for 35 days. Their mortality and the development of their broods were monitored. The results showed that DnBP at environmental dose increases mortality to 20% within 72 hours of contact exposure in isolated workers, an effect absent in individuals kept in microcolonies. Moreover, repeated exposure in microcolonies show effects of DnBP that tend to increase the lipid level in adult workers after 35 days and to increase the weight of certain larval stages from the same microcolonies. In light of these results, it seems important to deepen research and characterize the effects of phthalates on the regulatory pathways of pollinating insects.

BENTHIC FOOD WEBS IN ANTARCTICA: WOULD YOU CARE FOR SOME MORE (MICRO)ALGAE?

Martin DOGNIEZ[1,2,3*], Davide CADONICI[1,6], Camille MOREAU[4], Lea KATZ[4], Bruno DANIS[4], Axelle BRUSSELMAN[5], Bruno DELILLE[5], Loïc N. MICHEL[6], Isa SCHÖN[2,3], Gilles LEPOINT[1]

[1] Laboratory of Trophic and Isotope Ecology (Freshwater and Oceanic sCiences Unit of reSearch), Université de Liège, 4000 Liège, Belgium

[2] Freshwater Biology Unit (Operational Directorate Natural Environment), Institut Royal des Sciences Naturelles de Belgique, 1000 Bruxelles, Belgium

[3] Centre for Environmental Sciences, Universiteit Hasselt, 3590 Diepenbeek, Belgium

[4] Marine Biology Laboratory, Université Libre de Bruxelles, 1050 Bruxelles, Belgium

[5] Chemical Oceanography Unit (Freshwater and Oceanic sCiences Unit of reSearch), Université de Liège, 4000 Liège, Belgium

[6] Animal Systematics & Diversity Laboratory (Freshwater and Oceanic sCiences Unit of reSearch), Université de Liège, 4000 Liège, Belgium

***Presenting author, martin.dogniez@uliege.be**

Keywords: Trophic ecology, Antarctica, Stable isotopes, Climate change

The West Antarctic Peninsula (WAP) is experiencing rapid warming, which will impact ecosystem processes, particularly sympagic algae dynamics. As these ice-associated microalgae are a vital food source for primary consumers, this disruption is likely to cascade through the communities via trophic interactions. To study these effects, we sampled benthic communities along the WAP in February 2023, focusing on macroalgae forests (n=2) and soft bottoms (n=3) at Dodman Island and Blaiklock Island. Basal resources and benthic invertebrates (n=410, 49 morphospecies) were collected for carbon and nitrogen stable isotope analysis to explore differences in food webs structure between macroalgae forests and soft bottoms, addressing three questions: 1) Are sympagic algae more crucial as basal resources in one of the two habitats? 2) Is there a difference in trophic diversity between macroalgae forests and soft bottoms? 3) How does the vertical food web structure differ between the two habitats? In soft bottoms communities, consumers' stable isotope ratios showed a switch toward higher $\delta^{13}C$ values, typical of sympagic algae in Antarctica. This may suggest a higher vulnerability of WAP soft bottoms communities to alterations of sympagic algae dynamics. Trophic diversity was generally higher in communities with a wider range of basal resources. However, significant local-scale variations in trophic diversity surpassed habitat-related differences, limiting conclusions about habitat influence on trophic diversity. Finally, soft bottoms consumers tended to occupy a higher trophic position than those in macroalgae forests, resulting in a higher mean trophic position at the community scale. This could reflect a diet shift by generalist invertebrates—common in Antarctica—towards increased consumption of more degraded organic matter or necrophagy in habitats with fewer basal resources. Overall, these results underscore the complexity of trophic dynamics in Antarctica, where both local variability and large-scale environmental changes influence food web structure and community resilience to climate change.

INTERSPECIFIC VARIATION IN THE EFFECT OF PESTICIDES ON WILD POLLINATORS

Luca DORIO[1]*, Manon FIEVET[1]*, Kevin TOUGERON[2], Denis MICHEZ[1]

[1] Laboratory of Zoology, University of Mons, 7000, Belgium

[2] Ecology of Global Change and Interactions, University of Mons, 7000, Belgium

***Presenting authors**, Luca.DORIO@umons.ac.be, Manon.FIEVET2@umons.ac.be**

Keywords: Pesticides, Wild pollinators, Ecotoxicology

Human imprint on earth leads to massive changes in earth ecosystems, including the introduction of a multitude of chemicals in the environment. These pollutants are primary drivers in the sharp decline of wildlife. For wild pollinator species, these xenobiotics come mainly from the development of intensive agricultural practices, including the spread of pesticides.

Wild pollinators provide unmatched ecosystemic services by ensuring the sexual reproduction of wild plant communities and improve crop yields (i.e. pollination). Given their importance, understanding pesticide effects on wild pollinators is essential. However, current testing protocols primarily focus on a few models of domesticated species (e.g. honeybees, bumblebees), excluding a wide range of wild pollinators — a discordant approach, considering that wild pollinating insects exhibit significant morphological and physiological differences.

Assessing and characterizing these interspecific differences among pollinators exposed to pesticides is one of the main objectives of the European WildPosh project (Horizon program, 2024-2028). Lethal and sublethal effects of three pesticides from main product categories (i.e. Acetamiprid, Cypermethrin and Tebuconazole) are tested in controlled conditions on different species of wild bees and butterflies, at different life stages (larvae and adults), when possible, and compared with a domesticated reference species, the buff-tailed bumblebee (*Bombus terrestris* L.). First results indicate that wild bees appear to be more sensitive to pesticides than its domestic counterpart.

CLIMATE CHANGE THREATS AND CONSERVATION CHALLENGES FOR THE ENDANGERED JAPANESE GIANT SALAMANDER (*Andrias japonicus*)

Clément DURET[1*], Tiphanie BARTET[1], Alain HAMBUCKERS[2], Osamu KISHIDA[3], Sumio OKADA[4], Yuki TAGUCHI[5], Mizuki K. TAKAHASHI[4,6] and Mathieu DENOËL[1]

[1] Laboratory of Ecology and Conservation of Amphibians (LECA), Freshwater and OCeanic science Unit of reSearch (FOCUS), University of Liège, 4000, Liège, Belgium

[2] Unit of Research SPHERES, University of Liège, 4000, Liège, Belgium

[3] Wakayama Experimental Forest, Field Science Center for Northern Biosphere, Hokkaido University, Sapporo, 001, Hokkaido, Japan

[4] The Hanzaki Research Institute of Japan, Asago, 652–0000, Hyogo, Japan

[5] Asahi Hanzaki Research Association, 730-0000, Hiroshima, Japan

[6] Department of Biology, Bucknell University, 17837, Lewisburg, Pennsylvania, USA

***Presenting author, clement.duret@uliege.be**

Keywords: Climate change, Ecology, Giant salamanders, Habitat suitability

Giant salamanders are the world's largest species of amphibians and play a key role as large predators in riverine environments. Like many other amphibians, they are experiencing population declines and are particularly vulnerable to various threats. Identifying environmental variables influencing their distribution is crucial for their conservation, and predicting the impacts of climate change on their future distribution is essential for making informed and appropriate conservation decisions. This study assesses the current habitat suitability and distribution of the Japanese giant salamander (*Andrias japonicus*) and predicts changes under future climate scenarios. Using species distribution models including a large number of occurrence data points and multiple environmental predictors, we projected habitat suitability maps, identified key contributing variables, and calculated shifts in suitable areas for three future time periods under projected climate conditions. Climatic variables were the dominant factors influencing salamander distribution, with preferences for areas with moderate precipitation and mild summer temperatures. Local topography also influenced their distribution, while land cover had less influence. Our results highlight the serious risks posed by climate change, which is predicted to significantly reduce suitable habitat for giant salamanders. By identifying the variables that influence species distribution and examining the effects of climate change, we expose the global threats facing this species. These results provide important insights for future conservation strategies, helping to delineate priority areas that are less vulnerable to climate change and emphasizing the urgent need for further research on local habitat disturbances to better protect giant salamanders.

STUDY OF THE SOUND-PRODUCING APPARATUS OF TWO CARIBBEAN BOXFISHES, *LACTOPHRYS TRIQUETER* AND *ACANTHOSTRACION POLYGONIUS*

Louise ECHE[1*], Marc THIRY[2], Eric PARMENTIER[3]

[1] Laboratory of Functional and Evolutionary Morphology, Department of Biology, Ecology, Evolution, FOCUS, University of Liège, 4000 Liège, Belgium.

[2] Cellular Biology, Department of Life sciences, GIGA, University of Liège, 4020 Liège, Belgium.

[3] Laboratory of Functional and Evolutionary Morphology, Department of Biology, Ecology, Evolution, FOCUS, University of Liège, 4000 Liège, Belgium.

***Presenting author, louise.eche@uliege.be**

Keywords: Bioacoustics, Morphology, Sound production, Ostraciidae

The first studies on the production of sounds in different Indo-Pacific Ostraciidae species from *Ostracion* and *Lactoria* genera have highlighted different unique features. One intriguing morphological feature is the presence of two muscles positioned at right angles to each other, located at the anterior region of the swim bladder. This unique anatomical arrangement enables them to produce two distinct types of sounds in a sequential manner, with prolonged hums interspersed by pronounced clicks.

In this study, our focus shifts to the Atlantic Ostraciidae, investigating for the first time the sound-producing mechanism of *Lactophrys triqueter* and *Acanthostracion polygonius*. Both species have demonstrated the capacity to generate sounds. The sound-producing mechanism in Atlantic species displays an entirely novel and distinctive design. Whereas sound-producing apparatus using the swimbladder are usually composed of the latter and sonic muscles inserted on it, the system in Atlantic Ostraciidae comprises two spherical masses applied to the swim bladder fenestra, a region lacking the tunica externa, situated at the dorso-rostral end of the swimbladder. These spherical masses are entirely enveloped by sound-producing muscles possessing characteristics typical of fast-contracting muscles. The contraction of these muscles propels the spherical masses within the swimbladder, thus initiating the production of sounds. Histological investigations showed that the spherical masses are composed of connective tissue evaginating from the submucosa of the tunica externa. This new kind of sound-producing mechanism in Atlantic species diverges significantly from that observed in their Pacific counterparts. Additional comprehensive studies on the acoustic abilities of Ostraciidae and the evolutionary origins of this unique sound-producing mechanism are required to gain a comprehensive understanding of these intriguing biological adaptations.

HIDING INEQUALITIES BEHIND RICHNESS: HOW URBAN LANDSCAPES SHAPE WILD BEE COMMUNITIES

William FIORDALISO[1]*, Sara REVERTE[2], Guillaume GHISBAIN[2,3], Thomas WOOD[2], Eulalie RUELLE[2], Alexandre LEFEBVRE[2], Alexandre REESE[2], Martin LOOCKX[2], Denis MICHEZ[2+], Kévin TOUGERON[1+]

[1]Laboratory of Interaction Ecology and Global Change, University of Mons, 7000 Mons, Belgium.

[2]Laboratory of Zoology, University of Mons, 7000 Mons, Belgium.

[3]Spatial Epidemiology Lab (SpELL), Free University of Brussels, 1000 Brussels, Belgium

[+] Co-last authors.

***Presenting author**, **william.fiordaliso@umons.ac.be**

Keywords: Urban ecology, Wild bees, Nature reserves, Threatened species.

Post-industrial landscapes such as the one found in Northern Europe Belgium are home to an impoverished community of pollinators, probably as a byproduct of ever-increasing urbanization and intensive agriculture. Yet, cities within this type of environment have been found to host surprisingly diverse assemblages of bees around the globe. This observation suggests that urban areas might serve as unconventional refuges for pollinators, potentially informing local conservation strategies beyond traditional nature reserves. However, the apparent richness found in urban areas may hide ambiguous patterns of diversity, especially when it comes to the distribution of rare or endangered species.

Our aim was to determine the effect of urbanization on wild bee richness and evenness using increasing orders of entropic diversity. Conservation significance was also assessed by quantifying IUCN threatened species. The relative significance of protected areas in the conservation of wild bees was examined by comparing their patterns of diversity to the one found in unprotected areas. Our findings indicate that while urbanization may not have a positive effect on raw species richness, urban areas harbor a more diverse set of dominant species, albeit with a conspicuous absence of threatened ones. In contrast, flower-rich grasslands, though similar in overall diversity to other habitats, tend to concentrate rare and declining species. Surprisingly, nature reserves in this landscape show lower diversity indices, a pattern likely driven by their predominantly forested habitats.

Our results suggest that the decline of threatened species in urban environments may be masked by high diversity among abundant species, a pattern detectable only through multiple metrics of conservation value. In addition, we reveal that existing networks of protected areas in the landscape may not be able to mitigate this decline, as reserves are not necessarily designed for the conservation of all species and may be biased towards certain types of environments.

HOW SEAHORSES GOT SACKED: STRUCTURAL AND FUNCTIONAL ANALYSIS OF THE TAIL MUSCLE SAC IN A PREHENSILE TAIL

Danial FOROUHAR[1,2*], Barbara DE KEGEL[1], Francis WYFFELS[2], Dominique ADRIAENS[1]

[1] Ghent University, Evolutionary Morphology of Vertebrates, Department of Biology, 9000, Belgium.

[2] Ghent University— imec, IDLab-AIRO, Faculty of Engineering and Architecture, 9052, Belgium.

***Presenting author, Danial.forouhar@ugent.be**

Keywords: Prehensile tail, Musculoskeletal Adaptation, Seahorse, Biomimetics

Seahorses and pipehorses exhibit prehensile capabilities, using their tails to hold onto objects or mates. This functional adaptation is facilitated by unique musculoskeletal structures, including large gaps between bony plates (BP), highly specialised joints and a unique hypaxial muscle architecture. The prehensile tail actuates through a combination of active and passive mechanisms, with a capacity for extensive ventral bending. Active actuation in ventral bending is primarily driven by axial forces generated by the medioventral muscle and parallel hypaxial muscle bundles. While medioventral muscles are found in prehensile seahorses and pipehorses and not in non-prehensile pipefishes, the parallel hypaxial muscle organisation is unique to seahorses. This hypaxial muscle complex is enclosed in a thin connective tissue layer, seemingly forming a long "muscle sac" detached from the surrounding skeleton. Yet, hypaxial muscle forces are transferred to the skeletal components via parallel myosepta, extending diagonally over multiple segments inside the sac and inserting into the body armour plates. However, the precise morphology and function of this sac, particularly its attachment points to the vertebral column (VC) and BP and, hence, its role in force transfer, remain unclear. At the same time, it can play an important role in force and pressure distribution inside the bony plate cage. To investigate the morphology of the sacs and their attachment points, we employed contrast-stained, high-resolution micro-computed tomography (µCT) scans to visualise the musculoskeletal structures of the seahorse tail in 3D. The µCT data were compared with dissected specimens to observe patterns and gain insights into how the muscle sac mechanically interacts with the VC and BP. This combined approach provided a clearer understanding of the muscle sac's structural arrangement and its potential role in enhancing the tail’s prehensile capabilities. These findings are crucial for further understanding the biomechanics of seahorse tail prehension, as supported by recent studies on musculoskeletal adaptations in prehensile structures across various species and forming a well-integrated base for robotic designs.

BREEDING HABITAT SELECTION AND MORPHOLOGY OF THE GREAT CRESTED NEWT (*TRITURUS CRISTATUS)*, THE MARBLED NEWT (*TRITURUS MARMORATUS)*, AND THEIR HYBRIDS AT THE SOUTHERN EDGE OF THEIR CONTACT ZONE

Mathilde FOUCTEAU[1,2*], Yann SELLIER[3], Nicolas TITEUX[1], Olivier LOURDAIS[2],

[1] Luxembourg Institute of Science and Technology, 4422 Belvaux, Luxembourg.

[2] Centre d'Etudes Biologiques de Chizé, CNRS UMR 7372, Villiers en Bois, France

[3] Réserve Naturelle Nationale du Pinail, GEREPI, 86210 Vouneuil-sur-Vienne, France.

***Presenting author, mathilde.foucteau@list.lu**

Keywords: Habitat selection, Morphometry, Amphibians

Amphibians are increasingly vulnerable to climate change, particularly at range edges where environmental conditions are most constraining. Examining how organisms respond there to environmental pressures offers key insights into ecological factors shaping their resilience, persistence and interactions. While habitat selection reflects species' requirements along abiotic gradients and biotic interactions, morphological traits provide insight into physical characteristics that may influence ecological roles and competitive dynamics. Contact zones between parapatric species, such as the cold-adapted great crested newt (*Triturus cristatus*) and warm-adapted marbled newt (*Triturus marmoratus*), offer a unique opportunity to study biotic interactions, including competition and hybridization. The Pinail National Natural Reserve which encompasses over 6000 ponds, provides an ideal setting to study these processes at the southern range margin of T. cristatus, where environmental conditions may exert differing pressures on each species.

In this study we examined (i) breeding habitat selection and (ii) morphological traits (body size, body proportions) in *T. cristatus*, *T. marmoratus*, and their hybrids. Amphicapt traps were deployed to assess newt's presence and distribution in ponds. Morphometric data were collected from captured individuals, including measurements of body length, head width, and tail length. Statistical analyses showed that *T. cristatus* probability of occupancy was associated to ponds with lower water conductivity, while *T. marmoratus* preferred small ponds. *T. cristatus* strictly avoided ponds with fish, while *T. marmoratus* showed occasional presence in fish-inhabited ponds, suggesting a higher tolerance to this biotic constraint. Morphometric analyses revealed that *T. cristatus* is characterized by an elongated snout-vent length, while *T. marmoratus* has a large mouth, potentially advantageous for consuming large prey items. Hybrids exhibit intermediate traits proportions but an increased height and body mass relative to the parental species. This study provides support for future work on ecomorphology and habitat use of parapatric newt species in the Pinail National Natural Reserve.

HIT ME (SWIM) BLADDER ONE MORE TIME

Romane FREY[1*], Philippe COMPERE[1], Eric PARMENTIER[1]

[1] Laboratory of Functional and Evolutionary Morphology, University of Liège, 4000 Liège, Belgium.

***Presenting author**, **romane.frey@uliege.be**

Keywords: Biomechanics, Bioacoustics, Morphology

In teleost fishes, the swim bladder is an organ filled with gaz that, in addition to providing buoyancy, plays a role in hearing and, in some species, in acoustic communication. Although several studies in different species have demonstrated that the swim bladder has a prominent role in sound production, its function in this process remains largely unknown in the absence of extensive studies on the subject. A first approach, borned in the 60's, considered the swim bladder as a « resonant bubble » which describes it as an omnidirectional resonant gaz bubble, i.e. an acoustic monopol. This theory has been rarely discussed even though literature described, since then, an unusual high damping rate for a free bubble. Wrongly justified by the properties of the surroundings tissues, we show that this damping property is in fact an intrinsic property of the swim bladder, the organ fails to resonate. For the species with sonic muscles, sounds are more likely to be the result of a forced response to muscular contraction and should not be amplified at the eigenfrequencies of the swim bladder.

SOCIAL SELECTION DRIVES THE EVOLUTION OF FACIAL COLOR PATTERNS IN COOPERATIVE BREEDING CICHLIDS

Jarne MELIS[1,2], Toon VERBEECK[1,2], Hannah WELLER[3], Steven VAN BELLEGHEM[1], Hugo F. GANTE[1,2*]

[1] Department of Biology, KU Leuven, 3000 Leuven, Belgium.

[2] Department of Biology, Royal Museum for Central Africa, 3080 Tervuren, Belgium.

[3] Helsinki Institute of Life Sciences, University of Helsinki, 00790 Helsinki, Finland.

*** Presenting author, hugo.gante@kuleuven.be**

Keywords: Social selection, Pigmentation, Animal communication, Honest signaling

Color patterns in animals serve diverse functions, from camouflage to communication in social and mating contexts, particularly in visually oriented species. In cichlid fishes, color patterns are especially varied, often varying between but also within species. Lake Tanganyika cichlids of the *Neolamprologus savoryi* complex are the only known cooperatively breeding fishes, forming tightly knit families that live and defend a common territory on rocky shore habitat.

Many species of this complex display striking differences in facial color patterns despite occupying similar ecological niches. In two species, *N. brichardi* and *N. pulcher*, facial color patterns are known to be involved in the signaling of fighting ability and individual recognition. While sexual selection is a known driver of the evolution of color patterns in many cichlids, these *Neolamprologus*species are sexually monochromatic, making sexual selection an unlikely mechanism behind the observed phenotypic variation.

Using over 500 photographs of the entire complex from across Lake Tanganyika, and employing an analysis workflow that involves image alignment, color segmentation and color analysis, we demonstrate that two species display the majority of observed variation in facial colors in this complex. Importantly, we found that the levels of between-population variation exceed those of within-population variation. This observation is consistent with social selection driving the evolution of this color pattern. We discuss these findings in light of social selection, cooperative breeding, and honest signaling.

THE NEW EUROPEAN RED LIST OF BEES

Guillaume GHISBAIN[1*], Mira BOUSTANI[1], Ahlam SENTIL[1], Denis MICHEZ[1]

[1] Laboratory of Zoology, Department of Biology, University of Mons (UMONS), 7000 Mons, Belgium.

***Presenting author**, **guillaume.ghisbain@umons.ac.be**

Keywords: Wild bees, Conservation, Global change biology

Biodiversity provides essential resources and ecosystem services that are foundational for sustainable development. Consequently, its degradation represents one of the most urgent global challenges, and robust data on biodiversity status is critical for informing policies and developing frameworks to mitigate this loss. In this context, insect pollinators have become a focal point of conservation efforts. Under the guidance of the International Union for Conservation of Nature (IUCN), the University of Mons, in collaboration with partners across Europe, has led the development of a new Red List assessment for the continent's >2000 bee species. In this presentation, we share preliminary findings from this ongoing project, scheduled for publication in 2025. We report on the proportion of species currently classified under various IUCN categories, from Least Concern to Extinct in the Wild, and examine the drivers of wild bee decline across Europe, focusing on the proximate mechanisms driving declines at the community level among these crucial pollinators.

TO COLOUR OR NOT TO COLOUR: COLOUR PATTERNS AND PIGMENTS IN INVERTEBRATES FROM THE PALAEOZOIC OF BELGIUM

Stijn GOOLAERTS[1*], Christian BURLET[1], Pierre GUERIAU[2,3], Aurore MATHYS[1,4,5],
Sebastian SCHOEDER[6], Mathieu THOURY[2], Bernard MOTTEQUIN[1]

[1] OD Earth & History of Life, Royal Belgian Institute of Natural Sciences, Vautierstraat 29, 1000 Brussels, Belgium.

[2] IPANEMA, site du Synchrotron SOLEIL, BP 48 Saint-Aubin, 91192 Gif-sur-Yvette, France.

[3] Institute of Earth Sciences, University of Lausanne, CH-1015 Lausanne, Switzerland.

[4] Royal Museum for Central Africa, Leuvensesteenweg 13, 3080 Tervuren, Belgium.

[5] Faculty of Architecture, Art, Archaeology and Heritage unit, University of Liège, Boulevard de la Constitution, 4020 Liège, Belgium.

[6] PUMA Beamline, Synchrotron SOLEIL, L'Orme des Merisiers, 91190 Saint-Aubin, France.

***Presenting author**, **sgoolaerts@naturalsciences.be**

Keywords: Evolution, Shell, Mollusca, Brachiopoda

Almost nothing is known about the evolution of shell colour in invertebrates. This is largely due to the ultra-rarity of fossils in which colour patterns and pigments are preserved and immediately visible, and therefore easy to identify, especially when these are hundreds of millions of years old. This hampers our understanding of the role and function of colour in extinct animals, their ecology, mode of life, interactions, development, and evolution. A good example for this ultra-rarity is the Palaeozoic of Belgium, world-renowned for its exquisitely preserved fossils of the Devonian and Carboniferous, enabling to document major transitions in ecosystem dynamics and the evolution of life on Earth (e.g. nekton revolution, terrestrialisation, major climate changes, anoxic events, biodiversity crises) but from which only a few cephalopod, bivalve and gastropod mollusc and brachiopod shells were historically documented preserving coloured traces (mostly by L.-G. de Koninck and P. de Ryckholt, mid to late 19th century). However, recently, it was discovered that many more specimens preserve these traces, in particular those from Tournaisian–Viséan shallow marine reef environments, allowing to investigate its occurrence in different evolutionary lineages of marine invertebrates exactly during one of the main periods of revolution in geologic history.

In Brain project B2/P233/P2 nicknamed COLOURINPALAEO financed by Belspo, after gathering all the specimens available in the main Belgian collections, we use different techniques (multispectral photogrammetry and spectro-imaging) to better visualise the preserved colour patterns and pigments. Furthermore, advanced spectroscopic techniques, namely Raman micro-probe spectroscopy, synchrotron trace elemental mapping and absorption spectroscopy, are used to identify the chemical signature of the pigments as well as their mode and pathways of preservation. Some of the first results on this multidisciplinary study on a unique set of Belgian fossils will be presented.

THE GREAT PUZZLE OF THE GREAT LAKES: UNCOVERING THE COMPLEX HYBRID ORIGINS OF THE LAKE MALAWI CICHLID RADIATION

Sophie GRESHAM[1*], Bosco RUSUWA[2], Maxon NGOCHERA[3], F. George TURNER[4], J. Martin GENNER[5], Milan MALINSKY[6], Hannes SVARDAL[1,7]

[1] Evolutionary Ecology Group, Department of Biology, University of Antwerp, 2610 Wilrijk, Belgium.

[2] Department of Biological Sciences, Chancellor College, University of Malawi, Zomba, Malawi.

[3] Department of Fisheries, Ministry of Natural Resources & Climate Change, P.O. Box 593 Lilongwe, Malawi.

[4] School of Natural Sciences, Bangor University, LL57 2TH Bangor, United Kingdom.

[5] School of Biological Sciences, University of Bristol, BS8 1TQ Bristol, United Kingdom.

[6] Department of Biology, Institute of Ecology and Evolution, University of Bern, 3012 Bern, Switzerland.

[7] Naturalis Biodiversity Centre, 2333 Leiden, The Netherlands.

***Presenting author, sophie.gresham@uantwerpen.be**

Keywords: Adaptive radiation, Lake Malawi cichlid, Introgression, ABBA BABA

In the new era of genomics, a growing number of studies have revealed that gene flow between closely related species is surprisingly common across the tree of life. Although gene flow was traditionally seen as a barrier to speciation, evidence from many animal and plant systems, particularly those involving adaptive radiations, now supports the role of gene flow in promoting ecological adaptation and speciation by spreading beneficial variants amongst diverging lineages. In the case of the Lake Malawi cichlid fish radiation – comprising ~800 ecologically and phenotypically diverse species that evolved within the last 800 KY – gene flow has been identified as an important factor in its early formation. However, many potential gene flow sources into the radiation remain unexamined.

Here, we used whole genome sequencing data from 239 cichlid species from Lake Malawi and a comprehensive dataset of 76 species from surrounding African riverine and lake systems to discover and map previously unknown introgression events into the Malawi cichlid radiation. Using genome-wide excess allele sharing (D-statistics) and window-based analyses, we discovered three new independent riverine cichlid lineages showed consistent signatures of gene flow with the Malawi radiation. Amongst Malawi species we found low variability in the measured levels of gene flow, indicating that these gene flow events occurred before or during the formation of the radiation and that introgressed haplotypes are distributed evenly across Malawi species. We also find the first evidence of contemporary gene flow between Malawi and riverine species, which could potentially further fuel ongoing adaptation.

Overall, our results point towards several previously unknown lineages that contributed to the formation of the Malawi radiation, raising the total number of contributing lineages to five - the largest known for any adaptive radiation.

GENERATING FAIR AND OPEN BIODIVERSITY DATA IN THE FIELD: A CASE STUDY ON BOLIVIAN FISH DIVERSITY

Pascal I HABLÜTZEL[1,2*], Robert BLANCO HUANTO[3], Els L. R. DE KEYZER[4]

[1] Research Department, Flanders Marien Institute (VLIZ), Jacobsenstraat 1, 8400 Oostende, Belgium

[2] Biology Department, Vrije Universiteit Brussel, Pleinlaan 2, 1050 Elsene, Belgium

[3] Department of Eco-pisciculture, UNIBOL Guaraní y Pueblos de Tierras Bajas "Apiaguaiki Tüpa", Ivo, Bolivia

[4] EVECO, Universiteit Antwerpen, Universiteitslaan 1, 2020 Antwerpen, Belgium

***Presenting author, pascal.hablutzel@vliz.be**

Keywords: Molecular genetics, Nanopore sequencing, Conservation, Freshwater

Biodiversity science cannot keep up with the demand for data on occurrence, abundance and distributions of species. Data which is vital for effective species and ecosystem conservation should have been available to us years ago, and every delay in obtaining this information increases the risk for irreplaceable loss of species and ecosystem functions. Fortunately, there is continuous technological advancement to enable us to generate increasingly large amounts of data at an unprecedented rate. For example, hand-held DNA sequencers even enable obtaining genetic barcodes of collected specimens on site. If we take the FAIR principles at heart, we will be able to generate a digital data ecosystem from which ecologists, taxonomists and conservationists can source the data vital to their activities. In this project, we conducted a rapid biodiversity assessment in an understudied, biodiverse region. We collected fishes in the northern Pantanal in Bolivia across the watershed to the Amazon. This area has only very rarely been visited by ichthyologists. In total, we observed more than 150 fish species over the course of two weeks, several of them new to science. We photographically documented the life colouration and took tissue samples for genetic analysis. We then applied a customized sequencing protocol to barcode the fishes at the COI gene using nanopore technology. By involving students from indigenous communities in every step, from sampling over sequencing and storage, we take a small but significant step towards empowering local scientists to be at the forefront of cataloguing their own biodiversity using current technology and practices. Samples were deposited in the ichthyological collection of the fish collection of the UNIBOL Guaraní y Pueblos de Tierras Bajas "Apiaguaiki Tüpa". In order to serve the data to many researchers in an efficient manner, we adhere to common metadata standards and present the data as a knowledge graph using a resource description framework (RDF) representation.

THE REDOX-GUIDED BLUEPRINT OF REGENERATION: LESSONS FROM PLANARIANS

Martijn HELEVEN[1]*, M. DOLORES MOLINA[2], Vincent JAENEN[1], Karolien BIJNENS[1], Francesc CEBRIA[3,4], Karen SMEETS[1]

[1] Zoology: Biodiversity and Toxicology; Centre for Environmental Sciences at Hasselt University, Agoralaan Gebouw D 3590 Diepenbeek, Belgium.

[2] Department of Bioengineering, IQS School of Engineering, University of Ramon Llull, Barcelona, Catalonia, Spain.

[3] Department of Genetics, Microbiology & Statistics; Faculty of Biology; University of Barcelona, Barcelona, Catalonia, Spain.

[4] Institute of Biomedicine of the University of Barcelona (IBUB); University of Barcelona, Barcelona, Catalonia, Spain.

***Presenting author, martijn.heleven@uhasselt.be**

Keywords: Regeneration, Stem cells, Planarians, Reactive oxygen species

Regeneration is a fascinating process that allows organisms to restore and replace damaged or lost body parts following injury. Reactive oxygen species (ROS) have been shown to play important signaling roles in the cellular events underlying tissue renewal. An amputation-induced ROS burst has been observed in many regenerative models, and its absence often results in significant regenerative defects. In this project, the highly regenerative planarian *Schmidtea mediterranea* was used to study the interaction between adult pluripotent stem cells and redox signals during tissue regeneration. Planarians possess remarkable plasticity, enabling them to regrow an entire functional body from small tissue fragments within 7 to 14 days after injury, making them ideal for investigating cellular and molecular mechanisms of tissue renewal. Using real time in vivo imaging, we identified a rapid accumulation of ROS, such as superoxide and hydrogen peroxide, at the injury site immediately after wounding. Amputation-induced ROS production was shown to be critical for regeneration as blocking ROS production significantly impaired regeneration. Both superoxide and hydrogen peroxide activity levels fluctuate based on the wound location along the anterior-posterior body (AP) axis. These positional redox differences resulted in AP-dependent activation of the MAPK/ERK pathway, thereby influencing polarity decisions as early as 3–6 hours post-amputation. ROS-mediated, AP-dependent activation of ERK was maintained by wound-dependent antioxidant levels and potentially regulated via the MAPK/ERK-related transcription factor egr-4. Finally, we identified functional and/ or positional links between amputation-induced redox changes, pERK, and other redox-induced transcription factors. Overall, this research provides deeper insights into the role of ROS-mediated MAPK/ERK activation in coordinating positional information after injury in *Schmidtea mediterranea*, shedding light on potential broader mechanisms in regenerative biology.

A PICTURE IS WORTH A THOUSAND WORDS: THE ROLE OF MACROPHOTOGRAPHY IN WILD BEE CONSERVATION BIOLOGY IN LUXEMBOURG

Fernanda HERRERA-MESÍAS[1-3*], Antonio CRUZ[1,3], Anna HAUPRICH[1,3,4], Amanda LUTTRINGER[1,3], Alexander WEIGAND[1,3]

[1] Zoology Department, Musée national d'histoire naturelle de Luxembourg (MNHNL), 25 rue Münster, 2160, Luxembourg, Luxembourg

[2] Department of Animal Ecology, Evolution and Biodiversity, Ruhr-Universität Bochum, Universitätsstraße 04/495, 44801, Bochum, Germany

[3] Fondation Faune-Flore, 25 Rue Münster, 2160 Luxembourg, Luxembourg

[4] University of Hohenheim, 70593 Stuttgart, Germany

***Presenting author, Fernanda.Herrera@ext.mnhn.lu**

Keywords: Hymenoptera, Pollinators, Taxonomy, Keartonian impediment

Developing evidence-based, targeted conservation strategies require not only to be aware of the existing knowledge regarding the taxa of interest, but also of its potential limitations and gaps, thus, to ultimately identify the right questions to be answered. The more robust the body of data, the more straightforward it is to define proper conservation priorities. However, for many groups of insect pollinators, there are still important biodiversity information gaps that hinder our capacity to answer some of the most crucial questions on this matter. Despite wild bees being among the better-studied insect groups in Europe, there are still significant data shortfalls that increase the level of uncertainty of conservation initiatives. One of these shortfalls is the "Keartonian impediment," meaning the absence of high-quality and publicly available visual representations of the appearance of several wild bee species. This impediment affects the accuracy of taxonomic identification and biases our understanding of other aspects of wild bee research, including biogeographical distribution, ecological interactions, and evolutionary relationships. Therefore, it is fundamental to improve current reference data on relevant diagnostic characters for identification purposes. Here we describe the concept and preliminary results of the beelibre project, which intends to fill in these gaps on a local scale by building the first repository of high-quality visual reference material of the wild bee fauna of Luxembourg. This project addresses the limitations imposed by the Keartonian impediment by building a collection of high-resolution, open access *in situ* photographs of local species. By doing so, the beelibre project aims not only to help solve some of the most pressing shortfalls on the study of European wild bees, but also to lay the foundations for the development of new technologies for insect monitoring and to promote social change in favor of local pollinator groups.

CAMERA TRAP SAMPLING DESIGN MODIFICATIONS IN LONG-TERM ECOLOGICAL MONITORING: IMPLICATIONS ON WILDLIFE ACTIVITY ESTIMATION

Siebe INDESTEGE[1]*, Martijn BOLLEN[1,2], Jim CASAER[2], Natalie BEENAERTS[1]

[1] Centre for Environmental Sciences, Hasselt University, Martelarenlaan 42 Hasselt, 3500, Belgium.

[2] Research Institute for Nature and Forest (INBO), Havenlaan 88 Brussels, 1000, Belgium.

***Presenting author**, **siebe.indestege@uhasselt.be**

Keywords: Sampling designs, Activity patterns, Camera traps, Long-term ecological monitoring

Long-Term Ecological Monitoring (LTEM) is essential to study ecological phenomena over extended temporal scales, though it is challenging due to its long wait for results, high costs, labor intensity, and restrictions of their sampling designs. The possibility to alter the sampling design within a LTEM framework to address specific ecological questions may increase attractiveness, affordability and feasibility of LTEM research. We investigated the difference in activity levels and patterns of roe deer *Capreolus capreolus* and wild boar *Sus scrofa* as inferred from two different camera trap sampling designs within the same LTEM project in National Park Hoge Kempen (Belgium). From May 2017 to May 2020, a systematic random sampling design was employed, followed by a stratified random sampling design from May 2020 to May 2023. The sampling designs differed in number of camera traps deployed, deployment times, and amount of spatial variation and temporal replication. Activity levels and patterns were analyzed over three-year periods for each design and across individual sampling years to compare inferred differences between and within sampling designs. We reveal significant variability in activity patterns, though not in activity levels, for both species across sampling designs. However, activity patterns for either species differed significantly between most pairwise year-to-year comparisons, and some activity levels as well. Hence, we discovered highly variable activity pattern estimations between and within sampling designs. Despite the sequential rather than parallel use of the sampling designs, our results indicate the differences in inferred activity patterns are more likely attributable to ecological and environmental factors than methodological differences. Hence, within the context of one long-term ecological monitoring project, the sampling design may be altered to address specific ecological questions concerning wildlife activity.

ENERGIZED AND EFFICIENT: HOW MITOCHONDRIA AND DIGESTIVE EFFICIENCY DRIVE FASTER PACE-OF-LIFE IN A RANGE-EXPANDING SPECIES

Sarah JORISSEN[1]*, Lieve DEWALLEF[1], Tibo GILLET[1], Eléonore POTTIER[1], Bram DECRU[2], Pieter VERMEERSCH[2], Nicolas PICHAUD[3,4], Steven VAN BELLEGHEM[5], Janne SWAEGERS[1], Robby STOKS[1]

[1] Evolutionary Stress Ecology and Ecotoxicology, University of Leuven, Charles Deberiotstraat 32, B-3000, Leuven, Belgium

[2] Department of Cardiovascular Sciences, University of Leuven, and Department of Laboratory Medicine, University Hospital Leuven, B-3000, Leuven, Belgium

[3] New Brunswick Centre for Precision Medicine, Moncton, NB-E1A 3E9, New Brunswick, Canada

[4] Department of Chemistry and Biochemistry, Université de Moncton, NB-E1A 3E9, Moncton, New Brunswick, Canada

[5] Eco-Evolutionary Genomics, University of Leuven, Charles Deberiotstraat 32, B-3000, Leuven, Belgium

***Presenting author,* sarah.jorissen@kuleuven.be**

Keywords: Pace-of-life, Mitochondrial efficiency, Food digestive metabolism, Range expansion

It is hypothesized that, apart from food digestive metabolism, mitochondrial efficiency contributes to variations in pace-of-life (POL) across different thermal regimes in insects. To explore this relationship, we investigated the Spanish range expansion of the damselfly *Ischnura elegans*, where populations encounter warmer temperatures. Alongside the ancestral populations from colder regions in France, we studied two additional populations from warmer regions in Spain: (i) ‘new edge populations’ founded ~10 years ago in Salamanca and (ii) ‘old edge populations’ founded ~70 years ago in Murcia-Alicante. In a common garden experiment, larvae and adults from the three regions were exposed to the summer temperatures of both the ancestral French region and the invaded Spanish regions. Our results confirmed that the old edge Spanish populations evolved a faster POL than the ancestral French region. In contrast, the new Spanish edge populations showed unexpectedly maladaptive traits to a slower POL. Moreover, as hypothesized, the old edge populations had both a higher mitochondrial and food digestive efficiencies to support their evolved fast POL. Conversely, the new edge populations showed only a higher food intake which was likely a response to thermal stress. In conclusion, our study provides evidence that mitochondrial efficiency along with the traditional food intake and metabolic rate traits mediate the POL. This suggests a more nuanced interpretation of the traditional POL framework.

WHY NOT STRONG AND FAST? THE BIOMECHANICS OF HIGH-FREQUENCY FINGER OSCILLATIONS

Cas JORISSEN[1*], Sam VAN WASSENBERGH[1]

[1] Laboratory of Functional Morphology, University of Antwerp, Universiteitsplein 1, 2610 Antwerp, Belgium

***Presenting author,** Cas.Jorissen@uantwerpen.be

Keywords: High-frequency, Oscillations, Antagonistic muscle pairs

The vertebrate body contains many lever systems operated by antagonistic muscle pairs. Some of these lever systems are involved in tasks with conflicting mechanical demands. To better understand these demands, insight into the biomechanical basis of performance trade-offs is needed. For example, humans use their fingers for a multitude of reasons; some tasks require the fingers to exert high static forces (e.g., climbing) or others rely on fast, repetitive movements (e.g., playing piano). People excelling in one of these tasks are expected to show differences in forearm musculature at different levels, e.g. anatomy, fibre type, and/or activation patterns. In some people, the flexor muscles can be much stronger than the extensor muscles, leading to a larger antagonistic torque imbalance. This imbalance might influence rapid finger movement, as fully activating the flexor muscle will inevitably result in delayed finger extension while the powerful flexors are relaxing. Muscle activation levels and timings may compensate for this effect. This mechanism might suggest that there is a torque-frequency trade-off present. We measured maximal force and torque output of the index finger in both flexion and extension directions of 137 people to estimate the torque imbalance. High-speed videos of standardised index finger oscillations are used to quantify maximal frequency and surface-EMG provides comparative data on activation patterns. In contradiction to our hypothesis, we found a positive correlation between finger torque and frequency output, meaning that stronger people are able to produce higher frequencies. The duration of flexion movements is shorter than that of extension movement, and further decreases with an increase in finger torque. Our first results indicate that there is no torque-frequency trade-off in rapid finger movements. However, further analysis of finger kinematics and muscle activation patterns will indicate how people who produce larger torques can also produce more rapid finger oscillations.

STUDYING GENOMES TO SAVE THE SPECIES: HUMAN AND NATURAL EFFECTS ON THE GLOBAL GENETIC DIVERSITY OF MAMMALS

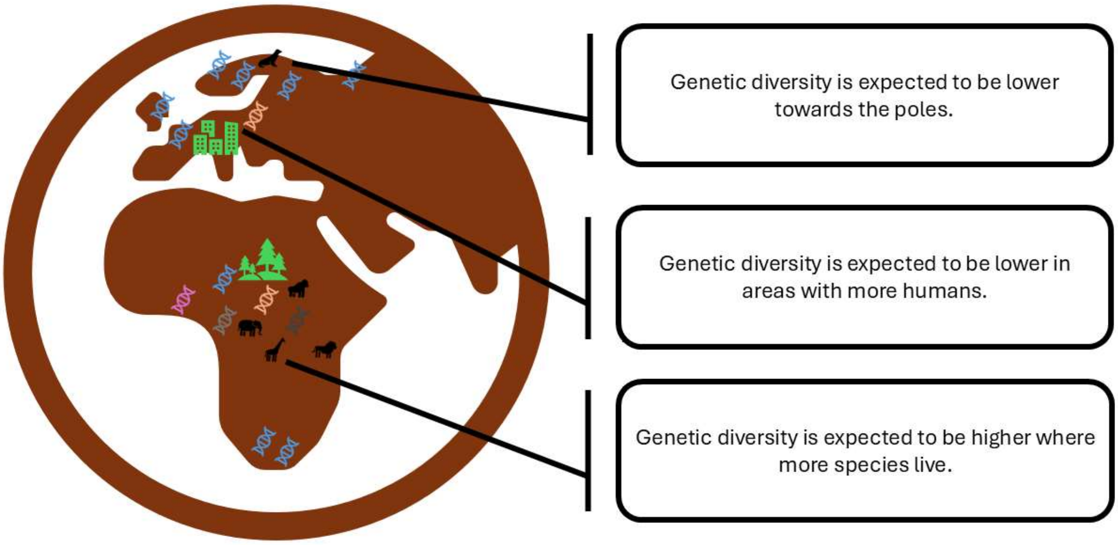
Christos KAROULIS[1*], Patrick MEIRMANS[1]

[1] Institute for Biodiversity and Ecosystem Dynamics (IBED), University of Amsterdam, Sciencepark 904, 1098 XH, Amsterdam, Netherlands.

***Presenting author**, **christos.karoulis@student.uva.nl**

Keywords: RADseq, Nucleotide diversity, Mammalia, Macrogenetics

We are now midst what has been called by many a “Sixth Mass Extinction”. Species are being lost at unprecedented rates and as a response a lot of effort is attributed to their conservation. However, since biodiversity is a result of genomes interacting with environment such efforts can only be truly comprehensive if genetic diversity patterns within species are addressed too. For that, the study of genetic patterns at large taxonomic, temporal or spatial scales (i.e. macrogenetics) can be really valuable. Under this scope, several studies have tried to investigate the relationship of global genetic diversity in mammals with latitude, local mammal species richness, human footprint, and anthromes (i.e. human built biomes). However, for every single one of these factors, the findings have been contradictory. That has mainly been attributed to differences in the used genetic markers, mostly microsatellites and mitochondrial genes. A more appropriate, but yet untested, method would be to use genome-wide diversity estimates to clarify what shapes mammals’ genetic diversity globally. Here, we use the genome-wide nucleotide diversity (π) for a large number of mammalian species, estimated from publicly available RADseq data or collected directly from the literature. Generalized linear mixed effect models were used to test the effects of latitude, local mammal species richness, human footprint, anthromes and global biomes on the level of π. To the best of our knowledge, this study is the first available test of genetic diversity in mammalian nuclear genomes on a global scale. We discuss the results of the study, and its limitations, under the scope of how the field of mammalian macrogenetics and thus our ability to protect mammals could be improved.



Best supported theoretical expectations for genetic diversity patterns on a global scale. Different studies on mammals support or go against these expectations so far.

CONNECTIVITY OF CORAL REEFS AND MANGROVES IN THE INDIAN OCEAN

Marc KOCHZIUS[1*], Debora MUSSA BENJAMEN[1], Axel DE PAUW[1], KUSHLANI DISSANAYAKE[1,2], Min HUI[3], Filip HUYGHE[1], Winnie A. NG'ENDO IKINYA[1,4], Agus NURYANTO[5], Levy OTWOMA[1,4], Hajaniaina A. RATSIMBAZAFY[1,6], Rosa VAN DER VEN[1,7], Annelore VAN NIEUWENHOVE[1]

[1] Marine Biology – Ecology, Evolution & Genetics, Biology Department, Vrije Universiteit Brussel (VUB), Brussels, Belgium

[2] Faculty of Fisheries and Marine Sciences & Technology, University of Ruhuna, Sri Lanka

[3] Key Laboratory of Experimental Marine Biology, Institute of Oceanology, Chinese Academy of Sciences, Qingdao, China

[4] Kenya Marine and Fisheries Research Institute (KMFRI), Mombasa, Kenya

[5] Faculty of Biology, Jenderal Soedirman University, Purwokerto, Indonesia

[6] Institut Halieutiques et des Sciences Marines, University of Toliara, Toliara, Madagascar

[7] Marine Animal Ecology Group, Wageningen University, Wageningen, The Netherlands

[*]Presenting author, marc.kochzius@vub.be

Keywords: COI, Larval dispersal, Genetic markers, Marine coastal ecosystems

So far, connectivity of populations in the Indian Ocean (IO) was rather understudied and no comprehensive picture could be drawn based on the available data. However, this has changed in recent years and meanwhile a growing number of connectivity studies based on genetic data (mtDNA and microsatellites) are published or under way. Even though there are differences in spatial scale, study region and genetic markers used, some general pattern of gene flow are emerging from these different studies on a growing number of coral reefs and mangrove dwelling animals. On the large scale of the IO and adjacent seas, the following genetically differentiated regions can be observed: (1) Western Indian Ocean (WIO), (2) Red Sea (RS), (3) Persian Gulf (PG), (4) South Indian Shelf and Bay of Bengal (BoB), and (5) Eastern Indian Ocean (EIO). This genetic structure is congruent with large-scale oceanographic pattern, such as the narrow connections of the RS and PG to the IO, the gyre in the BoB and the large stretches of open ocean between the WIO and EIO. Prevailing currents, gyres and isolation-by-distance are apparently shaping the genetic structure of all these different taxa in the same way. The emerging pattern of a common genetic structure in coral reef and mangrove fauna of the WIO could be summarised as follows: (1) North/East Madagascar, (2) South/Southwest Madagascar, (3) Southwest Madagascar and northern Mozambique Channel, (4) South Mozambique and (5) Tanzania and Kenya.

Future studies utilising genome-wide SNPs analysed by Next-Generation-Sequencing are needed to receive a comprehensive picture of connectivity in the WIO. This is needed for a proper spatial arrangement of marine protected areas in a WIO-wide network that matches the general connectivity pattern. This will enable sustainable management of marine living resources in the WIO in order to reach SDG 14 (life below water).

THE IMPACT OF DIFFERENT RECREATION TYPES ON SEASONAL SPATIOTEMPORAL BEHAVIOUR OF WILDLIFE – APPLICATION TO A SMALL, HIGHLY VISITED NATIONAL PARK

Wim KUYPERS[1]*, Martijn BOLLEN[2], Jim CASAER[2], Natalie BEENAERTS[1]

[1] Centre for Environmental Sciences, Hasselt University, 3590 Diepenbeek, Belgium.

[2] Research Institute for Nature and Forest, 1000 Brussels, Belgium.

***Presenting author**, **wim.kuypers@uhasselt.be**

Keywords: Human-wildlife interaction, Recreation, Protected area, Camera traps

Protected areas face the challenge of balancing conservation goals with increasing recreational use, which can strongly influence behavioural changes of wildlife and, consequently, affect ecosystem functioning. Understanding the specific impacts of various recreational activities on wildlife behaviour is essential for guiding targeted management strategies and supporting sustainable conservation practices.

In the 60km² highly visited Hoge Kempen National Park (Belgium), we assessed habitat preferences and the seasonal impact of officially designated hiking, mountain biking, and tarmac cycling trail densities on the land-use of western roe deer, wild boar, and red fox. From May 2018 until May 2019 camera traps were used to monitor wildlife. Since individual animals could not be uniquely identified and the detection is imperfect, we used N-mixture models to estimate spatial variation in land-use, while accounting for detection probability.

We revealed species-specific habitat preferences and seasonal differences in how recreational activities impact wildlife. Hiking trails had a negative impact on roe deer and wild boar space use in summer, autumn and winter. The impact of cycling and mountain biking trails on land use by roe deer and wild boar varied by season. Hiking trails had a more negative impact on space use of roe deer during the day than at night. In contrast, red fox preferred areas with high recreational trail density, especially mountain biking trails. These findings underscore the difference and seasonality in the impact of different forms of recreation on land-use by wildlife, highlighting the need for recreation monitoring and adaptive management strategies to mitigate or leverage recreational pressures on wildlife. This is especially important in highly visited parks with limited spatial refuges.

INDIVIDUAL ACOUSTIC SIGNATURES IN THE DAMSELFISH *DASCYLLUS ALBISELLA*?

Salomé LABOURY[1*], Eric PARMENTIER[1], Phillip LOBEL[2]

[1] Laboratory of Functional and Evolutionary Morphology, Department of Biology, Ecology and Evolution, FOCUS, University of Liège, 4000 Liège, Belgium.

[2] Department of Biology, Boston University, 02115 Massachusetts, U.S.

***Presenting author, S.Laboury@uliege.be**

Keywords: Bioacoustics, Acoustic communication, Individual recognition, Pomacentridae

Many animal species are known to show individuality in their acoustic communication. This variation in individual male signatures can be decisive for female choice. Within the damselfishes, *Dascyllus* species are known for prolific sound production during the realization of movements associated with courtship (i.e., the signal jump) and spawning (mating sounds). However, whether males of this taxon have individually distinguishable sounds is unknown. We investigated the variability in the courtship and mating sounds of seventeen males of *Dascyllus albisella* at Johnston Atoll, Central Pacific Ocean, to determine if it was possible to distinguish them from one another and thus have information on their ability to convey individual information. Acoustic analyses confirmed that courtship sounds differed from mating sounds. Comparative analyses suggest that acoustic signals cannot serve as distinctive traits unless the individuals are of different sizes. Males of *Dascyllus albisella* do not use individual signatures in a reproductive behavioral context. However, it cannot be ruled out that variations in the sound production rate may serve as a discriminative feature.

SPECIES DELIMITATION AND GENOME SIZE VARIATION IN TROPICAL MARINE SPONGES

Ninon LECOQUIERRE[1]*, Maryeme BENOUNOU[1], Mohammed M. TAWFEEQ[1], Dirk ERPENBECK[2,3], Gert WÖRHEIDE[2,3,4], Jean-François FLOT[1,5]

[1] Evolutionary Biology & Ecology, Université libre de Bruxelles (ULB), 1000 Brussels, Belgium.

[2] Department of Earth and Environmental Sciences, Palaeontology and Geobiology, Ludwig-Maximilians-Universität München, 80539 Munich, Germany.

[3] GeoBio-Center, Ludwig-Maximilians- Universität München, 80539 Munich, Germany.

[4] Bavarian State Collections of Palaeontology and Geology, 80539 Munich, Germany.

[5] Interuniversity Institute of Bioinformatics in Brussels – (IB)², 1000 Brussels, Belgium.

*<u>**Presenting author**</u>, **lecoquierre.ninon@ulb.be**

Keywords: Genome size, Intraspecific variation, *Stylissa*, Species delimitation

Genome size is a fundamental biological trait that shapes the evolutionary path of species, their adaptability to environmental pressures, and even their ecological niche. Studies suggest that larger genomes are often associated with a higher risk of extinction. In early-diverging animal lineages such as sponges, genome size data are limited, and intraspecific variation remains underexplored. This study investigates intra- and interspecific genome size variation within the sponge genus *Stylissa*, with samples collected from Indonesia and Saudi Arabia, with a focus on species delimitation among specimens.

Using the mitochondrial mt-IGR and ribosomal ITS2 markers, we assessed species boundaries among 26 samples, identifying two genetically distinct putative species with congruent results across both markers. Interestingly, spicule length—a key morphological character in sponge taxonomy—did not differ significantly between these two putative species.

Genome size estimates obtained using Feulgen Image Analysis Densitometry (FIAD) revealed a 3.6-fold variation in C-values, ranging from 0.075 pg to 0.27 pg. The highest mean genome size was found in *Stylissa carteri* (0.22 pg, with a 1.6-fold variation), followed by *Stylissa massa* (0.20 pg, with a 3.3-fold variation). Additionally, a positive association was observed between nucleotide polymorphism (π) and genome size variance.

This study provides the first insights of intra- vs. interspecific genome size variations within tropical *Stylissa* sponges and paves the way for efficient specimen selection for whole-genome sequencing.

LENS ISOTOPIC COMPOSITIONS AS A TRACER OF CORAL FISH ECOLOGICAL ONTOGENY

Gilles LEPOINT[1]*, Victor CORNET[1,2], Bruno FRÉDÉRICH[2]

[1] Laboratory of Trophic and Isotope Ecology, UR FOCUS, University of Liège, 4000 Liège, Belgium.

[2] Laboratory of Evolutionary Ecology, UR FOCUS, University of Liège, 4000 Liège, Belgium.

***Presenting author, G.Lepoint@uliege.be**

Keywords: Diet shift, Habitat shift, Madagascar, SW Indian Ocean

Coral reef-associated teleost fishes have complex life cycles, often involving the use of several habitats and changes in diet during their ontogeny. Stable isotope ratios of carbon and nitrogen are potential tracers of these ontogenetic changes. In this study, we use the crystalline lens of six species of coral reef fish to trace the variation of their habitat and diet during their ontogeny. The crystalline lens of adult fish is made up of successive layers, each formed during a different part of the individual's life. Once formed, these layers retain their initial isotopic composition, making it possible to trace the isotopic ontogeny of the individual and, potentially, to interpret this in terms of habitat use and diet. Aiming to study their ecological ontogeny, we selected six fish species (n = 5 specimens per species, 5 - 36 layers per individual, n = 600 isotopic measurements) from different families with contrasting trophic ecologies (herbivore, invertivore, piscivore) and habitat uses (e.g. external reef slope, reef flat, water column, seagrass ecosystems) at the adult stage. These species are all targeted by artisanal fishing on the Great Reef of Toliara (SW Madagascar). The results not only enabled us to compare these species showing very contrasted ecological strategies during their ontogeny but also enabled us to reveal intraspecific variation in the isotopic trajectories. Diversity of individual trajectory differed among species. For example, some species (e.g. *Strongylura incisa*) displayed very low intraspecific variability with individuals having the same isotopic trajectory, indicating that individuals exploited the same habitat and the same food sources during their ontogeny. By contrast, other species (e.g. *Lethrinus harak*) showed a high intraspecific variability, indicating more inter-individual variability in habitat/food sources use during their life. These data have the potential to guide conservation decisions as all these species are potentially overfished on the Great Reef of Toliara but do not have the same ecological ontogeny.

UNRAVELING CHROMOSOMAL INVERSIONS AND THEIR EVOLUTIONARY DANCE IN A WING POLYMORPHIC BEETLE

Maria MADRID-RESTREPO[1*], Frederik HENDRICKX[2], Steven VAN BELLEGHEM[1]

[1] Eco-Evolutionary Genomics Lab, KU Leuven, 3000 Leuven, Belgium.

[2] Royal Belgian Institute of Natural Sciences, 1000 Brussels, Belgium.

***Presenting author**, **maria.madrid@kuleuven.be**

Keywords: Evolutionary genomics, Adaptation, Bioinformatics, Population genetics

Evolutionary adaptation can rapidly occur in response to environmental changes, driven by mechanisms ranging from allele frequency shifts at a few loci to polygenic scenarios across multiple chromosomes. Adaptation, especially under high levels of gene flow, is particularly interesting, and recent advances in whole-genome sequencing can shed light on these processes. *Pogonus chalceus*, a saltmarsh beetle, provides a compelling case of rapid adaptation and parallel evolution on a microgeographical scale. These wing polymorphic beetles exhibit short- and long-winged ecotypes presumably adapted to different hydrological regimes. Short-winged beetles inhabit regularly flooded tidal marshes, while long-winged beetles reside in seasonal marshes that are periodically inundated for months. Despite being found as close as 10-20 meters apart with ample opportunity for gene flow, these ecotypes remain distinct.

New genomes were assembled for both ecotypes using PacBio HiFi reads and Hi-C chromatin capture, producing assemblies of over 1 Gb in length. These assemblies are significantly less fragmented than the previously published draft genome, with BUSCO scores of over 98%, and synteny analysis that reveal high conservation across ten of eleven chromosomes. These genomes were also found to be over 75% repetitive. Population genetic analyses identified several regions of high divergence, hinting at large-scale inversions that facilitate adaptation in multiple traits. These regions cover at least 7% of the genome and were identified in five chromosomes. The high repetitiveness of the genome, alongside the high heterozygosity in sampled individuals, may contribute to the fragmentation seen at potential inversion breakpoints. Further research is needed to confirm the presence of these inversions, and despite the challenges, our study provides important insights into how genetic architecture drives adaptation and speciation.

SHAPE VARIATION IN THE PATELLA OF MODERN PERISSODACTYLS: DECIPHERING THE INFLUENCE OF EVOLUTIONARY LEGACY AND FUNCTIONAL CONSTRAINTS ON SESAMOID BONES

Christophe MALLET[1,2*], Alexandra HOUSSAYE[3]

[1] Faculty of Engineering, Department of Geology and Applied Geology, University of Mons, 8000 Mons, Belgium.

[2] Institute of Natural Sciences, Operational Directorate Earth and History of Life, 1000 Brussels, Belgium.

[3] Adaptative Mechanisms and Evolution (UMR 7179 MECADEV), Muséum National d'Histoire Naturelle, 75005 Paris, France.

***Presenting author**, cmallet@naturalsciences.be**

Keywords: Rhinocerotidae, Tapiridae, Equidae, 3D geometric morphometrics

In mammals, the patella is the biggest sesamoid bone of the skeleton and is of crucial importance in posture and locomotion, ensuring the role of a pulley for leg extensors while protecting and stabilizing the knee joint. Despite its central biomechanical role, the relation between the shape of the patella and functional factors, such as body mass or locomotor habit, in the light of evolutionary legacy, are poorly known. Here, we propose a morphofunctional investigation of the shape variation of the patella among modern rhinoceroses and more generally among perissodactyls, this order of ungulates displaying a broad range of body plan, body mass and locomotor habits, to understand how the shape of this sesamoid bone varies between species and relatively to these functional factors. Our investigation, relying on three-dimensional geometric morphometrics and comparative analyses, reveals that, within Rhinocerotidae and between the three perissodactyl families, the shape of the patella strongly follows the phylogenetic affinities rather than variations in body mass. The patellar shape is more conservative than initially expected both within and between rhinoceroses, equids and tapirs. The development of a medial angle, engendering a strong mediolateral asymmetry of the patella, appears convergent in rhinoceroses and equids, while tapirs retain a symmetric bone close to the plesiomorphic condition of the order. This asymmetric patella is likely associated with the presence of a "knee-locking" mechanism in both equids and rhinos. The emergence of this condition may be related to a shared locomotor habit (transverse gallop) in both groups. Our investigation underlines unexcepted evolutionary constraints on the shape of a sesamoid bone usually considered as mostly driven by functional factors.

SHARKS OF TAIWAN: EXPLORING THEIR TROPHIC ECOLOGY THROUGH THE RESOLUTION OF THREE ISOTOPES

Ulrich MARTIN[1*], Gilles LEPOINT[2], Jérôme MALLEFET[3]

[1] Laboratoire de biologie marine, University of Louvain, 1348 Louvain-la-Neuve, Belgium.

[2] Départment de biologie, écologie et évolution, University of Liège, 4031 Liège, Belgium.

[3] Laboratoire de biologie marine, University of Louvain, 1348 Louvain-la-Neuve, Belgium.

***Presenting author, ulrich.martin@uclouvain.be**

Keywords: Sharks, Taiwan, Stable isotopes

Stable isotope analysis (SIA) is a valuable tool to study the trophic ecology of species living in remote ecosystems, like the deep parts of the oceans. Deep-water sharks are currently poorly known, and studies using SIA are more and more used to understand their role in their food web. Here, we study the trophic structure of six species living in the deep ocean around Taiwan: *Etmopterus molleri*, *Etmopterus brachiurus*, *Etmopterus splendidus*, *Deania profundorum*, *Squaliolus aliae*, *Galeus sauteri*. We used stomach content analysis and muscle samples for SIA. Most studies on the subject focus on the stable isotopes ^{13}C and ^{15}N, but here, we added ^{34}S to add another level of resolution to the analysis. Incidentally, we discovered that the six species have similar isotopic niches when considering the muscle samples with the first two stable isotopes, indicating reliance on similar trophic resources, with a common primary production in their food network and similar trophic levels. However, when considering the third isotope and refining the analysis in three dimensions, some species separated from the others, demonstrating the interest of using other isotopes to reveal otherwise hidden differences.

GENETIC DIVERSITY ACROSS THE CAT FAMILY (FELIDAE)

Michaël MEEUS[1*], Jonas LESCROART[1,2], Hannes SVARDAL[1,3]

[1] Department of Biology, University of Antwerp, 2610 Wilrijk, Belgium.

[2] School of Health and Life Sciences, Pontifical Catholic University of Rio Grande do Sul, 90619-900 Porto-Alegre, Brazil.

[3] Naturalis Biodiversity Center, 2333 Leiden, The Netherlands.

***Presenting author**, **michael.meeus@uantwerpen.be**

Keywords: Heterozygosity, Felidae, Genomics, Conservation

As the world is hit by the sixth mass extinction, it is critical to understand the factors that are important to the conservation of species, so that we may protect biodiversity to the best of our abilities. Although genetic diversity is known to underlie population health and adaptability, it is not explicitly used in assessments for the International Union for the Conservation of Nature (IUCN) Red List. Additionally, studies comparing diversity estimates between species often rely on summarizing results across studies, which often use different methodologies and may thus not be suited for direct comparison. In this study we performed a family-wide assessment of genomic diversity in Felidae, covering most extant species. We used publicly available whole-genome sequencing data and subjected all samples to an identical quality filtering and mapping pipeline to obtain unbiased, intercomparable estimates of autosomal heterozygosity. We then tested for correlations between genomic diversity and ecological traits of the various (sub)species, as well as whether a subspecies' genomic diversity was associated with its IUCN category. We found a strongly positive correlation for heterozygosity with both geographic range size and population density, but not with population census size. Furthermore, although heterozygosity was not significantly correlated with IUCN status overall, threatened species had significantly lower levels of genomic diversity than non-threatened species. Our results confirm the association of population parameters and assessment of extinction risk with genetic diversity in one of the most iconic and threatened family of land carnivores. While mechanisms and causality behind these associations will need to be the subject of further investigation, our study adds further credence to the importance of incorporating genomic approaches in conservation efforts and risk assessments.

INFRAFADA: UPGRADING THE TAXONOMIC BACKBONE OF GLOBAL FRESHWATER ANIMAL BIODIVERSITY RESEARCH INFRASTRUCTURES

Géraldine MERTENS[1*], Astrid SCHMIDT-KLOIBER[2], Koen MARTENS[1]

[1] OD Nature - Freshwater Biology, Royal Belgian Institute of Natural Sciences (RBINS), 1000 Brussels, Belgium.

[2] Institute of Hydrobiology and Aquatic Ecosystem Management, BOKU University, 1180 Vienna, Austria.

***Presenting author**, **gmertens@naturalsciences.be**

Keywords: Taxonomy, Assessment, Biodiversity, Database

The current Freshwater Animal Diversity Assessment (FADA) comprises an extensive set of global taxa lists for freshwater animal groups. At present, more than 125 thousand described freshwater animal species in more than 11 thousand genera have been documented. However, taxonomy is a living scientific discipline, where new taxa are continuously being described, and existing taxa are being placed in new taxonomic positions. Therefore, after a period of relative inactivity, the BELSPO (Belgian Science Policy) project “infraFADA” (2023-2026) re-establishes the global FADA consortium of taxonomic experts, so that all taxa lists will be brought up to date, both technically and in terms of content. infraFADA will develop a living, updated, and global FADA database, fully in open access and according to the FAIR principles. The infraFADA database is intended for use and consultation by the scientific freshwater community, as well as for interested stakeholders, for example, freshwater ecosystem managers, biodiversity conservationists, and others. Most importantly, FADA will also serve as a taxonomic backbone for other global biodiversity data infrastructures, such as the Catalogue of Life (CoL), the Global Biodiversity Information Facility (GBIF), the Freshwater Information Platform (FIP), and others. As such, FADA will provide a digital and living heritage of freshwater data, building bridges between science and society and helping to sustainably maintain freshwater resources.

DINING IN THE DEEP: UNRAVELING ENERGY ACQUISITION STRATEGIES IN SYNTOPIC COLD-WATER CORALS

Loïc N. MICHEL[1*], Margaux MATHIEU-RESUGE[2], Louis AMAND[3], Eve-Julie ARSENAULT-PERNET[2], Alizé BOURIAT[2], Jonas BOUSQUET[2], Sandra FUCHS[2], Corentin LE GOFF[2], Gilles LEPOINT[4], Maxime MARINIER[2], Valentine MEUNIER[2], Fabrice PERNET[5], Joëlle ROBBE[3], Bruce SHILLITO[3], Logan THERASSE[1], Julie TOUROLLE[2], Magali ZBINDEN[3], Lénaïck MENOT[2]

[1] Animal Systematics and Diversity, FOCUS research unit, University of Liège, 4000 Liège, Belgium.

[2] UMR 6197 BEEP, University of Western Brittany, CNRS, Ifremer, 29280 Plouzané, France.

[3] Equipe Adaptation aux Milieux Extrêmes (AMEX), Laboratoire Biologie des Organismes et Ecosystèmes Aquatiques (BOREA), MNHN, CNRS 8067, SU, IRD 207, UCN, UA, 75005 Paris, France.

[4] Laboratory of Trophic and Isotope Ecology, FOCUS research unit, University of Liège, 4000 Liège, Belgium.

[5] UMR 6539 LEMAR, University of Western Brittany, CNRS, IRD, Ifremer, CS10070, 29280 Plouzané, France.

***Presenting author, loic.michel@uliege.be**

Keywords: Trophic tracers, Niche segregation, Food webs, Deep Sea

Cold-water corals (CWCs) are reef-building foundation species occurring worldwide in the aphotic zone of the ocean. Those reefs are considered biodiversity hotspots in the deep-sea. In the absence of autochthonous production, CWCs mostly depend on exported photosynthetic production for their nutrition. Energy acquisition is therefore a major challenge for CWCs. In this context, we investigated feeding habits of three syntopic CWC species forming reefs in the Lampaul Canyon (Bay of Biscay) at depths ranging from 800 to 1600 m: *Desmophyllum pertusum*, *Madrepora oculata* and *Solenosmilia variabilis*. Specifically, we tackled the following questions: 1) What is the realized trophic niche of CWCs in the Lampaul Canyon?; 2) Do the three species rely on the same resources?; and 3) Are the trophic niches of CWCs overlapping with those of associated fauna, particularly suspension feeders?

Joint carbon, nitrogen and sulfur stable isotope analysis showed that CWC exhibit marked resource segregation with associated fauna. Coral niches partly overlapped in some sampling years, but trophic interactions showed important interannual variations, hinting at an ecologically dynamic system. Species-specific trends in niche size were also present, suggesting variable trophic diversity. Fatty acid analysis suggested that all three species were selective plankton feeders, with interspecific differences in consumption of zoo- and bacterioplankton, likely increasing niche segregation. Furthermore, pulse-chase experiments in pressurized tanks suggested that all species are, to some extent, able to function as holobionts. They notably obtain part of their nitrogen from mutualistic relationships with the microbiome living in the mucus secreted by the polyps. Ultimately, reliance upon these multiple, non-mutually exclusive ecological mechanisms could be a key factor to facilitate CWCs future survival under changing environmental conditions.

EUROPEAN INITIATIVES FOR POLLINATOR MONITORING

Denis MICHEZ[1*], Guillaume GHISBAIN[1], Sara REVERTE[1], Simone FLAMINIO[1], Romain LE DIVELEC[1], Paolo ROSA[1]

[1] Laboratory of Zoology, University of Mons, Place du parc 20, 7000 Mons, Belgium

***Presenting author, denis.michez@umons.ac.be**

Keywords: Conservation biology, Taxonomy, Nature Restauration law, Bees

Several studies have now shown at different spatial scales that certain pollinator species are in decline in Europe. In response, some European countries and the European commission are implementing action plans to mitigate these negative population trends. To evaluate the efficiency of these actions, we need an accurate estimation of their populations. One of the first actions proposed is therefore an ambitious monitoring program, which involves the development of taxonomic / recognition tools and training to use them. Several projects started in 2021 and concern the whole of European continent. We will present here the initiatives on taxonomy (ORBIT project) and on capacity building (SPRING project). ORBIT and SRPING are three-year projects commissioned by the General Directorate for Environment of the European Commission. Orbit aims to develop taxonomic resources for facilitating European bee inventory and monitoring. SPRING aims to strengthen the taxonomic capacity in EU Member States, and support preparation for the implementation of the EU Pollinator Monitoring Scheme "EU-PoMS", notably by organising training sessions for different levels of expertise. The trainings are aimed at 4 different levels: (i) identifying large pollinator groups, (ii) identifying bees and hoverflies to genus level, (iii) identifying bees or hoverflies to species group level, (iv) identifying bees or hoverflies to species level. Trainings at level (i) were developed at the national scale; levels (ii) and (iii) were covering multiple countries; and level (iv) considered the whole Europe. Moreover, the project created a series of e-learing materials on pollinator identification at different levels, focusing on the needs of people involved on the monitoring. All this material will be open to the public on the online portal 'Pollinator Academy,' which will act as a hub to centralise information about already available tools related to pollinator identification (articles, online keys, books, interesting links, other courses, etc.).

ECOMORPHOLOGICAL DIVERSIFICATION OF GOATFISH HYOID BARBELS

Laurent MITTELHEISER[1*], Gilles LEPOINT[2], Denis BAURAIN[3], Bruno FREDERICH[1]

[1] Laboratory of Evolutionary Ecology, FOCUS, University of Liège, Liège, Belgium

[2] Laboratory of Trophic and Isotope Ecology (LETIS), FOCUS, University of Liège, Liège, Belgium

[3] Unit of Eukaryotic Phylogenomics, UR InBioS, University of Liège, Liège, Belgium

***Presenting author**, **lmittelheiser@uliege.be**

Keywords: Coral reef, Trophic ecology, Taste buds, Phylogeny

Coral reefs act as catalysts for morphological diversification, producing extreme body shapes like trumpetfish and boxfish, or unique adaptations such as the beak of parrotfish. Goatfishes (Mullidae) provide another example of morphological innovation with their hyoid barbels, which are articulated finger-like structures covered of sensory cells organized into taste buds. Commonly categorized as benthic invertivores, goatfish use their barbels to detect and extract prey from soft sediments or coral crevices. While similar types of barbels were studied in catfishes, little is known about the morphological diversity of goatfish barbels especially concerning the characteristics and the distribution of taste buds. The proximity of barbels to the mouth and their role in feeding behavior suggests a link between barbel morphology and goatfish trophic ecology. Thus, we first checked the relationship between barbel morphology (*i.e.* size and distribution of taste buds, and barbel length) and trophic ecology of 14 species from the Toliara Reef (Madagascar) assessed by using stable isotopes of carbon, nitrogen, and sulfur. Surprisingly, Phylogenetic Generalized Least Squares (PGLS) analysis revealed no significant relationships between stable isotopes and barbel morphology, except between δ^{15}N and barbel length. Then, we aimed to explore the diversification of barbel morphology across the family by studying 34 species from major genera. A moderate phylogenetic signal (Kmult = 0.63, $P < 0.05$) suggested some conservatism of barbel traits within the family. The mapping of barbel morphology onto the evolutionary tree revealed that a monophyletic subclade within the *Upeneus* genus exhibited a unique barbel morphology, made of a high density of small taste buds. While barbel morphology is relatively conserved throughout goatfish evolution, some variation exists deeper in the phylogeny. However, the facet of trophic ecology grasped by stable isotopes appears to play a limited role in driving this diversification.

MIMETIC CRUSTACEANS: PIGMENTATION CHANGES AND CHEMICAL INVESTIGATION OF *SCLERACTINIAN* ECTOSYMBIONTS

Lisa MUSSOI[1,2*], Alexia LOURTIE[1,3], Killian VER HOEYE[1], Laetitia HEDOUIN[4], Julie MAIRE[1], Louis GROIGNET[2], Pascal GERBAUX[+2], Guillaume CAULIER[+1]

[1] Biology of Marine Organisms and Biomimetics Unit, University of Mons, 6 Avenue du Champs de Mars, Mons, Belgium.

[2] Organic Synthesis and Mass Spectrometry Laboratory, University of Mons, 6 Avenue du Champs de Mars, Mons, Belgium

[3] Culture and Patrimony unit, University of Mons, 24 Place du Parc, 7000, Mons, Belgium

[4] PSL Research University, USR 3278 CRIOBE, BP 1013, 98729, Papetoai, Mo'orea, French Polynesia.

+ These two authors shared the supervision of the study

***Presenting author**, **lisa.mussoi@umons.ac.be**

Keywords: Symbiosis, Coloration, Decapod, Coral

Color mimicry is a common phenomenon in marine species, often used for camouflage. This process may rely on pigments, such as carotenoids, contained in chromatophores in many organisms. This strategy is notably used by symbiotic decapods to camouflage themselves on their hosts in order to reduce their predation rate. In addition, it has also been described that when symbionts are separated from their hosts, the latter can suffer from 'Host separation syndrome', leading to a decline in health and sometimes discoloration of the symbiont. This study explores the effects of the 'Host separation syndrome' between ectosymbionts (*Alpheus lottini* and *Trapezia serenei)* and their host, the coral *Pocillopora acuta* in Mo'orea (French Polynesia). Two questions arise: do these ectosymbionts undergo separation-related discoloration? And what impact does this have on their carotenoid content? To answer these questions, the ectosymbionts were placed in different environmental conditions and their color evolution was monitored using standardized photography. Chemical analysis of the carotenoids was carried out by HPLC-MS to identify the nature of the pigments and to discover if the symbionts and the host share similar pigmented molecules. This analysis was also used to assess potential differences in the quantity of these pigments between control symbionts and those suffering from host separation syndrome. The results revealed significant discoloration patterns after isolation and the presence of similar pigments in both partners, such as astaxanthin. The results of the photographic analyses showed various color changes for the 2 ectosymbiont species studied under the different conditions. Discoloration and a decline in survival were observed in individuals physically isolated from their host. These phenomena could be explained by a trophic link between the symbionts and their host.

THE FUNCTION AND EVOLUTION OF IRIDESCENT COLOURATION IN BIRDS

Michaël NICOLAÏ[1,2,3*], Gerben DEBRUYN[4], D'Alba LILIANA[1,4], Matthew, SHAWKEY[1]

[1] Biology Department, Evolution and Optics of Nanostructures Group, Ghent University, Ghent, Belgium

[2] Department of Recent Vertebrates, Royal Belgian Institute of Natural Sciences, Brussels, Belgium

[3] Museum of Comparative Zoology, Harvard University, Cambridge, MA 02138, USA

[4] Evolutionary Ecology Group, Naturalis Biodiversity Center, Leiden, the Netherlands

***Presenting author, michael.nicolai@ugent.be**

Keywords: Birds, Colour, Evolution

Iridescent colours are responsible for some of the most brilliant and diverse colours in the animal kingdom. Paradoxically, it remains one of the least understood mechanisms responsible for bird colouration. Unlike pigment-based colouration, where colour is produced by absorption of light, iridescent colouration is created by scattering of light by photonic structures where pigment organelles called melanosomes are the building blocks. Using a database, scoring the presence of iridescence in 71.536 body patches, from 8942 representative skins of 5755 species of birds (more than 50% of all species) spanning all but 36 genera (98%) from all families, we retraced the evolution of iridescent colouration in birds. We found that multiple ecological and biological factors contribute to the presence and intensity of iridescence, but that only sexual selection is a consistent predictor. Finally, we use this dataset, in combination with Finite Domain Time Difference models to show that ancestral birds, and dinosaurs, were most likely iridescent but only in a restricted set of body patches.

DIVERSITY OF OPSINS AND PHOTOSENSORY STRUCTURES IN SEA CUCUMBERS (HOLOTHUROIDEA, ECHINODERMATA)

Youri NONCLERCQ[1*], Anneke WIRTH-YAP[2], Igor EECKHAUT[1], Megan PORTER[2], Patrick FLAMMANG[1], Jérôme DELROISSE[1,4]

[1] Laboratory of Biology of Marine Organisms and Biomimetics, Research Institute for Biosciences, University of Mons, 7000 Mons, Belgium

[2] Porter Vision Laboratory, University of Hawai‘i at Mānoa, Honolulu HI 96822, USA

[3] Laboratory of Molecular Biology of Sensory Systems, GIGA, University of Liège, 4000 Liège, Belgium.

[4] Laboratory of Cellular and Molecular Immunology, GIGA, University of Liège, 4000 Liège, Belgium

***Presenting author, youri.nonclercq@umons.ac.be**

Keywords: Holothurian, Apodida, Photoreception, Echinoderm, Opsin, Ocelli

Photoreception mediated by opsins is a fundamental sense in most Eumetazoans. These opsins are generally expressed in visual structures (eyes or ocelli). However, it is not the case for the most echinoderm species which present an extraocular photoreception. Currently, photoreception was poorly studied in sea cucumbers (Holothuroidea). Although most sea cucumber species are eyeless, many of them remain sensitive to daylight. On the other hand, the possible presence of ocelli has been suggested in several species belonging to the order of Apodida. We have conducted comparative morpho-functional and molecular study of the photosensory structures in these Holothurians. The comparative genomic study carried in 3 different lineages of sea cucumbers revealed the presence of a large diversity of opsin genes almost equivalent to those of other echinoderms (5 to 6 different opsin types). Immunostaining performed in a European eyeless sea cucumber species: *Holothuria forskali*, revealed the expression of rhabdomeric opsins at the tips of its oral tentacles and tube feet. We have also investigated a great epibenthic Apodida species from Madagascar which presents dark spots at the base of oral tentacles: *Euapta godeffroyi*. The morphological study of these ocelli by light and electron microscopy revealed the presence of a dense neuroepithelium composed of sensory cells with numerous apical elongated microvilli and some atypical cilium. Immunolabelling highlighted the expression of one ciliary opsin inside these photosensory cells. Finally, we have investigated a small European burrowing species: *Oestergrenia digitata*. This species is devoid of eyespots but presents sensory cups on the oral face of tentacles. Immunostaining has highlighted the presence of a ciliary opsin in these cupules that could been involved in light perception in this species.

MELAMPUS JAUMEI: THE METABOLOMIC ANALYSIS OF A PULMONATED GASTROPOD TO REVEAL THE MECHANISMS OF ADAPTATION TO ENVIRONMENTAL CHANGES

Jessica ODY[1], Alice DENNIS[1]

[1] Department of biology, UNamur, rue de Bruxelles 61, 5000 Namur, Belgium.

***Presenting author, jessica.ody@unamur.be**

Keywords: Gastropod, Genomics, Metabolomics, Environment

The *Melampus sp*. cryptic species complex is found on the western Atlantic coast and in the northern Caribbean. These snails are often very abundant and are found under plant debris in salt marshes and across a range of salinities. Three species have been identified in this cryptic complex and provide an interesting model to understand specific responses to multiple environmental changes including salinity and temperature.

It was previously described that each of these species can resist freezing temperature with no significant distinction that would explain their geographical distribution. To better understand this resistance, we selected one of the species from the cryptic complex, *Melampus jaumei* and performed a multi-omic approach with genomic, transcriptomic and metabolomic analyses. As no genome is available for Melampus, we assembled the first genome of *M. jaumei* and the impact of salinity and temperature changes was also evaluated with transcriptomic analysis with a view to discovering the mechanisms of this adaptation. In this study, we will focus on shifts in metabolomic contents to environmental changes in *M.jaumei*.

The experiment consisted of acclimating 62 specimens of *M. jaumei* to three different salinities (5ppt, 20ppt, 35ppt). Then, to simulate the effect of sudden freezing conditions, 28 individuals underwent a cold shock for one hour at -8°C. For every specimen, an un-targeted metabolic analysis was performed. Comparisons of metabolites suggests an impact of salinity on the metabolic response to cold shock. The sucrose metabolism pathway is impacted by the cold shock and may play a role in management of energy reserve, resistance to damage due to freezing, or to prevent damage. These parallel findings in the transcriptomic part of this study, and are the first step to better understand the ability of *M. jaumei* to adapt to fluctuating environmental conditions.

EXPLORING THE GENETIC POPULATION STRUCTURE OF INDO-PACIFIC CORAL REEFS: A WHOLE GENOME SEQUENCING APPROACH UTILIZING THE CLOWNFISH AMPHIPRION CLARKII AS A MODEL

Lode OP'T ROOD L[1*], Filip HUYGHE F[1], Kushlani DISSANAYAKE[2], Marc KOCHZIUS[2]

[1] Marine Biology – Ecology, Evolution & Genetics (bDIV), Vrije Universiteit Brussel (VUB), Pleinlaan 2, 1050 Brussels, Belgium

[2] Department of Oceanography and Marine Geology, Faculty of Fisheries and Marine Sciences & Technology, University of Ruhuna, Matara, Sri Lanka

[*] **Presenting author, lode.opt.Roodt@vub.be**

Keywords: Anemonefish, Larval dispersal, Principal Component Analysis (PCA), Sunda shelf

Clownfish, members of the family Pomacentridae, are iconic coral reef inhabitants with complex social structures. Despite their conservation importance, mechanisms governing coral reef fish dispersal are still not completely understood. Previous studies have shown high genetic differentiation among Amphiprion clarkii populations, indicating substantial regional isolation or potential cryptic speciation. Additionally, human-induced stressors, including overexploitation (e.g., ornamental fisheries) and climate change, have led to declining population sizes. To protect reef fish species effectively, understanding their genetic structure and connectivity is essential, providing a foundation for targeted management strategies.

This study examines the population genetic structure of A. clarkii across the Indo-Pacific, with a focus on previously underexplored areas in the Central Indian Ocean. Using samples from five distinct regions - Taiwan (6), Japan (7), Sri Lanka (73), the Indo-Malay Archipelago (62), and the Maldives (33) - we employed next-generation sequencing (NGS) and analysed single nucleotide polymorphisms (SNPs) to assess genetic diversity. Our findings reveal significant population structure.

Our findings reveal significant population structure, with four clearly differentiated population clusters spanning six geographic regions: Sri Lanka, the Maldives, Eastern and Western Indonesia, and the western Pacific. One cluster is composed of individuals from eastern Indonesia and the western pacific, not representing geographic separation. This large-scale study on A. clarkii's genetic structure, expands prior research in the Indo-Pacific.

The restricted connectivity identified here underscores the need to manage A. clarkii populations as separate units. Conservation strategies, such as establishing and enforcing marine protected areas (MPAs), must consider this genetic structure to ensure the species' long-term survival and resilience in the face of environmental challenges.

MICROPLASTICS ON THE MENU; EXPLORING INTERACTIONS BETWEEN TWO MOSQUITO SPECIES AND MICROPLASTICS

Léa POIRIER[1], Thierry LEFEVRE[1], Kévin TOUGERON[2], Olivier ROUX[3]

[1] MIVEGEC, IRD, 911 Avenue Agropolis, 34394 Montpellier, France.

[2] Ecologie des Interactions et Changements Globaux, Umons, Campus Plaine de Nimy, 7000 Mons, Belgium.

[3] MIVEGEC, IRD, 911 Avenue Agropolis, 34394 Montpellier, France.

***Presenting author, lea.poirier@yahoo.fr**

Keywords: Microplastics, Mosquitoes, Interaction

Microplastic pollution exposes organisms to severe alterations in their life history traits. Once ingested, microplastics can fragment further, facilitating their dispersal in ecosystems. However, the risk of ingestion and the capacity for fragmentation vary among organisms based on their ecology.

In this study, we used two mosquito species with different larval ecologies: *Anopheles gambiae*, which filters particles at the surface, and *Aedes albopictus*, which grazes on biofilm on submerged surfaces. We exposed them to various concentrations, sizes, and densities of microplastics (polystyrene, which sinks, and polyethylene, which floats). We assessed the probability of ingestion, the quantities ingested, and the impacts on survival, sex ratio and individual size. We also investigated whether these larvae could physically or chemically alter the microplastics during digestion.

The risk of microplastic ingestion primarily depends on particle size rather than larval ecology. Only the survival of *An. gambiae* adults exposed during larval development was affected by microplastics, and this was only at the highest concentration. Microplastics had no impact on other measured traits. No physical or chemical alteration of the microplastics was detected following ingestion.

THE ICHTHYOLOGICAL SYMPHONY OF MESOPHOTIC CORAL REEFS: HOW LIGHT REDUCTION SHAPES FISH ACOUSTIC COMMUNICATION

Xavier RAICK[1], Julien CAMPISI[1*], Under The Pole Consortium[2], Frédéric BERTUCCI[3], David LECCHINI[4,5], Lucia DI IORIO[6], Eric PARMENTIER[1]

[1] Laboratory of Functional and Evolutionary Morphology, Freshwater and Oceanic Science Unit of Research, University of Liège, 4000 Liège, Belgium.

[2] Under the Pole Expeditions, 29900 Concarneau, France. Members: G. Bardout, J. Fauchet, A. Ferucci, F. Gazzola, G. Lagarrigue, J. Leblond, E. Marivint, A. Mittau, N. Mollon, N. Paulme, E. Périé-Bardout, R. Pete, S. Pujolle and G. Siu.

[3] UMR MARBEC, University of Montpellier-CNRS-IFREMER-IRD, 34200 Sète, France.

[4] EPHE-UPVD-CNRS, UAR 3278 CRIOBE, PSL University, BP 1013 98729 Papetoai, Moorea, French Polynesia.

[5] Laboratoire d'Excellence ‘CORAIL’, 66860 Perpignan, France.

[6] CEFREM-CNRS/UMR 1510, University of Perpignan Via Domitia, 66860 Perpignan, France.

***Presenting author**, **Julien.Campisi@student.uliege.be**

Keywords: Mesophotic coral ecosystems, Passive acoustic monitoring, Biophony, Acoustic niche hypothesis

According to the Acoustic Niche Hypothesis, the sound spectrum is a limited resource that species or communities share to minimize acoustic competition. This theory has been proven in birds, frogs, arthropods and has recently begun to be shown in fishes. However, the partitioning of acoustic activity in ichthyological communities of Mesophotic Coral Ecosystems (MCEs) and how abiotic factors shape this partitioning is poorly known. This research focuses on studying the ecological role of light reduction on the acoustic behavior of fish in mesophotic coral reefs. The study specifically investigates the lower and upper mesophotic coral reefs from the Tuamotu Archipelago (French Polynesia). Three key complementary objectives are pursued: investigating how fish share the acoustic soundscape, how depth shapes the diel cycles of fish sounds with GAM models and analyzing their ‘realized acoustic niches’ (i.e., the range of acoustic resources). The study showed that the MCEs acoustic community exhibited temporal and frequential partitioning. Moreover, depth exerts a significant impact on the community dynamics of fish sounds. As depth increases, the nocturnal character of frequency modulated sounds is more pronounced while the contrary is observed for pulse series sounds. Depth also affects realized acoustic niches. At the community level, acoustic activity becomes more focused during specific time periods at greater depths, particularly during the night. There is a broader exploitation of the frequency spectrum. On the contrary, for certain sound types, acoustic niches become narrower for frequency resources at deeper depths. Overall, this study showed that light reduction, both with depth and diel cycle, has a significant influence on the acoustic characteristics and community dynamics of fish sounds in MCEs, deepening our understanding of the ecology of MCEs' communities.

HABITAT-USE OF THE RABBITFISH, *SIGANUS SUTOR* AT THE GREAT REEF OF TOLIARA (SW MADAGASCAR)

Helga Berjulie Ravelohasina[1,2*], Richard Rasolofonirina[1], Henitsoa Jaonalison[1,2], Jamal Angelot Mahafina[1], Gilles Lepoint[3], Bruno Frédérich[2]

[1] Institut Halieutique et des Sciences Marines (IH.SM), Université de Toliara, Madagascar.

[2] Laboratoire d'Ecologie Evolutive, FOCUS, Université de Liège, Belgique

[3] Laboratoire d'Ecologie Trophique et Isotopique (LETIS), FOCUS, Université de Liège, Belgique

***Presenting author, helga.ravelohasina@doct.uliege.be**

Keywords: Habitat selection, Fish recruitment, Nursery grounds, Small-scale fishery

Coastal marine fish often transition between habitats throughout their ontogeny, utilizing sometimes mangroves and seagrass beds as juveniles and coral reefs as adults. These habitats are vital for providing food and protection, making them essential for fish development. The rabbitfish *Siganus sutor* (Siganidae) is a key species in the Western Indian Ocean, where it is heavily targeted by small-scale fisheries. Unfortunately, overfishing of juveniles, particularly through destructive practices like mosquito seine nets, threatens both fish populations and the sustainability of coastal fisheries. In order to protect these fish stocks, we must identify their resource needs by studying their ecology. Accordingly, the present study aims to examine the habitat use of *S. sutor* at Toliara reefs (Madagascar). To do so, fish samples were collected from diverse habitats, including mangroves, seagrass meadows in the fringing reef, an intermediate area of patchy reefs mixed with seagrass, and coral reefs. Monthly surveys of juvenile *S. sutor* were conducted over one year, in collaboration with local small-scale fishermen using mosquito nets. Adults were sampled from the Great Barrier Reef using gillnets over three consecutive months. The results revealed significant spatial differences in the abundance and size of juvenile *S. sutor*, with the highest abundance in seagrass meadows near the fringing reef. Two primary recruitment periods for juveniles were identified in August and January. Adults (over 22 cm SL) were primarily found on the outer reef slope, while subadults (under 20 cm SL) were more observed in the fringing reef. Our results highlight the habitat succession of *S. sutor* over its ontogeny, emphasizing its preference for seagrass areas and coral reefs, which underscores the need for spatial management strategies for its sustainable use.

OUTCOMES FROM THE EUROPEAN PROJECT SPRING: CAPACITY BUILDING IN POLLINATOR TAXONOMY

Sara REVERTE[1*], Denis MICHEZ[1]

[1] Laboratory of Zoology, Research Institute for Biosciences, University of Mons, Place du Parc 20, 7000 Mons, Belgium

***Presenting author**, **sara.revertesaiz@umons.ac.be**

Keywords: Capacity building, Pollinator academy, Taxonomy, Trainings

The skills for pollinator identification, especially bees and hoverflies, are restricted to a small number of people and not covering homogeneously the European territory. There is a strong need for increasing the number of people that will be able to identify the samples coming from the future EU Pollinator Monitoring Scheme, particularly at the species level. One of the main objectives of the European project SPRING (2021-2024) was to strengthen taxonomic capacity in EU Member States regarding pollinators, and support preparation for the implementation of the EU Pollinator Monitoring Scheme, in relation to the European Nature Restoration Law. A series of training courses have been organized to connect the people working on pollinator identification across different geographical scales; and to increase the taxonomic skills of the local people across the EU27 member states. The training courses aimed at 4 different levels: (i) identifying large pollinator groups, (ii) identifying bees and hoverflies to genus level, (iii) identifying bees or hoverflies to species group level, (iv) identifying bees or hoverflies to species level. Training courses at level (i) were developed at the national scale; levels (ii) and (iii) covered multiple countries; and level (iv) considered the whole of Europe. Moreover, the project created a series of e-learning materials on pollinator identification at different levels, focusing on the needs of people involved in monitoring programs. All this material is open to the public on the online portal ‘Pollinator Academy’, that will act as a hub to centralize information about already available tools related to pollinator identification (articles, online keys, books, interesting links, other courses, etc.).

ORBIT: THE EUROPEAN TAXONOMIC INITIATIVE FOR POLLINATOR MONITORING

Paolo ROSA[1*], Guillaume GHISBAIN[1], Sara REVERTE[1], Simone FLAMINIO[1], Romain LE DIVELEC[1], Denis MICHEZ[1]

[1] Laboratory of Zoology, University of Mons, 7000 Mons, Belgium.

***Presenting author**, **paolo.rosa@umons.ac.be**

Keywords: Taxonomy, Bees

Europe has an important international responsibility in bee conservation, hosting over 2,000 bee species, including 400 endemic ones. Recent research has shown that pollinators are in decline and, in response, the European Commission (EC) is implementing monitoring projects that require taxonomic resources for accurate species identification and the effective execution of monitoring schemes. However, a lack of taxonomists and taxonomic resources for identifying bee species significantly hinders conservation efforts in this hotspot of bee diversity. To address the need for taxonomic tools, the Directorate-General for Environment of the EC commissioned the ORBIT project, a three-year initiative aimed at developing resources to support European bee inventory and monitoring. Here, we present results from the project, which synthesizes taxonomic information into comprehensive factsheets for each of the 2,138 species. These include diagnoses, high-resolution images, photographs of bees in nature, and summaries of their biology (such as host-plant associations and ecological/behavioural traits), along with information on distribution and conservation status. This data will be accessible to the public through an open-access online platform, conceptualized and designed in collaboration with an expert workshop and the EC's IT team at the project's outset. Outputs also include the new checklist of the European species and National checklists which serve as foundational tools for biodiversity assessment, conservation planning and research.

MULTI-WAY METHODS FOR WIREWORMS' CONTROL: VOLATILE ORGANIC COMPOUNDS, POTATO VARIETAL PREFERENCES AND ENTOMOPATHOGENIC FUNGI

Fanny RUHLAND[1*], Andrea Chacon HURTADO[1], Ismahen LALAYMIA[2], Antoine BOULLIS[1], Nolan REGNIER[2], Stéphane DECLERCK[2], François J. VERHEGGEN[1]

[1] Chemical and Behavioural Ecology, Gembloux Agro-Bio Tech, University of Liège, 5030 Gembloux, Belgium.

[2] Earth and Life Institute, Applied Microbiology, Mycology, Catholic University of Leuven, 1348 Louvain-la-Neuve, Belgium.

***Presenting author**, **fanny.ruhland@uliege.be**

Keywords: *Agriotes,* Attractivity, Semiochemicals, Virulence

Wireworms are a major threat to agriculture worldwide. These soil-dwelling insect pests cause major economic losses. Following the recent ban on neonicotinoids, it has become crucial to develop integrated management strategies targeting this insect. In this study, we sought to (i) assess the feeding preferences of wireworm larvae for different potato varieties and (ii) identify new strains of effective entomopathogenic fungi. We selected three potato varieties that exhibit varying levels of susceptibility to wireworm damage in the field: Monalisa (high damage), Spunta (moderate damage), and Charlotte (low damage). In one-choice bioassays, we observed that wireworms displayed higher feeding activity on Monalisa tubers compared to the other varieties. Additionally, after 50 weeks, we found that wireworms experienced an accelerated life cycle on Monalisa compared to Charlotte. Since wireworms rely on volatile organic compounds (VOCs) to locate hosts, we hypothesized that Monalisa's susceptibility might be linked to specific VOC emissions. However, dual-choice bioassays revealed an unexpected pattern: while Monalisa sustained the highest damage, Spunta showed greater attraction. Using non-destructive headspace dynamic sampling and gas chromatography, we identified a blend of 63 VOCs released by tubers in the rhizosphere. No significant differences in VOCs composition were found across varieties. These findings suggest that the variety most susceptible to damage is not the most attractive but rather the one that promotes higher wireworm foraging activity, implicating other olfactory cues (such as CO_2 and secondary metabolites) in host selection. In a further step, we tested the biocidal activity of 11 strains of entomopathogenic fungi on wireworms, and after 12 weeks of continuous exposure, two new strains significantly reduced wireworm survival. Encapsulating these two strains in a biodegradable matrix optimized for field application showed that one strain was particularly effective in killing wireworms. Collectively, these findings contribute valuable insights toward integrated management strategies for wireworm control.

POPULATION ASSESSMENT AND FORAGING ECOLOGY OF THE RARE SOLITARY BEE *MEGACHILE CYPRICOLA* ON THE ISLAND OF CYPRUS

Rémi SANTERRE[1+], Jordan BENREZKALLAH[1+*], Androulla I. VARNAVA[2], Denis MICHEZ[1], Menelaos STAVRINIDES[2,3]

[1] Laboratory of Zoology, Research Institute for Biosciences, University of Mons, 7000 Mons, Belgium.

[2] Biotechnology and Food Science, Department of Agricultural Sciences, Cyprus University of Technology, 3036 Limassol, Cyprus.

[3] Eratosthenes Centre of Excellence, 3012 Limassol, Cyprus.

[+]First authors

***Presenting author, remi.santerre@umons.ac.be jordan.benrezkallah@umons.ac.be**

Keywords: Solitary bee, Conservation, Population ecology, Foraging ecology

Megachile cypricola is a solitary bee endemic to Cyprus, which was assessed as Critically Endangered in 2014 following IUCN criteria. Recent records suggest that the species is still occurring in a few locations, however information on its ecology and population size is required to revise its status and implement conservation measures. For this purpose, samplings were carried out in four areas during spring 2022. We evaluated (i) the habitat of *M. cypricola* (ii) its foraging ecology and the importance of *Onobrychis venosa* (endemic Fabaceae reported as its main host plant) in its diet; (iii) its nesting biology; (iv) its population size. *O. venosa* represented over 95% of the pollen loads of female *M. cypricola* on average, confirming its narrow oligolecty. The nests consisted of external structures made of a dried mortar of sand and secretions regurgitated. A mark-recapture study resulted in an estimate of 849.4 female individuals across three assessment locations. Overall, this study highlights the high degree of specialisation of *M. cypricola* on a single endemic plant species. It also provides evidence that the species, which is known from a restricted number of localities, is relatively abundant locally.

Implications for insect conservation: Although *M. cypricola* does not appear to be at imminent risk of extinction, population monitoring should be conducted as this highly specialised species may be particularly vulnerable to habitat modifications, especially those driven by tourism development in coastal areas. This study highlights a few sites of interest and a potential method to implement such a monitoring.

OYSTERS AS A MODEL ORGANISM FOR SETTLEMENT OF REEF-BUILDING ORGANISMS IN RESPONSE TO COMPLEX SENSORY LANDSCAPES OF CHEMICAL, TACTILE, AND SOUND CUES

Sarah SCHMIDLIN[1,2*], Jan MEES[1,2], Pascal I. HABLÜTZEL[1,3]

[1] Flanders Marine Institute, InnovOcean Campus, 8400 Oostende, Belgium.

[2] Marine Biology, Ghent University, 9000 Gent, Belgium.

[3] Department of Biology, Vrije Universiteit Brussel, 1050 Brussels, Belgium.

***Presenting author, sarah.schmidlin@vliz.be**

Keywords: Behavioral ecology, Plankton ecology, Larvae settlement, Settlement cues

Substrate colonization by planktonic larvae is a complex process. As larvae near the end of their pelagic period, they rely on environmental cues to evaluate habitat quality for permanent settlement. Most invertebrate species with a larval phase depend on settlement cues to identify ideal environments. These cues are highly species specific, can have various origins, and influence larvae at different spatial scales. Understanding larvae responses to these cues, especially when multiple cues interact, not only advances fundamental knowledge of larval settlement strategies but also provides critical insights for habitat restoration, aquaculture, and antifouling efforts.

Through a series of controlled laboratory experiments, we investigated known or predicted settlement cues of the Pacific oyster (*Magallana gigas*).

In the first set of experiments, we examined how larvae modify optimization strategies in response to multiple and conflicting cues (e.g., from conspecifics or predators). Our findings suggest that larval settlement under conflicting cues depends on the cue origin (waterborne vs. substrate-bound). Notably, larvae can ignore predator cues when faced with preferred substrates but not when exposed to waterborne conspecific cues.

In a second experiment, we explored the influence of marine soundscapes on larval settlement, using sounds associated with oyster reefs and anthropogenic noises from marine vessels. Our results indicate an increased settlement response to sounds from healthy reefs. We propose that acoustic diversity is crucial for larval settlement, emphasizing not just an increase in decibel level but also the acoustic complexity of different sounds.

A third experiment investigated how changes in surface microtopography and the resulting biofilm alterations affect larval settlement patterns.While these experiments contribute to our understanding of larval settlement, a significant gap remains in conceptual frameworks that explain observed patterns. Developing such frameworks is essential for generating new hypotheses and advancing this field of research.

AN OPPORTUNE MOMENT: INVESTIGATING INERTIAL PROPERTIES OF THE DISTAL LIMB OF HORSES THROUGH AN ICONIC EVOLUTIONARY TRANSITION

Anastasia SELINI[1,2*], Tim DE RIDDER[2], Peter AERTS[2], Jamie A. MACLAREN[2]

[1] Evo-Eco-Paleo Laboratory, University of Lille, 59655 Lille, France.

[2] Functional Morphology Laboratory, University of Antwerp, 2180 Antwerp, Belgium.

***Presenting author, Anastasia.Selini@uantwerpen.be**

Keywords: Equidae, Digit reduction, Locomotion, Biomechanics

Horse side-digit reduction is used as a textbook example of adaptative evolution. A principal hypothesis for the reduction (and eventual loss) of side-digits in horses (family Equidae) has been to minimize energetic cost during locomotion, linked to reducing inertial load of the limbs (inertial load hypothesis). The inertial load (or moment of inertia (MOI)) of the equid distal limb would intuitively have decreased with side-digit loss, as side-digits account for mass at the furthest point from the rotation center of e.g. the forelimb (at the scapula). In this study, we aimed to experimentally test this hypothesis by estimating and comparing inertial loads of tridactyl (three-toed) equid limbs, both with and without side-digits. Additionally, we compared the results of the tridactyl and monodactyl equids, while accounting for differences in limb size, to investigate the effect of side-digit loss across equid evolution. A validation analysis using cadaver specimens was performed to verify the predictability of soft tissue reconstructions, later implemented in the extinct species. We demonstrate that side-digits did not account for significant additional inertial load in the distal limb segments, and MOI was further minimized when the inertial load of the full limb was considered. Additionally, we find no significant differences in relative mass of the pastern segment (comprising the proximal phalanges) between tridactyl and monodactyl equids; monodactyl forms sometimes surpassed the mass of the tridactyl species. Size-corrected MOI between monodactyl and tridactyl taxa suggested significant differences (monodactyl equids with lower MOI); however, allometric differences in segment proportions likely caused this reduced MOI, rather than the effect of side-digit presence. Our study refutes the theory that side-digit reduction in derived tridactyl equids was linked to inertial load minimization. We are currently expanding our study to incorporate more different phylogenetic groups, which will doubtless provide greater evolutionary resolution to our current findings.

RELATION BETWEEN HONEYBEE ABUNDANCE AND WILD BEES COMMUNITIES IN MOROCCAN AGRO-ECOSYSTEMS

Ahlam SENTIL[1*], William FIORDALISO[1], Denis MICHEZ[1]

[1] Laboratory of Zoology, University of Mons, 7000 Mons, Belgium.

***Presenting author**, **ahlam.sentil@umons.ac.be**

Keywords: Competition, Conservation, Pollinator, Niche-partitioning, Marketable plants

The expansion of entomophilous crops over the last decades has been accompanied by a growing demand for managed honey bee colonies to provide pollination services. The massive introduction of honey bee in agro-ecosystems has raised concerns about a negative effect on wild bee communities. Here we assess following a standardized sampling the relation between honey bee abundance and wild bee abundance/species richness in six pollinator dependent crops across 201 sites in four different regions in Morocco and during two consecutive years. We also evaluate how multi-croping can modulate the impact of honey bee on wild bees. Our results show that wild bee abundance and richness were not influenced by honey bee abundance regardless of the crop. The response of wild bees to honey bee did not vary between monoculture fields and fields with additional crops. These findings suggest that the current Moroccan agro-ecosystems are not experiencing a strong competition between wild and honey bees and they might co-exist even in the absence of additional habitat plants. However, the effect of honey bee on wild bees remains context-dependent, and we therefore urge caution when generalizing the results.

EVALUATING CONSERVATION EFFORTS FOR THE EUROPEAN HAMSTER: INSIGHTS FROM PREDICTIVE MODELLING

Imke TOMSIN[1]*, A. Bradley DUTHIE[2], Nils BUNNEFELD[2], Herwig LEIRS[3], Jim CASAER[4], Natalie BEENAERTS[1]

[1] Centre for Environmental Sciences, Hasselt University, 3500 Hasselt, Belgium.

[2] Biological and Environmental Sciences, University of Stirling, FK9 Stirling, UK.

[3] Evolutionary Ecology group, University of Antwerp, 2000 Antwerpen, Belgium.

[4] Research Institute for Nature and Forest (INBO), 1000 Brussel, Belgium.

***Presenting author, imke.tomsin@uhasselt.be**

Keywords: Wildlife management, Predictive modelling, Conservation, European hamster

Does the European hamster (*Cricetus cricetus*) still have a future in our landscapes? To date, no conservation program has succeeded in establishing a minimum viable, stable, or growing European hamster population. This study aimed to evaluate the effectiveness of current conservation strategies and to explore alternative management actions that could lead to population recovery. We developed a predictive model using the Generalised Management Strategy Evaluation (GMSE) R package to simulate the impact of changes in population parameters, as could be the result of specific management actions, on the population dynamics of the European hamster. Our findings indicate that, under current conditions and without significant management interventions, the European hamster population will continue its decline, ultimately leading to extinction. However, scenarios that include substantial increases in reproductive output and survival rates for hamsters living in fields managed with hamster-friendly practices show potential for population recovery. This study underscores the urgent need for more ambitious, targeted conservation strategies to ensure the long-term survival of the European hamster and highlights the value of predictive modelling tools like GMSE in guiding future conservation efforts for the European hamster and other endangered species.

SYMBIOTIC INTERACTIONS CHALLENGED BY ENVIRONMENTAL STRESS IN AQUATIC TRANSITIONAL HABITATS

Martina TOPIĆ[1*], Nikol KMENTOVÁ[1,2], Maarten VAN STEENBERGE[3], Maarten P.M. VANHOVE[1]

[1] Zoology: Biodiversity and Toxicology group, Centre for Environmental Sciences, Hasselt University, 3590 Diepenbeek, Belgium.

[2] OD Natural Environment, Royal Belgian Institute of Natural Sciences, 1000 Brussels, Belgium.

[3] OD Taxonomy and Phylogeny, Royal Belgian Institute of Natural Sciences, 1000 Brussels, Belgium.

***Presenting author, martina.topic@uhasselt.be**

Keywords: Climate change, Parasites, Killifishes, Estuaries

Estuaries present transitional habitats between freshwater and marine ecosystems. They are known for their changing abiotic conditions, influenced by daily and seasonal changes in sea levels, changes in temperature, and river influx. Estuaries are also significantly impacted by climate change, which affects them through changes of sea levels, water temperature, salinity and acidity. These changes will increase the environmental stress experienced by aquatic organisms and their symbiotic communities, which include bacteria and metazoan parasites, and influence their symbiotic relationships. The impact of climate change and environmental stress on aquatic estuarine organisms is underexplored on the level of symbiotic communities. This project is focused on understanding the effects of global climate change on these communities. We will research the diversity present in fish-parasite-microbiome communities on the east coast of the United States of America using the Atlantic mummichog (*Fundulus heteroclitus)* as a fish host model species; identify mechanisms of stress response to salinity change in fish ectoparasites; describe the genomic landscape of salinity tolerance in a symbiont community; and model the possible direction of change in a symbiont community under the influence of climate change. The project started with the research of ectoparasites of estuarine fishes from South Carolina. Species of *Anchoa*, *Fundulus*, *Gambusia*, *Gobiosoma, Menidia* and *Mugil* (n=11) were screened for the presence of ectoparasites. In total, 15 species belonging to different lineages of monopisthocotylan flatworms (*Gyrodactylus*, *Ligophorus*, *Salsuginus*), polyopisthocotylan flatworms (*Metamicrocotyla*) and copepods (*Bomolochus*, *Caligus*, *Ergasilus*, *Naobranchia*). From all screened hosts species *Ligophorus* have the highest mean intensity and prevalence. Furthermore, *M. cephalus* harbors the highest parasite species richness (seven). Some of the parasites identified present new records for the study area. These parasites show strong patterns of host-specificity and can be found in different habitats within the estuary, such as creeks, small lakes and water reservoirs.

GLOBAL MODELS OF HERBIVORY VARIABILITY: DATA FROM THE HERBVAR PROJECT

Kévin TOUGERON[1*], The Herbivory Variability Network[2]

[1] EICG laboratory, Research Institute in Biosciences, University of Mons, 7000 Mons, Belgium.

[2] Full author list can be found at doi: 10.1126/science.adh8830

***Presenting author**, **kevin.tougeron@umons.ac.be**

Keywords: Interaction, Plants, Global, Biogeography

Herbivory is a major selection pressure on plants, which have evolved many different physical and chemical adaptations to prevent animals from eating their tissues. Mean herbivory patterns have been well studied in ecology. However, herbivory pressure can be highly variable, among different species of plants, and even between plants in the same population. The Herbivory Variability Network consortium used standardized surveys to compare herbivory variability within populations at 790 sites across five continents, on various families of plants. With these data, we show that within-population variability in herbivory increases with latitude, decreases with plant size, and is phylogenetically structured. Such patterns of variability in herbivory-related selection pressures could explain variations in plants' induced or constitutive defense capacities across latitudes, families or individual sizes. Differences in the magnitude of variability are thus central to how plant-herbivore biology varies across macroscale gradients. These findings highlight how variation in species interactions can influence eco-evolutionary outcomes. We argue that increased focus on interaction variability will advance understanding of patterns of life on Earth.

EFFECT OF HEATHER FLAVONOIDS ON THE BUFF-TAILED BUMBLEBEE

Clément TOURBEZ[1*]

[1] Laboratory of Zoology, University of Mons, 7000 Mons, Belgium.

***Presenting author**, **clement.tourbez@umons.ac.be (mailto: smile@whysoserious.com)**

Keywords: Plant-pollinator interaction, Specialised metabolite, Bumble bee health, Parasite.

There is evidence that specialised metabolites of flowering plants occur in both vegetative parts and floral resources (*i.e.*, pollen and nectar), exposing pollinators to their biological activities. While such metabolites may be toxic to bees, it may also help them to deal with environmental stressors. One example is heather nectar which has been shown to limit bumble bee infection by a trypanosomatid parasite, *Crithidia* sp., because of callunene activity. Besides in nectar, heather harbours high content of specialised metabolites in pollen such as flavonoids, but they have been poorly investigated. In this study, we aimed to assess the impact of *Crithidia* sp., heather pollen and its flavonoids on bumblebees using non-parasitised and parasitised microcolonies fed either control pollen diet (*i.e.*, willow pollen), heather pollen diet, or flavonoid-supplemented pollen diet. We found that heather pollen and its flavonoids significantly affected microcolonies by decreasing pollen collection as well as offspring production, and by increasing male fat body content while parasite exposure had no significant effect except for an increase in male fat body. We did not find any medicinal effect of heather pollen or its flavonoids on parasitised bumble bees. Our results provide insights into the impact of pollen specialised metabolites on heather-bumble bee-parasite interactions. They underline the contrasting roles of the two floral resources for bumble bees and emphasize the importance of considering both nectar and pollen when addressing medicinal effects of a plant for pollinators.

LINKING FISH ECOLOGY TO OTOLITH DIVERSITY AT A BROAD PHYLOGENETIC SCALE

Arthur VAN DAMME[1,2]*, Antoni LOMBARTE[3], Bruno FRÉDÉRICH[2], Éric PARMENTIER[1], Effrosyni FATIRA[4], Tanja SCHULZ-MIRBACH[5], Aline Paiva M. DE MEDEIROS[6], Ricardo BETANCUR-R[7], Victor M. TUSET[4]

[1] Laboratory of Functional and Evolutionary Morphology, University of Liège, 4000 Liège, Belgium.

[2] Laboratory of Evolutionary Ecology, University of Liège, 4000 Liège, Belgium.

[3] Institut de Ciències del Mar (ICM-CSIC), 08003 Barcelona, Spain.

[4] Instituto de Oceanografía y Cambio Global (IOCAG), Universidad de Las Palmas de Gran Canaria (ULGPC), Unidad Asociada ULPGC-CSIC, 35214 Telde, Canary Islands, Spain.

[5] Department Biologie II, Ludwig Maximilians Universitaet Muenchen, 82152 Planegg-Martinsried, Germany.

[6] Programa de Pós-Graduação em Ciências Biológicas, Universidade Federal de Paraíba, 58051-900 João Pessoa, Brazil.

[7] Scripps Institution of Oceanography, UC San Diego, 92037 La Jolla, San Diego, CA, U.S.A.

***Presenting author**, **arthur.vandamme@uliege.be**

Keywords: Actinopterygii, Otolith, Diversification, Ecomorphology

Ecomorphology explores the links between species morphology and its environment to better understand the adaptive value of a given phenotype. Different studies have applied this approach trying to explain intra- and interspecific variability of fish otolith shape but they did not reach a consensus about the major factors influencing this structure of the inner ear. The present study aims to uncover the major influence of teleost ecology on otolith diversification at a large taxonomic scale, spanning the fish tree of life. To do so, we (1) redefine the main axes of otolith diversity, (2) compare levels of ecological and otolith morphological diversity among orders and (3) quantify the effect size of ecological variables on otolith shape and size while accounting for phylogeny. We gathered ecological variables for 697 fish species. Collected information included species ecology (position in the water column, habitat light conditions, feeding mode, mobility and gregariousness) including traits related with acoustic communication (hearing specializations and sound production). Otolith shape was quantified with landmark-based geometric morphometric methods and phylogenetic information was retrieved from the megaphylogeny of Betancur et al. (2013). Our analysis showed that the major axes of otolith disparity involve elongation, sulcus shape, rostro-caudal thickness and curvature. Next, we found that the order-level ecological diversity is decoupled from otolith morphological diversity. Finally, we demonstrated that otolith morphology is influenced by fish occupation of the water column, habitat light conditions, and mobility. We concluded that fish otolith morphology reflects a compromise between various life history traits and cannot be summarized as a function of one aspect of a fish's ecology.

ENVIRONMENTAL FACTORS AND UV EXPOSURE AFFECT GENE ACTIVITY IN THE PUTATIVE ANCIENT ASEXUAL OSTRACOD *DARWINULA STEVENSONI*

Yelle VANDENBOER[1,2*], Koen MARTENS[1,3], Franscesc MESQUITA-JOANES[4], Isa SCHÖN[1,2]

[1] Freshwater Biology, ATECO, OD Nature, Institute of Natural Sciences, 1000 Brussels, Belgium.

[2] Department of Biology, Hasselt University, 3500 Hasselt, Belgium.

[3] Department of Biology, Ghent University, 9000 Ghent, Belgium.

[4] Institut Cavanilles de Biodiversitat i Biologia Evolutiva, University of Valencia, 46980 Paterna, Spain.

***Presenting author, yvandenboer@naturalsciences.be**

Keywords: Freshwater, Ostracods, Adaptation, Genomics

The non-marine ostracod *Darwinula stevensoni* (Ostracoda, Crustaceae) is one of the last remaining examples of an ancient asexual and has probably abandoned sexual reproduction approximately 20 million years ago. In spite of the limited genetic diversity of *D. stevensoni*, its cosmopolitan distribution in different aquatic habitats indicates that this species can survive asexually in the long-term, possibly because it developed a general purpose genotype. To unravel the genetic background of this general purpose genotype, we have studied gene activity of *D. stevensoni* via the RNA-sequencing of transcriptomes. The transcriptome is the collection of all active genes which have been transcribed from DNA to RNA under certain conditions. Statistically comparing the genetic composition of transcriptomes allows us to identify differences in active (or expressed) genes, which inform on host adaptations to specific conditions. We characterised transcriptomes of *D. stevensoni* from natural populations in Spain, England and Belgium. In total, 11.197 *D. stevensoni* gene transcripts were detected, many of which were repressed in the English population. To summarize results in our multi-gene approach, genes were grouped by function using the “gene ontology” (GO) classification system. These groups revealed no clear link with adaptive mechanisms, suggesting the ancient asexual’s adaptive strategy is more elusive than hypothesized. In addition to this, living *D. stevensoni* individuals from Belgium were experimentally exposed to UV radiation. This experimental set-up minimizes confounding variables, and we therefore expected to detect adaptations specific to UV radiation. Overall, ostracods activated (rather than repressed) genes in response to UV radiation. The functions of affected genes can be linked mitosis and the septin cytoskeleton. UV-radiation can thereby affect the growth of *D. stevensoni*, but the species appears to lack a specific mechanism based on gene expression for adapting to UV radiation. Further experiments and analyses are planned in 2025 to support these results.

Fig. 1. Female *Darwinula stevensoni* with three eggs in the brood chamber at the rear (length: 0.8 mm). Image modified from Lake Biwa Museum website.

STUCK IN THE SPOTLIGHT: GLOW-WORM LARVAE SLOW DOWN UNDER ARTIFICIAL LIGHT

Mira VAN DEN BROECK[1*], Sander VANDORMAEL[1], Thomas MERCKX[2], Raphaël DE COCK[1], Erik MATTHYSEN[1]

[1] Evolutionary Ecology Group, Universiteit Antwerpen, 2610 Antwerp, Belgium.

[2] Department of Biology, Vrije Universiteit Brussel, 1050 Brussels, Belgium.

***Presenting author, mira.vandenbroeck@uantwerpen.com**

Keywords: ALAN, Glow-worms, Activity

Artificial light at night (ALAN) forms a threat to wildlife on a global scale, potentially affecting all species that evolved under predictable light-dark cycles, with nocturnal species being particularly vulnerable. We investigated the effects of different artificial light colours on the activity and movement behaviour of the European common glow-worm (*Lampyris noctiluca* L.) larvae, a nocturnal and bioluminescent beetle. Two arena experiments were carried out, one in spring and one in fall. We hypothesized that (i) larvae have a reduced activity under artificial illumination, and (ii) that female larvae might be attracted to light during the dispersal phase, just before pupation, using it as a cue for a suitable display site to attract a mate in the adult phase. We found no evidence for positive or negative phototaxis towards artificial light. However larval activity decreased significantly under artificial illumination, especially under short-wavelength dominated light (blue and white). These findings were consistent across both seasons. We found no evidence that female larvae were attracted to light. Reduced activity during the larval foraging stage could have severe consequences on reproductive success, as glow-worms are capital breeders building up reserves in the larval phase and ceasing to feed during adulthood, and female fecundity is linked to body weight. Our findings highlight the potential risks ALAN poses to glow-worm populations by disrupting key life stages essential for reproduction and population sustainability.

IMPACT OF ENDOCRINE DISRUPTION ON THE NUMBER OF HAIR CELLS IN NEUROMASTS OF THE LATERAL LINE ORGAN OF ZEBRAFISH LARVAE

Ellen VANDEPUTTE[1*], Evelyn STINCKENS[1], Lucia VERGAUWEN[1], Dries KNAPEN[1]

[1] Zebrafishlab, Veterinary Physiology and Biochemistry, Department of Veterinary Sciences,
University of Antwerp, 2610 Wilrijk, Belgium.

***Presenting author**, **Ellen.Vandeputte@uantwerpen.be**

Keywords: Endocrine disruption, Thyroid hormone system, Lateral line system, Zebrafish embryo

Research on the potential adverse effects of endocrine distrupting compounds (EDCs) on biological systems has received progressively more attention worldwide. While there have been some indications of effects of endocrine disruption on the lateral line (LL) system such as the presence of hormone receptors in the LL, the effect of EDCs on this system has not received a lot of attention. The LL system detects water movements and pressure gradients in water via hair cells (HCs) that are positioned along the body of the fish. The current study examines this system in zebrafish larvae until 5 days post fertilization (hpf), which are non-protected animals according to the European Directive (2010/63/EU). Embryos were exposed to a model compound for disruption of LL (copper sulfate pentahydrate, positive control) and model EDCs: an estrogen receptor agonist (17α-ethinylestradiol), an estrogen receptor antagonist (fulvestrant), two different thyroid hormone (TH) system disruptors (methimazole, a thyroid peroxidase inhibitor, and iopanoic acid, a deiodinase inhibitor) and an aryl hydrocarbon receptor agonist (β-naphthoflavone). LL development was evaluated by counting the number of HCs in selected neuromasts. Only methimazole (MMI) affected this endpoint: a decline in the number of HCs was observed. To elucidate the effect of TH synthesis disruption on the LL, embryos were exposed to MMI during two time windows (TWs): 0-72 hpf and 72-120 hpf. Due to the thyroid only becoming active around 72 hpf, the embryo is dependent on maternally transferred THs prior to this time point. No effect was observed in the 0-72 hpf TW, but disrupting TH synthesis between 72 and 120 hpf resulted in less HCs. These results suggest that the observed effect on the LL system is the consequence of reduced endogenous TH synthesis and additional research is being performed to confirm this, including the study of environmentally relevant thyroid peroxidase inhibitors.

THE THYROID HORMONE SYSTEM DISRUPTING POTENTIAL OF RESORCINOL IN FISH

Imke VAN DINGENEN[1*], Emma ANDERSEN[2], Sina VOLZ[2], Monica CHRISTIANSEN[2], Jiří NOVAK[3], Ann-Cathrin HAIGIS[1], Emma STACY[4], Brett BLACKWELL[4], Daniel VILLENEUVE[4], Lucia VERGAUWEN[1], Klára HILSCHEROVA[3], Henrik HOLBECH[2], Dries KNAPEN[1]

[1] Zebrafishlab, Veterinary Physiology and Biochemistry, Department of Veterinary Sciences, University of Antwerp, 2610 Wilrijk, Belgium.

[2] Department of Biology, University of Southern Denmark, 5230 Odense M, Denmark.

[3] RECETOX, Faculty of Science, Masaryk University, 625 00 Brno, Czech Republic.

[4] United States Environmental Protection Agency, Great Lakes Toxicology and Ecology Division, Duluth, 55804 Minnesota, U.S.

***Presenting author, imke.vandingenen@uantwerpen.be**

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

An increasing number of environmental pollutants have been shown to interfere with the thyroid hormone (TH) system, raising concern for both human and environmental health. Recently, resorcinol was identified as a compound of high concern, due to its endocrine disrupting properties. It is capable of inhibiting thyroperoxidase (TPO), an enzyme crucial for TH synthesis. In humans, therapeutic use of resorcinol has been linked to hypothyroidism. Evidence concerning ecotoxicologically relevant effects of resorcinol in fish, on the other hand, is limited. Recently, a set of adverse outcome pathways (AOPs) has been developed linking thyroid hormone system disruption (THSD) to impaired swim bladder inflation and eye development in fish. These AOPs were used in the current study to provide the background for testing potential THSD effects of resorcinol in zebrafish eleutheroembryos. Zebrafish eleutheroembryos were exposed to resorcinol and effects on TH levels, swim bladder inflation and eye development were assessed. As a TPO inhibitor, resorcinol exposure is expected to alter TH levels and eye morphology but not affect swim bladder inflation during embryonic development. Thyroxine (T4, the main synthetized TH) levels were indeed significantly decreased following resorcinol exposure. Contrary to our hypothesis, swim bladder inflation was impaired and no effects on eye morphology were observed. Therefore, *in vitro* assays were performed to identify potential additional thyroid hormone system disruption-related mechanisms through which resorcinol may act. Two new mechanisms were identified: TH receptor (TR) antagonism and transthyretin (TTR) binding inhibition. Both of these mechanisms can plausibly be linked to impaired swim bladder inflation and could, therefore, explain the observed effect. Overall, our study contributes to the knowledge of the THSD potential of resorcinol both *in vivo* in the zebrafish model as well as *in vitro*.

PHYLOGENOMICS OF *ENYALIUS* LIZARDS REVEALS CRYPTIC DIVERSITY IN THE ATLANTIC FOREST AND MIOCENE RAINFOREST CONNECTIONS WITH THE AMAZON

Mariana VASCONCELLOS[1 2*], Roberta DAMASCENO[1], Ísis ARANTES[3], Katia PELLEGRINO[4], Miguel RODRIGUES[1], Ana Carolina CARNAVAL[4]

[1] Departamento de Zoologia, Universidade de São Paulo, 05508-090 São Paulo, Brazil.

[2] Department of Biology, University of Antwerp, 2610 Wilrijk, Belgium.

[3] Department of Biology, University of Mississippi, 38677 Oxford, U.S.

[4] Departamento de Ciências Biológicas, Universidade Federal de São Paulo, 09920-000 Diadema, Brazil.

***Presenting author, marimiravasc@gmail.com**

Keywords: RADseq phylogeny, Biogeography, South America, Molecular species delimitation

Next-generation sequencing has enabled the collection of genomic-scale data for evolutionary studies across numerous taxa, including non-model organisms. This technological advance has revolutionized phylogenetic inference, increasing the resolution of species relationships that were previously uncertain or limited by sparse data from a few genes. Using the *Enyalius* lizards of South America as a model group to test the suitability of reduced-representation genomic data (RADseq) for deep phylogenetic inference, we estimated the evolutionary relationships among all species in this genus, including multiple populations per species. Using over 70,000 SNPs (genetic polymorphisms), our study provides strong nodal support for all species, dividing the genus into two major clades: one comprising seven species occupying the northern Atlantic Forest and gallery forests of the Cerrado savanna, and another comprising six species from the southern Atlantic Forest or the western Amazonia. Our model-based species delimitation approach confirmed three undescribed cryptic species in the Atlantic Forest, previously suggested by mitochondrial data. Additionally, the deep phylogenetic relationships between clades differed slightly from previous findings, likely resulting from our genome-wide dataset, which enhanced the resolution of previously weakly supported relationships. The most recent common ancestor of *Enyalius* likely evolved in the Atlantic Forest in the late Oligocene, around 27 million years ago (95% HPD = 33.37–21.01 Mya). Our ancestral range reconstruction inferred dispersal to the Amazon Forest around 22.8 Mya. This finding corroborates Miocene rainforest connections between the southern Atlantic Forest and western Amazon Forest. Our study highlights RADseq as a powerful tool for resolving phylogenetic relationships at both population and species levels, providing robust insights into the deep evolutionary history and biogeography of this arboreal lizard genus in South America.

SYNTHESIS OF ANIMAL TRAIT DATA ACROSS THE TREE OF LIFE WITH SHARETRAIT: PROBLEMS, PITFALLS AND POSSIBILITIES

Wilco VERBERK[1], Matty BERG[2], Iris VAN DE POL[1*], Jacintha ELLERS[2]

[1] Department of Ecology, Radboud Institute for Biological and Environmental Sciences, 6525 AJ Nijmegen, The Netherlands.

[2] Department of Ecological Sciences – Animal Ecology, Vrije Universiteit Amsterdam,1081 HZ Amsterdam, The Netherlands.

***Presenting author, iris.vandepol@ru.nl**

Keywords: Animal traits, FAIR principles, Database, Metadata

Here we present ShareTrait, a user-friendly platform that makes animal trait data not only Findable and Accessible, but also Interoperable and Reusable, thus embracing FAIR principles. To date, the ShareTrait database holds over 30,000 records on three traits universal to animal life: metabolic rate, development time and fecundity. A key feature is the wealth of metadata that is included in a standardized manner, which we demonstrate greatly enhances data interoperability and reusability. For instance, after accounting for differences in common covariates such as size and temperature, intraspecific trait variation was similar to variation in traits across species for both fecundity and metabolic rate, while variation in development rates was ~3 fold smaller within species, compared to across species. This makes ShareTrait a valuable resource for researchers collaborating in large-scale syntheses projects, which are urgently needed to address the complex, global environmental challenges of our time.

INTEGRATING GENETIC CONNECTIVITY AND LOCAL ADAPTATION IN EFFECTIVE MARINE PROTECTED AREA DESIGN: A CASE STUDY ON SOUTHERN OCEAN *TREMATOMUS* FISHES

Marie L. VERHEYE[1*], Henrik CHRISTIANSEN[1,2], Anton VAN DE PUTTE[3,4], Isa SCHÖN[3], Enora GESLAIN[1], Bart HELLEMANS[1], Franz MUETER[5], Filip. A.M. VOLCKAERT[1]

[1] Laboratory of Biodiversity and Evolutionary Genomics, KU Leuven, 3000 Leuven, Belgium.

[2] Greenland Institute of Natural Resources, 3900 Nuuk, Greenland.

[3] Directorate Natural Environment, Royal Belgian Institute of Natural Sciences, 1000 Brussels, Belgium.

[4] Marine Biology Lab, Université Libre de Bruxelles, 1050 Brussels, Belgium.

[5] College of Fisheries and Ocean Sciences, University of Alaska, 99775-7220 Fairbanks, U.S.

***Presenting author, marie.verheye@kuleuven.be**

Keywords: Population genomics, Connectivity, Adaptation, Southern Ocean

Polar ecosystems support a distinctive, cold-adapted biodiversity that faces significant threats from rapid environmental changes and escalating human impacts. To effectively manage and conserve these living resources, multi-scale data on connectivity and adaptation are essential. Marine protected areas (MPAs) are most effective when designed as interconnected networks that account for both functional diversity and connectivity within and among species. In this study, 607 individuals from ten *Trematomus* species were analyzed through ddRAD sequencing, yielding thousands of genomic markers to examine patterns of divergence and connectivity on the Southern Ocean shelf, both within and between species. Genomic SNPs showing evidence of selection, identified as "outlier loci," were further analyzed to explore potential local adaptations to varying environmental conditions. Population structure analyses of four species — *T. loennbergii*, *T. eulepidotus*, *T. scotti*, and *T. newnesi* — indicate extensive dispersal across the Weddell Sea and along the West Antarctic coast, likely facilitated by the Weddell Sea Gyre and the Antarctic Coastal Current. A genetic discontinuity was detected near the Filchner Trough in several species, likely due to the strong outflow from the Filchner-Ronne ice shelf, which may isolate the trough region from the broader Weddell Sea habitat. Additionally, evidence of previously unrecognized cryptic diversity was observed in *T. eulepidotus* and *T. loennbergii*. These findings contribute to our understanding of diversity, connectivity, and adaptation on the Southern Ocean shelf, a critical foundation for conservation amid unprecedented global change.

WHAT DO GRAZERS REALLY GRAZE ON?

Anthony VOISIN[1,2*], Martin DOGNIEZ[2,3,4], Camille MOREAU[5], Julien THÉBAULT[1], Gauthier SCHAAL[1], Loïc N. MICHEL[6], Gilles LEPOINT[2]

[1] Laboratory of Environmental Marine Sciences (LEMAR), University of Western Brittany, 29200 Brest, France.

[2] Laboratory of Trophic and Isotopes Ecology (LETIS), FOCUS, University of Liège, 4020 Liège, Belgium

[3] Center of Environmental Science (CMK), University of Hasselt, 3500 Hasselt, Belgium.

[4] Freshwater Biology Department, Operational Directorate Natural Environment, Royal Belgian Institute of Natural Sciences (RBINS), 1000 Brussels, Belgium.

[5] Marine Biology Lab, Université Libre de Bruxelles (ULB), 1000 Brussels, Belgium.

[6] Animal Systematics and Diversity (ASD), FOCUS, University of Liège, 4020 Liège, Belgium.

***Presenting author, anthony.voisin@univ-brest.fr**

Keywords: Trophic ecology, Benthic grazer, Fatty acid, Antarctica

Sea ice dynamics strongly influence primary production and its availability for local communities in polar ecosystems. In spring, sea ice melting promotes phytoplanktonic and benthic (i.e. macroalgae and microphytobenthos) primary production, and causes a massive export of sea ice algae. All of these represent potential food sources for benthic organisms. Along the West Antarctic Peninsula, two gastropods (*Nacella concinna* and *Margarella antarctica*) and a sea urchin (*Sterechinus neumayeri*) represent some of the most abundant benthic grazing species. Understanding their trophic plasticity when faced with such a diversity of potential food sources is necessary to understand the flow of energy within these communities. To address this objective, analysis of fatty acid composition was carried out on primary food sources and consumers. A clear distinction was observed in the fatty acid composition of the three benthic species. The limpet *N. concinna* showed higher proportions of fatty acids described as macroalgal biomarkers (i.e.,18:1n-9, 20:4n-6, 20:5n-3) than the other two species. *M. antarctica* had higher proportions of fatty acids described as a biomarker of microorganisms (i.e., 16:1n-7, 16:4n-1, ante or iso, C16 or C18 PUFA). *S. neumayeri*, meanwhile, contained a higher proportion of fatty acids described as copepod biomarkers (i.e., 20:1n-9, 20:1n-11, 22:1n-9). Given these results, it would appear that these three grazers feed on different food sources. *N. concinna* may feed more on macroalgae, *M. antarctica* on microorganisms and *S. neumayeri* may have a more mixed diet ranging from sources to primary consumers, such as filter feeders, which might explain the proportion of zooplankton biomarkers. These differences could be driven by both morphological differences in feeding structures and different prey selections, interactively modulating the role of grazers in Southern Ocean food webs.

WHEN ENVIRONMENTAL CHANGES INFLUENCE DISEASE DEVELOPMENT: THE CASE OF THE ENDANGERED SEA CUCUMBER *HOLOTHURIA SCABRA*

Noé WAMBREUSE[1*], Mabel CASTIAUX[1], Vanessa TAGLIATTI[2], Igor EECKHAUT[1,3],
Lafforest TSINDESY[3], Laurence FIEVEZ[4], Fabrice BUREAU[4], Guillaume CAULIER[1,3+],
Jérôme DELROISSE[1,4+]

[1] Biology of Marine Organisms and Biomimetics Unit, University of Mons, 7000 Mons, Belgium.

[2] Human Biology and Toxicology Laboratory, University of Mons, 7000 Mons, Belgium.

[3] Belaza Marine Station, IHSM-UMONS-ULIEGE, 601 Toliara, Madagascar.

[4] Molecular and Cellular Immunology Laboratory, GIGA Institute, University of Liège, 4000 Liège, Belgium.

[+] These two authors shared the supervision of the study

***Presenting author, noe.wambreuse@umons.ac.be**

Keywords: Stress, Immune response, Metabolism, Gene expression

Sea cucumbers are key organisms in marine ecosystems, playing a similar role to earthworms, but in the seas and oceans. Among them, *Holothuria scabra* is a tropical species living in the shallow seabed of Indo-Pacific waters and is endangered due to over-exploitation. Although aquaculture of these species has been successfully developed in emerging countries, *H. scabra* can develop a particular syndrome called skin ulceration syndrome (SUS), which consists of a progressive degradation of the integument leading to the death of individuals. Previous research has shown that the prevalence of the disease increases during the austral winter when seawater temperatures are the coldest. These temperature changes are thought to have the effect of weakening immunological defences. However, it remains unclear whether exposure to pathogenic bacteria is necessary for the onset of the disease. In this study, juveniles of *H. scabra* were maintained at different temperatures, namely 22°c (cold), 27°c (optimal) and 33°c (warm), and half of the individuals were injected with non-sterile seawater to expose them to potential pathogenic bacteria from their environment (Fig. 1). The development of the disease was then monitored for three weeks and the response to the different stress conditions was studied using various indicators, including behaviour, energy metabolism, and immune cell abundance and gene expression. The results show that more juveniles developed the SUS under cold and warm conditions, mainly within a few days after the temperature change, but that the injection had no significant effect on the development of the disease. In addition, the different stress indicators provide clues to explain how *H. scabra* copes with stress and how the SUS appears. Overall, this study provides an example of how thermal changes can influence the emergence of disease in marine environments, which is a major concern for biodiversity in our changing world.

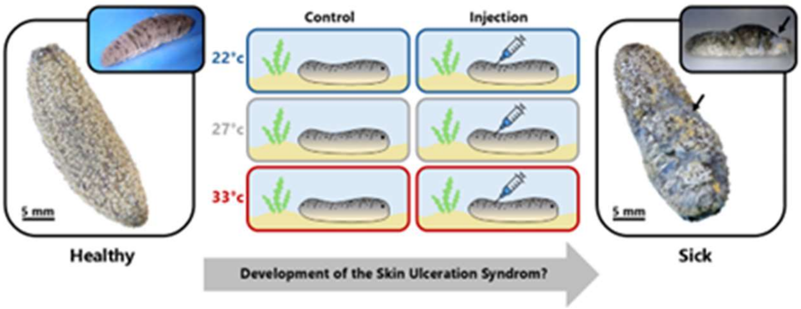


Fig. 1. Graphical abstract showing the experimental design of the study.

Abstracts of Posters Communications

PHYLOGEOGRAPHIC PATTERNS OF THE GIANT CLAM *TRIDACNA MAXIMA* ACROSS THE INDO-PACIFIC

Sezgi AKBAL KESKIN[1*], Filip HUYGHE[1], Kushlani DISSANAYAKE[1,2], Marc KOCHZIUS[1]

[1] Marine Biology – Ecology, Evolution & Genetics (bDIV), Vrije Universiteit Brussel (VUB), 1050 Brussels, Belgium.

[2] Oceanography and Marine Geology, University of Ruhuna, Matara, Sri Lanka.

Poster 1

***Presenting author, sezgiaa@gmail.com, sezgi.akbal@vub.be**

Keywords: Connectivity, Population genetics, Whole genome sequencing

Giant clams provide food, shelter, and protection for various marine species, economic benefits for local communities, and are valuable targets for the international aquarium trade. Despite their importance, giant clam species are declining in abundance. Understanding their genetic population structure is important for their conservation and management. Here, we provide insight into the genetic population structure of the giant clam *Tridacna maxima* across its entire range, spanning the Indo-Pacific.

Samples were collected from Red Sea, Kenya, Tanzania, Madagascar, Sri Lanka, Indonesia, and French Polynesia and analysed using genome wide SNPs obtained by whole genome sequencing, aiming to investigate both genetic diversity and the genetic population structure.

Seven distinct genetic groups, with two subgroups in the Western Indian Ocean (WIO) were identified. Indonesia itself shows substantial genetic structure, with four subgroups, some of which are highly differentiated. Overall, *T. maxima* populations from the Red Sea, Tanzania, and Madagascar show marked differentiation from each other, underscoring the species' genetic diversity across its range and highlighting the need for more specific conservation strategies.

EXPLORATION OF THE POTENTIAL LINKS BETWEEN THE GUT MICROBIOTA AND THE BEHAVIOUR OF *KRYPTOLEBIAS MARMORATUS*

Sarah AYOUB-LAMBIN[1*], Jérôme LAMBIN[1], Valérie CORNET[1], Frédéric SILVESTRE[1]

[1] Biology Department, Institute of Life-Earth-Environment (ILEE), B-5000 Namur, Belgium.

Poster 2

***Presenting author, sarah.ayoublambin@student.unamur.be**

Keywords: Gut microbiota, Behavior, Phenotypic plasticity, Rivulus

Kryptolebias marmoratus is one of the only two vertebrates known to be able to self-fertilize. This explains why certain populations, particularly the Emerson Point Preserve (EPP) population, the population of interest, are highly isogenic. Despite this unique characteristic among vertebrates, these populations display various phenotypes, particularly in terms of behavioral traits. Studies have demonstrated a link between these traits and the epigenome state of each individual, indicating that epigenetics compensate for the low genetic diversity. However, the source of these epigenetic differences observed in these organisms remain unclear. Evidence on other organisms shows that the gut microbiota can influence the host's epigenome by producing, for example, enzymes involved in DNA methylation. Moreover, the gut microbiota can influence the host's behavior through the gut-brain axis, while, conversely, the host's behavior can impact the gut microbiota. The aim of this study is to explore whether the gut microbiota composition of *K. marmoratus* could be a compelling candidate to explain the variation in behavioral traits by examining individuals reared in the same environment. In fish, the gut microbiota is primarily influenced by their environment and diet. The behavior of these fish is assessed using a shelter test. The gut microbiome of the six bolder fish and the six shyer fish was extracted using the 16S kit to amplify and sequenced the V1-V9 region using the Nanopore MinION™.

CROCODYLIA IN THE PALAEONTOLOGICAL FILHOL COLLECTION OF KU LEUVEN

Anne BASTEN[1], Pascal VAN DER BIJ[1*], Wouter BERINGS[1*], Sophie BOERMAN[1,2], Johan VELLEKOOP[1,2]

[1] Earth and Environmental Sciences, KU Leuven, Celestijnenlaan 200E, 3001 Leuven, Belgium.

[2] OD Earth and History of Life, Institute of Natural Sciences, Vautierstraat 29, 1000 Brussels, **Belgium.**

Poster 3

***Presenting authors**, **pascal.vanderbij@student.kuleuven.be, wouter.berings@student.kuleuven.be**

Keywords: *Diplocynodon*, Crocodylia, Palaeontology

Diplocynodon is an enigmatic extinct genus that is thought to be part of the Alligatoroidea, Crocodylia. While Alligatoroidea originated in North America, *Diplocynodon* only has a fossil record in Europe, where it occurred in the Eocene to Miocene (~45-15 million years ago). It is so far unclear how and when the group dispersed to Europe. The study of *Diplocynodon* remains curated in paleontological collections could aid research on the phylogeny, evolution and biogeography of this genus. This study therefore focuses on the crocodylian remains in the Filhol collection of KU Leuven, comprising abundant *Diplocynodon* material.

The Filhol collection is a largely unknown and inadequately described collection of vertebrate remains from the Cenozoic, collected from various localities in France. Here we describe the crocodylian remains in this collection, found in Saint-Gérand-le-Puy and Ronzon. The remains are expected to belong to the genus *Diplocynodon*. From Saint-Gérand-le-Puy, the species *Diplocynodon ratelii* has already been described, while specimens from Ronzon may belong to *Diplocynodon gervaisi*, a species currently considered invalid pending further review. The aim of the study was to identify which remains reside in the Filhol collection and to deduce the systematics behind the remains, making the collection more accessible to future projects. All crocodylian items in the collection were cleaned and sorted, amounting to a total of 787 skeletal elements, including both cranial and post-cranial bones. A catalogue of all items was made, and the most complete and anatomically representative fossils were photographed. Based on characteristic features, the remains from Saint-Gérand-le-Puy could be diagnosed as *Diplocynodon ratelii*, while the remains from Ronzon, potentially belonging to *Diplocynodon gervaisi*, could not be confidently determined in the present study.

EFFECTS OF BIFENTHRIN ON NEUROLOGICAL DEVELOPMENT, BEHAVIOUR AND THE EXPRESSION OF BIOMARKERS ASSOCIATED WITH ALZHEIMER'S DISEASE IN *NOTHOBRANCHIUS FURZERI*

Théo AZAMA SHALIE RODOMA[1]*, Julie HETRU[1,2], Melissa PAGE[2], Frédéric SILVESTRE[1]

[1] Laboratory of Evolutionary and Adaptative Physiology, University of Namur, 5000 Namur, Belgium.

[2] Louvain Institute of Biomolecular Science and Technology, UCLouvain, B-1348 Louvain-la-Neuve, Belgium.

Poster 4

Presenting author**, **theo.azamashalie@student.unamur.be

Keywords: *Nothobranchius furzeri*, Neurodegenerative disease, Bifenthrin, Aging

Neurodegenerative diseases such as Alzheimer's are influenced by various environmental factors, including exposure to neurotoxic pesticides. In this context, *Nothobranchius furzeri*, which is characterised by an accelerated ageing process, represents a model of choice for studying the effects of these substances on neuronal ageing, due to its similarities with mammals. The specific aim of this study was to assess the effects of bifenthrin, a neurotoxic pesticide widely used in the agri-food industry, on the behaviour, neurological development and gene expression of this model fish. In this study, larvae were exposed for 7 days, from day 7 post-hatching, to two concentrations of bifenthrin (5 µg/L and 10 µg/L) and compared with a control group. We examined behavioural effects using light-dark and tapping tests on days 14 (2 weeks) and 42 (6 weeks), to capture the immediate and long-term effects of exposure. To complete these tests, we selected genes involved in Alzheimer's disease-related syndromes, including APP, PSEN1, PSEN2, SYN2A, MANF, HTR1B, GFAP, SLC6A4A and ELAVL3. These genes were analysed by qPCR to identify any changes in their expression associated with exposure to the pollutant. Our results will contribute to understanding the mechanisms by which bifenthrin affects neuronal development and associated behaviours, as well as assessing its potential implications in neurodegenerative disorders.

UNLOCKING THE GENETIC DYNAMICS OF THE GREAT CRESTED NEWT (*TRITURUS CRISTATUS*) POPULATIONS: INSIGHTS FOR EFFECTIVE CONSERVATION STRATEGIES

Anaïs BEAUMARIAGE[1*], Alix ATTAQUE[1], Lise-Marie PIGNEUR[1], Éric GRAITSON[2], Johan MICHAUX[1]

[1] Laboratoire de génétique de la conservation (GeCoLab), Université de Liège, 4000 Liège, Belgium.

[2] Natagora, 5002 Namur, Belgium.

Poster 5

***Presenting author, anais.beaumariage@gmail.com**

Keywords: Conservation, Population genetics, Microsatellite, *Triturus cristatus*

The Great crested newt (*Triturus cristatus*) is a dispersal-limited amphibian affected by habitat fragmentation and associated genetic erosion. The objectives of this study were to assess the status of the genetic structuring of Walloon populations (Belgium), evaluate gene flow between populations, estimate risks of inbreeding, and assess potential disruptions in genetic connectivity among these populations to propose effective conservation measures. As part of the Life BNIP project (Belgian Nature Integrated Project), samplings were conducted in 2019 and 2023. Buccal DNA from 540 individuals from 40 widely distributed sites in Wallonia was collected. Eight microsatellite markers were used for genotyping, allowing for in-depth genetic analysis.

Our results reveal heterogeneous genetic structure of the crested newt in Wallonia, highlighting a major division between the populations of western Wallonia (province of Hainaut) and others. We also identify at least eight distinct genetic clusters, with particularly pronounced genetic diversity and gene flow for the group located in western Wallonia. Although inbreeding issues are limited to a fraction of the sampled stations, gene flow between distant populations is generally low, except for sites connected by a network of ponds. These findings underscore the importance of considering genetic structure and gene flow in the conservation of the crested newt. Furthermore, they highlight the need for continued measures to improve the genetic health status of the species.

WILD AT RISK: TRACKING HYBRIDIZATION BETWEEN WILDCAT AND DOMESTIC CAT IN LUXEMBOURG

Anaïs BEAUMARIAGE[1*], Alix ATTAQUE[1], Lise-Marie PIGNEUR[1], Johan MICHAUX[1]

[1] Laboratoire de génétique de la conservation (GeCoLab), Université de Liège, 4000 Liège, Belgium.

Poster 6

***Presenting author**, **anais.beaumariage@gmail.com**

Keywords: Hybridization, Luxembourg, SNPs, Wildcat

This study focuses on the hybridization between wildcats (*Felis silvestris*) and domestic cats (*Felis catus*) in Luxembourg, where the wildcat is the only native feline species. Hybridization with domestic cats is a growing concern for the conservation of wildcats, as it threatens their genetic integrity. Since 2011, 1,345 hair samples have been collected and analysed using genetic markers (microsatellites and SNPs). The analysis reveals that hybridization rates remain low, fluctuating between 1% and 9% over the years, except for a peak of 17% in 2022. Most hybrids identified are later-generation crosses, with few recent (F1) hybrids detected, indicating that recent hybridization events are rare.

Geographic analysis reveals that hybrid cats are unevenly distributed, with urban areas emerging as potential hybridization hotspots due to increased contact between wild and domestic cats, while forest-dense regions are less affected. These results suggest that human infrastructure may play a significant role in facilitating this crossbreeding.

While the current hybridization rate does not pose an immediate threat, ongoing monitoring is crucial to prevent long-term genetic dilution. Conservation efforts, such as sterilisation campaigns, public awareness programs, and the establishment of ecological corridors, are essential to protect wildcat populations from further introgression. This project is conducted in collaboration with the Luxembourg Institute of Science and Technology (LIST) and the Ministry of Environment, Climate, and Biodiversity.

ORIGIN OF ANDROGENETIC LINEAGES AND SPERM COMPETITION IN THE CLAM GENUS *CORBICULA*

Mohammed BENBACHIR[1]*, Marc GUERINEAU[1], Serge ARON[1], Karine VAN DONINCK[1]

[1] Département de Biologie des Organismes, Université Libre de Bruxelles, 1050 Bruxelles, Belgium.

Poster 7

***Presenting author**, **mohammed.benbachir@ulb.be**

Keywords: Androgenesis, Sperm Competition, *Corbicula*, Bivalve

Androgenesis is a reproductive mode where only paternal nuclear genome is transmitted to the offspring, the maternal nuclear genome is either absent (non-nucleated oocyte) or extruded from the oocyte as two polar bodies after fertilization. The clam genus *Corbicula* includes both sexual and androgenetic species. The sexual species are dioecious, producing reduced, monoflagellate sperm, and are geographically restricted to their native range in Asia, Africa, or Australia. In contrast, the androgenetic lineages are hermaphroditic, produce biflagellate unreduced sperm, and are distributed across both their native ranges and invasive areas in the Americas and/or Europe.

Recently, a study revealed an extensive allele sharing between invasive androgenetic lineages, and native species in Lake Biwa (Japan) and Mooi River (South Africa), leading to the hypothesis about the existence of two distinct biogeographical origins of the androgenetic lineages. Interestingly, the males of *C. sandai*, a dioecious, sexually reproducing species endemic to Lake Biwa, that shares alleles with 3 androgenetic invasive lineages, produce both monoflagellate reduced and biflagellate unreduced spermatozoa in equivalent proportions.

My PhD project aims to explore the potential sperm competition between biflagellate and monoflagellate sperm in *Corbicula*, by comparing their swimming patterns, quality and quantity. Additionally, I will investigate the South African origin of androgenetic lineages, by studying the reproductive characteristics (sperm ploidy and morphotype, sex, reproductive mode) of the South African *Corbicula* population.

During the first months of my PhD, I successfully induced the spawning in individuals sampled from the Vidourle River (France) and the Waal River (Netherlands) in the lab. The preliminary observations suggest androgenesis in the spawned gametes and zygotes, as indicated by signatures consistent with androgenesis in *Corbicula* (simultaneous polar bodies in oocyte and biflagellate sperm). These preliminary findings will be further validated with confocal microscopy observation and ploidy assessment of the spermatozoa through flow cytometry.

COMPUTED TOMOGRAPHY (CT) SCANNING IN PALEONTOLOGY: SHEDDING NEW LIGHT ON A 70-MILLION-YEAR-OLD FOSSIL CROCODYLIAN

Sophie A. C. BOERMAN[1,2*], Paul M. J. BURKE[3], Johan VELLEKOOP[1,2], Gwendal PERRICHON[4], Philip D. MANNION[3], Thierry SMITH[2], Jeremy E. MARTIN[4]

[1] Department of Earth and Environmental Sciences, KU Leuven, 3001 Leuven, Belgium.

[2] Directorate Earth and History of Life, Royal Belgian Institute of Natural Sciences, 1000 Brussels, Belgium.

[3] Department of Earth Sciences, University College London, WC1E 6BT London, United Kingdom.

[4] Université Claude Bernard Lyon 1, LGL-TPE, UMR 5276, 69100 Villeurbanne, France.

Poster 8

***Presenting author**, sophie.boerman@kuleuven.be**

Keywords: Computed tomography, Phylogeny, Paleoecology, Crocodylia

The study of fossil specimens is fundamental for understanding the evolution of life on Earth and the origins of modern animal lineages. However, a persistent challenge in paleontology is that data are limited due to the scarce and often fragmentary nature of the fossil record. In recent developments, computed tomography (CT) scanning of fossils has become more common practice, unlocking previously inaccessible anatomical data, and offering new perspectives on long-standing evolutionary questions. Here, we present the first CT data of a skull of *Thoracosaurus isorhynchus*, a fossil crocodylian that inhabited coastal waters of Europe around the time of the Cretaceous/Paleogene (K/Pg) mass extinction, 66 million years ago. This taxon has been suggested to be a close relative of extant gharials (Gavialidae), and thus plays a pivotal role in understanding the evolutionary history of this clade of crocodylians, but its phylogenetic placement has been disputed. Segmentation of the CT scans enabled us to reconstruct the endocast, the inner ear, the nasal cavity, the pneumatic system connected to the middle ear and the pharynx (paratympanic sinus system), and several cranial nerves and arteries. These structures reveal promising new insights into the phylogenetic position and paleoecology of *Thoracosaurus isorhynchus*.

BREAKING THE RED MYTH: CAROTENOIDS IN HOLOTHUROID COELOMOCYTES

Estelle BOSSIROY[1*], Noé WAMBREUSE[1], Frank DAVID[2], Céline VANWINGE[3], Sandra ORMENESE[3], Fabrice BUREAU[4], Jérôme DELROISSE[1,4], Igor EECKHAUT[1], Guillaume CAULIER[1]

[1] Biology of Marine Organisms and Biomimetics Unit, University of Mons, 7000 Mons, Belgium.

[2] Marine Station of Concarneau (MNHN), 29900 Concarneau, France.

[3] GIGA Research Institute affiliated with the University Hospital (CHU) of Liège, 4000 Liège, Belgium.

[4] Cellular and Molecular Immunology, University of Liège, 4000 Liège, Belgium.

Poster 9

***Presenting author**, **estelle.bossiroy@umons.ac.be**

Keywords: Holothuroids, Coelomocytes, Pigmentation, Carotenocytes

Coelomocytes are known to be circulating cells within coelomic cavities, and to play a role in the immune response in different invertebrates including holothuroids, also known as sea cucumbers (Echinodermata). Among the various types of coelomocytes, haemocytes are distinguished by their intense red pigmentation, which has been attributed to the presence of intracellular haemoglobin for over a century. In contrast to other coelomocytes found in the hydrovascular and perivisceral fluids, haemocytes circulate exclusively in the hydrovascular fluid or are associated with internal organs membranes. The presence of haemoglobin indicated a potential role in oxygen transport, which could be particularly valuable for endobenthic species. However, our research on the haemocytes of *Holothuria forskali* revealed unexpected carotenoid concentrations instead of haemoglobin in this European epibenthic species. These findings led us to rename those cells as "carotenocytes" and to propose that they may act as immune regulators thanks to their antioxidant properties. This study focuses on the localization of carotenocytes and their pigments within the various tissues of holothuroids, with the objective of providing insight into their site of production and action. Furthermore, the aim is to extend the investigation into the pigment origin and the role of carotenocytes in diverse sea cucumber species of varying taxonomy and ecology. The study has already demonstrated the presence of carotenoids in the haemal system of *H. forskali*, which is otherwise populated by pigmented coelomocytes. Moreover, similar carotenoids have been identified in the Polian vesicle (a hydrostatic organ filled with hydrovascular fluid) of the tropical species *H. atra*. In conclusion, our studies support the hypothesis that the red pigmentation of pigmented coelomocytes has been incorrectly associated with haemoglobin across all holothuroids, or at least in certain species.

A NEW SPECIES OF *AGAPOSTEMONOIDES* (HYMENOPTERA: HALICTIDAE) FROM MEXICO

Thomas BRAU[1]*, Stephania SANDOVAL-ARANGO[2], Ruben Dario MARTIN ROJAS[2], Sarah KANIA[2], Denis MICHEZ[1], Margarita M. LÓPEZ-URIBE[2]

[1] Laboratory of Zoology, Research Institute for Biosciences, University of Mons, 7000 Mons, Belgium.

[2] Department of Entomology, The Pennsylvania State University, 16802 Pennsylvania, United States.

Poster 10

Presenting author**, **thomas.brau@student.umons.ac.be

Keywords: Biodiversity, Pollinators, Taxonomy, Anthophila, Apoidea, Halictidae

A new species of *Agapostemonoides* has been discovered at Xalapa in the Mexican state of Veracruz. We describe the species from four females collected on *Cucurbita pepo* that were planted in an area of Mexican cloud forest. This species is the first of its genus to be found in Mexico. Following this discovery, we provide a discussion on the characteristics of the genus *Agapostemonoides* and a determination key.

TURNING SCIENCE UPSIDE DOWN: WHY THE UPSIDE-DOWN JELLYFISH COULD BE A GAME-CHANGER IN ENVIRONMENTAL RESEARCH

Noémie BURATTO[1*], Eli THORÉ[1,2,3]

[1] Laboratory of Adaptive Biodynamics, Research Unit in Environmental and Evolutionary Biology (Department of Biology), Institute of Life, Earth, and Environment, University of Namur, Rue de Bruxelles 61, 5000 Namur, Belgium.

[2] Department of Wildlife, Fish, and Environmental Studies, Swedish University of Agricultural Sciences, Skogsmarksgränd 17, 907–36 Umeå, Sweden.

[3] TRANSfarm, Science, Engineering, and Technology Group, KU Leuven, Bijzondereweg 12, 3360 Bierbeek, Belgium.

Poster 11

***Presenting author**, **noemie.buratto@unamur.be**

Keywords: *Cassiopea xamachana*, Ecotoxicology, Bioindicator, Symbiotic relationship

The mangrove jellyfish, *Cassiopea xamachana*, also known as the upside-down jellyfish, is a benthic cnidarian living in close symbiosis with photosynthetic dinoflagellates. *Cassiopea* is an established model to study symbiosis-driven development and evolution and, owing to several valuable characteristics, holds great promise as a suitable study system for a wide range of other disciplines, including environmental science. However, despite its potential, few studies have explored the use of *Cassiopea* in environmental research, particularly in ecotoxicology. Here, I explore what *C. xamachana* has to offer and outline a key objective of my PhD research. First, as an ancient metazoan with a relatively simple body structure, the species belongs to one of the earliest-diverging lineages in the evolution of animal life, thus occupying a key evolutionary position. At the same time, the species plays a significant ecological role in mangroves and coastal ecosystems, where they mediate benthic-pelagic coupling of nutrient cycles and serve as an important link in the trophic network. Research has shown that *C. xamachana* bioaccumulate and are sensitive to various chemical pollutants, highlighting its potential as a biomonitor and/or bioindicator species. This, combined with the relative simplicity of culturing *Cassiopea* and generating clonal laboratory lines, makes for a highly amenable system for ecotoxicology research in both the field and the laboratory. In my upcoming PhD research, I will assess the impact of two major forms of pollutants plastics and pharmaceuticals on the biology and ecology of *C. xamachana*. I will start by studying the impact of these pollutants on *Cassiopea*'s relationship with endosymbiotic dinoflagellates, focusing particularly on photosynthetic activity and the recruitment of symbionts. As such, this study will provide an important baseline for my follow-up research, aimed at unraveling the impacts of pollution on these organisms and their ecosystems.

COMPARING MATERNAL CARE IN CAPTIVE PAN: A MULTI-GROUP STUDY

Tuana BÜYÜKGÜNER[1*], Jonas VERSPEEK[2,3], Nicky STAES[2,3]

[1] Master student, Biology Department, Vrije Universiteit Brussel (VUB) Brussels, Pleinlaan 2, 1050, Elsene, Belgium.

[2] Antwerp Zoo Centre for Research and Conservation, Royal Zoological Society of Antwerp, Koningin Astridplein 26, 2018, Antwerp, Belgium

[3] Behavioural Ecology and Ecophysiology, University of Antwerp, Universiteitsplein 1, 2610, Wilrijk, Belgium

Poster 12

***Presenting author**, **tuana.buyukguner@vub.be, tuanabuyukguner@gmail.com**

Keywords: Maternal care, Bonobo (*Pan paniscus*), Chimpanzee (*Pan troglodytes*), Interspecies differences

Maternal care is critical for primates, who produce limited offspring with long inter-birth intervals and extensive dependency periods. The divergence of maternal behaviours is especially pronounced between species that exhibit species-specific social structures such as bonobos (*Pan paniscus*) and chimpanzees (*Pan troglodytes*). In this study, we investigate six maternal behaviours: body contact, proximity, maternal approach, maternal leave, groom, and play, focusing on the influence of species, mother and offspring age, and sex of offspring. Utilizing data from 48 mother-offspring dyads across European zoos, we applied linear mixed models to dissect the inter- and intraspecific variation in maternal care strategies. Our results illustrate species-specific differences in body contact, proximity, and grooming, supporting the delayed behavioural maturation of bonobo infants. These behaviours were significantly negatively influenced by offspring age in both species, more pronounced in chimpanzees, excluding stable levels of maternal groom in bonobos. Additionally, our findings revealed a universal bias of maternal investment towards male offspring, in terms of play, potentially linked to reproductive strategies of male-philopatric primate societies. The differences in maternal care between humans and two of the closest living relatives are discussed to gain a better understanding of the adaptive nature of maternal care strategies in response to socio-environmental pressures.

UNDERSTANDING THE EFFECTS OF EOCENE WARMING ON MARINE FISH: A DIVE INTO FISH DIVERSITY AND DISTRIBUTION UNDER YPRESIAN WARMING

Jonas CALLAERTS[1*], Hugo GANTE[1,2], Johan VELLEKOOP[3,4]

[1] Department of Biology, KU Leuven, 3000 Leuven, Belgium.

[2] Section Vertebrates, Royal Museum for Central Africa, 3080 Tervuren, Belgium.

[3] Department of Earth and Environmental Sciences, KU Leuven, 3000 Leuven, Belgium.

[4] OD Earth and History of Life, Institute of Natural Sciences, 1000 Brussels, Belgium.

Poster 13

***Presenting author, jonas.callaerts@student.kuleuven.be**

Keywords: Ypresian, Otolith, Warming, Diversity

The Ypresian (early Eocene, ~56-47.8 million years ago) is a time interval in Earth history characterised by several global warming events, such as the Paleocene-Eocene Thermal Maximum (PETM) and Early Eocene Thermal Maximum (EETM), representing potential analogues for the warming our planet is facing today. Therefore, these warming events could provide useful insights into the impacts of climate change on marine ecosystems. However, current knowledge of the Ypresian paleoenvironment and its effects on marine fish populations is limited. Here we use fossil otoliths, inner ear stones present in all bony fish, to study changes in marine fish populations during the Ypresian. Otoliths assist with both balance and hearing in fish, and can be identified at the genus and, in some cases, species level, allowing for a detailed mapping of populations. The otoliths analysed in this study were collected from the Aizy-Jouy outcrop in the Northeast of France, which, during the Ypresian, was a shallow marine system characterised by tropical temperatures. Preliminary results based on the benthic foraminiferal Mg/Ca temperature proxy indicate an increase in sea water temperature of ~5 °C between the lower and upper sections of the Aizy-Jouy outcrop, likely representing a global warming event. This temperature shift seems to correlate with changes in fish population dynamics, including variations in both diversity and distribution patterns. The observed dominance of juveniles in the local fossil record provides further insights into the paleoecology of this region, suggesting that it may have served as a nursery habitat. These preliminary findings indicate the potential to enhance our understanding of the effects of warming events on marine fish populations in the past, present, and future.

RECONSTRUCTING THE DEMOGRAPHIC HISTORY OF THE ADAPTIVE RADIATION OF SILVERSIDES IN THE MALILI LAKES

Francisco CAMPUZANO JIMÉNEZ[1*], Els L. R. DE KEYZER[1], Hannes SVARDAL[1]

[1] Evolutionary ecology group (EVECO), Department of Biology, University of Antwerp, 2610 Wilrijk, Belgium.

Poster 14

***Presenting author**, **curro.campuzanojimenez@uantwerpen.be**

Keywords: Adaptive radiation, Demographic inference, Hybridization

Adaptive radiations, the rapid diversification into multiple lineages, are important in shaping the world's biodiversity. Although they are central to the development of evolutionary theory, the mechanisms by which they take place are still largely unknown. The hybrid origin hypothesis suggests that hybridization between divergent populations increases the likelihood of adaptive radiation if it coincides with an ecological opportunity. We take advantage of the unique study system of sailfin silverside fishes (genus *Thelmaterina*) from the Malili Lake system in Sulawesi (Indonesia). The silverside radiation took place within the last 2 million years. It consists of ~20 species that show high phenotypic and genetic diversity and are adapted to different habitats and diets. Surprisingly, previous studies have revealed strong evidence of ongoing introgression. Could this imply that gene flow did not cease after the adaptive radiation, or, perhaps, that it has increased more recently? Currently, silversides are threatened by several factors including, most recently, the proliferation of invasive species. We hypothesize that alien species have altered the demographic dynamics of silversides, as the increase in competition may select specialized or intermediate individuals (either decreasing or increasing interspecies gene flow). We will analyze whole-genome sequencing data to infer the ancient and recent demographic history of silversides. To do so, we will take advantage of the advances in model-based and simulation-based methods. By considering a set of plausible scenarios and incorporating genomic estimates informative of different timescales, we hope to make an accurate reconstruction of silversides' evolutionary history. These estimates might shed light on the underlying mechanisms of adaptive radiation and guide conservation management plans.

BEE-ING UNIQUE: UNVEILING A NEW CASE OF GYNANDROMORPHY IN THE PARASITIC BEE GENUS *NOMADA*

Frédéric CARION[1], Thomas BRAU[1*], Denis MICHEZ[1], Guillaume GHISBAIN[1]

[1] Laboratory of Zoology, University of Mons, 7000 Mons, Belgium.

Poster 15

***Presenting author**, **thomas.brau@student.umons.ac.be**

Keywords: Nomad Bee, Development, Gynandromorphs, Teratology

Gynandromorphy is a type of teratological aberration that occurs at a low frequency under natural conditions and in which individuals display both male and female morphological traits. Three classes are established depending on the distribution of these traits: (i) Mosaic (disordered traits distribution), (ii) Bilateral (ordered traits distribution on each side of the sagittal plan) and (iii) Transversal (ordered traits distribution on each side of a transversal plan). These types of aberrations can be used for describing developmental differences between male and female structures (*i.e.* sexual dimorphism) but also for pairing individuals in poorly known species. This poster aims to present a second case of gynandromorphy for the species *Nomada lathburiana*, with a specimen found in Tournai (Belgium) on April 5th, 2024. This specimen was classified as a mosaic gynandromorph due to the asymmetrical distribution of different sexual traits on the head.

EFFECTS OF PHOTOSYMBIOSIS ESTABLISHMENT ON CNIDARIAN REDOX HOMEOSTASIS

Enora CARNAC[1*], Stéphane ROBERTY[1]

[1] Laboratoire de Physiologie Animale et Ecophysiologie, Université de Liège, 4 Chemin de la Vallée, 4000 Liège, Belgium.

Poster 16

***Presenting author**, **enora.carnac@student.uliege.be**

Keywords: Corals, *Symbiodiniaceae*, Antioxidants, Oxidative stress

In cnidarian-*Symbiodiniaceae* symbioses, the presence of photosynthetic dinoflagellates inside the host tissues causes daily local hyperoxia and promotes the generation of reactive oxygen species (ROS), which can damage cellular components, trigger cell death and, under certain conditions, lead to the collapse of the symbiotic interaction (bleaching). This implies that the establishment and maintenance of a symbiotic relationship with algae relies in part on regulatory mechanisms that maintain redox homeostasis at the holobiont level. This project aims to better understand how ROS and redox changes affect the development and maintenance of the cnidarian-*Symbiodiniaceae* symbiosis. Specifically, using the Aiptasia model, we propose to (I) detect and monitor in vivo intracellular H_2O_2 production across different stages of symbiosis by developing a genetically encoded biosensor (HyPer7) and introducing it into larvae and pedal lacerates of our anemones; (II) assess the importance of redox homeostasis for the establishment of the symbiosis by comparing the antioxidant capacity of the host according to its symbiotic state and by modifying the balance between ROS production and its antioxidant capacity. A better understanding of these processes is necessary if we are to conserve coral reefs in the coming decades. In addition, the developments in this project will provide a powerful methodological platform to study the dynamics of H_2O_2 in complex processes in cnidarians such as development, regeneration, interactions with pathogens and symbionts, and stress responses.

DECODING SKIN ULCERATION SYNDROME IN THE AQUAFARMED SEA CUCUMBERS: AN INTEGRATIVE TRANSCRIPTOMIC AND METABOLOMIC ANALYSIS

Mabel CASTIAUX[1*], Vanessa TAGLIATTI[2], Raphael CONOTTE[2], Guillaume CAULIER[1], Igor EECKHAUT[1,3], Noé WAMBREUSE[1], Jérôme DELROISSE[1,4]

[1] Biology of Marine Organisms and Biomimetics Unit, University of Mons, 6 Avenue du Champ de Mars, 7000 Mons, Belgium

[2] Human Biology and Toxicology Laboratory, University of Mons, 6 Avenue du Champ de Mars, 7000 Mons, Belgium

[3] Belaza Marine Station (IH.SM-UMONS-ULIEGE), 601 Toliara, Madagascar

[4] Molecular and Cellular Immunology Laboratory, GIGA Institute, ULiège, 4000 Liège, Belgium

Poster 17

***Presenting author**, **Mabel.Castiaux@student.uliege.be**

Keywords: Marine disease, Echinoderms, Omics, Aquaculture

The expansion of large-scale aquaculture has led to the rise of diseases affecting species like the sea cucumber *Holothuria scabra*, farmed in Madagascar. These sea cucumbers suffer from "skin ulceration syndrome" (SUS), characterised by degradation of the cuticle, epidermis, and connective tissue, with symptom peaks during austral winter. Despite detailed morphological data, molecular insights into SUS remain limited for the species. We conducted integrated transcriptomic and metabolomic analyses of *H. scabra* affected by skin ulceration syndrome. Transcriptome analyses indicate overexpression of stress-responsive genes, particularly those coding for heat shock proteins, as well as genes associated with inflammation, including NLRP10 and BHMT1. Other genes with high expression, such as TNF receptor-associated factors and NF-kappa-B inhibitors, suggest increased pro-inflammatory signalling and apoptosis. Upregulation of matrix-associated proteins like Fibropellin and Fibroleukin also suggests tissue remodelling linked to inflammation or healing. Additionally, genes involved in pathogen recognition, including C-type mannose and macrophage mannose receptors, are overexpressed, could indicate an importance of microorganisms in the development of the disease. Metabolomic analyses reveal a significant increase in fumarate levels in SUS-affected individuals, potentially indicating disrupted energy metabolism. Fumarate accumulation, a marker of tricarboxylic acid cycle dysfunction, suggests altered ATP production in the context of skin ulceration syndrome. Our findings provide a molecular framework to investigate marine diseases in the aquaculture context, shedding light on inflammatory, immune, and metabolic disruptions, and offering insights into the syndrome’s potential environmental triggers and mechanisms in aquafarmed echinoderms.

ASSESSMENT OF THE CONSERVATION STATUS OF THE OLIVE COLOBUS POPULATION (*PROCOLOBUS VERUS*) IN SOUTHERN BENIN

Raimi CHABI OTA[1*], Sylvie DJOSSOU DJEGO[2], Toussaint LOUGBEGNON[3]

[1] Laboratoire d'Ecologie Appliquée, Faculté des Sciences Agronomiques, Université d'Abomey-Calavi, 443 Abomey-Calavi, Benin.

[2] Département de Zoologie, Faculté des Sciences et Techniques, Université d'Abomey-Calavi, 443 Abomey-Calavi, Benin.

[3] École de Foresterie Tropicale, Université Nationale d'Agriculture, Kétou, Benin

Poster 18

Presenting author**, **raimichabiota@gmail.com

Keywords: *Procolobus verus*, Conservation status, South-Bénin

Knowledge of the conservation status of animal biodiversity, especially primates, is crucial for sustainable conservation efforts. This study, entitled "Assessment of the Conservation Status of the Olive Colobus Population (*Procolobus verus*) in Southern Benin," aims to deepen our understanding of the distribution, identification of primary core groups of olive colobus, and the ecological factors that influence their presence. To conduct this research, we first carried out individual and group surveys with hunters, wine tappers, farmers, and charcoal producers. Forest surveys were then undertaken to confirm or refute the responses of the interviewees, assess the group sizes encountered, and investigate the ecological factors favoring their presence. For this purpose, linear trails ranging from 500 meters to 2 kilometers were walked several times a day. We used GIS (Geographic Information System) to characterize the distribution and ecological permeability of the habitat. Our findings indicate that localities such as Sotikame, Go, Domè, Dèmè, Lokoli, Goita, Gohissanou Bolamè, Koussoukpa, Adogbé, Aklissa, and Sehoué have a strong awareness of the species. However, field surveys confirmed the species' presence specifically in the swamp forest of Lokoli in the Dèmè area, the Domè community forest, and the Mahessou community forest (now a municipal protected area), which may be the primary core from which smaller populations observed in surrounding forests originate. The encounter rate is 0.07 groups/km. The habitat is characterized by marshy grasslands and primary swamp forests where the olive colobus coexists with other primate species, such as the mona monkey, *Cercopithecus mona*, which often serves as a leading species. For sustainable conservation of the olive colobus, it is necessary to engage in education, habitat restoration, and the creation of ecological corridors.

INTEGRATIVE CONTROL STRATEGIES FOR CHICORY APHID PESTS

Thomas COCHENILLE[1,2*], Arnaud AMELINE[1], Roman SALMON[1], Laurent CASSAN[3], Régis CATTEAU[3], Géraldine DOURY[1], Kevin TOUGERON[2]

[1] Ecologie et Dynamique des Systèmes Anthropisés UMR CNRS 7058, Université Picardie Jules Verne, 33 Rue Saint-Leu, 80000 Amiens, France.

[2] Ecologie des Interactions et Changements Globaux, Institut de Recherche en Biosciences, Université de Mons, Av. du champ de mars 6, 7000 Mons, Belgique.

[3] APEF, Association des producteurs d'endives de France, 2 Rue des fleurs, 62000 Arras, France.

Poster 19

***Presenting author,** **thomas.cochenille@outlook.fr**

Keywords: Climate change, *Pemphigus bursarius*, *Cichorium intybus*, Thaumatomyia.

The woolly root aphid, *Pemphigus bursarius*, is the main aphid of chicory (*Cichorium intybus*). This pest, which causes endive mosaic disease, threatens crops in the European production basin between France and Belgium. Climate change such as rising temperatures and water restrictions can modulate aphid pressure on crops. As part of the INTERREG 'REFLECHI' program, our project aims to increase our knowledge about the consequences of climate change on chicory-aphid interactions, to develop integrated strategies for the control of the aphid pest of the aerial parts (*Myzus persicae*), and the root part (*P. bursarius*) of chicory. These strategies will be based on the use of biopesticides (essential oils and entomopathogenic fungi), the identification of resistance factors in chicory varieties, and the optimisation of *P. bursarius* control by predatory flies of the genus Thaumatomyia (Chloropidae).

ASSESSING THE HABITAT SUITABILITY OF MASON BEES IN EUROPE TO GUIDE CONSERVATION EFFORTS

Bastien DE TANDT[1,2*], Guillaume GHISBAIN[2], Diana ERAZO[1], Simon DELLICOUR[1,3], Denis MICHEZ[2]

[1] Spatial Epidemiology Lab (SpELL), Université Libre de Bruxelles, 1050 Brussels, Belgium.

[2] Laboratory of Zoology, University of Mons, Av. du champ de mars 6, 7000 Mons, Belgium.

[3] Laboratory of Clinical and Epidemiological Virology, Rega Institute for Medical Research, Department of Microbiology, Immunology and Transplantation, KU Leuven, 3000 Leuven, Belgium.

Poster 20

***Presenting author**, bastien.de.tandt@ulb.be*

Keywords: Wild bees, Ecological niche modelling, Conservation biology

Bees are important pollinators in both natural and agricultural ecosystems. Yet, increasing anthropogenic pressures threaten their populations, eroding the numerous ecosystemic services they provide to society. Following this decline, numerous projects, particularly in Europe, have been launched to understand and document the threats to which wild bees are exposed. However, despite these efforts, some groups of bees remain understudied, and their conservation needs therefore remain overlooked. This is particularly true for mason bees (Megachilidae, tribe Osmiini), a diverse group of bees with unique life-history traits related to their nesting biology and flower preferences. As part of broader conservation efforts, this study aims to investigate the ecologically suitable areas for osmiine bees across Europe. Using an ecological niche modelling approach, the ecological niche of osmiine bee species was predicted based on various environmental variables and occurrence records in Europe. The results demonstrate that the Mediterranean and mountainous areas of western Europe have highly suitable environmental conditions for these species. Consequently, effective conservation measures should be concentrated towards these areas.

HIERARCHICAL ECO-EVO DYNAMICS MEDIATED BY THE GUT MICROBIOME

Ellen DECAESTECKER[1,2*], Broos VAN DE MOORTEL[1*], Shinjini MUKHERJEE[2,3], Aditi GURUNG[2], Robby STOCKS[4], Luc DE MEESTER[2,5,6]

[1] Laboratory of Aquatic Biology, Interdisciplinary Research Facility Life Sciences, KU Leuven, 8500 Kortrijk, Belgium.

[2] Laboratory of Aquatic Ecology, Evolution, and Conservation, Department of Biology, KU Leuven, 3000, Belgium.

[3] Laboratory of Reproductive Genomics, Department of Human Genetics, KU Leuven, 3000, Belgium.

[4] Laboratory of Evolutionary Stress Ecology and Ecotoxicology, Department of Biology, KU Leuven, 3000, Belgium

[5] Leibniz Institute of Freshwater Ecology and Inland Fisheries (IGB), D-12587 Berlin, Germany

[6] Institute of Biology, Freie Universität Berlin, D-14195 Berlin, Germany

Poster 21

***Presenting author, ellen.decaestecker@kuleuven.be**

Keywords: Hierarchical eco-evolutionary dynamics, Microbiome-mediated phenotypic plasticity, Host-microbiome interactions, Global change

The concept of eco-evolutionary (eco-evo) dynamics, stating that ecological and evolutionary processes occur at similar time scales and influence each other, has contributed to our understanding of responses of populations, communities, and ecosystems to environmental change. Phenotypes, central to these eco-evo processes, can be strongly impacted by the gut microbiome. The gut microbiome shapes eco-evo dynamics in the host community through its effects on the host phenotype. Complex eco-evo feedback loops between the gut microbiome and the host communities might thus be common. Bottom-up dynamics occur when eco-evo interactions shaping the gut microbiome affect host phenotypes with consequences at population, community, and ecosystem levels. Top-down dynamics occur when eco-evo dynamics shaping the host community structure the gut microbiome.

BLACK CORAL SHALLOW-WATER COMMUNITIES OF MADAGASCAR: THE FUNCTIONAL LINK BETWEEN HABITAT AND DIVERSITY

Alexia DIMOPOULOS[1*], Bruno DANIS[1], Lucas TERRANA[2]

[1] Laboratory of Marine Biology, Université Libre de Bruxelles, Laboratory of Marine Biology, CP160/15, 1050 Bruxelles, Belgium.

[2] Natural History Museum & Vivarium, 7500 Tournai, Belgium

Poster 22

***Presenting author, alexia.dimopoulos@ulb.be**

Keywords: Black corals, Diversity, Functional niche

In the context of global change, reef communities are undergoing reorganization in response to rapid changes in environmental parameters. These variations can lead to a loss of specific and functional diversity, which may alter ecosystem functions and services. The concept of niche links biodiversity to these changes. Communities can be assessed by their functional redundancy, which ensures stability and resilience in the face of environmental disturbance. Conservation measures have been implemented for some scleractinian species. However, other foundation species have been neglected, despite their crucial ecological role. In Madagascar, antipatharians, also known as black corals, are major components of shallow-water reefs, where they form heterospecific assemblages. They are found in heterogeneous habitats such as coral reefs, caves, and river mouths, where environmental parameters are highly variable and dependent on human activity. This thesis aims to examine the current state of antipatharian communities by studying several sites in Madagascar: The Great Reef of Toliara with its north and south passes, the fringing reefs of Soalara and the reefs surrounding the island of Nosy Be. Although these sites have different environmental and anthropogenic contexts, they are home to the same black coral species. The abundance, taxonomic and functional diversities of antipatharians will be assessed using morphology and genetics. The study will determine and monitor the environmental features such as bathymetry and slope. Temperature, currents and sedimentation will also be monitored for a year to capture seasonal variations. This knowledge is crucial for comprehending future community changes and is a prerequisite for monitoring black coral populations in an evidence-based conservation framework.

PONDS TO PATTERNS: PARASITE AND KILLIFISH DIVERSITY IN TEMPORARY POOLS

Nichole DONOUGH[1,2,3*], Marliese TRUTER[1,2], Victor WEPENER[1], Luc BRENDONCK[1,3], Eli THORÉ[4,5,6], Nico J SMIT[1,2]

[1] Water Research Group, Unit for Environmental Sciences and Management, North-West University, 2531, Potchefstroom, South Africa.

[2] South African Institute for Aquatic Biodiversity, Somerset Street, 6139, Makhanda, South Africa

[3] Animal Ecology, Global Change and Sustainable Development, KU Leuven, 3000, Leuven, Belgium

[4] Laboratory of Adaptive Biodynamics, Research Unit of Environmental and Evolutionary Biology, Institute of Life, Earth and Environment, University of Namur, 5000, Namur, Belgium

[5] Department of Wildlife, Fish, and Environmental Studies, Swedish University of Agricultural Sciences, 901 30, Umeå, Sweden

[6] TRANSfarm – Science, Engineering, & Technology Group, KU Leuven, 3000, Lovenjoel, Belgium.

Poster 23

* **Presenting author, nicholesasha-lee.donough@kuleuven.be**

Keywords: Wetlands, Parasitism, Biodiversity

Nothobranchius killifish are keystone species in temporary ponds. Since these habitats are seasonal, killifish have evolved distinctive traits to cope with the recurring drying of their habitat, including a rapid life cycle and the production of drought-resistant eggs. While this unique life history may influence parasite dynamics, research on parasites associated with *Nothobranchius* spp. is scarce and there is only limited information on *Nothobranchius* spp.'s role in parasite transmission. As a step towards filling this knowledge gap, we determined the digenean parasitic community of *Nothobranchius* spp. We sampled five natural populations of killifish in Karingani Game Reserve in southern Mozambique, dissecting and screening the fish for parasites. Molecular data revealed at least three different *Nothobranchius* spp. in the pools—*N. furzeri*, *N. orthonotus* and *N. pienaari*. All five sites had fish that were infected with encysted metacercaria throughout the tissues [intensity of infection (IF 1–192)], and four individual fish had free metacercaria in the cranial cavity [IF 1–14]. A minimum of seven parasite genotypes was found and preliminary molecular data indicate that two encysted metacercaria individuals correspond to sequences of described adults in two different final hosts. Altogether, these results provide new insights into parasite diversity and their distribution in *Nothobranchius* populations, enhancing our knowledge of killifish's role in parasite transmission.

A SINGLE GENETIC POPULATION OVER 24,000 KM: THE UNUSUAL COHESIVE GENETIC PATTERN IN *ABYSSORCHOMENE DISTINCTUS* (BIRSTEN & VINOGRADOV, 1960)

Deborah W. E. DUPONT[1*], Tasnim PATEL[2], Marie VERHEYE[1], Marc KOCHZIUS[3], Isa SCHÖN[1,4]

[1] ATECO-FWB, Belgian Institute of Natural Sciences, 1000 Brussels, Belgium.

[2] ATECO-MARECO, Belgian Institute of Natural Sciences, 1000 Brussels, Belgium.

[3] Marine Biology, Vrije Universiteit Brussels, 1050 Ixelles, Belgium.

[4] Zoology Research Group, Universiteit Hasselt, 3500 Hasselt, Belgium.

Poster 24

***Presenting author**, **deborahw.dv@gmail.com**

Keywords: Population expansion, Cryptic diversity, Deep sea, Amphipoda.

Cryptic diversity among deep-sea malacostracans is increasingly unveiled through molecular analyses, helping to reassess biodiversity in abyssal and hadal zones and establish baselines before inevitable mineral exploitation. Cryptic diversity, which is the presence of morphologically similar but genetically distinct lineages within what appears as a single species, is marked by genetic variation, structured populations, and high differentiation among geographically distant populations, often isolated over evolutionary timescales. Although cryptic diversity is prevalent in Lyssianassoidea amphipods, *Abyssorchomene distinctus* emerges as an exception.

Analysing mitochondrial COI and nuclear 28S genes from 373 specimens across three ocean basins, we observed no cryptic diversity in *A. distinctus*. Instead, our results indicate a single, widely distributed population spanning ~24,000 km across the Southeastern Indian and Northeastern Pacific Oceans. Evidence includes a predominant ancestral haplotype in a star-shaped COI network, a skewed nucleotide mismatch distribution, and deviations from neutrality tests, all suggesting a unique population expansion event. This finding positions *A. distinctus* as one of only five known deep-sea amphipod species with confirmed wide cross-ocean distribution.

To explore if this genetic pattern extends to other Lyssianassoidea amphipods, we are conducting similar analyses on *Orchomenella pinguides*, a circumpolar Antarctic species with minimal prior genetic characterization. Our preliminary study includes 48 specimens from the Ronne Ice Shelf, examining COI and 28S genes to assess genetic structure, cryptic diversity, and intraspecific variation. We plan to expand our sample size to compare genetic differentiation between populations from the Ronne Ice Shelf and publicly available COI sequences databases from the Australian Antarctic Territory, and Southeastern Filchner area in the Weddell Sea.

UNDERSTANDING THE EFFECTS OF CHANGING ENVIRONMENTAL CONDITIONS AND CLIMATE EVENTS ON PLANKTON COMMUNITIES USING AUTOMATED IMAGE SENSORS

Annika I. ESKE[1,2*], Carlota MUÑIZ[1], Pascal I. HABLÜTZEL[1,3], Ilias SEMMOURI[2], Jonas MORTELMANS[1], Colin JANSSEN[4]

[1] Flanders Marine Institute (VLIZ), 8400 Ostend, Belgium

[2] Ghent University, Laboratory of Environmental Toxicology and Aquatic Ecology, Faculty of Bioscience Engineering, 9000 Ghent, Belgium

[3] Biology Department, Vrije Universiteit Brussel, 1050 Elsene, Belgium

[4] Blue Growth Research Lab, Ghent University, Bluebridge Building, 8400 Ostend, Belgium

Poster 25

***Presenting author, annika.eske@vliz.be**

Keywords: Plankton ecology, Climate change, Heatwaves, Plankton imaging

In marine ecosystems, plankton comprise the base of trophic webs and serve as an integral part of chemical cycles such as carbon sequestration. Due to their foundational role in these systems, plankton are highly useful for monitoring and anticipating abiotic effects on marine communities. In the Belgian Part of the North Sea (BPNS), where the shallow waters are already subject to various anthropogenic influences, changes such as marine heatwaves have also started to affect plankton dynamics. In recent years, warmer summers in the BPNS have led to phenology changes such as unprecedented blooms of *Bellerochea* spp., while groups such as copepods see dramatic dips in abundance. The current study expands on such findings using a long-term time series from the Belgian contribution to LifeWatch. Plankton samples are collected monthly (nine coastal stations) and seasonally (with an additional eight offshore stations) on board the RV Simon Stevin, with zooplankton data from 2012 onwards and phytoplankton data from 2017 onwards. Zooscan and FlowCam imaging sensors were used to study changes in zooplankton and phytoplankton communities, respectively, in relation to climate-driven events. The aim of this investigation was to highlight community dynamics and taxon interactions related to climate, particularly testing whether there were any downstream impacts of HABs or shifts in the gelatinous zooplankton community. This investigation provides preliminary insight into the health of the broader BPNS ecosystem in the face of climate change. Future research will further elucidate the effects of marine heatwaves on plankton using continuous imaging data as well as laboratory tests of genetic heat stress responses.

ITALIAN POLLINATORS: STEPS FORWARD TOWARD THE FUTURE ITALIAN RED LIST

Simone FLAMINIO[1*], Natasha DE MANINCOR[1]

[1] Laboratory of Zoology, Research Institute for Biosciences, University of Mons, 7000, Mons, Belgium

Poster 26

***Presenting author**, **Simone.FLAMINIO@umons.ac.be**

Keywords: Historical data, Italy, Red List, Wild bees

Mediterranean areas constitute one of the world's main biodiversity hotspots for numerous taxa, including wild bees. The Italian peninsula, due to its considerable latitudinal and altitudinal gradient and geological complexity, presents a great diversity of climates and natural environments, i.e. ecological niches, that can host a high diversity of species. Furthermore, its geographical location in the center of the Mediterranean basin, explains the presence of marginal populations from species that are abundant in different biogeographical sub-regions, such as the Balkans, or the westernmost portion of Europe. These factors contribute to making the Italian bee fauna one of the richest in the world in relation to the surface area of the country. Despite its enormous potential, a comprehensive knowledge of Italian wild bee fauna is still limited, mainly due to the lack of aggregated historical and current data that would help to accurately assess the wild bee diversity. The scope of this project is to (1) recover and combine historical and current information on spatial and temporal distribution, (2) to map and document historical changes in wild bee species and populations, in order to (3) reassess their status and trends which will pave the way for the future Italian Red List of bees.

AN UNKNOW ALIEN: CHARACTERIZATION OF THE FIRST INVASIVE POPULATION OF SEA SPIDERS

Antoine FLANDROIT[1*], Louis SIMON[1], Benjamin DECOUX[1], Naomie GEERINCKX[1], Igor EECKHAUT[1], Guillaume CAULIER[1]

[1] Biology of Marine Organisms and Biomimetics Unit, Research Institute for Biosciences, University of Mons (UMONS), 7000 Mons, Belgium.

Poster 27

***Presenting author**, **antoine.flandroit@umons.ac.be**

Keywords: Invasive, Arthropod, Phenology, Belgium

Invasive species are a major threat to biodiversity. They are defined as species that occur outside their native range, complete their life cycle in the non-native ecosystem, and become locally dominant there. Among the 1,400 extant species of sea spiders (*i.e.*, pycnogonids), ubiquitous yet understudied marine chelicerates, none of them fell under the definition of invasive species. That was until a population of *Ammothea hilgendorfi* (Böhm, 1879) was discovered in 2022 in Belgium. Native from the North Pacific Ocean (*i.e.*, Japan, USA), *A. hilgendorfi* was introduced in the late 1970s in Italy and the UK, then extended its range to several other European countries. While every record only consisted of punctual observations of a few specimens, the present study demonstrates that, in Belgium, this species meets all the criteria to be defined as invasive.

More than 1,000 individuals were collected in a monthly monitoring over a 24-month period. By discriminating juveniles, females, males, and males bearing eggs, the phenology of *A. hilgendorfi* was elucidated, and a periodicity in their life cycle was highlighted. In addition, each larval instar was observed in microscopy and morphologically described, a first for this species.

The present study also raises concern on their invasiveness and potential impact. Since no similar case exists elsewhere in the world, there is nothing this population can be compared with, and everything must be studied from scratch. Yet, this population represents a unique opportunity to deepen the general knowledge on sea spiders, understanding how *A. hilgendorfi* has become so successful, and assessing its impact on invaded ecosystems.

A PROBABLE NEW SPECIES OF EULIMID (GASTROPODA, MOLLUSCA) INFESTING FARMED *HOLOTHURIA SCABRA* IN MADAGASCAR

Loic GAUMEZ[1,2*], Igor EECKHAUT[1,3], Jérôme DELROISSE[1,4]

[1] Biology of Marine Organisms and Biomimetics, Research Institute for Biosciences, University of Mons, 7000 Mons, Belgium

[2] Indian Ocean Trepang, Toliara, 601, Madagascar

[3] Belaza Marine Station (IH.SM-UMONS-ULIEGE), Toliara, 601, Madagascar

[4] Cellular and Molecular Immunology, University of Liège, 4000, Liège, Belgium.

Poster 28

Presenting author**, **loic.gaumez@iotrepang.com

Keywords: *Eulimidae*, Sea cucumber, Parasitic gastropod, Aquaculture

In southwest Madagascar, an aquaculture company is dedicated to breeding tropical Indo-Pacific sea cucumbers, *Holothuria scabra*, commonly known as 'sandfish'. Farming trials began in the late 1990s, but Indian Ocean Trepang has been producing this species on a large scale since 2012. Since 2020, a parasitic gastropod has emerged in the offshore grow-out sites. This parasitosis develops progressively over time, culminating in an infestation of 15.9% at the company's first offshore grow-out site, and 9.6% at the second. To date, and to the best of our knowledge, no observation of parasitism of *Holothuria scabra* by a gastropod has been documented in the scientific literature. This study aims at identifying and describing the gastropod responsible for the parasitism of aquacultivated *H. scabra* in Madagascar. We used both traditional and molecular taxonomic approaches. For the traditional taxonomy, we provided a detailed description of all the morphological characteristics, including the structure of the gall created and its content. We then compared these observations with the descriptions of potential families and genera. For molecular taxonomy, parasitic individuals were preserved in 100% ethanol before being subjected to DNA extraction. Gene segments of interest were selected, amplified, purified, and sequenced to obtain the COI, 18S and 16S gene sequences. These sequences were then compared with those in the NCBI (National Center for Biotechnology Information) database. The results of the molecular taxonomy show that the COI, 18S and 16S sequences are respectively 80, 100 and 63% identical to the sequences of the genus *Melanella* Bowdich, 1822. *Melanella* is a genus of gastropods belonging to the family *Eulimidae* R. A. Philippi, 1853. Eulimids are gastropod parasites of echinoderms, characterized by a conical, straight, solid shell, generally uncolored and poorly sculptured, with the presence of growth lines. The results of the molecular taxonomy are corroborated by the morphological study of the shell. The shell is conical with helical winding, a perfectly straight winding axis, and the last turn of the shell is half its height. The shell is 15 mm high and has a maximum diameter of 7.5 mm. It is wound dexterously on a solid columella that does not open into an umbilicus. The shell is smooth with seven turns, the first of which are whitish in color.

We have examined the 212 *Melanella* species data existing in literature (geographical area, bathymetry, number of shell turns, size, size-to-diameter ratio and a shell lacking curvature) but none of them matches perfectly with the Malagasy species which strongly suggests that it is a new species to Science. The gastropod lies in the integument of the sea cucumbers, forming galls where, in each, are a large individual and 0 to 20 smaller ones. The largest individual always sends its proboscis deeper into the host tissues while, surrounding this individual, several smaller individuals and ovigerous sacs filled with eggs or veliger larvae are present.

COMPARATIVE STUDY OF OCULAR MORPHOLOGY IN FOUR SPECIES OF TROPICAL LIZARDS (SCINCIDAE) LIVING IN DIFFERENT ECOLOGICAL NICHES

Sébastien GENNAUX[1*], George DOLINSKII[1], Sébastien BOUTRY[2,3], Denis NONCLERCQ[1]

[1] Laboratory of Histology, University of Mons, 7000 Mons, Belgium.

[2] General, Organic and Biomedical Chemistry Unit, NMR and Molecular Imaging Laboratory, University of Mons (UMONS), 7000 Mons, Belgium

[3] Center for Microscopy and Molecular Imaging (CMMI), 6041 Gosselies, Belgium

Poster 29

***Presenting author, Sebastien.GENNAUX@umons.ac.be**

Keywords: Skinks, Fovea, Histology, Visual ecology

Scincidae represents one of the most diverse families within Squamates, exhibiting considerable variations in behavior and lifestyle. However, limited research has been conducted on the visual system of these reptiles.

The aim of this study was to better understand the visual system of Scincidae. Four tropical species were selected: *Tribolonotus gracilis*, *Mochlus fernandi*, *Tiliqua gigas*, and *Tiliqua scincoides*. Foraging in tropical forests, which are enclosed and dim environments, may drive animals to develop specific adaptations. Eye morphology was studied using histological methods, RMI, and examination of fresh retinal samples. The photoreceptor types were identified by immunohistochemistry using specific anti-opsin antibodies.

Our results show that *T. gracilis* and *M. fernandi* possess a well-developed fovea, which is an unusual feature of Scincidae. In contrast, *T. gigas* and *T. scincoides* have no fovea but present a high density of photoreceptors in the central part of the retina. *T. scincoides* possesses a low depression in the central retina, suggesting a sketched fovea. The main cone populations identified in all the species are sensitive to long wavelengths (opsin LWS). Most cones possess a colored or colorless oil droplet that allows the focalization of light rays to the opsins present in the discs of the cone external segment. A small population of photoreceptor cells showed immunoreactivity to rhodopsin, which is highly sensitive under scotopic conditions. RMI analysis of the morphology of the cornea and lens reflects an adaptation to photopic vision, but in a habitat where the light intensity is moderate. We also observed a linear connection between photoreceptors and ganglion cells favoring visual acuity. The morphological differences, including the presence of fovea, observed in *Tribolonotus gracilis* and *Mochlus fernandi* could be linked to their modes of predation and ecological niches.

IMPACT OF TEMPERATURE ON BUMBLEBEE COGNITION

Maxence GERARD[1,2*], Emily BAIRD[2]

[1] Laboratory of Zoology, University of Mons, 7000 Mons, Belgium

[2] Department of Zoology, University of Stockholm, SE-106 91 Stockholm, Sweden

Poster 30

***Presenting author**, **maxence.gerard@umons.ac.be**

Keywords: Bees, Behaviour, Climate change, Learning

Cognitive abilities are essential for pollinators, as they influence foraging efficiency, navigation, and adaptation to changing environmental conditions. Despite concerns about rising global temperatures, the impact of heat on insect pollinator cognition – critical for ecosystem stability – remains underexplored. This study examines how temperature influences the associative learning capabilities of bumblebees (*Bombus terrestris*) while foraging in free flight. We tested bumblebees in climate-controlled rooms at 24°C and 32°C using colour-conditioned learning tasks with artificial flowers. While the impact of exposure to elevated temperatures for a few minutes while foraging did not impair learning performance, bees foraging in warmer conditions drank significantly more water when it was available, indicating behavioural plasticity. These results suggest that, although the associative learning capabilities of foraging bees may be robust to changes in ambient temperature, heat causes them to adapt their foraging choices. These findings have consequences for our understanding of how pollinator foraging choices may change as environmental temperatures increase with global warming.

THE GENOME SEQUENCE OF THE COMMON SOLE, *SOLEA SOLEA*

Enora GESLAIN[1*], Filip A.M. VOLCKAERT[1*], Ann M. MC CARTNEY[2], Giulio FORMENTI[3], Alice MOUTON[4], Wellcome Sanger Institute Tree of Life Management, Samples and Laboratory team[5], Wellcome Sanger Institute Scientific Operations: Sequencing Operations[6], Wellcome Sanger Institute Tree of Life Core Informatics team[7], Tree of Life Core Informatics collective[8], Darwin Tree of Life Consortium[9]

[1] Department of Biology, KU Leuven, B-3000 Leuven, Belgium.

[2] Genomics Institute, University of California, Santa Cruz, CA 95060, USA.

[3] The Vertebrate Genome Laboratory, The Rockefeller University, New York, NY 10065, USA

[4] InBios-Conservation Genetics Laboratory, University of Liège, B-4000 Liège, Belgium.

[5]https://doi.org/10.5281/zenodo.12162482

[6]https://doi.org/10.5281/zenodo.12165051

[7]https://doi.org/10.5281/zenodo.12160324

[8]https://doi.org/10.5281/zenodo.12205391

[9]https://doi.org/10.5281/zenodo.4783558

Poster 31

***Presenting authors, Enora.geslain@kuleuven.be, filip.volckaert@kuleuven.be**

Keywords: Evolution, Pleuronectiformes, Reference genome, Structural variation

We present a genome assembly from an individual female *Solea solea* (Linnaeus, 1758) (the common sole; Chordata; Actinopterigii; Pleuronectiformes; Soleidae). The genome sequence spans 643.80 megabases. Most of the assembly (97.81%) is scaffolded into 21 chromosomal pseudomolecules. The mitochondrial genome has also been assembled and is 17.03 kilobases in length. Gene annotation of this assembly on Ensembl identified 21,646 protein-coding genes. We compare the common sole genome with Senegal sole *Solea senegalensis* and thickback sole *Microchirus variegatus* in a synteny, structural variation and phylogenetic analysis. This reference genome represents a valuable resource to understand the biology of common sole and teleost fishes, support conservation, fisheries management and a budding aquaculture industry.

Wolbachia Invasion: From Aphid cells to Plant tissue – It's Everywhere!

François GILBERT[1*], Stefan BRANDL[1], Marie-Christine ELOY[2], Thierry HANCE[1], Daisuke KAGEYAMA[3], François RENOZ[1]

[1] Earth and Life Institute, Université Catholique de Louvain, Croix du Sud, 1348 Louvain-la-Neuve, Belgium

[2] Louvain Institute of Biomolecular Science and Technology (LIBST), Université Catholique de Louvain, Croix du Sud, 1348 Louvain-la-Neuve, Belgium

[3] National Agriculture and Food Research Organization (NARO), Institute of Agrobiological Sciences, Japan.

Poster 32

***Presenting author**, **francois.gilbert@student.uclouvain.be**

Keywords: Symbiosis, *Wolbachia*, Horizontal transmission, Aphids

Wolbachia is an intracellular bacterium widely known for its extensive host range amongst arthropods and for manipulating host reproduction. This bacterium's remarkable capacity for manipulation has led to its integration into numerous pest control programs. However, little is known about the complete spectrum of its tissue distribution in many hosts. We also know that *Wolbachia* must have a strong capacity for horizontal transmission to explain such a wide distribution, but the mechanisms behind are still largely unknown. Using Fluorescent in situ Hybridization (FISH) microscopy, we examined *Wolbachia* localization across embryonic stages and various tissues of the banana aphid, *Pentalonia nigronervosa*. Our findings reveal the bacterium's presence in all embryonic stages, in a large part of digestive tracks, and many other somatic tissues such as antennae, legs and rostrum. This extensive tissue tropism could suggest a highly adaptive and invasive lifestyle for *Wolbachia* in *P. nigronervosa*. Additionally, *Wolbachia* have been detected in all banana tissues in contact with aphids, from the leaves to the roots. All these elements, given the phloem-sucking feeding of aphids, suggest that the bacterial symbiont could be transferred between host populations via plant phloem, thus providing elements to understand the mechanisms behind that remarkably wide distribution amongst phylogenetically distant arthropod species.

EMBRYOS AT RISK: EARLY EMBRYONIC DEVELOPMENT OF AQUATIC ECTOTHERMS IN A WARMING AND POLLUTED WORLD

Nicole GOEDE[1,2], Eli THORÉ[3,4,5], Luc BRENDONCK[2,6], Lendert GELENS[1]

[1] Department of Cellular and Molecular Medicine, KU Leuven, 3000 Leuven, Belgium.

[2] Laboratory of Animal Ecology, Global Change and Sustainable Development, KU Leuven, 3000 Leuven, Belgium.

[3] Laboratory of Adaptive Biodynamics, Research Unit in Environmental and Evolutionary Biology (Department of Biology), Institute of Life, Earth, and Environment, University of Namur, 5000 Namur, Belgium.

[4] Department of Wildlife, Fish, and Environmental Studies, Swedish University of Agricultural Sciences, SE-907 36 Umeå, Sweden.

[5] TRANSfarm, Science, Engineering, and Technology Group, KU Leuven, 3360 Bierbeek, Belgium.

[6] Water Research Group, Unit for Environmental Sciences and Management, North-West University, 2520 Potchefstroom, South Africa.

Poster 33

***Presenting author**, **nicole.goede@kuleuven.be**

Keywords: Global change, Chemical pollution, Mixed-stressors, Ecotoxicology

Animals increasingly face harsh environmental conditions, including exposure to rising temperatures and chemical pollutants. Egg-laying, ectotherm animals—including many fishes and amphibians—may be particularly vulnerable to such environments during early embryonic stages. Yet, the effects of temperature and chemical exposure on their early embryonic development have received only little attention and remain poorly understood. Predicting such effects is made even more complicated given that simultaneous exposure to rising temperatures and chemicals—a common situation in natural settings—can result in complex interactive effects beyond the sum of their individual impact.

With the goal of filling this knowledge gap, my PhD research will use advanced imaging techniques to capture high-resolution spatiotemporal data on embryonic development in three model species: *Xenopus laevis*, *Danio rerio*, and *Nothobranchius furzeri*. Specifically, my objective is to quantify the temperature-dependent scaling of key embryonic developmental events and evaluate its interaction with chemical exposure.

To reach this objective, I will first establish a baseline by characterizing how a wide temperature range affects developmental rates across various early embryonic stages. Then, I will assess how chemical exposure may disrupt this temperature scaling and characterize temperature-dependent sensitivities of embryos to pollutants. Additionally, I will investigate how daily temperature fluctuations impact early embryonic development and their potential interactive effects with chemical stressors. Finally, I will examine potential carry-over effects of transient temperature and chemical exposure during early embryonic stages on the development, physiology, and behavior in later life stages.

Ultimately, this research will advance our understanding of the fundamental principles that regulate early life. These insights will allow for more accurate predictions of how aquatic animals respond to global change, particularly under combined temperature and chemical stress.

INCOMPLETE SOCIAL CUES AND NAVIGATIONAL DECISION-MAKING IN SOCIAL AND SEMI-SOCIAL INSECTS

Frida HILDEBRANDT[1*], James FOSTER[1], Einat COUZIN-FUCHS[1]

[1] Neurobiology, Konstanz University, 78464 Konstanz, Germany.

Poster 34

***Presenting author**, **frida.hildebrandt@uni-konstanz.de**

Keywords: Collective behaviour, Navigation, Polarized light, Decision-making

Socially-acquired information is often incomplete and may be both uncertain and ambiguous. How does this incomplete information affect the individual decisions within the group, and the behaviour of social groups as a whole? It is likely that all insects can perceive and use the polarized light pattern in the sky for navigation. Polarized light is characterized by two properties: the angle of polarization (directional component) and the degree of polarization (signal strength). As uncertainty and ambiguity are inherent properties of polarized light, social animals that use polarized light for navigation, such as locusts and honeybees, are excellent models for investigating how incomplete information propagates through social groups.

Locusts are semi-social animals in which communication between individuals occurs passively in the form of inadvertent social cues. The desert locust possesses polarization sensitive photoreceptors in the dorsal rim area of their compound eye and it is highly likely that they use a celestial compass system to aid navigation. Although this species has been a model for the neuronal processing of polarized light, there is yet scarce behavioural evidence on the orientation of locusts to polarized light, limited mostly to single individuals. Unlike locusts, honeybees are central place foragers that actively communicate the location of a food source to their nest-mates through the waggle dance. Even when presented with uncertain and ambiguous information, e.g. from a polarized light stimulus, a dancing bee will still dance the location to a food source, according to her own estimate. However, little is known about how this incomplete information propagates to her nest-mates.

Here, we investigate how locusts and honeybees interpret and make navigational decisions using uncertain and ambiguous information from their peers by altering the directional component, signal strength and the light intensity of an artificial polarized light stimulus.

IMPROVING FISH BIODIVERSITY MONITORING IN AFRICA: BUILDING A COMPREHENSIVE EDNA METABARCODING REFERENCE LIBRARY

Alexander HILL[1*], Manon GEERTS[1], Hugo GANTE[1,2]

[1] Department of Biology, KU Leuven, 3000 Leuven, Belgium.

[2] Section Vertebrates, Royal Museum for Central Africa, 3080 Tervuren, Belgium.

Poster 35

***Presenting author**, **alexander.hill@student.kuleuven.be**

Keywords: environmental DNA, freshwater, barcode databases, primer sets

Environmental DNA (eDNA) metabarcoding has emerged as a crucial tool for studying and monitoring (fish) biodiversity, especially in regions where logistical challenges and/or limited funding restrict access to (remote) areas, such as various regions in Africa. However, the effectiveness of eDNA metabarcoding heavily relies on high-quality reference libraries that link DNA sequences to known species. While reference libraries for fishes are relatively well developed for some regions and for specific markers like COI, genetic resources for African freshwater species remain underrepresented. By creating a comprehensive reference library, our aim is to 1) identify species with missing genetic data and 2) evaluate the efficacy of current primer sets. Additionally, we can determine whether novel primer sets need to be developed.

To start with, we acquired a species list from FishBase using the rfishbase package. Based on this list, we extracted sequence data from the NCBI and BOLD repositories. We conducted searches for both mitochondrial and nuclear DNA, employing multiple relevant loci such as COI, 12S, 16S, and S7. Sequences were aligned using Hidden-Markov models, and phylogenetic trees were generated for each barcode using RAxML. Finally, a species coverage report was created allowing for the assessment of the completeness of the respective barcode databases (NCBI and BOLD) across different molecular markers commonly used in eDNA studies. This methodology is built upon the existing pipeline known as meta-fish-lib.

Preliminary results show that the number of accepted species is projected to be around 4,000, with the total number of names, including synonyms, exceeding 15,000. We found that reference genetic information is still lacking for many African freshwater fish species, which has a large impact on the feasibility and accuracy of biodiversity studies (including metabarcoding).

THE INFECTIOUS STATE OF *APHIS FABAE* BY *SERRATIA SYMBIOTICA* IMPACTS THE FORAGING BEHAVIOUR OF *APHIDIUS COLEMANI*?

Maxence JACQUET[1*], Alisa HAMIDOVIC[1], Thierry HANCE[1]

[1] Earth and Life Institute, Biodiversity Research Centre, UCLouvain, ELIB – Croix du sud, 1348 Louvain-la-Neuve, Belgium

Poster 36

***Presenting author**, **maxence.jacquet@student.uclouvain.be**

Keywords: *Serratia symbiotica*, Aphid-parasitoid, Foraging behaviour, Symbiont

Aphids (Hemiptera: Aphididae) have emerged as an outstanding model for studying the functional interactions with bacterial symbionts, offering insight into environmental adaptation mechanisms. In addition to an obligate nutritional symbiont, *Buchnera aphidicola*, aphids carry a number of facultative but heritable symbionts. These heritable symbionts are known to have multiple ecological functions that alter host physiology, including effects on nutrition, reproduction, resistance to stresses such as heat, fungi, and parasitoids. Specifically, the facultative symbiont *Serratia symbiotica* provides aphids with defence benefits against parasitoids, leading to the emergence of possible strategies that depend on its presence in the context of optimal foraging theory. Recently, a cultivable, non vertically transmitted strain of *S. symbiotica (*CWBI-2.3T) has been discovered to be present in the aphid digestive tract, and appears to be basal in the evolution of the symbiosis as it retains a pathogenic character. We hypothesise that its regular presence in aphids in the wild, despite its negative effect, is linked to a form of positive compensation provided by the protection it offers against parasitoids. Consequently, the aim of this study was to identify whether the infectious state of the black-bean aphid *Aphis fabae* by *S. symbiotica* affects the foraging behavior of the generalist parasitoid *Aphidius colemani* (Hymenoptera: Braconidae). Olfactometry assays in a Y-shaped tube were performed and behavioural activity related to patch allocation was recorded between *A. fabae* orally infected with an artificial diet containing *S. symbiotica* and non-infected individuals. The parasitoid wasp tends to show a marked preference for non-infected aphids. This preferential orientation is likely to be enabled by perceived chemical cues that alter their foraging behaviour, influencing its timing and sequence of behaviours within a patch. This work demonstrates the likely behavioural adaptation to infection status by a facultative symbiont and highlights the implications for the aphid-parasitoid relationship.

THE ROLE AND REGULATION OF REACTIVE OXYGEN SPECIES (ROS) AND ANTIOXIDANTS (AOX) DURING TISSUE REGENERATION IN *SCHMIDTEA MEDITERRANEA*

Bob KAUFFMANN[1*], Martijn HELEVEN[1], Karolien BIJNENS[1], Karen SMEETS[1]

[1] Center for Environmental Sciences, University Hasselt, 3590 Diepenbeek, Belgium

Poster 37

***Presenting author**, **bob.kauffmann@uhasselt.be**

Keywords: Regeneration, Reactive oxygen species (ROS), Antioxidants (AOX), *Schmidtea mediterranea*

Animal multicellularity could only be this efficient due to the capacity for healing and regenerating damaged body parts. Throughout history, regeneration has emerged in various animals, but not in all. Among those that can regenerate, some species possess a remarkable capacity for regeneration, while others have a much more limited ability, resulting in a spectrum from simple to complex forms of regeneration.

One organism with outstanding regenerative capacity is the flatworm *Schmidtea mediterranea*, which belongs to the taxon Tricladida (planarians), and is part of the clade Adiaphanida. Within this clade, the capacity for regeneration varies among families and species; however, *Schmidtea mediterranea* is considered one of the species regarded as a 'holy grail' candidate in the regeneration spectrum. It can regrow an entire animal from a small fragment of its body.

Regeneration begins when tissue experiences damage or loss, activating a cellular response. One of the earliest of these responses is a cellular stress reaction. In *Schmidtea mediterranea*, it has been demonstrated that reactive oxygen species (ROS) are essential. Recent research has primarily focused on the role of ROS (reactive oxygen species), but understanding the other side of this balance – antioxidants – is essential. Antioxidants, often understudied, are crucial for maintaining stable ROS levels and ensuring cellular homeostasis.

Understanding how AOX regulates redox balance in a regenerative context provides valuable insights into the underlying mechanisms. By utilizing immunohistochemistry and functional interference to disrupt the glutathione and thioredoxin cycles, this study will investigate the role of AOX and identify the specific cell types involved in regeneration within a redox-balanced background.

POPULATION DYNAMICS OF PREDATORY SPIDERS OF COTTON FIELDS FROM DISTRICT FAISALABAD, PUNJAB, PAKISTAN

Bilal Saeed KHAN[1*], Muhammad Aneeb SHAHZAD[2], Tariq MUSTAFA[2]

[1] Department of Entomology, University of Agriculture, 38000 Faisalabad, Pakistan

[2] Department of Entomology, University of Agriculture, Faisalabad, Sub-Campus Depalpur
56300 Okara, Pakistan

Poster 38

***Presenting author**, **bsk_1703@yahoo.com**

Keywords: Population dynamics, Predatory spiders, Abiotic factors, Faisalabad

Spiders are one of the outstanding and admired bio-control agents that belong to class Arachnida. The current study has enumerated the population dynamics of predatory spiders in relation to some abiotic factors. Random sampling was done under a Randomized Complete Block Design with three replications in six cotton-cropping areas (Faisalabad City, Faisalabad Saddar, Khurrianwala, Chak Jhumra, Makkuana and Samundri) of District Faisalabad, Punjab, Pakistan. Spiders were collected using different methods, such as pitfall traps, hand picking, and aerial netting. The identification of spiders was made through taxonomic keys and online literature. During April-September 2023, a total of 1273 specimens of spiders belonging to 10 families, 20 genera and 27 species were recorded. Lycosidae (34%) and Salticidae (20%) were the most abundant spider families while Oxyopidae made smallest contribution with 7% of total population. Correlation matrix analysis of the population of predatory spider families with abiotic factors demonstrated that they exhibit a significant positive correlation with minimum temperature. However, certain predatory spider families such as Salticidae, Araneidae and Linyphiidae displayed a non-significant negative correlation (-0.060, -0.056 and -0.159) with relative humidity. Thomisidae only exhibited positive non-significant correlation (0.013) with rainfall, but an overall significant negative correlation existed between rainfall and the total predatory spider population. In conclusion, predatory spiders generally flourish under stable environmental conditions, with high temperatures and rainfall negatively impacting their populations. These findings underscore the significance of stable environmental conditions for the prosperity and predatory activities of predatory spiders, supporting biodiversity, and promoting sustainable cotton production.

UNCOVERING GENE REGULATORY NETWORKS UNDERLYING BEHAVIOURAL PLASTICITY IN *DAPHNIA MAGNA* THROUGH SINGLE-CELL MULTI-IOMICS

Aaron KIGGEN[1*], Steven VAN BELLEGHEM[1]

[1] Eco-Evolutionary Genomics Lab, KU Leuven, 3000 Leuven, Belgium

Poster 39

***Presenting author, aaron.kiggen@kuleuven.be**

Keywords: Genomics, Behaviour, Plasticity, Single-cell

Behavioural plasticity allows organisms to rapidly adapt to environmental changes, serving as an immediate response mechanism on short time scales. Understanding these adaptive behaviours is essential, as they provide insights into how organisms adapt to shifting environments. However, the variation and evolution of behavioural plastic responses, along with their underlying molecular mechanisms—particularly the gene regulatory networks (GRNs) driving these responses—remain largely unexplored.

The phototactic behaviour —defined as the movement toward or away from light— of *Daphnia magna* serves as a prime example of an adaptive response that can be rapidly altered by environmental factors, such as the presence of fish. Phototaxis is a relatively simple behaviour that lends itself to easy study, making it an ideal model for investigating how sensory inputs influence behavioural responses. This simplicity enables researchers to examine how *Daphnia* integrate sensory information with motor outputs through GRNs. Populations adapted to high predation pressure exhibit a significant negative phototactic response to fish kairomones, swiftly switching from positive to negative phototaxis to seek refuge in deeper waters. This rapid response to predator cues suggests a fast-acting GRN, raising fundamental questions about the molecular mechanisms governing this plasticity.

To address these gaps, this project will develop a high-throughput, multidimensional behavioural assay to capture detailed data on behavioural patterns in response to kairomone exposure in *D. magna*. We will then utilize single-cell multi-omics sequencing to investigate the GRNs involved in *Daphnia*'s behavioural plasticity. Due to the clonal nature of *Daphnia*, this approach allows us to disentangle environmental and genetic influences on behaviour, offering insights into the evolution and developmental regulation of plasticity. By elucidating these regulatory mechanisms, our study aims to enhance understanding of how behavioural plasticity is expressed and evolved in response to ecological challenges, ultimately advancing predictions about organismal responses to rapid environmental changes.

THE EVOLUTION OF PESTICIDE RESISTANCE IN *DAPHNIA MAGNA*; A POPULATION, COMPARATIVE AND FUNCTIONAL GENOMICS APPROACH

Alexandros KOURTIDIS[1*], Styliani ZETTA[1], Steven VAN BELLEGHEM[1]

[1] Division of Ecology, Evolution and Biodiversity Conservation, KU Leuven, 3000 Leuven, Belgium

Poster 40

***Presenting author**, **alexandros.kourtidis@kuleuven.be**

Keywords: Genomics, Adaptation, Pesticides

Characterising the genetic basis of adaptation is a central goal in evolutionary biology. Despite the enormous advancements in molecular and computational methods, landscape-level evolutionary studies that combine genome sequencing with functional assays remain scarce. Here, we will use the water flea *Daphnia magna* and its distribution in an agricultural-vs-natural pond system in Flanders, Belgium, to comprehensively study the genetics behind pesticide tolerance evolution. This will be done in four steps. First, we will describe the populations' demography and structure, and identify parts of the genome that are under selection against high pesticide concentration (population genomics). Second, we will assemble a pangenome of *D. magna* in this system to identify structural variations and analyse them in relation to pesticide concentration (comparative genomics). Third, we will combine RNA-seq with chromatin accessibility assays (ATAC-seq) to identify the genes and regulatory regions that are involved in the functional response against organophosphate pesticides (functional genomics). Finally, we will integrate these results to assess the evolution of gene regulatory networks that are involved in the adaptation of *D. magna* against pesticide use in Flanders. This study is going to provide a novel insight into the evolution of the genome's sequence, structural variation and gene regulation in a landscape that is highly exposed to a prevalent anthropogenic stressor.

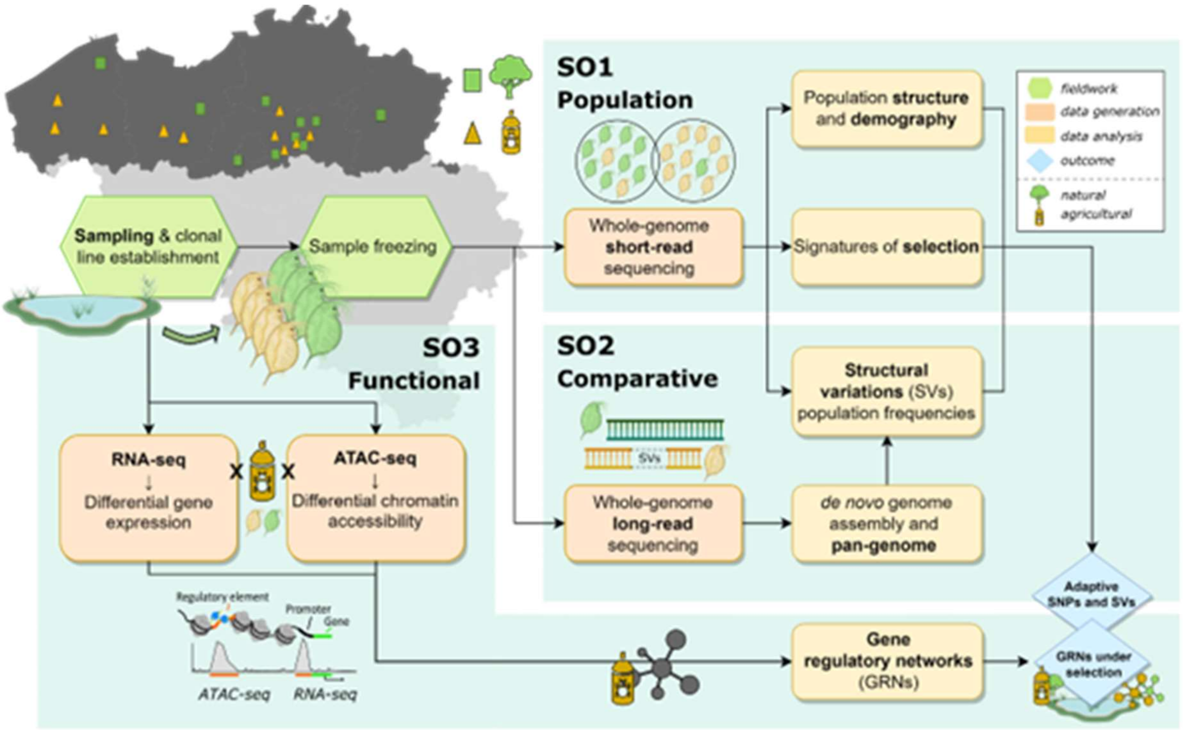


Fig 1. Flowchart of the work packages, illustrating the three complementary genomic approaches.

EXPLORING THE INFLUENCE OF INVASIVE PLANT SPECIES ON PLANT-BEE COMMUNITIES, FUNCTIONAL TRAITS, AND INTERACTIONS

Clara LECONTE[1*], Alice NAVEAUX[1*], Clément TOURBEZ[1], Denis MICHEZ[1]

[1] Laboratory of Zoology, Research Institute for Biosciences, University of Mons, 7000 Mons, Belgium.

Poster 41

***Presenting authors**, **clara.leconte@student.umons.ac.be, alice.naveaux@student.umons.ac.be**

Keywords: Bee conservation, Invasive species, Plant and pollinator communities, Pollination networks

Since the Industrial Revolution, globalisation has led to the intentional or accidental introduction of exotic species into new environments. Some of these species become invasive, degrading ecosystems by outcompeting native species and disrupting native mutualisms. One prominent invasive species, *Buddleja davidii* (butterfly bush), is characterised by its abundant seed production, rapid growth, and high environmental tolerance. Originally from China, *B. davidii* has colonised various ecosystems, including the species-rich pioneer habitats of spoil tips in Europe. Its spread poses significant threats to ecosystems, where competition with native flora may reduce pollinator diversity and disrupt plant-pollinator interactions. This poster summarises our master's thesis project, which aims to assess the impacts of *B. davidii* on (i) the plant community, (ii) the bee community, and (iii) pollination networks in Belgian spoil tips. To explore this, we conducted plant surveys, floral unit counts, and bee samplings across 30 sites representing a gradient of *B. davidii* invasion over a six-month period beginning in April 2024. Across the sampling season, we recorded 94 bee species (from six families, totalling 2,898 individuals) and 85 plant species (from 21 families, representing over 470,000 floral units). To further examine potential impacts, we will measure plant and bee functional traits to determine if *B. davidii* invasion influences functional diversity or promotes particular traits. Additionally, palynological analysis of pollen carried by bees will be conducted to identify bee-plant interactions, model pollination networks, and assess the impact of *B. davidii* invasion on these networks. The expected results will enhance our understanding of the impacts of *B. davidii* in spoil tip habitats and contribute to conservation strategies to protect native pollinator and plant communities from invasive species.

POLLINATOR DIVERSITY ON ROADSIDES AND TRAFFIC-RELATED IMPACTS

Sarah LESCOT[1], William FIORDALISO[1], Tea SKENDŽIĆ[2], Denis MICHEZ[1]

[1] Laboratory of zoology, University of Mons, 7000 Mons, Belgium.

[2] Department of biology and ecology, University of Novi Sad, 21000 Novi Sad, Serbia.

Poster 42

***Presenting author**, **sarah.lescot@umons.ac.be**

Keywords: Bees, Hoverflies, Butterflies, Anthropocene

The diversity and abundance of wild pollinators are declining. One of the primary drivers behind this decline is the fragmentation of their habitats. Roads contribute to this fragmentation by posing physical barriers and lethal threats to pollinators. As part of the Safeguard project, this research investigates the effects of road traffic on pollinators in Belgium and Serbia, two European countries selected for their contrasting road densities: Belgium's road network being eight times denser than Serbia's.

Our study first evaluates pollinator diversity along roadsides, focusing on bees, hoverflies, and butterflies to assess ecological quality. Subsequently, it analyzes the risks of collision-related mortality among these pollinators. Using line transect, we surveyed 24 sites in each country, three times along both high- and low-traffic roads in agricultural and semi-natural landscapes. During each survey, bees, hoverflies, and butterflies are net-sampled along the roadside. Additionally, road sampling is conducted using a sticky trap mounted under the vehicle's license plate.

The results reveal low pollinator diversity along roadsides, although these habitats do support endangered species. In Belgium, the species richness across the three pollinator groups studied is significantly higher along minor roads than major roads, with increases of 66% in bee species, 76% in hoverfly species, and 46% in butterfly species. This pattern is not observed in Serbia, likely due to its lower road density and use. Among the insects involved in vehicle collisions, Thysanoptera, Diptera, and Hymenoptera are the most frequently affected, while collisions involving bees, hoverflies, and butterflies are less numerous. These findings suggest that collisions mainly affect small insects.

THE ADAPTATIONAL AND EVOLUTIONARY HISTORY OF SPECTRAL SENSITIVITY IN ECDYSOZOAN R-OPSINS

Minglei MA[1], James F. FLEMING[2], Marjorie A. LIENARD[1*]

[1] Department of Life Sciences, Laboratory of Molecular Biology of Sensory Systems, GIGA-R, University of Liege, 4000 Liege, Belgium.

[2] Japan Agency for marine-Earth Science and Technology, 23700061 Kanagawa, Japan.

Poster 43

***Presenting author,** **marjorie.lienard@uliege.be**

Keywords: Vision, Spectral sensitivity, Terrestrialisation, Invertebrates

Visual r-opsins originated more than 600Ma in the common ancestor of all protostomes and underwent multiple duplications within the evolutionary history of Ecdysozoa, leading to a remarkable number of visual pigments in extant insect and crustacean species. Combining phylogenetic, computational and molecular approaches we explore the evolution of visual pigment functions across major duplications throughout Arthropoda (insects, crustaceans, chelicerates, myriapods).

A comprehensive phylogeny was built combining large-scale opsin datasets of modern UV-SW-MWS-LWS-Rh7 paralog lineages across arthropods and non-arthropod ecdysozoans. Ancestral states were robustly calculated using Lazarus with additional Gap Correction, alongside a novel comparative approach to better approximate flanking regions, providing 8 ancestral sequences (around 370-aa long) at key internal nodes representing duplication events preceding modern arthropod opsin lineages.

Our first ancestral sequence is placed at the origin of all modern opsin lineages, incorporating arthropod-specific families Rh7, UV, SWS, LWS and MWS and non-arthropod ecdysozoans (ancestral 1). Ancestral 2 represents the common ancestor of all arthropod-specific visual r-opsin families, which upon duplication around 599Ma, gave rise to LWS/MWS opsins (ancestral 3) in Chelicerata-Pancrustacea-Myriapoda, and Rh7/UV/SWS opsins in Chelicerata-Pancrustacea (ancestral 4). The LWS/MWS lineage evolved into MWS+LWS opsins 590Ma before the split between Chelicerata-Pancrustacea-Myriapoda, with an internal division between Chelicerate and Mandibulate LWS opsins (ancestral 5). Duplications of the RH7/UV/SWS (ancestral 4) lineage resulted in Rh7 and a combined UV/SWS (ancestral 6) 570Ma, followed by evolution of the Chelicerate UV family (ancestral 7), then the UV/SWS split into modern UV+SWS opsins (ancestral 8).

The four LWS-MWS-Rh7 and UV/SWS opsin families shared across Arthropoda originated prior to terrestrialisation of arthropods but also of vascular plants. For shallow water and coastal organisms, the water would likely have been red-shifted, owing to sediment influx without roots to bind the soil. The LWS/MWS to LWS+MWS duplication (second opsin duplication) might have resulted in a bathochromatic LWS opsin adapted to Cambrian coastal environments. As the ancestral ecdysozoan opsin is likely blue-green sensitive, the evolution of LWS and UV/SWS pigments should tell us about the early ecologies of Cambrian shallow marine environments.

By capturing key evolutionary transitions, including the terrestrialisation of insects, tardigrades and chelicerates and exploring functionally these resurrected opsins by heterologous expression, we can assess the spectral range of early light-sensitive receptors, giving a functional view of opsin adaptation to new visual environments.

DOES DIFFERENT KARYOTYPE MAINTAIN CRYPTIC SPECIES BOUNDARIES?

Louise MALICE[1*], Alice DENNIS[1]

[1] URBE, Department of Biology, University of Namur, 5000 Namur, Belgium.

Poster 44

***Presenting author**, **malouliceise@gmail.com**

Keywords: Karyotype, Cryptic species, Gastropods

Studies of chromosome number are a key to understanding evolution, adaptation, and biodiversity. Variations in this number can provide insights into evolutionary histories and help distinguish closely related species which is useful in conservation to identify management units, especially in endangered species. Chromosomal differences can also serve as reproductive barriers, aiding in the study of speciation. Moreover, these differences can reflect species-specific adaptations showing how species survive in particular environments.

Several studies have been conducted to investigate the chromosomal count within the class of gastropods. These studies have revealed that there is a large diversity in chromosome number, and that this value alone is a limited indicator and cannot definitively determine whether an organism belongs to one species. However, while the chromosome count may not be sufficient for species identification on its own, it does provide valuable insight into the evolutionary relationships and genetic diversity among different organisms within this class.

The *Melampus* species can be studied to understand the speciation process. This complex of salt marshes snails, including a cryptic species complex divided in three different species that are *Melampus bidentatus, jaumei and gundlachi*, presents an interesting system for study, especially as their chromosome number hasn't been reported yet. The aim of the study is to observe if this factor does have an impact in the speciation process in this complex.

DIVERSITY OF THE REEF FISH COMMUNITY WITHIN AND OUTSIDE A FISHING ZONE IN THE BALANDRA BAY MARINE PROTECTED AREA (LA PAZ, MEXICO)

Héloïse MANIQUET[1,2*], Bruno FREDERICH[2], Damien OLIVIER[1]

[1] Departamento Académico de Ciencias Marinas y Costeras, Universidad Autónoma de Baja California Sur, 23000 La Paz, Mexico.

[2] Laboratory of Evolutionary Ecology, University of Liège, 4000 Liège, Belgium.

Poster 45

***Presenting author**, **Heloise.maniquet@student.uliege.be**

Keywords: Biological conservation, No-take marine reserve, Gulf of California, Ichthyology

The establishment of marine protected areas (MPAs) is the most widely used tool for protecting marine biodiversity. However, many of these areas have no active controls, leaving room for illegal fishing and thus failing to achieve their objectives. This illegal fishery can negatively impact the ecosystem by targeting some fish species which can have cascading trophic effects. In regions where governmental authorities do not have the means to conduct active controls, collaboration with local populations is essential. This situation is present in the Bay of La Paz in Mexico. There, the multi-use MPA of Balandra includes fishing and no-fishing areas. San Rafaelito is a no-fishing zone, where numerous ecotourism activities take place, while in La Gaviota artisanal and sport fishing are permitted. Thanks to ecotourism activities in San Rafaelito, this area could benefit from the almost permanent control by the population, and this could increase the effectiveness of this area. Here, we studied the effect of the absence of fishing on reef fish communities, controlled by ecotourism. Specific richness, composition of assemblages, total biomass, as well as the biomass and the density of fish targeted by fishery were compared between the two sites. The total biomass, biomass and the density of large individuals of targeted species were significantly higher at San Rafaelito. More specifically, the biomass and density of large individuals of parrotfish (Scaridae) and groupers (Serranidae *Mycteroperca rosacea*) were significantly higher at San Rafaelito. The lower biomass and density of large piscivores and herbivores at La Gaviota may affect the reef ecosystem functioning. Indeed, the key roles of herbivory and bioerosion operated by Scaridae as well as the top-down control achieved by predatory Serranidae could be reduced at this site. Accordingly, our work revealed the effectiveness of the San Rafaelito no-fishing zone, unlike multi-use areas such as La Gaviota.

SOIL AND POLLINATOR CONSERVATION: CAN URBAN SAND BEDS PARTICIPATE TO THE CONSERVATION OF GROUND NESTING BEES?

Bodil MATTSSON[1*], Denis MICHEZ[1]

[1] Laboratory of zoology, University of Mons, 7000 Mons, Belgium

Poster 46

Presenting author**, **bodil.mattsson@umons.ac.be

Keywords: Ground nesting bees, Pollinators, Nesting, Conservation

Wild bees provide crucial ecosystem services through the pollination of flowers, ensuring healthy ecosystems and stable food production. However, with increasing threats such as habitat loss and land fragmentation bees are declining. As an example, rapid urbanization is diminishing ground nesting bees' habitats. This group makes up 64-83% of all known bee species, and they're all dependent on permeable surfaces for nesting. To mitigate the problem, local initiatives are developed to provide alternative nesting resources. However, practitioners sometimes appear to lack basic knowledge on species requirements and some initiatives can fail because of wrong management. This finding posed further questions whether ground nesting bees need specific soil characteristic requirements for nesting. An ongoing PhD study focuses on revealing the nesting ecology of this group of bees by looking at soil variables at the nest level. Five European species (*Andrena vaga, A. cineraria, Colletes cunicularius, Dasypoda hirtipes,* and *Lasioglossum calceatum*) will be examined through five European countries (Sweden, Great Britain, Germany, Belgium, and France) in search of possible inter- and intraspecific variations in nesting ecology. Three populations/species/country will be sampled. Field sampling will be done with soil cores at the nest sites which will provide information on particle size distribution, pH, and carbon (C) and nitrogen (N) content. Additional measurements will be taken such as seasonal temperature and humidity variability measured with iButtons, and soil compaction. Not only will some of the knowledge gaps on ground-nesting bees' ecology be filled in by this study, but with the information of whether different species have different soil characteristics requirements, more efficient conservation measures can be taken. Areas fulfilling the soil requirements of certain species can be protected against habitat loss and sand beds aiming at conservation can be adapted to the bees' needs and help populations rise again.

COMPARISON OF THE POLLINATOR MICROBIOME: MANAGEMENT PRACTICES, ALTITUDE AND SEX AS DRIVERS FOR CHANGE

Nele MULLENS[1,2*], Sija KABOTA[3,4], Marc DE MEYER[2], Maulid MWATAWALA[3], Hannes SVARDAL[1,5], Carl VANGESTEL[6,7], Kurt JORDAENS[2]

[1] University of Antwerp, Department of Biology, 2180 Antwerp, Belgium.

[2] Royal Museum for Central Africa, Biology Department, 3080 Tervuren, Belgium.

[3] Sokoine University of Agriculture, Department of Crop Science and Horticulture, 672 Morogoro, Tanzania.

[4] National Sugar Institute, Academic, Research and Consultancy Section, 672 Morogoro, Tanzania.

[5] Naturalis Biodiversity Center, 2333 Leiden, The Netherlands.

[6] Royal Belgian Institute of Natural Sciences, Biology Department, 1000 Brussels, Belgium.

[7] Ghent University, Department of Biology, 9000 Ghent, Belgium.

Poster 47

***Presenting author**, **nele.mullens@uantwerpen.be**

Keywords: Microbiomics, Pollinators, Hoverflies, Tanzania

While *Apis mellifera* (Western honeybee) is a well-studied pollinator, many hoverfly species (Syrphidae) -the most significant group of dipteran pollinators- remain understudied. The gut microbiome plays a crucial role in insect health, behaviour, and response to stressors such as pesticides. Given this and the global decline in insect populations, this study examines the effects of management practices (conventional vs. agroecological farming) on the microbiomes of different pollinator species from Tanzania. For the first time, we compare the microbiomes of the three most common syrphid species (*Paragus borbonicus*, *Toxomerus floralis*, and *Ischiodon aegyptius*) with that of *A. mellifera*. We found substantial differences between hoverflies and honeybees, with hoverflies exhibiting higher microbiome diversity and greater individual variation. Although sex-specific feeding patterns were expected to impact the hoverfly microbiome, a sex-specific microbial difference was only observed in *I. aegyptius* where females had significantly higher microbiome diversity than males. Other notable differences included shifts in beta diversity of female *P. borbonicus* and *A. mellifera* at different altitudes and higher dispersion in male *P. borbonicus* compared to females. Differences in microbiomes based on management practices were evident in *A. mellifera* but not in hoverflies, suggesting that honeybees are more affected by management practices than the target hoverfly species.

OPSIN-MEDIATED PHOTORECEPTION IN THE MOST BASAL ECHINODERM GROUP: THE CRINOIDS (CRINOIDEA, ECHINODERMATA)

Youri NONCLERCQ[1*], Marjorie LIENARD[2], Alexia LOURTIE[1], Emilie DUTHOO[1], Lise VANESPEN[1], Igor EECKHAUT[1], Patrick FLAMMANG[1], Jérôme DELROISSE[1,2]

[1] Laboratory of Biology of Marine Organisms and Biomimetics, Research Institute for Biosciences, University of Mons, 7000 Mons, Belgium.

[2] Laboratory of Molecular Biology of Sensory Systems, GIGA, University of Liège, 4000 Liège, Belgium.

[3] Laboratory of Cellular and Molecular Immunology, GIGA, University of Liège, 4000 Liège, Belgium.

Poster 48

Presenting author**, **youri.nonclercq@umons.ac.be

Keywords: Crinoid, Photoreception, Echinoderm, Opsin, Vision

Light perception is a fundamental sense in most metazoan lineages. This capacity is mainly mediated by photoreceptor proteins known as opsins. While photoreception is well understood in many animal groups with specialized visual organs, such as eyes or ocelli, it remains relatively underexplored in organisms which primarily rely on extraocular photoreception, such as echinoderms. Paradoxically, these eyeless marine animals possess one of the greatest diversities of ancestral opsin types among bilaterian lineages. To gain a deeper understanding of opsin evolution in this group of deuterostomes, it is essential to study the most phylogenetically basal echinoderm class, the crinoids. These filter-feeder animals use branched arms to capture small planktonic particles in their feeding grooves, which lead to the mouth. Their photoreception remains largely understudied, although it is known that some shallow-water comatulid species are sensitive to daylight.

We conducted a comprehensive study of the photoreception in the European species *Antedon bifida*, examining both morpho-functional and molecular aspects. An analysis of its chromosome-scale genome revealed the presence of only three opsin genes, all of which belong to the rhabdomeric type (i.e., the type containing most arthropod visual opsins). The low opsin diversity contrasts with that observed in other echinoderm classes. The three crinoid opsins were expressed *in vitro,* and their measured absorbance corresponded to blue and green light (respectively 464, 426 and 525nm). These results are largely consistent with behavioural tests that revealed a negative phototaxis with a large peak sensitivity to blue light (463nm) in this species. Finally, two of these opsins have been localised through immunostaining, one in the basiepithelial nervous system of the feeding grooves and the second at the tip of the tube feet. This opsin expression pattern suggests a complex extraocular photoreception system in these feather stars, like that observed in other echinoderms, such as sea urchins and brittle stars.

REVISION OF THE GENUS *BALTOPLANA* (RHABDOCOELA: SCHIZORHYNCHIA: CHELIPLANIDAE) WITH THE DESCRIPTION OF TWO NEW SPECIES

Jhoe REYES[1*], Marlies MONNENS[1,3], Tom ARTOIS[1]

[1] Hasselt University, Centre for Environmental Sciences, Research Group Zoology: Biodiversity and Toxicology, Agoralaan Gebouw D, B-3590 Diepenbeek, Belgium.

[2] Royal Zoological Society of Antwerp, Center for Research & Conservation, Koningin Astridplein 20-26, B-2018 Antwerp, Belgium.

[3] Royal Belgian Institute of Natural Sciences, OD Taxonomy and Phylogeny, Vautierstraat 29, B-1000 Brussels, Belgium.

Poster 49

***Presenting author, jhoe.reyes@uhasselt.be**

Keywords: Marine meiofauna, Taxonomy, Phylogeny, Rhabditophora, Free-living flatworms

Marine microturbellarians are important components of the meiofauna and contribute significantly to the processes and functioning of marine ecosystems. Microturbellarians of the taxon Cheliplanidae are, among other things, characterized by a proboscis with protractile hooks. Within Cheliplanidae, the genus *Baltoplana* currently includes four described species: *B. bisphaera* from Kenya, *B. cupressus* from South Africa, *B. magna* from the Mediterranean and the European Atlantic coasts, and *B. valkanovi* from the Black Sea. However, the phylogeny of *Baltoplana* within Cheliplanidae and Schizorhynchia remains unresolved. This study revises the genus *Baltoplana* from an integrative framework, using morphology and, for the first time, DNA sequences (18S, 28S, cox1). A preliminary phylogeny of *Baltoplana* was constructed based on newly collected material, confirming its position within Cheliplanidae. We also provide new distributional data for *B. magna*, and two new species of *Baltoplana* are described based on DNA sequences and the morphology of the male copulatory organ, particularly of the cirrus and accessory cirri. In *Baltoplana* **n. sp. 1**, the male copulatory organ has an armed cirrus adjacent to an accessory armed cirrus. The ejaculatory duct connects to the cirrus, which has small, robust spines that gradually increase in length from the proximal to the distal region. The accessory cirrus is also armed with long and robust spines extending to the distal area. *Baltoplana* **n. sp. 2**, on the other hand, has an armed cirrus with three accessory cirri. The cirrus has short spines in its proximal region, which increase in length towards the distal end. One of the accessory cirri is long, while the other two are oval. All three of them have equally sized spines. These morphological features set these species apart from previously described species of *Baltoplana*.

DE-NOVO GENOME ASSEMBLIES OF HYBRID CICHLID SPECIES GIVE INSIGHTS INTO GENOME DIVERGENCE PATTERNS DUE TO HYBRIDISATION

Jaysmita SAHA[1*], Valentina PEONA[2], Hannes SVARDAL[1]

[1] Department of Biology, University of Antwerp, Prinsstraat 13, 2000 Antwerp, Belgium.

[2] Department of Organismal Biology – Systematic Biology, Uppsala University, Dag Hammarskjölds väg 7, 753 10 Uppsala, Sweden.

Poster 50

***Presenting author**, **jaysmita.saha@uantwerpen.be**

Keywords: Cichlid, Hybrid, Genome structure, ONT

Hybridisation plays a major role in speciation and formation of adaptive radiations. The cichlid radiations in the Eastern African Great Lakes are known to have evolved from hybrid swarms of divergent lineages. Hybridisation can have a wide range of consequences. It can give rise to species with novel adaptive traits and improved fitness compared to the parental species. It can also facilitate accumulation of deleterious mutations that reduce the fitness of the hybrid species. How genomes from distantly related lineages interact to produce this variation remains incompletely understood.

In this study we focused on a hybrid species that was produced by breeding two eco-morphologically similar species but from distantly related lineages: Maylandia emmiltos from Lake Malawi and Neochromis omnicaeruleus from Lake Victoria. Both of these parental species are rock-dwelling algae scrappers. We used long read nanopore sequences for our de novo assemblies of the hybrid individuals. One of the challenges in our study was the unavailability of the reference genomes of the parental species. By using phased genome assemblies, we were able to reconstruct the parental haploid genomes.

Our analysis shows the variations segregating in the chromosomes in the hybrids are not always completely heterozygous. But there is an over-representation of a specific donor in certain regions of the genome. Additionally, we explored the occurrence of transposable elements (TE) and their propagation across generations. Preliminary results indicate that there is a substantial amount of putative de novo transpositions that accumulate and requires to be verified further.

HOST-BACTERIOME TRANSPLANTS OF THE SCHISTOSOME SNAIL HOST *BIOMPHALARIA GLABRATA* REFLECT SPECIES-SPECIFIC ASSOCIATIONS

Ruben SCHOLS[1], Isabel VANOVERBERGHE[2*], Tine HUYSE[1], Ellen DECAESTECKER[2]

[1] Department of Biology, Royal Museum of Central Africa, 3080 Tervuren, Belgium.

[2] Laboratory of Aquatic Biology, Interdisciplinary Research Facility Life Sciences, KU Leuven, 8500 Kortrijk, Belgium.

Poster 51

***Presenting author, ellen.decaestecker@kuleuven.be (All authors contributed equally)**

Keywords: Freshwater snail, Microbiome, Parasite, Schistosiomasis, Transplant, Tripartite interaction

Microbial symbionts can affect host phenotypes and, thereby, ecosystem functioning. The microbiome is increasingly being recognized as an important player in the tripartite interaction between parasitic flatworms, snail intermediate hosts, and the snail microbiome. To better understand these interactions, transplant experiments are needed, which rely on the development of a reliable and reproducible protocol to obtain microbiome-disturbed snails. Here, we report on the first successful snail bacteriome transplants, which indicates that *Biomphalaria glabrata* can accrue novel bacterial assemblies depending on the available environmental bacteria obtained from donor snails. Moreover, the phylogenetic relatedness of the donor host significantly affected recipients' survival probability, corroborating the phylosymbiosis pattern in freshwater snails. The transplant technique described here, complemented by field-based studies, could facilitate future research endeavors to investigate the role of specific bacteria or bacterial communities in parasitic flatworm resistance of *B. glabrata* and might ultimately pave the way for microbiome-mediated control of snail-borne diseases.

DEEP LEARNING APPROACHES TO INVESTIGATE OLFACTORY RESPONSES IN BEHAVIORALLY DIVERGENT DEER MICE

Thorbjörn SIEVERT[1], Long MA[1], Jean-Marc LASSANCE[1*]

[1] GIGA Research & Faculty of Veterinary Medicine, University of Liège, 4000 Liège, Belgium.

Poster 52

***Presenting author**, **jmlassance@uliege.be**

Keywords: Natural behavior, Deer mouse, Olfactory exploration, Machine learning

Deciphering olfactory cues for sex and species identification is a critical aspect for the survival of mammalian populations. Furthermore, the impact of mating systems on the response to social olfactory cues remains uncertain. In our investigations, we selected *Peromyscus polionotus* and *P. maniculatus*, two closely related species of North American deer mice characterized by divergent mating systems. Specifically, *P. polionotus* is a rare example of a genetically and socially monogamous species whereas *P. maniculatus* is a typical example of promiscuous rodents. These two sister species serve as essential study systems for exploring variations in social behavior in correlation with the divergence of mating system. During experimental trials, individuals of both sexes were systematically exposed to the scent of a conspecific or heterospecific in a full-factorial design. All trials were recorded using a high-speed overhead camera for subsequent analysis. For the automated detection of 20 anatomical landmarks in our high-framerate videos, we employed DeepLabCut, a deep-learning-based software that allows the automation of precise animal tracking while requiring minimal manual input. We analyzed behavioral patterns in the absence or presence of odor cues. Our integrated approach facilitates a high-throughput analysis of video recordings, reducing the need for a priori knowledge of anticipated behaviors or concerns related to biases introduced by multiple observers. It allows us to identify key differences in the olfactory exploration of the two investigated sister species.

STUDYING ECHINODERM ADHESIVE PROTEIN EVOLUTIONARY HISTORY

Leandro Smacchia[1,2*], Jérôme Delroisse[1,3], Denis Baurain[2], Patrick Flammang[1]

[1] Biology of Marine Organisms and Biomimetics Unit, Research Institute for Biosciences, University of Mons (UMONS), 7000, Mons, Belgium.

[2] Unit of Eukaryotic Phylogenomics, InBioS–PhytoSYSTEMS, University of Liège (ULIEGE), 4000, Liège, Belgium.

[3] Laboratory of Cellular and Molecular Immunology, GIGA Institute, University of Liège, 4000, Liège, Belgium

Poster 53

***Presenting author**, **leandro.smacchia@umons.ac.be**

Keywords: Adhesive proteins, Echinoderms, Phylogeny, Evolution

Biological adhesives are widely used by metazoans. In particular, marine invertebrates produce strong adhesive secretions that allow them to attach to the sea floor, even in intertidal environments characterized by strong current forces. Maintenance of position is not the only ecologically relevant use of marine adhesive secretions, which may also serve food capture, locomotion, building or protection purposes. Because biological adhesives consist mainly of proteins, 'omics technologies have been used extensively to characterize adhesive protein repertoires from marine species. Abundant data have thus been generated over the years, and that is particularly true for echinoderms, especially asteroids.

Our project aims at deciphering the evolutionary history of echinoderm adhesive proteins through different questions. At the class level, what is the correlation between adhesive protein repertoires and sea star ecology and phylogeny? At the phylum level, what are the conserved adhesive proteins whose evolutionary history can be traced across all five echinoderm classes? How did this protein group develop as echinoderms diversified? Finally, from which proteins have the main functional domains of echinoderm adhesive proteins originated? Preliminary results have already been produced for sea stars. Public proteomic, genomic and transcriptomic datasets have been extensively mined to retrieve homologs to adhesive proteins from the reference repertoires of *Asterias rubens* and *Asterina gibbosa*. Numerous adhesive protein homologs have been found throughout the asteroid class. Additionally, an evolutionary framework of the asteroid clade has been established using phylogenomic approaches. The resulting supertree displays a subdivision into what would be three superorders, in accordance with recent literature. Moreover, this tree supports the polyphyletic nature of big traditional orders, as exposed in recently published phylogenies.

The goal of this communication is to present the whole project, including the planned laboratory and bioinformatics experiments, as well as some preliminary results.

INTEGRATED TAXONOMIC-TAPHONOMIC INVESTIGATION OF A COMPLEX LATE PLEISTOCENE MOLLUSC FAUNA: A CASE STUDY FROM ZEEBRUGGE

Michael STEENHUYSE-VANDEVELDE[1,4*], Frank P. WESSELINGH[2,3], Johan VELLEKOOP[1,4], Stijn GOOLAERTS[4]

[1] Department of Earth & Environmental Sciences, Katholieke Universiteit Leuven, Celestijnenlaan 200E, 3001 Heverlee, Belgium.

[2] Naturalis Biodiversity Center, Darwinweg 2, 2333 CR Leiden, The Netherlands.

[3] Faculty of Science and Engineering, Maastricht University, Paul-Henri Spaaklaan 1, 6229 EN Maastricht, The Netherlands

[4] Royal Belgian Institute of Natural Sciences, Vautierstraat 29, 1000 Brussels, Belgium

Poster 54

***Presenting author**, michael.steenhuyse-vandevelde@student.kuleuven.be**

Keywords: Mollusca, Taxonomy, Taphonomy, Pleistocene

Due to the mixed nature of (sub)fossil shelly faunas in coastal regions, it is difficult to reconstruct past environments. Within the Belgian coastal part of the North Sea, the inherent reworking of shelly faunas makes this rather rule than exception. This case study presents a now buried and fossilized mollusc shell fauna found during excavations in the Port of Zeebrugge. The shell layer was sampled in a construction pit at -7.5 mTAW (Belgian reference height) and likely represents Late Pleistocene deposits (+/- 115.000 – 100.000 years ago; exact age under study).

Bivalvia like Macoma balthica, Cerastoderma edule, Donax vittatus and Spisula subtruncata are dominant within this fauna. In today's North Sea, these species are characteristic of marine littoral to upper sublittoral environments. Yet, also material from other environments and ages seemed present, hampering straightforward interpretations. Therefore, detailed taxonomic and taphonomic analysis was undertaken of > 2000 mollusc shells extracted from three samples.

We identified 72 mollusc species, 42 Bivalvia species, and 31 Gastropoda species, and established 6 (tapho)classes and 2 (tapho)subclasses of preservation state, ranging from shells with periostracum up to discoloured, weathered, bioeroded specimens. While some species occur in multiple taphoclasses, others are restricted to one. Our taphonomic analysis helps discriminating autochthonous elements from allochthonous elements (= reworked from older deposits), some up to 50 million year old. The autochthonous part indicates an environment with water depths < 20 m, most probably sand- or mudflats within an estuary or bay.

This study reveals the necessity of an integrated taxonomic – taphonomic approach to correctly interpret the composition and diversity of (sub)fossil mollusc faunas from the North Sea, especially since our shells also place in ongoing climate change research: as indicators of past trends in marine biodiversity or environmental changes and as records for paleotemperature through stable isotopes within the shell material.

IMPACT OF INVASIVE PLANT SPECIES ON WILD BEE CONSERVATION

Clément TOURBEZ[1*], Denis MICHEZ[1]

[1] Laboratory of Zoology, Research Institute for Biosciences, University of Mons, 7000 Mons, Belgium.

Poster 55

***Presenting author**, **clement.tourbez@umons.ac.be**

Keywords: Wild bee conservation, Invasive species, Pollination networks, Bee fitness

The Anthropocene is characterised by a major decline in pollinators, particularly affecting bees. Conversely, on the other side of the mutualism that lies behind the pollination activity, some plant species are taking advantage of anthropogenic activity to expand their distribution. These invasive plant species can modulate plant-pollinator interactions and therefore constitute a disturbance factor for communities. This poster summarises à PhD project that aims to characterise how invasive plant species alters the floral resource profile at the local landscape level, as well as their consequences on bee floral choices and fitness. To answer this question, we will study along an invasion gradient, the summer lilac (*Buddleja davidii*), an invasive species rich in floral resources. We will first describe how the diversity, abundance and quality of floral resources are affected. We will then investigate the repercussions of these changes on the interaction profile of bee species with the plant community using pollination networks. Finally, the consequences on bee fitness will be evaluated via an experimental approach with sentinel bumblebee individuals placed on the sites. In the current context of pollinator decline, the multidisciplinary approach of this project will make it possible to precisely characterise the impact of invasive species and help to define effective conservation strategies.

GLOBAL POPULATION GENOMICS OF AN AGRICULTURAL PEST: INSIGHTS INTO HAPLOTYPE VARIATION AND POTENTIAL DRIVERS OF INVASION

Sam VANBERGEN[1,2*], Steven VAN BELLEGHEM[2], Pablo DESCHEPPER[1], Massimiliano VIRGILIO[1], Marc DE MEYER[1]

[1] Department of Biology, Royal Museum for Central Africa, Leuvensesteenweg 80, 3080, Tervuren, Belgium.

[2] Department of Biology, KU Leuven, Charles Deberiotstraat 32, 3000 Leuven, Belgium.

Poster 56

***Presenting author**, **sam.vanbergen@africamuseum.be**

Keywords: Invasive species, Population genomics, Evolution, Inversion, Structural variation

As a near globally invasive agricultural pest, the oriental fly, *Bactrocera dorsalis* (Diptera, Tephritidae), has posed significant challenges to crop production and food security, particularly in Africa. Understanding the population genetic structure of this fly is crucial to uncovering the mechanisms driving its adaptability and global spread. A genomic dataset has revealed haplotype variation that may provide insights into its invasion success.

Using local PCA, Fst and nucleotide diversity along genomic windows in an Illumina short read resequencing dataset consisting of 500+ individuals, we discovered large haplotypes that cluster individuals in three groups, consistent with large chromosomal inversions.

The minor alleles associated with putative inversions on chromosome 2 and chromosome 4 are widespread but exhibit regionally variable frequencies, being absent in East Asia. The chromosome 2 variant is most common on the Indian subcontinent, recently inferred as the species' most likely origin. Hence, this variation is likely ancestral, predating the recent range expansion in Africa. The chromosome 4 haplotype minor allele distribution aligns with populations historically described as a distinct species, based on phenotypes exhibiting a paler thorax. In addition, mitogenome haplotypes suggest introgression of a sympatric species. To further investigate the origin of these inversions, a resequencing dataset including congeneric species is screened for these variants, testing the possibility of adaptive introgression.

One estimated inversion breakpoint coincides with a hemicentin-like gene on chromosome 2. Hemicentin genes are down-regulated in insect cells infected with polydnaviruses hosted by Braconid parasitoid wasps. We thus speculate that the observed haplotype variation might be adaptive and maintained by balancing selection driven by parasitism. Investigation of this dataset exposes multiple potential mechanisms related to the invasion success of this species, which may serve as a foundation for hypothesis-driven experimental research to pinpoint key genes and their relevance for fitness.

JUMPING GENES IN ANCIENT CRUSTACEANS: OSTRACODA

Yelle VANDENBOER[1*], Fernando RODRIGUEZ[2], Irina ARKHIPOVA[3], Koen MARTENS[1], Isa SCHÖN[1]

[1] Freshwater Biology, OD Nature, Royal Belgian Institute of Natural Sciences, Vautierstraat 29, 1000 Brussels, Belgium.

[2] Thomas H. Gosnell School of Life Sciences, College of Science, Rochester Institute of Technology, Rochester, NY, USA

[3] Marine Biological Laboratory, 7 MBL Street, MA 02543, Woods Hole, USA.

Poster 57

***Presenting author**, **yvandenboer@naturalsciences.be**

Keywords: Ostracods, Transposons, Parthenogenesis, Genomes

Ostracods are microscopic, bivalved crustaceans with the best fossil record of all living arthropods. Their fossil record, starting 450 million years ago, together with a high prevalence of parthenogenetic reproduction and putative ancient asexuality, make non-marine ostracods fascinating evolutionary model organisms. Transposons or jumping genes are components of all metazoan genomes and can have both deleterious and positive effects on their hosts. In the absence of high-quality ostracod reference genomes, we here compare transposon landscapes between two Illumina genome assemblies from the putative ancient asexual *Darwinula stevensoni* and the fully sexual ostracod *Notodromas monacha*. Because homology-based programs are not sensitive enough to detect families of transposable elements (TEs) in species missing from Repbase or Dfam, we used three different pipelines for de novo analyses: REPET, RepeatModeler2 (RM2) and EarlGrey (RM2-based, with automated curation).

TE diversity between the two genomes differed substantially regardless which pipeline was used. In the Illumina assembly of *N. monacha,* LTR retrotransposons stood out with 6.5%, together with some DNA transposons (3.7%), whereas DNA (15.5%), LINE-like (5.9%) and rolling circle Helitron elements (1.5%) were most abundant in the assembly of *D. stevensoni*. Our results on the dominance of DNA- and LINE-like TEs in *D. stevensoni* parallel earlier findings from a partial genomic library and differ from those of other asexuals. TE copies with a low number of nucleotide substitutions, which could indicate active TEs, were only observed with the REPET pipelines in both genomes. TE activity patterns are currently further investigated with dnapipeTE based on Illumina raw sequencing reads.

Although the presented results may underestimate TE abundance, they indicate pronounced differences of the transposon landscapes and diversity between these two ostracod species. Analysis of related species should determine whether the differences are correlated with the reproductive mode or are lineage specific.

STUDY OF THE IMPACT OF ENVIRONMENTAL CHANGES ON WILD BOAR MICROBIOME INVOLVING HEALTH RISKS

Jérôme VANDROMME[1*], Johan MICHAUX[1]

[1] Laboratoire de Génétique de la Conservation, University of Liège, Chemin de la vallée 4, 4000 Liège,Belgique

Poster 58

* **Presenting author, jerome.vandromme@uliege.be**

Keywords: Microbiome, Wild boar, Zoonosis

European wild boar (*Sus scrofa*) populations have risen sharply as a result of climate change or inappropriate hunting management. As a result of this population explosion, the species has been forced to colonise new highly anthropised areas, leading to much more frequent contact with domestic species and humans. However, ungulates (including wild boar) are the animals that host the most pathogens transmissible to humans. Wild boars can host or be affected by numerous zoonotic diseases (brucellosis, tuberculosis, salmonellosis, yersiniosis, etc.). Better knowledge of the circulation of these pathogens among wild boar populations is therefore essential to prevent future threats to public health and that of domestic animals. Little is also known about the risk of an increase in the prevalence of these pathogens as a result of the changes to which wild boar are exposed: change of habitat (and hence diet), increase in densities, increase in contact with humans and domestic animals, etc. Nothing is also known about the relationship between these factors and the diversity of the bacterial microbiota of wild boar, which is so important for the health of individuals.

The aim of our study is to gain a better understanding of the circulation of bacterial communities (commensal and pathogenic) in ten selected areas of Belgium, with contrasting characteristics (wild boar population densities, proximity to livestock, different habitats, etc.) by : 1) developing a non-invasive detection method for pathogenic bacteria 2) studying the impact of environmental changes on the bacterial diversity of wild boar.

GENOMIC APPROACHES TO IMPROVE EX SITU CONSERVATION OF THE TUFTED DEER (*ELAPHODUS CEPHALOPHUS*)

Sam VAN GIESSEN[1*]

[1] A-life, VU University Amsterdam, De Boelelaan 1108, 1081 HZ Amsterdam, The Netherlands.

Poster 59

***Presenting author**, **sam.van.giessen@student.uva.nl**

Keywords: Genomics, Inbreeding, Outbreeding, Conservation

Ex situ populations are crucial to animal reintroduction efforts, yet using captive-bred populations as source stock can risk inbreeding and outbreeding depression. This project aimed to inform the European Endangered Species Program (EEP) of the tufted deer (*Elaphodus cephalophus*) on these problems using whole genome sequencing data. A de novo whole genome and mitogenome assembly were constructed from Oxford Nanopore Technologies (ONT) longread sequences of a tufted deer living in Rotterdam Zoo. To see the possible effects of inbreeding nucleotide diversity was calculated and Runs of Homozygosity (ROHs) were identified on the genome of the tufted deer. To prevent outbreeding depression in future mixing of populations the subspecies was identified and the relative divergence time among available samples of tufted deer were studied. These analyses showed that the individual in Rotterdam Zoo exhibits signs of recent inbreeding: a lot of long ROHs with relatively high background genetic diversity outside of these ROHs. Additionally, the animal is most closely related to the *michianus* subspecies and the phylogeny showed large divergence times between the different samples of tufted deer, supporting the current differentiation of the subspecies in captive breeding programs. All these results inform the EEP of the tufted deer to make informed management decisions ensuring a viable insurance population. This study shows the effectiveness of genomic approaches in *ex situ* conservation efforts.

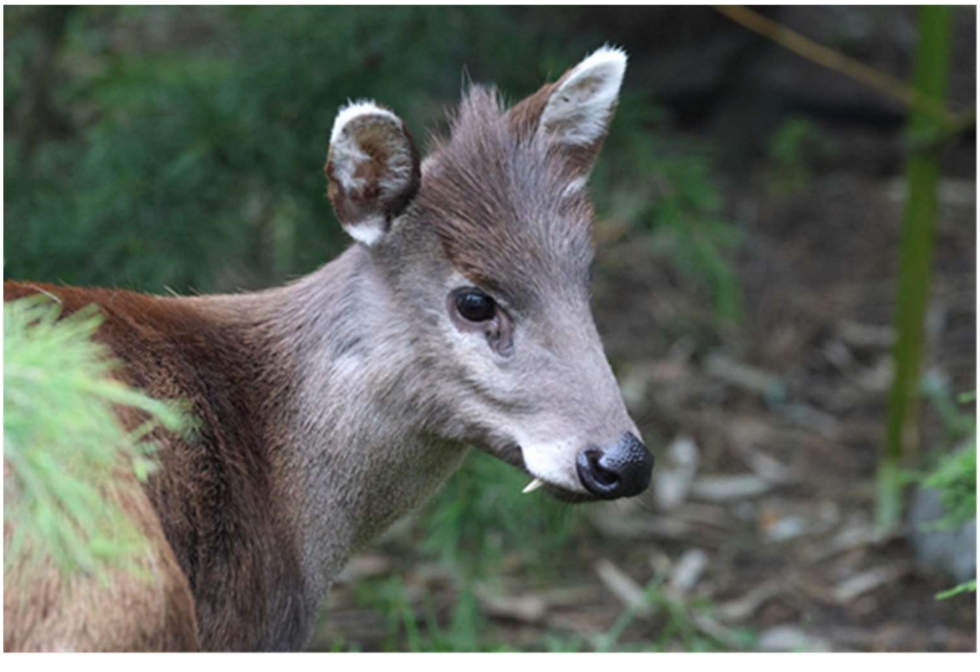


Figure 1: A tufted deer living in Rotterdam Zoo. Photo by Jurian de Brouwer

3D-CALIBRATED MULTI-VIEW HIGH-SPEED VIDEOGRAPHY OF MANOEUVRING BOXFISH

Merel VAN GORP [1], Pim BOUTE [2], Sam VAN WASSENBERGH [1]

[1] Functional Morphology, Department of Biology, University of Antwerp, Universiteitsplein 1, 2610 Antwerpen, Belgium.

[2] Biomimetics, Energy and Sustainability Research Institute Groningen, Faculty of Science and Engineering, University of Groningen, Bernoulliborg, Nijenborgh 9, 9747 AG Groningen, the Netherlands

Poster 60

***Presenting author**, **merel.vangorp@uantwerpen.be**

Keywords: manoeuvring, kinematics, multi-view high-speed videography, 3D tracking.

Boxfish serve as valuable model systems for the bioinspired design of autonomous underwater vehicles, particularly for slow-speed manoeuvring. However, there is a lack of fundamental biomechanical knowledge regarding how boxfish execute their manoeuvres using their five fins. To address this gap, we need information from live boxfish during manoeuvring. The three-dimensional movement paths of their rigid bodies, along with the bilaterally asymmetric actions of their fins, make it challenging to quantify the kinematics of these manoeuvres comprehensively. To tackle this issue, we developed an aquarium setup equipped with eight synchronised cameras for the 3D tracking of both body and fin movements. We captured videos at 200 frames per second from six different viewpoints around the fish in the horizontal plane, as well as from dorsal and ventral perspectives. This was done for two individuals of the boxfish genus *Ostracion* during various manoeuvres. The videos collected will be used to quantify the kinematics of both the body and fins, ultimately enabling us to analyse the dynamics of manoeuvring in great detail.

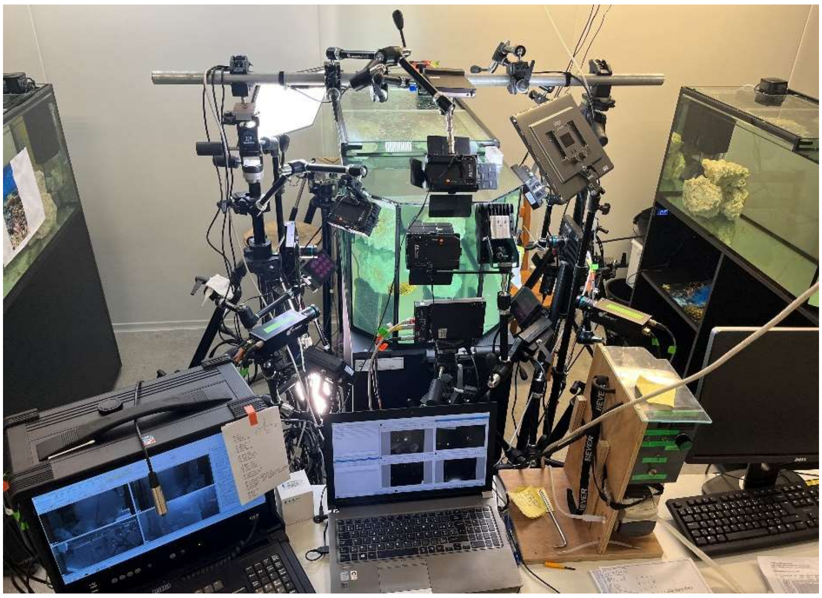


Figure 1: Setup equipped with eight synchronised high-speed cameras

THE WESTERN JACKDAW'S FLIGHT TO THE CITY : A MULTI-DISCIPLINARY APPROACH TO STUDY THE IMPACT OF HUMAN ACTIVITIES ON BIRD POPULATIONS

Margaux VANHUSSEL[1], Fany BROTCORNE[2], Alex THORNTON[3]

[1] Department of Biology, Ecology & Evolution, University of Liège, Place du XX Août, 4000 Liège, Belgium

[2] Department of Biology, Ecology & Evolution, University of Liège, Place du XX Août, 4000 Liège, Belgium

[3]Department of Ecology and Conservation, University of Exeter, Penryn TR10 9FE, UK

Poster 61

***Presenting author**, margaux.vanhussel@doct.uliege.be

Keywords: urban ecology, ornithology

With increasing urbanisation worldwide, many species are compelled to either leave their habitats or adapt to survive. Those that manage to adjust are often categorised as "urban adapters." But do all individuals within an "urban adapter" species truly tolerate and maintain adequate fitness in such heavily human-modified environments? This doctoral research project aims to investigate this question through a multidisciplinary approach, examining behaviour, genetics, cognition, and diet among jackdaw colonies exposed to various types and levels of human activity.

The central hypothesis of this work is that intense urban pressures act as an ecological filter, limiting the dispersal and habitat occupation capacity of jackdaws that cannot efficiently adapt. Through this approach, the project seeks to determine whether urban environments impact specific traits in jackdaws and, if so, to what extent these pressures drive selective adaptations in urban populations. Ultimately, this research intends to improve our understanding of how human activities influence "urban adapter" birds, facilitating the development of more effective management and conservation strategies for these populations.

THE GREEN HEART OF AFRICA, THE LOMAMI PRIMER

Maarten VAN STEENBERGE[1,2]*, Klaas-Douwe B. DIJKSTRA[3], Wilson MAYO ILODIRI[4], Guy Crispin GEMBU[4], Filip VANDELOOK[5], François NGERA[6], Koko BISIMWA[7], Raffael ERNST[8]

[1] Vertebrates Group, OD Taxonomy and Phylogeny, Royal Belgian Institute for Natural Sciences, 1000 Brussels, Belgium.
[2] Centre for Environmental Sciences, Hasselt University, 3500 Hasselt, Belgium.
[3] Naturalis Biodiversity Center, Postbus 9517 2300RA Leiden, the Netherlands.
[4] Centre de Surveillance de la Biodiversité, Faculté des Sciences et Technologies, University of Kisangani, 59303 Kisangani, Democratic Republic of the Congo.
[5] Meise Botanic Garden, 1860 Meise, Belgium.
[6] Centre de Recherche en Sciences Naturelle (CRSN-LWIRO), DS Bukavu, Democratic Republic of the Congo.
[7] Frankfurt Zoological Society, Kindu, Democratic Republic of the Congo.
[8] Zoology, Senckenberg Geselschaft für Naturforschung, 01109 Dresden, Germany.

Poster 62

Presenting author**, **mvansteenberge@naturalsciences.be

Keywords: Capacity building, Congo Basin, Biodiversity monitoring, Taxonomy

The "Green Heart of Africa" initiative aims to bolster sustainable research in the Congo Basin, focusing on biodiversity monitoring and management. Despite being the world's second-largest rainforest and river system, the region remains largely unexplored and reliable biodiversity data is often lacking. As an African-European consortium, we teamed up with the vision of training a new generation of biodiversity experts. Our network includes both academic and governmental institutions, which guarantee the employment of trained experts and the translation of high-quality research into policy. This aligns with the AU-EU innovation agenda (including NaturAfrica) and the implementation of biodiversity credits. The initiative connects expert knowledge with traditional and semi-automated monitoring, including remote sensing. The activities started around Lomami NP, the newest protected area in the DR Congo, created to protect two recently discovered endemic primate species. It is the nation's only park with a buffer zone, and the only one established following consultation with local communities. This huge conservation landscape (30,000km^2) straddles the forest and savanna biomes, and is dissected by the Lomami, a large Congo tributary. The start of the GHoA initiative coincides with the implementation of the park's first management plan, allowing us to immediately embed our activities in an existing conservation framework, thus establishing Lomami NP as a model for future research across the Congo Basin.

Besides monitoring of the park's flagship species, no biodiversity monitoring is currently taking place in Lomami NP. Preliminary explorations in 2013 provided data for the park's establishment. The GHoA team conducted fieldwork in November 2024, which resulted in an updated species list for fishes, reptiles, amphibians and aquatic insects from the southernmost sector of the park. We will present the outcome of this expedition.

SIMULATIONS OF WATER FLOW THROUGH GEOMETRICALLY SIMPLIFIED MODELS OF FILTER-FEEDING MOUTH CAVITIES

Sam VAN WASSENBERGH[1*]

[1] Department of Biology, University of Antwerp, 2610 Antwerpen, Belgium.

Poster 63

***Presenting author**, **sam.vanwassenbergh@uantwerpen.be**

Keywords: Filtration, Fish, Biomimetics, Feeding

Understanding the mechanics of filtration and clogging resistance in filter-feeding fish can pave the way for future designs of fish-inspired filters. One of the model organisms of bio-inspired filtration is the paddlefish, a ram-filter-feeding species. However, the hydrodynamic processes involved in plankton filtration are still not fully understood. When water enters the mouth, it first encounters the plate-like branchial arches arranged in a step-like pattern. Deeper inside slots in between the adjacent branchial arches, gill rakers form a comb-like porous layer. In this study, flow is simulated in morphologically simplified models of mouth cavities, including realistic flow dynamics at the porous layer using Ansys Fluent software. The simulations show that multiple filtration mechanisms are at play: from ricochet filtration at the level of the medial flow passing the branchial arches to both cross-flow and dead-end sieving near the porous layer modeled after the gill rakers. The models also indicated that the rear slots draw in water in significantly different ways and are more likely to become clogged. Further research on models with a more realistic shape and with backwash flows is needed to fully understand the feeding mechanism of paddlefish.

ESTIMATING THE IMPACT OF WIND TURBINES MORTALITY ON THE RED KITE (*MILVUS MILVUS*) POPULATION IN WALLONIA

Arnaud VANSTEENKISTE[1], Arnaud BECKERS[2], Dorothée DENAYER[3], D. Jean-Yves PAQUET[4], Nicolas MAGAIN[1*]

[1] Biologie de l'évolution et de la conservation, UR InBioS, University of Liège, 4000 Liège, Belgium.

[2] CSD Ingénieurs Conseils SA, 5100 Jambes, Belgium.

[3] SEED, Etude et gestion du vivant. University of Liège, 6700 Arlon, Belgium.

[4] Natagora, 5000 Namur, Belgium.

Poster 64

Presenting author**, **Nicolas.magain@uliege.be

Keywords: Birds, PVA, Demographics, Renewable energy

The Red Kite (*Milvus milvus*) is a European species of bird of prey, which, after sharp decline, showed rapid growth in Europe and Wallonia over the past two decades. The Walloon population is very unevenly distributed, with high densities in East Ardenne, while the species is almost absent from the Western half. Wind turbines are a cause of mortality for birds including the Red Kite (*Milvus milvus*). However, the actual impact of this mortality on populations remains poorly understood. We have estimated present, past and future mortality of wind turbines on Red Kites in Wallonia. We estimated mortality by searching two wind parks for carcasses for one year. We then generalized these results to Wallonia based on number of wind turbines and Red Kite densities. For 2023, we estimate a mortality of ca. 20 birds in Wallonia, which represents 1.1% of an estimated population of ca. 1900 birds. We then estimated past mortality and modelled future impact of wind turbines based on several scenarios of wind energy development. We inferred Population Viability Analyses using EolPop. Due to the species' current high growth rates, the Walloon population does not appear threatened in any of the wind energy development scenarios considered. However, wind turbines expansion will have an impact on the overall size of the population, as well as on the number of fatalities. We advocate for continued monitoring of the species to detect future trends in the population, as well as further data gathering to improve models. High uncertainties remain, including on how the species will adapt to new habitats, and how current favorable habitats will change in the future. The Red Kite also represents a special case because of its current high growth rate, and more sensitive species (bats, black stork, harriers…) should also be studied.

IS ANTARCTICA AN EVOLUTIONARY INCUBATOR? PHYLOGENETIC COMPARATIVE STUDY OF THE AMPHIPOD FAMILY IPHIMEDIIDAE ON THE ANTARCTIC SHELF

Marie L. VERHEYE[1,2*], Anthony HERREL[3], Gilles LEPOINT[1], Pablo MARTINEZ-SOAREZ[1,2], Isa SCHÖN[4], Bruno FREDERICH[2]

[1] Laboratory of Trophic and Isotopes Ecology (LETIS), University of Liège, 4000 Liège, Belgium.

[2] Laboratory of Evolutionary Ecology (LEE), University of Liège, 4000 Liège, Belgium.

[3] Adaptive Mechanisms and Evolution (UMR 7179 MECADEV), Muséum National d'Histoire Naturelle, 75005 Paris, France.

[4] Operational Directorate Natural Environment (OD Nature), Royal Belgian Institute of Natural Sciences, 1000 Bruxelles, Belgium.

Poster 65

***Presenting author, mverheye@uliege.be**

Keywords: Macroevolution, Morphometrics, Diversification, Southern Ocean

Around 40 million years ago, Antarctica's geographic isolation led to a dramatic cooling of its marine shelf, causing many lineages to go extinct whilst others adapted and flourished. Among the successful ones is the amphipod family Iphimediidae. Here, we apply advanced phylogenetic, comparative, and morphometric methods to explore the evolutionary processes which generated the exceptional diversity of this clade. To this purpose, three types of data were collected: (1) a novel phylogeny of the family was reconstructed from a multigene molecular dataset, (2) 3D shape data were obtained by applying geometric morphometric methods on micro-CT scans, and (3) stable isotope ratios ($\delta^{13}C$ and $\delta^{15}N$) were measured and used as proxies for trophic ecology. First, possible evolutionary correlations between mouthpart shapes and stable isotope ratios were examined. Significant correlations suggest that mouthpart shapes are adapted to the food source. Second, species boundaries were investigated using a combination of DNA-based delimitation methods and detailed morphological/morphometric analyses, revealing that Iphimediidae species diversity is greatly underestimated. Most described species were found to be complexes of multiple, morphologically similar species. Finally, changes in lineage diversification rates were explored alongside the evolution of morphological traits. Late bursts of lineage diversification (appr. 7-3 Mya) combined with a late partitioning of mouthparts' shape diversity might result from the invasion of novel ecological niches. Plio-Pleistocene glacial cycles, which have been hypothesized to act as a diversity pump, might also have promoted such late diversification events in Antarctic iphimediids. This integrative approach, applied here for the first time in Antarctic invertebrates, enhances our understanding of the evolutionary dynamics shaping Antarctic shelf biodiversity.

CORAL DWELLING DECAPODS IN THE FACE OF HOST BLEACHING AND HABITAT LOSS

Killian VER HOEYE[1]*, Laetitia HEDOUIN[2], Guillaume CAULIER[1]

[1] Biology of Marine Organisms and Biomimetics Unit, Research Institute for Biosciences, University of Mons, 7000 Mons, Belgium.

[2] EPHE-CNRS-UPVD, USR 3278 CRIOBE, 98729 Papetoai, French Polynesia.

Poster 66

***Presenting author**, **killian.verhoeye@umons.ac.be**

Keywords: Coral reefs, Crustaceans, Invertebrates, Symbiosis

Coral reefs are under growing threats from different (a)biotic causes, notably causing bleaching (*i.e.*, the loss of endosymbiotic zooxanthellae from coral tissue) that may lead to coral death. While much research has focused on corals' relationships with zooxanthellae to understand this phenomenon, corals also host numerous ectosymbiotic organisms that are largely understudied. Without these partners, corals may suffer from excess of stress due to diseases, predation, and bleaching. But what happens to this symbiotic community if their coral host dies or bleaches? The goal of this study is to assess the adaptive responses of ectosymbiotic decapods associated with *Pocillopora* and *Acropora* corals as they experience decline.

The scientific strategy involved measuring decapod abundance, diversity, reproduction rate, and migration patterns across healthy, bleached, and dead corals. Additionally, decapod survival and stress levels were monitored under three conditions of host separation — physical contact, chemical contact, and total separation — to explore any chemical dependency on their host that might explain potential declines in decapod populations.

The results indicate that decapods from the two host species exhibit different adaptive strategies in response to coral decline. Symbiotic decapods from *Pocillopora* show higher stress levels when in chemical contact with their host than when totally separated, suggesting that host stress in the absence of symbionts may affect ectosymbionts in the same aquarium, and that these decapods are not chemically dependent on their host. These individuals also exhibit low abundance, diversity, and reproduction rates, along with high emigration when their host begins to bleach. In contrast, bleaching of *Acropora* corals appears to have little impact on the associated decapod communities until the coral dies, at which time the decapods disappear.

In the context of coral reef degradation, understanding how these essential symbionts respond to stress becomes crucial to better assess the potential loss of coral-associated biodiversity.

NOSES FOR NATURE: SUPPLY AND DEMAND FOR ECOLOGICAL DETECTION DOGS IN FLANDERS

Hilde VERVAECKE[1]*, Ellen VAN KRUNKELSVEN[2], Kristof BAERT[3], Arno THOMAES[3]

[1] Agro-& Biotechnology, Salto research group, Odisee University of Applied Sciences, 9100 Sint-Niklaas, Belgium.

[2] Quercus, 1541 Herne, Belgium.

[3] Research Institute for Nature and Forest (INBO), 1000 Brussels, Belgium.

Poster 67

***Presenting author, hilde.vervaecke@odisee.be**

Keywords: Detection dogs, Monitoring

This study investigates the role of ecological detection dogs in Flanders, aiming to explore the needs within this emerging field, as well as the current state of supply and demand in this sector. By conducting interviews with key organisations, we assessed current needs for detection dogs for ecological monitoring. We engaged with various Flemish organisations to gauge their awareness and application of detection dogs for monitoring. To further drive collaboration, we hosted a networking event uniting the “demand” - nature organisations, government agencies, researchers - and the “supply” - dog trainers and handlers - fostering direct communication and sparking interest in future projects. These interviews and conversations revealed a growing interest in ecological detection dogs, and a current lack of understanding about their potential applications and limitations. On the other hand, the dog trainers and volunteers prioritize the need for coordination and quality control. We conclude that the development of the potential for the ecological detection dog sector in Flanders requires enhanced collaboration, coordination, certification, government support, and regular networking opportunities. Research on the complementarity of different detection methods is also needed. To bridge the information gap, a website was created offering information on ecological detection dogs to promote partnerships and knowledge sharing across the sector. Further, a strategic initiative was launched by the INBO to coordinate, filter and assist in the link between supply and demand in the sector. Ecological detection dogs present a promising tool for conservation and biodiversity monitoring, making the development of the Flemish expertise an asset for future ecological management. By fostering partnerships, we can advance the use of detection dogs in protecting Flanders' biodiversity.

UNRAVELING THE GENE REGULATORY NETWORKS OF PREDATOR-INDUCED DEVELOPMENTAL PLASTICITY WITHIN AND ACROSS GENERATIONS IN *DAPHNIA MAGNA*

Zorimar VILELLA-PACHECO[1]*, Steven VAN BELLEGHEM[1]

[1] Department of Biology, KU Leuven, 3000 Leuven, Belgium.

Poster 68

***Presenting author**, **zorimar.vilella-pacheco@kuleuven.be**

Keywords: Developmental plasticity, Chromatin accessibility, Gene regulation

The dynamic interplay between genetic and environmental factors has long captivated biologists aiming to understand phenotypic variation across environments. Developmental plasticity is a remarkable feature where a genotype may display multiple phenotypes in response to environmental factors, without changes to the DNA sequence. Moreover, developmental plasticity can occur through developmental changes within a single generation, termed within-generation plasticity (WGP), or involve environmental influences on one generation affecting the phenotypic traits of subsequent non-exposed generations, known as transgenerational plasticity (TGP). *Daphnia magna* is an ideal model for studying developmental plasticity, as its well-documented environmental responses and asexual reproduction enable clear separation of genetic and environmental effects. Notably, *Daphnia* adjust their morphology, behavior, and life history traits in response to predator cues, showing plasticity within and across generations. Recent research has highlighted gene expression changes during plastic responses, yet the gene regulatory mechanisms and how these connect into gene regulatory networks (GRNs) driving WGP and TGP remains largely unexplored. By combining traditional gene expression assays (RNA-seq) with Assays for Transposase-Accessible Chromatin sequencing (ATAC-seq) to assess gene regulation, this project will investigate the GRNs that control plastic responses to predator cues. Specifically, the project aims to (1) characterize regulatory mechanisms involved in WGP, (2) examine their persistence across generations in TGP, (3) explore small RNAs' role in epigenetic transmission, and (4) compare WGP and TGP. By leveraging *Daphnia*'s clonal reproduction, short generational cycles, and excellent standing as an ecological model, this study seeks to provide new insights into the epigenetic foundations of plastic development.

PRIDE LANDS IN PERIL: FORECASTING LION HABITATS ACROSS CHANGING AFRICAN LANDSCAPES

Fleur VISSER[1,2*], Christine N. MEYNARD[3], Johan R. MICHAUX[1]

[1] Laboratoire de génétique de la conservation, Institut de Botanique, University of Liège, 4000 Liège, Belgium.

[2] Department of Zoology and Entomology, Mammal Research Institute, University of Pretoria, 0028 Hatfield, South Africa.

[3] CBGP, INRAE, CIRAD, Institut Agro, IRD, University of Montpellier, 3400 Montpellier, France.

Poster 69

***Presenting author, fleur.visser@outlook.fr**

Keywords: Climate change, Fragmentation, *Panthera leo*, Species distribution models

The African lion (*Panthera leo*) has experienced significant range reduction due to habitat fragmentation, particularly in West and Central Africa. This study aims to model the potential distribution of lions in these regions under past, present, and future environmental conditions using Species Distribution Models (SDMs).

We utilized occurrence data from 1900-1990 and environmental variables from the CHELSA database to calibrate our models and generate a baseline map of potential distribution. We then projected into current (1981-2010) and future (2041-2070) climate conditions to assess potential shifts in habitat suitability. Two Global Circulation Models (IPSL-CM6A-LR and GFDL-ESM4) and two Shared Socioeconomic Pathways (SSP370 and SSP585) were considered to account for climate change scenarios.

Our preliminary results provide insights into the historical, current, and potential future distribution of suitable habitat for lions in West and Central Africa. The models highlight areas of high habitat suitability and potential range shifts under different climate change scenarios. These findings were overlaid with protected area and land use datasets to assess the implications for lion conservation.

This study contributes to our understanding of how climate change and habitat fragmentation may impact lion distribution in West and Central Africa. The results can inform evidence-based conservation strategies and policy decisions aimed at protecting lions and other endangered species in increasingly fragmented landscapes.

EVOLUTION IN THE TIDES: UNRAVELLING ADAPTIVE STRATEGIES IN *POGONUS CHALCEUS* BEETLES

Elke VOETEN[1]*, Maria MADRID-RESTREPO[1], Frederik HENDRICKX[2], Steven VAN BELLEGHEM[1]

[1] Eco-Evolutionary Genomics Lab, KU Leuven, 3000 Leuven, Belgium.

[2] Royal Belgian Institute of Natural Sciences, 1000 Brussels, Belgium.

Poster 70

***Presenting author**, **elke.voeten@student.kuleuven.be**

Keywords: Behavioural adaptation, Divergence, Evolutionary genomics, Demography

The saltmarsh beetle, *Pogonus chalceus*, provides an intriguing model for investigating rapid adaptation mechanisms in the presence of gene flow. This species exhibits two distinct ecotypes adapted to different hydrological regimes: short-winged individuals occur in daily inundated tidal salt marshes, while long-winged individuals occupy seasonally inundated habitats. Despite their proximity, which can be as close as 10-20m, these ecotypes maintain genetic differentiation through a combination of behavioural and genetic barriers.

To further explore the genetic and behavioural basis of this adaptation, beetles were sampled in southern Spain in September 2024, a region where we find the most distinct short and long-winged ecotypes, with no apparent overlap between them. We then explored behavioural and genomic elements between these ecotypes to identify barriers for reproductive isolation. First, behavioural experiments assessed both individual and population-level responses to inundation, a primary selective pressure driving ecotype differentiation. In response to inundation, we observed that long-winged beetles exhibit increased escape behaviour and generally display higher levels of activity compared to short-winged individuals. We argue that these behaviours contribute to maintaining reproductive barriers between the ecotypes despite their close proximity and ample opportunity for interbreeding. Second, to investigate the evolutionary history of *P. chalceus*, a Multiple Sequentially Markovian Coalescent (MSMC) analysis was performed on historical data from multiple European Atlantic coast localities and different parts of their genome, inferring past population sizes and possible admixture histories.

Our research is providing valuable insights into the complex interaction between genetic and ecological factors shaping rapid adaptation and evolution in this species.

TRAIT PLASTICITY OF MARINE PHYTOPLANKTON IN *SYNECHOCOCCUS SP.* IN RESPONSE TO LIGHT AND THERMAL VARIATIONS

Laura WILLAM[1*], Arunima SIDKER[2], Frédérik DE LAENDER[2,3]

[1] Interaction Ecology and Global Change Department, University of Mons, 7000 Mons, Belgium.

[2] Biology Department, Research Unit in Environmental and Evolutionary Biology (URBE), Institute of Life, Earth and Environment (ILEE), University of Namur (UNamur), 5000 Namur, Belgium.

[3] Namur Institute for Complex Systems (naXys), 5000 Namur, Belgium.

Poster 71

***Presenting author**, **Laura.WILLAM@student.umons.ac.be**

Keywords: Cyanobacteria, Phenotypic Plasticity, Environmental stress

Marine and coastal ecosystems face significant threats due to a rapidly changing climate, in forms of temperature fluctuations and destabilization of water column stratification. These variations in temperature and light exert strong pressure on the population dynamics of marine organisms and consequently on the balance of the ecosystem. In order to cope, shifting their geographical distribution towards higher latitudes could be a survival mechanism, however, their ability to adapt to new conditions could be limited by the imprint of their original environment. In this context, the study of rapid adaptive responses via phenotypic plasticity is crucial for understanding the evolutionary mechanisms of marine organisms.

In this study, we assessed the phenotypic plasticity of two *Synechococcus* strains, a key species for marine ecosystems belonging to the cyanobacteria. The selected strains had different habitats of origins, one from the Atlantic Ocean and another from the Indian Ocean and were exposed for 10 days to a range of environmental conditions (high/low light combined with four different temperatures). Comparison of the growth rates and variation in trait responses revealed species-specific patterns in coping with combined light and temperature stress.

The results of this research could help to improve our understanding of the short-term evolutionary adjustments of the phytoplankton population and highlight the importance of phenotypic plasticity in response to environmental stress.

UNRAVELING THE INTERPLAY OF GENETIC AND NONGENETIC TRAIT VARIATION IN RESPONSE TO GEOGRAPHIC MOSAICS OF STRESSORS

Kristina YEFIMAK[1]*

[1] Biology Department, KU Leuven, 3000, Leuven, Belgium.

Poster 72

***Presenting author**, **kristina.yefimak@gmail.com**

Keywords: Microbiome, Daphnia, Pesticide, Metagenomics

The impact of global change, including land-use changes such as agricultural intensification (especially pesticide use and fish stocks), is pervasive and affects all biological levels. In addition, natural populations and communities are increasingly threatened by a combination of global change stressors that can amplify each other's negative effects. There is, however, an increasingly influential understanding that the microbiome plays a crucial role in shaping host tolerance to such stressors. These microbial communities are organized into metacommunities. Both host metapopulations and microbial metacommunities are assembled through an interaction of local and regional processes, while they interact at different scales in time and space. This provides an important, but largely ignored, spatial aspect of host-microbiome interactions. We hypothesize that this contributes to spatial patterns of host tolerance, which in turn determine patterns of species adaptation and sorting along environmental gradients. This research question translates into specific objectives that we will develop using the water flea *Daphnia magna* and its microbiome in a natural zooplankton metacommunity. This PhD will test the hypothesis that genetic differentiation, phenotypic plasticity and microbiome-induced plasticity act on *Daphnia* tolerance in response to multiple stressors in a natural landscape. We will use landscape metagenomics to characterize the metagenomic structure of the free-living bacterioplankton of several ponds, as well as the microbiome communities of the *Daphnia* found in these ponds. More specifically, we will test the role of the microbiome in shaping stress-induced changes in phenotypic plasticity and adaptation by performing reciprocal microbiome transplantation experiments.

Index of Attendees

AKBAL KESKIN	Sezgi	VUB	sezgi.akbal@vub.be
ANDRIES	Tim	UAntwerpen	tim.andries@uantwerpen.be
ANSELMO	Abigaël	CRA-W	a.anselmo@cra.wallonie.be
AYOUB-LAMBIN	Sarah	UNamur	sarah.ayoub-lambin@student.uclouvain.be
AZAMA SHALIE R.	Théo	UNamur	theo.asr@hotmail.com
BALLÓN B.	Roxana	UvA)	roxana.ballon@live.nl
BAYAERT	Wendy-S.	UMONS	wendy-shirley.bayaert@umons.ac.be
BEAUMARIAGE	Anaïs	ULiège	anais.beaumariage@gmail.com
BÉLIK	Justine	UNamur	justine.belik@unamur.be
BENBACHIR	Mohammed	ULB	mohammed.benbachir@ulb.be
BENREZKALLAH	Jordan	UMONS	jordan.benrezkallah@umons.ac.be
BERGACKER	Stephen	ULB	stephen.bergacker@ulb.be
BERINGS	Wouter	KU Leuven	wouter.berings@student.kuleuven.be
BISSCHOP	Karen	KU Leuven	karen.bisschop@kuleuven.be
BOERMAN	Sophie	KU Leuven	sophie.boerman@kuleuven.be
BOOT	Max	UvA	maxboot98@gmail.com
BOSSIROY	Estelle	UMONS	estelle.bossiroy@umons.ac.be
BOYEN	Jens	UAntwerpen	jens.boyen@uantwerpen.be
BRANDL	Stefan	UCLouvain	stefan.brandl@uclouvain.be
BRAU	Thomas	UMons	thomas.brau@student.umons.ac.be
BURATTO	Noémie	UNamur	noemie.buratto@unamur.be
BÜYÜKGÜNER	Tuana	VUB	tuanabuyukguner@gmail.com
CADONICI	Davide	ULiège	david3cado@gmai.com
CALLAERTS	Jonas	KU Leuven	jonas.callaerts@student.kuleuven.be
CAMACHO G.	Julia	UAntwerpen	julia.camachogarcia@uantwerpen.be
CAMMERS	Louna	UMONS	louna.cammers@hotmail.com
CAMPISI	Julien	ULiège	Julien.campisi@student.uliege.be
CAMPUZANO J.	Francisco B.	UAntwerpen	curro.campuzanojimenez@uantwerpen.be
CARNAC	Enora	ULiège	enora.carnac@student.uliege.be
CASTIAUX	Mabel	UMONS	mabel_castiaux@hotmail.com
CAULIER	Guillaume	UMONS	guillaume.caulier@umons.ac.be
CEJAS	Diego	UMONS	denis.michez@umons.ac.be
CHACON-H.	Andrea	Agro-Bio Tech	achacon@uliege.be
CHEVALIER	Mélusine	UNamur	chevaliermelusine@gmail.com
COCHENILLE	Thomas	UMONS	thomas.cochenille@student.umons.ac.be
CORNET	Sarah	UNamur	sarcor236@gmail.com
CORNET	Victor	ULiège	victor.gorfou@gmail.com
COSA	Florian	UMONS	Florian.COSA@student.umons.ac.be
DE KEYZER	Els	UAntwerpen	els.dekeyzer@uantwerpen.be
DE KNOP	Cannelle	UMONS	Cannelledk@gmail.com
DE MANINCOR	Natasha	UMONS	natasha.demanincor@umons.ac.be
DE TANDT	Bastien	ULB	bastien.de.tandt@ulb.be
DEBOURCES	Maxime	UNamur	maxime.debources@student.unamur.be

DEBRUYN	Gerben	Ghent University	gerben.debruyn@ugent.be
DECAESTECKER	Ellen	KU Leuven	Ellen.Decaestecker@kuleuven.be
DECOUX	Benjamin	UMONS	Benjamin.DECOUX@student.umons.ac.be
DELROISSE	Jérôme	UMONS	jerome.delroisse@umons.ac.be
DEMOULIN	Ludivine	UMONS	200943@umons.ac.be
DENNIS	Alice	UNamur	alice.dennis@unamur.be
DENOËL	Mathieu	ULiège	Mathieu.Denoel@uliege.be
DEVIS	Max	VUB	Max.Wim.J.Devis@vub.be
DIMOPOULOS	Alexia	ULB	alexia.dimopoulos@ulb.be
DOGNIEZ	Martin	ULiège	martin.dogniez@uliege.com
DONOUGH	Nichole S.-L.	KU Leuven	conny.coeckelberghs@kuleuven.be
DORIO	Luca	UMONS	Luca.DORIO@umons.ac.be
DROSSART	Pierrot	ULiège	pierrotdrossart@gmail.com
DUPONT	Deborah W.E.	RBIN	deborah.dupont.valcy@gmail.com
DURET	Clément	ULiège	clement.duret@uliege.be
DUTHOO	Emilie	UMONS	emilie.duthoo@umons.ac.be
ECHE	Louise	ULiège	louise.eche@uliege.be
ESKE	Annika	VLIZ	annika.eske@vliz.be
FIEVET	Manon	UMONS	Manon.FIEVET2@umons.ac.be
FIORDALISO	William	UMons	william.fiordaliso@umons.ac.be
FLAMINIO	Simone	UMONS	simone.flaminio@umons.ac.be
FLAMMANG	Patrick	UMONS	Patrick.Flammang@umons.ac.be
FLANDROIT	Antoine	UMONS	antoineflandroit@hotmail.com
FOUCTEAU	Mathilde	LIST	mathilde.foucteau@list.lu
FREDERICH	Bruno	ULiège	bruno.frederich@uliege.be
FREY	Romane	ULiège	romane.frey@uliege.be
GANTE	Hugo	KU Leuven	hugo.gante@kuleuven.be
GASPARINI	Morena	KU Leuven	morena.gasparini@student.kuleuven.be
GEERTS	Manon	KU Leuven	manon.geerts@kuleuven.be
GENAUX	Sophie	Umons	Sophie.GENAUX@student.umons.ac.be
GENNARI	Sinji	ULiège	lassah@hotmail.be
GENNAUX	Sébastien	UMONS	535070@umons.ac.be
GÉRARD	Maxence	UMons	maxence.gerard@umons.ac.be
GESLAIN	Enora	KU Leuven	enora.geslain@kuleuven.be
GHISBAIN	Guillaume	UMONS	guillaume.ghisbain@umons.ac.be
GILBERT	François	UCLouvain	francois.gilbert@student.uclouvain.be
GOEDE	Nicole	KU Leuven	nicole.goede@kuleuven.be
GOOLAERTS	Stijn	RBIN	sgoolaerts@naturalsciences.be
GRESHAM	Sophie	UAntwerpen	sophie.gresham@uantwerpen.be
HAANE	Joyce	Radboud Un.	jjhaane@home.nl
HABLÜTZEL	Pascal	VLIZ	pascal.hablutzel@vliz.be
HAMIDOVIC	Alisa	UCLouvain	hamidovicalisa@gmail.com
HANOT	Léo	UMONS	Leo.Hanot@student.umons.ac.be
HELEVEN	Martijn	UHasselt	martijn.heleven@uhasselt.be
HERRERA-MESÍAS	Fernanda	FFF	Fernanda.Herrera@ext.mnhn.lu
HÉTRU	Julie	UNamur	julie.hetru@gmail.com

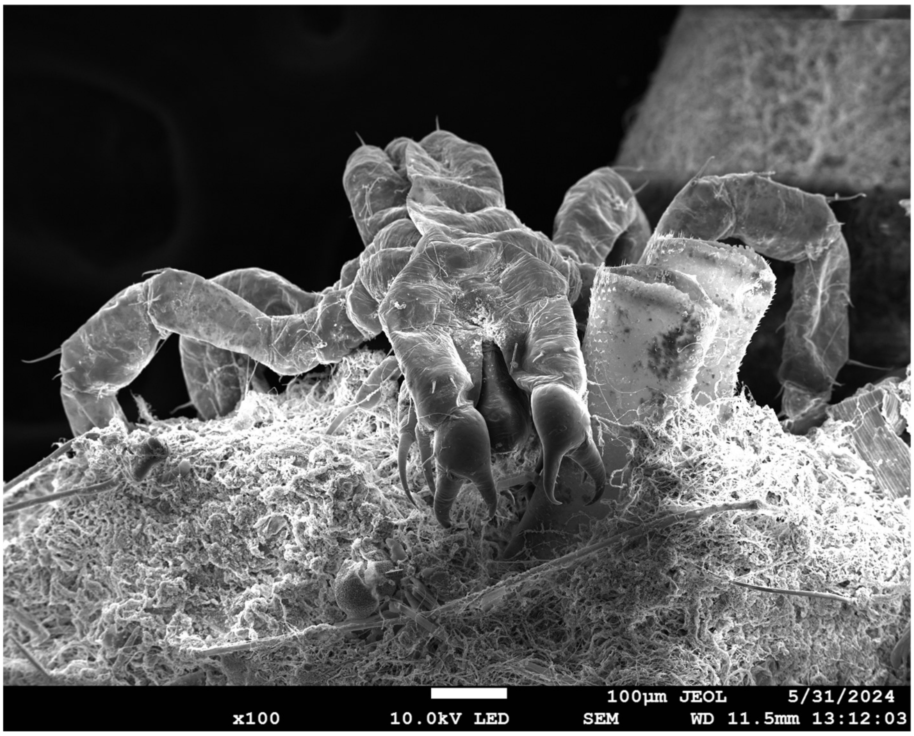
HILDEBRANDT	Frida	U. Konstanz	frida.hildebrandt@uni-konstanz.de
HILL	Alexander	KU Leuven	alexander.hill@student.kuleuven.be
INDESTEGE	Siebe	UHasselt	siebe.indestege@uhasselt.be
JACQUET	Maxence	UCL	maxence.jacquet@student.uclouvain.be
JANMAAT	Karline	IBED	K.R.L.Janmaat@uva.nl
JARADIN	Philippe	UMONS	philippejaradin@student.umons.ac.be
JOLY	Martin	UMONS	Martin.JOLY@student.umons.ac.be
JORISSEN	Sarah	KU Leuven	sarah.jorissen@kuleuven.be
JORISSEN	Cas	UAntwerpen	Cas.Jorissen@uantwerpen.be
JUSTINE	Dewaele	UMONS	justine.dewaele@umons.ac.be
KAROULIS	Christos	UvA	christos.karoulis@stuident.uva.nl
KAUFFMANN	Bob	UHasselt	bob.kauffmann@uhasselt.be
KIGGEN	Aaron	KU Leuven	aaron.kiggen@kuleuven.be
KIM	Elise	UMONS	elise.kim@student.umons.ac.be
KOCHZIUS	Marc	VUB	marc.kochzius@vub.be
KOURTIDIS	Alexandros	KU Leuven	conny.coeckelberghs@kuleuven.be
KOURTIDIS	Argyrios	Ghent Un.	argiriskourtidis@gmail.com
KUYPERS	Wim	UHasselt	wimkuypers@hotmail.com
LABOURY	Salomé	ULiège	S.Laboury@uliege.be
LADURNER	Peter	U. of Innsbruck	peter.ladurner@uibk.ac.at
LASSANCE	Jean-Marc	ULiège	jmlassance@uliege.be
LEBOURGEOIS	Solène	UMONS	210137@umons.ac.be
LECLERCQ	Sylvain	UNamur	sylvain.leclercq99@gmail.com
LECONTE	Clara	UMONS	Clara.LECONTE@student.umons.ac.be
LECOQUIERRE	Ninon	VUB	lecoquierre.ninon@ulb.be
LEMAIRE	Némo	UMONS	nemo.lemaire@student.umons.ac.be
LEPOINT	Gilles	ULiège	g.Lepoint@uliege.be
LESCOT	Sarah	UMONS	sarah.lescot@umons.ac.be
LIENARD	Marjorie	ULiège	marjorie.lienard@uliege.be
LIÉNARD	Alaïs	U. Paris 13	alais.lienard@gmail.com
LOURTIE	Alexia	UMONS	Alexia.LOURTIE@umons.ac.be
MADRID	Maria	KU Leuven	maria.madrid@kuleuven.be
MAGAIN	Nicolas	ULiège	nicolas.magain@uliege.be
MALICE	Louise	UNamur	malouliceise@gmail.com
MALLEFET	Jerome	UCLouvain	jerome.mallefet@uclouvain.be
MALLET	Christophe	UMONS	cmallet@naturalsciences.be
MANCUSI	Joseph	UvA	joseph.mancusi@student.uva.nl
MANIQUET	Héloïse	ULiège	heloise.maniquet@student.uliege.be
MARTIN	Norah	UMons	220306@umons.ac.be
MARTIN	Ulrich	UCLouvain	ulrich.martin@uclouvain.be
MARTOGLIO	Justine	Agro-Bio Tech	justine.martoglio@uliege.be
MATTSSON	Bodil	UMONS	bodil.mattsson@umons.ac.be
MEEUS	Michaël	UAntwerpen	michael.meeus@uantwerpen.be
MERGEN	Patricia	RMCA	Patricia.Mergen@plantentuinmeise.be
MERTENS	Géraldine	RBIN	gmertens@naturalsciences.be
MICHEL	Loic	ULiège	loic.michel@uliege.be
MICHEZ	Denis	UMONS	denis.michez@umons.ac.be
MINGUET	Caroline	UAntwerpen	carolinminguet@hotmail.com

MISSAWI	Omayma	UNamur	omayma.missawi@unamur.be
MITTELHEISER	Laurent	ULiège	lmittelheiser@uliege.be
MULLENS	Nele	UAntwerpen	nele.mullens@uantwerpen.be
MUSSOI	Lisa	UMONS	Lisa.mussoi@umons.ac.be
NADEAU	Nicola	U. of Sheffield	n.nadeau@sheffield.ac.uk
NAVEAUX	Alice	UMONS	Alice.NAVEAUX@student.umons.ac.be
NEELS	Nicolas	UMONS	170962@umons.ac.be
NICOLAÏ	Michaël	UGent	michael.nicolai@ugent.be
NONCLERCQ	Youri	UMONS	youri.nonclercq@umons.ac.be
ODY	Jessica	UNamur	jessica.ody@unamur.be
OP'T ROODT	Lode	VUB	Lode.opt.Roodt@VUB.be
PAULET	Maïlys	UMONS	Mailys.PAULET@student.umons.ac.be
PAULET	Lauralyne	UMONS	Lauralyne.PAULET@student.umons.ac.be
POIRIER	Léa	UMONS	lea.poirier@umons.ac.be
PUGLIESE	Carla	UMONS	Carla.pugliese16@gmail.com
RAVELOHASINA	Helga	ULiège	helga.ravelohasina@doct.uliege.be
REVERTE SAIZ	Sara	UMONS	sara.revertesaiz@umons.ac.be
REYES-PAJUELO	Jhoe	UHasselt	jhoe.reyes@uhasselt.be
RIGAUT	Blandine	Umons	220226@umons.ac.be
ROMEDENNE	Corentin	UNamur	coco112@hotmail.be
ROSA	Paolo	UMONS	paolo.rosa@umons.ac.be
RUHLAND	Fanny	ULiège	fanny.ruhland@uliege.be
SALMON	Lorie	UMONS	lorie.salmon.12@gmail.com
SALOMON	Luca	ULiège	luca.salomon@uliege.be
SANTERRE	Rémi	UMONS	remi.santerre@umons.ac.be
SCHMIDLIN	Sarah	VLIZ	sarah.schmidlin@vliz.be
SCHOLL	Michael	ULiège	michael.scholl@uliege.be
SELINI	Anastasia	UAntwerpen	anastacia.selini@gmail.com
SENTIL	Ahlam	UMONS	ahlam.sentil@gmail.com
SILVESTRE	Frédéric	UNamur	frederic.silvestre@unamur.be
SION	Anaïs	Agro-Bio Tech	anais.sion@doct.uliege.be
SMACCHIA	Leandro	ULiège	leandro.smacchia@umons.ac.be
SNIJDER	Yke	Utrecht U.	wysnijder@gmail.com
STEENHUYSE-V.	Michael	KU Leuven	michael.steenhuyse@student.kuleuven.be
TEUBEN	Aurora	UvA	aurora.teuben@gmail.com
THORÉ	Eli	UNamur	eli.thore@unamur.be
TOMSIN	Imke	UHasselt	imke.tomsin@uhasselt.be
TOPIC	Martina	UHasselt	martina.topic@uhasselt.be
TOUGERON	Kévin	UMONS	kevin.tougeron@umons.ac.be
TOURBEZ	Clément	UMONS	clement.tourbez@umons.ac.be
UKLEJA-CHABROS	Ignacy	KU Leuven	ignacyuklejachabros@gmail.com
VALADON	Cynthia	UvA	ct.valadon@gmail.com
VAN BELLEGHEM	Steven	KU Leuven	steven.vanbelleghem@kuleuven.be
VAN DAMME	Arthur	ULiège	arthur.vandamme@uliege.be
VAN DE POL	Iris	RIBES	iris.vandepol@ru.nl
VAN DEN ABEELE	Jean	UMONS	220097@umons.ac.be
VAN DEN BROECK	Mira	UAntwerpen	mira.vandenbroeck@uanwterpen.be
VAN DER BIJ	Pascal	KU Leuven	pascal.vanderbij@student.kuleuven.be

VAN DINGENEN	Imke	UAntwerpen	imke.vandingenen@uantwerpen.be
VAN ESPEN	Lise	UMONS	Lise.VANESPEN@student.umons.ac.be
VAN GIESSEN	Sam	UvA	sam.van.giessen@student.uva.nl
VAN GORP	Merel	UAntwerpen	merel.vangorp@uantwerpen.be
VAN HOECK	Clément	UMONS	vanhoeckclement@yahoo.be
VAN WASSENB.	Sam	UAntwerpen	sam.vanwassenbergh@uantwerpen.be
VANDENBOER	Yelle	IRBN	yvandenboer@naturalsciences.be
VANDEPUTTE	Ellen	UAntwerpen	Ellen.Vandeputte@uantwerpen.be
VANDROMME	Jérôme	ULiège	jerome.vandromme@doct.uliege.be
VANHUSSEL	Margaux	ULiège	margaux.vanhussel@doct.uliege.be
VANNECHEL	Pol	UMONS	polvannechel@outlook.fr
VANOVERBERGHE	Isabel	KU Leuven	isabel.vanoverberghe@kuleuven.be
VASCONCELLOS	Mariana	U. de São P.	marimiravasc@gmail.com
VER HOEYE	Killian	UMONS	Killian.VERHOEYE@umons.ac.be
VERHEYE	Marie	KU Leuven	marie.verheye@kuleuven.be
VERVAECKE	Hilde	Odisee Uni.	hilde.vervaecke@odisee.be
VILELLA-P.	Zorimar	KU Leuven	zorimar.vilella-pacheco@kuleuven.be
VISSER	Fleur	ULiège	fleur.visser@outlook.fr
VOETEN	Elke	KU Leuven	elke.voeten@student.kuleuven.be
VOLCKAERT	Filip	KU Leuven	filip.volckaert@kuleuven.be
VOS	Wicher	Wicher	wicher_vos86@hotmail.com
WAMBREUSE	Noé	UMONS	noe.wambreuse@umons.ac.be
WHAITE	Alessandra	UMONS	alessandra.whaite@umons.ac.be
WILLAM	Laura	UMONS	lauralns@outlook.be
WILLOT	Quentin	UNamur	will037@hotmail.com
YEFIMAK	Kristina	KU Leuven	maria.madrid@kuleuven.be
ZEEMAN	Adam	UvA	adamnzeeman@gmail.com
ZETTA	Styliani	KU Leuven	styliani.zetta@student.kuleuven.be

Photo Contest RBCZ 2024

The **Best Scientific Picture Contest** was held based on 73 images submitted. The award will be presented by the MUMONS team during the Reception Dinner. If the authors consent, the three best pictures will be included in the exhibition “**Explorer l’Invisible**”. Here the selection of the best three images voted by members of the jury from the Scientific Committee:

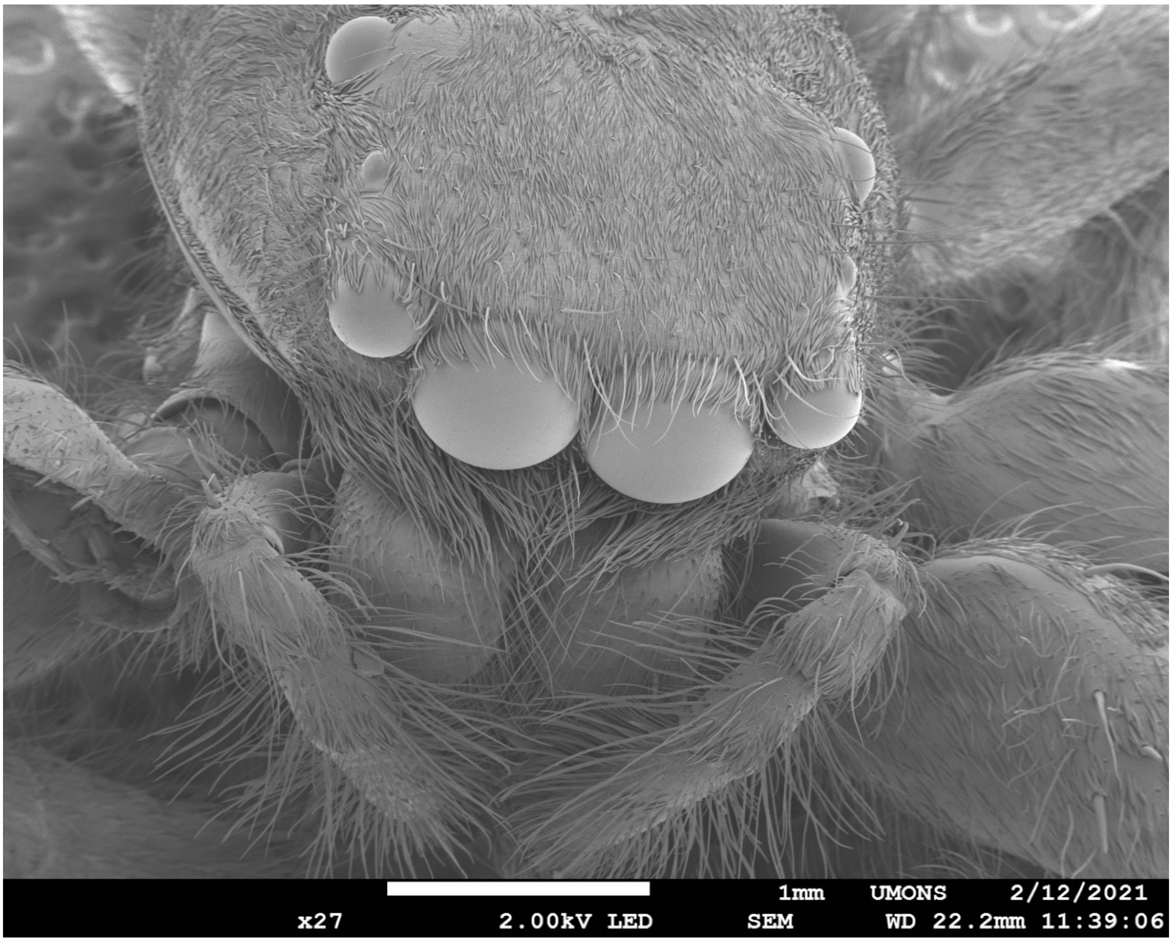


Alien Nursery by Benjamin DECOUX.

Third postlarval instar of the sea spider *Ammothea hilgendorfi*, an invasive species in the North Sea. The larval phase of this species is an ectoparasite of the hydrozoans on which it stands in the picture.

Seladonia by Ahlam SENTIL.

A *Seladonia* species foraging on a thistle plant in a vacant lot in Safi, Morocco.



Spider head by Youri NONCLERCQ.

Front view of jumping spider head (Salticidae *Marpissa muscosa*)

Special Mention

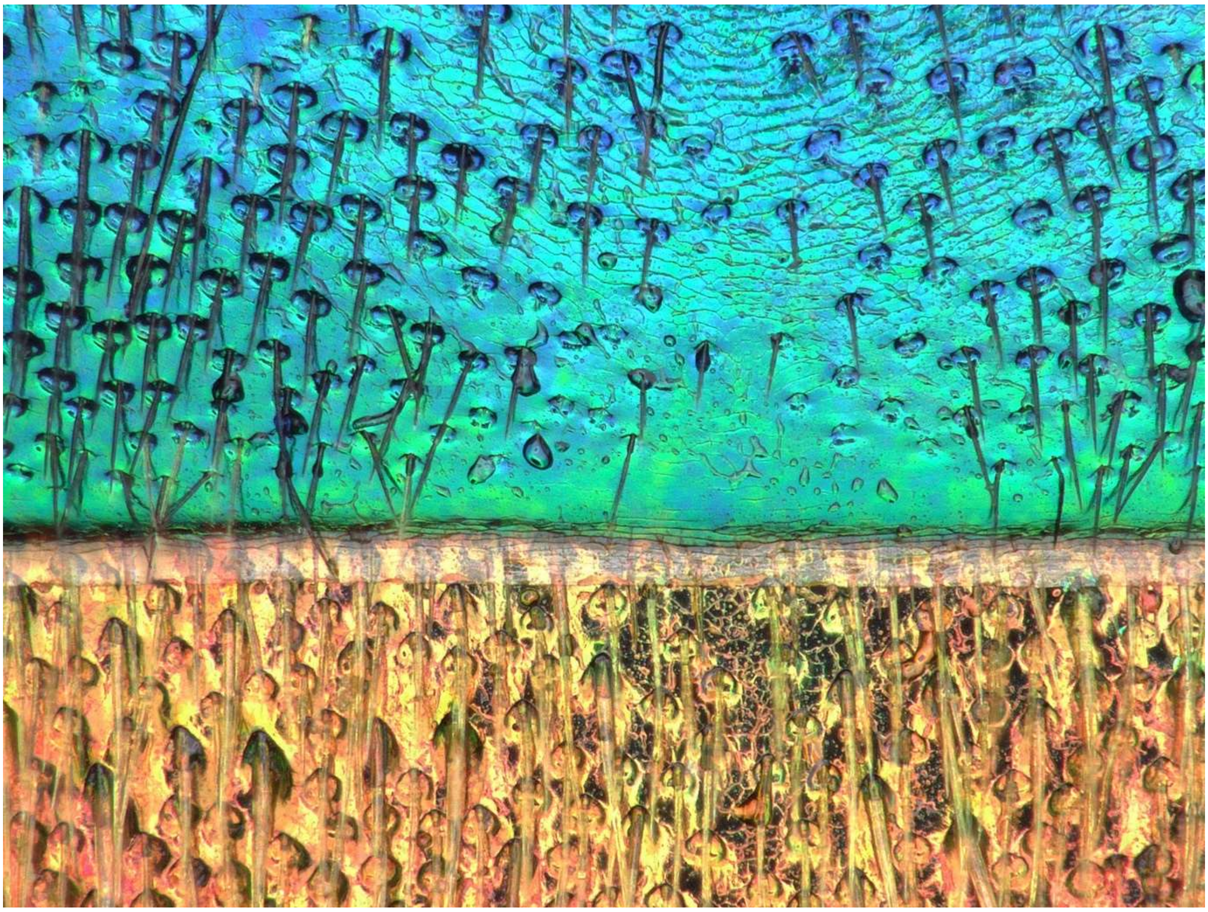
The following images received a “Special Mention” because they were voted by at least one member of the jury as “the best” for the Photo Contest 2024.

First encounter with an orchid bee by Clément TOURBEZ.

Macrophotography of *Exaerete frontalis.* Orchid bees are famous for their stunning metallic coloration, such as the bright metallic green of this specimen, as well as their long proboscis, which allows them to sample nectar from deep corollas. Species from the genus *Exaerete* are parasites of other orchid bees, meaning they do not collect pollen to feed their larvae but instead usurp the nest provisions of their host species. This specimen was collected by the author in December 2021 at the Patawa Camp in French Guiana.

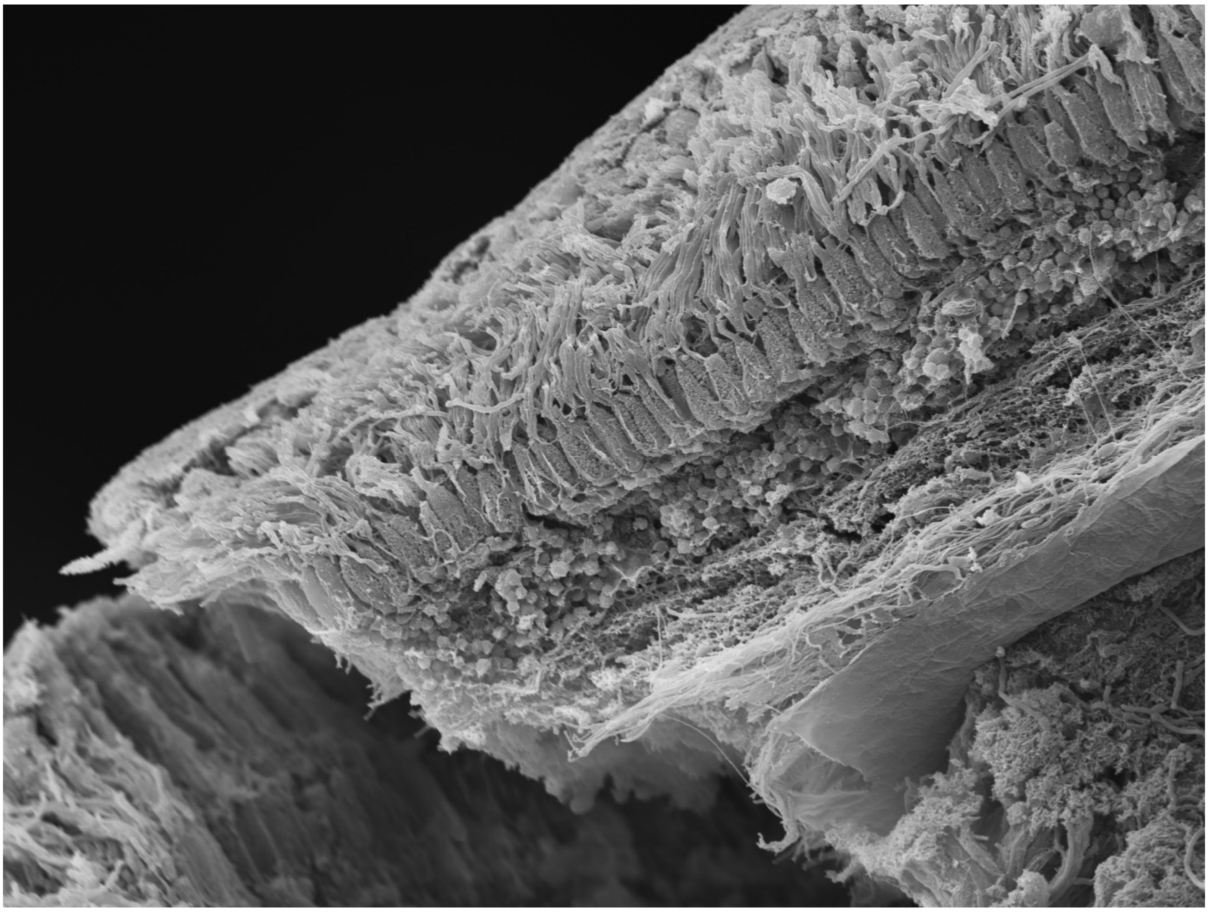
The cutting edge of conservation biology by Fernanda HERRERA-MESÍAS.

A female leaf-cutting bee (*Megachile willughbiella*) working to take a piece of maple leave from a nearby tree to use as building material for her nest. Overall, this piece celebrates the ingenuity of insects by depicting a commonly overlooked behavior of wild bees that makes them, at the same time, marvelous creatures of nature and relatable characters to the human experience.



Hidden flying beach by Clément TOURBEZ.

Microscope photography of an Eufriesea species. Orchid bees are renowned for their striking metallic coloration, such as the bright metallic gold and blue of this specimen, as well as their long proboscis, which enables them to access nectar from deep corollas. This photograph focuses on two dorsal abdominal segments (called tergites) of an orchid bee from the genus Eufriesea. It reveals the intricate micropores and hair covering this structure and highlight their remarkable coloration. This specimen was collected in 2023 in Ecuador.



Fish retina by Julia CAMACHO GARCIA , Timothy DUNSTAN and Domino JOYCE.

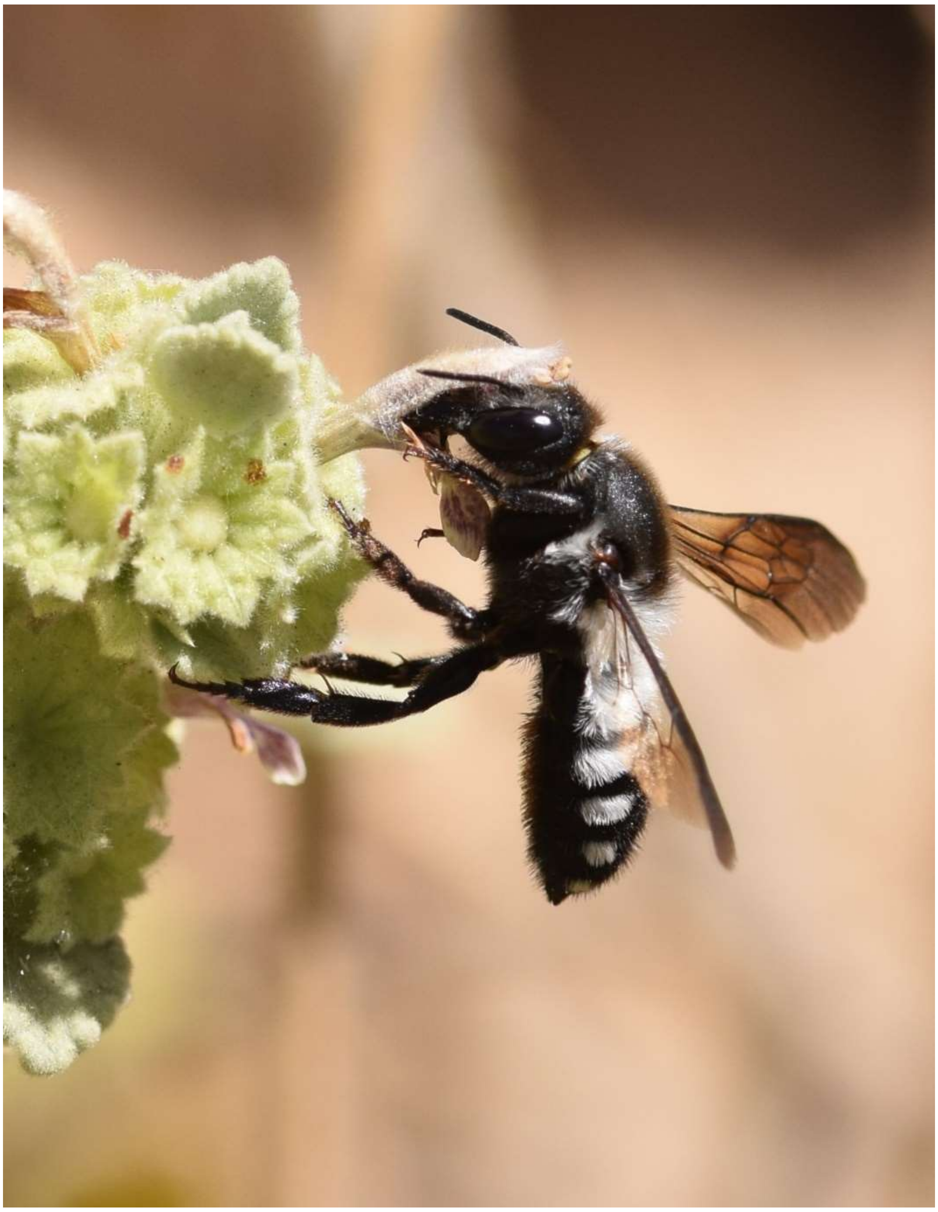
Scanning electron microscopy (SEM) image of a fish retina, taken at the University of Hull (UK).

Harlequin crab by Lisa MUSSOI.

Symbiotic crabs living in sea cucumber, this crab live in the digestive system of a lot of sea cucumbers in tropical area.

Megachile emerging from its nest by Ahlam SENTIL.

A wild bee male of *Megachile* emerging from its nest (a dead stem) on April 7, 2024.



Megachile lefebvrei on *Ballota hirsuta* by Ahlam SENTIL.

A wild bee *Megachile lefebvrei* foraging on the flower of *Ballota hirsuta* in a cemetery in Safi during late spring (May 14, 2024).