Master of Science Biology, incl. Educatieve Master Biologie - AJ 2025-2026

Goedgekeurde onderwerpen

Lijst gegenereerd op: Thu, 12 Dec 2024 04:04:31 +0100. *Laatst ingediende onderwerp: 42809*

42670: (Functionele) biodiversiteit van kevers in een beheer- en vegetatiestructuurgradiënt in Bos t'Ename

Promotor(en):	Jan Van Uytvanck
Begeleider(s):	Jan Van Uytvanck
Contactpersoon:	
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Insecten en ongewervelden in het algemeen staan in het huidige Europese landschap onder zware druk. In Duitsland werd recent een terugval van 75% (biomassa) geregistreerd. Alternatieve en adaptieve maatregelen in het natuurbeheer -zoals extensief graasbeheer- kunnen van belang zijn om deze terugval te temperen.

Doelstelling:

Als onderdeel van procesonderzoek in open extensief begraasde ecosystemen wordt de relatie onderzocht tussen (functionele) biodiversiteit van ongewervelden, zich ontwikkelende vegetatiestructuren en vegetaties en de habitatvoorkeuren van grote herbivoren zoals runderen en paarden.

In deze thesis ligt de focus op het natuurherstel op voormalige landbouwgronden (akkers, graslanden) van het natuurgebied Bos t' Ename. We onderzoeken de impact van variatie in vegetatiestructuur en alternatieve beheervormen (extensieve begrazing vs. traditioneel hooibeheer) op de (functionele) diversiteit van kevers. Beide factoren worden onderzocht in een gradiënt, m.a.w. van lage naar hoge structuurvariatie en van extensief naar intensief beheer. De variatie in vegetatiestructuur wordt afgeleid uit gedetailleerde vegetatie-hoogtemodellen die verkregen werden aan de hand van dronebeelden (fotogrammetrie). De beheerintensiteit wordt afgeleid uit de habitatvoorkeuren van grote herbivoren (GPS-data, verkregen via gps-collars bevestigd aan de dieren), met hooibeheer als (intensief) alternatief.

De voor natuurbehoud belangrijke responsvariabelen zijn diversiteit, aantal en biomassa van kevers (met behulp van automatische beeldverwerking) die in nauwe relatie leven met de bestudeerde vegetatiestructuren op verschillende schaalniveaus.

Locatie:

campus ledeganck of labo inbo (Sint-Denijs Westrem)

Website:

Meer informatie op: https://sites.google.com/inbo.be/procesbeheer

Samenwerking met bedrijf of non-profit organisatie

Bedrijf: Instituut voor Natuur- en Bosonderzoek
Samenwerking: promotor + begeleider

Onderwerp voorbehouden voor Wannes Wallijn

42702: 2. Investigating the transgenerational effects of ocean warming on the epigenetics of marine nematodes

Promotor(en): Rodgee Mae Guden, Tom Moens

Begeleider(s): Rodgee Mae Guden, Tom Moens
Contactpersoon: Rodgee Mae Guden
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Ocean warming is a significant threat to marine ecosystems. The increase in sea surface temperatures affects marine life at various levels, from individual organisms to entire populations and ecosystems. Marine nematodes, which are microscopic roundworms, play a crucial role in benthic ecosystems by contributing to nutrient cycling and organic matter decomposition. Understanding how these organisms respond to environmental stressors like ocean warming is essential for predicting the broader impacts of climate change on marine ecosystems.

Epigenetics, the study of heritable changes in gene expression that do not involve changes to the underlying DNA sequence, provides a valuable framework for understanding how organisms adapt to environmental changes. Epigenetic modifications, such as DNA methylation, histone modification, and non-coding RNA expression, can be influenced by environmental factors and can be passed on to subsequent generations. Investigating the transgenerational effects of ocean warming on the epigenetics of marine nematodes can provide insights into the mechanisms of adaptation and resilience of marine organisms.

Doelstelling:

In this study, we will investigate epigenetic variation in marine nematodes exposed to increased temperature across multiple generations. Here, we will use the marine nematode species complex Litoditis marina as our model system, and expose the nematodes to different temperature conditions for multiple generations. We will first develop a reference genome for Litoditis marina using Oxford Nanopore whole genome sequencing (WGS). Using the same technique, we will also detect and identify genomic modifications in nematodes exposed to different temperature conditions by mapping them to the reference genome of L. marina. By investigating microbiome changes and epigenetic mechanisms that underlie the responses of marine nematodes to increased temperature, we may gain better understanding on the adaptation of marine animals in the face of climate change.

Locatie:

campus Sterre (S8) en campus Ledeganck

42703: 3. Investigating the transgenerational effects of ocean warming on the life-history traits of marine nematodes

Promotor(en): Rodgee Mae Guden, Tom Moens
Begeleider(s): Rodgee Mae Guden, Tom Moens, Marie Cours
Contactpersoon: Tom Moens
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Ocean warming, a direct consequence of anthropogenic climate change, is causing unprecedented shifts in marine environments. The increase in sea surface temperatures affects the physical and chemical properties of the ocean, leading to altered habitats and ecosystems. Marine nematodes, which are among the most abundant and diverse metazoans in marine sediments, play a crucial role in nutrient cycling and energy flow within these ecosystems. Despite their ecological importance, the impact of ocean warming on marine nematodes, particularly across generations, remains poorly understood.

Marine nematodes exhibit a range of life-history traits, including growth rates, reproductive strategies, and survival mechanisms, which are essential for their adaptation to changing environmental conditions. These traits can be influenced by both direct environmental stressors and transgenerational effects, where the experiences of one generation affect the phenotypes of subsequent generations. However, the extent to which these changes are passed on to future generations, and the potential for adaptive responses, remains poorly understood. Understanding these transgenerational effects is vital for predicting how marine nematode populations will respond to ongoing and future ocean warming.

Doelstelling:

This study aims to examine the transgenerational effects of ocean warming on the life-history traits of marine nematodes. By conducting controlled laboratory experiments and analyzing multiple generations, we will assess how increased temperatures influence growth, reproduction, and survival across generations. Additionally, we will explore potential adaptive mechanisms that may enable marine nematodes to cope with ocean warming.

Locatie:

campus Sterre (S8) en campus Ledeganck

42684: A chemical genetics screen for highly specific inhibitors of nematode feeding site establishment

Promotor(en):	Tom Beeckman
Begeleider(s):	Saskia Proumen De Keyser
Contactpersoon:	Saskia Proumen De Keyser
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

A large proportion of the human and livestock food supply is provided by plants, since they make up about 80% of the food we eat. Unfortunately, crops face many challenges such as plant parasitic nematodes (PPNs) that cause about 12% yield loss in agriculture annually, with root-knot nematodes (RKNs) being among the most damaging nematodes. They invade the root and form nematode feeding sites (NFS) in the vascular cylinder by inducing a series of morphological, molecular and biochemical changes in plant root cells, causing severe biotic stress in plants.

Doelstelling:

The aim of this project is to identify compounds that can specifically protect plants from nematode infections by inducing resistance and inhibiting NFS formation, without affecting normal developmental processes. For this purpose, a chemical genetics screen in conditions representative for early stages of nematode infection, using a promoter-GUS-GFP reporter line in Arabidopsis thaliana, is being developed. The marker gene for the reporter line was selected based on its specifically upregulation upon RKN infection within the NFS, both in Arabidopsis and rice single-cell RNA sequencing data.

The effect of the selected compounds from the screen will have to be validated upon nematode infection in both Arabidopsis and rice, and through dose-response experiments in tomato and rice. Subsequently, these compounds will be subjected to a structure-activity relationship (SAR) analysis to generate more potent compounds. In addition, a first attempt to unravel the pathways to which the targets of these compounds belong will be provided through a functional genetic strategy, including RNA sequencing.

Depending on the progress of the project, the student will help validate the chemical genetics screen and/or functional characterization of the marker gene of early NFS formation. The selected marker gene belongs to the Glutathione S-transferase (GST) family and, in fact, little is known about the gene, especially within the nematode infection context.

Techniques to be used:

- cloning in Arabidopsis: Golden Gate for reporter- & overexpression lines, CRISPR/Cas for knock-out lines (TBD)
- RNA sequencing
- (q)PCR

- structure activity relationship analysis of compounds
- in vitro culture of plants
- pot experiments
- phenotyping
- microscopy
- gene expression analysis: GUS staining
- Technovit embedding & microtomy
- ...

Locatie:

VIB-UGent PSB (Technologiepark)

Website:

Meer informatie op: https://www.beeckmanlab.be/research/initiation-nematode-feeding-sites

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42719: A fungal monitoring project in Honduras: community ecology and taxonomy

Promotor(en):	Danny Haelewaters, Annemieke Verbeken
Begeleider(s):	Libelje Mortier, Danny Haelewaters
Contactpersoon:	Danny Haelewaters
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Background

Discovery of fungal biodiversity is ongoing with only 3-10% of the estimated 1.5 – 6 million species currently described. While biodiversity discoveries can be made anywhere, like for plants and animals, increased diversity and endemicity of soil fungi in many groups is concentrated in tropical environments, which generally have seen less formal scientific collecting than temperate regions. Beyond species discovery and inventories, documenting fungi allows comparisons with future data, which may be relevant for conservation planning. This is important as increasing calls are made to include fungi in conservation assessments and goals, yet baseline data is needed to evaluate the conservation status of fungal species. An effort to document the fungi in one tropical location, Cusuco National Park, began in 2019, in cooperation with Operation Wallacea. The park is a 23,440-ha protected area in the Merendón mountain range in northwestern Honduras with elevations ranging from 500 to 2,242 and various vegetation communities, including those dominated by ectomycorrhizal Pinus and Quercus species. Preliminary collecting in 2019 showed several species of fungi that may be new to science.

Problems

Biodiversity data on Honduran fungi is lacking, even compared with other Central American countries such as Panama and Costa Rica. Additionally, long-term fungal monitoring projects in the tropics that can detect rare species and monitor more common species in the face of climate change and increased risk of extinction are mostly non-existent. Finally, it is unclear if any environments are particularly species rich, nor what biotic and/or abiotic factors in general may drive fungal species richness and abundance.

Doelstelling:

A long-term fungal monitoring project began in Cusuco National Park in 2022 following incidental collecting in 2019. First, this student will join this project during the 2023 summer field season, learning fungal collection, identification, and processing skills in a remote location. Second, data from the 2022 and 2023 field seasons will be used to examine biotic and abiotic factors that may drive fungal diversity in Cusuco National Park, such as elevation, soil density, canopy cover, and presence of Pinus species. Finally, the student will have the opportunity to describe new species found during their fieldwork. The student will become familiar with analyzing biodiversity data and modern taxonomy and systematics in mycology. By completing this project, the student will continue biodiversity exploration of Honduras fungi that may be used in the future for conservation purposes, describe new species, and determine the drivers of fungal diversity in Cusuco National Park.

Locatie:

Campus Ledeganck, Honduras (pending funding)

Website:

Meer informatie op: www.dannyhaelewaters.com/a-fungal-monitoring-project-in-honduras-community-ecology-and-taxonomy/

Onderwerp voorbehouden voor Kira Tolstych

42808: A question of life and death: The molecular regulation of programmed cell death in plants

Promotor(en):	Moritz Nowack
Begeleider(s):	
Contactpersoon:	Moritz Nowack
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	2
Motivering voor deze opleiding:	

Probleemstelling:

Our research aims at understanding the molecular and cellular regulation of programmed cell death (PCD) in plants. In the biomedical field, PCD is intensely studied due to its implications in many human diseases and conditions, e.g. in the context of inflammation, (auto)-immunity, or cancer. By contrast, PCD research in plants still is pioneering work. Interestingly, plant PCD processes appear to have evolved independently from PCD in metazoans, and central players of major animal PCD pathways are not conserved in plant genomes. Nevertheless, PCD is as crucial for the development and health of plants as it is for animals. Without PCD, plants would not be able to efficiently transport water, form seeds and fruit, or defend themselves against pathogens. Hence, plant PCD is not only appealing as a frontier of fundamental research, but also provides a so far largely untapped agricultural potential to improve yield stability and stress resilience of crops.

Doelstelling:

You will be part of an international team performing cutting-edge research in plant developmental biology. We are using advanced technologies (e.g. CRISPR-based genome editing, advanced light-and electron-microscopy, live-cell imaging, protein biochemistry, protein interactomics, single-cell RNA sequencing, and many more) to answer the big biological question on how PCD is molecularly control in the context of plant development.

Your project will be situated in one of the ongoing projects on the Arabiodpsis root cap or on other experimental systems we are working on to decipher PCD control in plants (see our publications over the last years on https://scholar.google.com/citations?user=oPia24kAAAAJ&hl=en&oi=ao). If you are interested in plant PCD as a Master thesis topic, please contact me directly (moritz.nowack@vib.be or moritz.nowack@ugent.be) for a personal meeting. In this meeting we can discuss your interests and ambitions and tailor the optimal project regarding the biological question and the methodology used. I'm looking forward to meeting you!

Locatie:

Campus Ardoyen (Technologiepark Zwijnaarde)

42691: Analysing Strength Variation in Syngnathid Tail Segments for Bioinspired Robotic Applications

Promotor(en):	Dominique Adriaens, Francis wyffels

Begeleider(s):
Contactpersoon: Dominique Adriaens
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

The prehensile tails of syngnathid fishes, particularly seahorses, exhibit a unique skeletal structure composed of a vertebral column encased in segmental bony plates. Each segment consists of four bony plates connected by connective tissue, and their shape and size decrease distally along the tail. These morphological changes likely influence the mechanical strength of the bony plates. Understanding how strength varies along the tail and across species like seahorses, pipe horses, and pipefish is essential for material selection and structural constraints in bioinspired robotic designs.

Doelstelling:

The aim of this study is to analyze the mechanical strength variation in syngnathid tail bony plates along different levels of the tail and across multiple species. Using reconstructed µCT models in AMIRA, the student will apply Finite Element Method (FEM) analysis (eg, using ADAMS or SolidWorks) to evaluate strength differences. The results will provide critical insights into how tail morphology influences mechanical properties, contributing to the design of efficient, strength-optimized robotic systems inspired by syngnathid tails.

Locatie:

Ledeganck campuscampus Ledeganck, Research Group Evolutionary Morphology of Vertebrates

Website:

Meer informatie op: https://www.ugent.be/we/biology/evo-morph/en

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42698: Are nematodes eavesdropping on bacterial quorum sensing for finding food in marine sediments?

Promotor(en): Tom Moens
Begeleider(s): Marie Cours, Tom Moens
Contactpersoon: Tom Moens
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

In marine sediments, millions of mobility-restricted microorganisms live their lives in close vicinity of each other, using chemical communication to guarantee survival, and regulate physiology and ecological interactions such as foraging strategies and food selection. Quorum Sensing is the regulation of gene expression in response to fluctuations in cell-population density. At low cell densities, bacteria behave as a single cellular organism, but can shift their behaviour to ‘multicellular’ if their population density reaches a certain threshold level. At this point, they communicate through small signalling molecules which allow them to express genes for particular phenotypes. Using these secreted chemical messengers, bacteria are able to coordinate the behaviour of a group, including regulation of (rate of) cell division and other important key functions. Marine free-living nematodes, the most abundant metazoans on Earth, navigate their environment through chemotaxis, using olfactosensory organs called ‘amphids’. Bacterivorous nematodes contribute significant top-down effects on bacterial community structure, presumably shaping them with their grazing activities. Many nematode species indeed feed on bacteria and are able to locate patches of bacteria from a distance, but the mechanisms by which they detect bacteria are not yet understood. In 2012, Choe and co-authors showed that nematodes use a conserved family of signaling molecules, ascarosides, to communicate among eachother. The structural features and level of conservation of ascarosides are evocative of bacterial quorum sensing, where Nacyl homoserine lactones (AHLs) are both produced and sensed by many species of gram-negative bacteria. Ascarosides are assembled in a very similar fashion to AHLs. Both groups of signaling molecules have similar phylum-specific distribution and play significant roles in mediating survival strategies of the producing organisms. In addition, in a way similar to the regulation of bacterial behaviours by quorum sensing, ascarosides-mediated communication can regulate a variety of behaviours in nematodes. Furthermore, C. elegans is known to control the virulence of bacterial pathogens by inhibiting certain Quorum Sensing systems, and so there is evidence that within the phylum Nematoda, there are cross-Kingdom interactions that facilitate their survival using molecules that are akin to their own pheromone signals.

Doelstelling:

In this project, we investigate the possibility that marine bacterivorous nematode species can eavesdrop on QS communication between bacteria and use these QS molecules as a source of information which helps them to locate their bacterial food. In a first step, we will assess the chemotaxis of at least two species of marine nematodes to both wild-type (QS+) and QS deficient (QS-) strains of different bacterial species which are known to produce different types of QS molecules. Based on the result of these experiments, we will subsequently test nematode chemotaxis to the pure QS molecules (which can be obtained from several labs, including at UGent) to (dis)prove unambiguously whether observed responses can be ascribed to the QS molecules. This can be elaborated upon by (a) including more bacterial strains which produce yet other QS molecules, and/or (b) making the setting of these lab experiments more complex so as to include other stimuli that tend to trigger nematode chemotaxis in natural environments, since this could inform us on the hierarchy of different types of cues in shaping nematode behaviour in sediments.

Locatie:

campus Sterre, S8

Opmerkingen:

Samenwerking is voorzien met onderzoeksgroep van Prof. Tom Coenye* van de Faculteit Farmaceutische Wetenschappen.
*Specialist in microbiële QS.

42724: Assessing the capacity of tiger worms (Eisenia spp.) to compost stool containing Ascaris eggs to safe fertilizers

Promotor(en):	Bruno Levecke
Begeleider(s):	Nathalie De Wilde
Contactpersoon:	Bruno Levecke
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Soil-transmitted helminths (STHs, Ascaris lumbricoides, Trichuris trichura, Necator americanus and Ancylostoma duodenale) are intestinal worms that remain a threat to public health. Their transmission is characterized by a sequence of events: (i) infected individuals excrete worm eggs via their stool into the soil; (ii) under optimal conditions of moisture and temperature the excreted eggs will develop into infectious worm eggs (A. lumbricoides and T. trichiura) /larvae (hookworms); (iii) finally infection occurs through oral uptake (eggs) or skin penetration (larvae) of these infectious stages that reside in the soil. It was estimated that 900 million people worldwide are infected, the vast majority living in resource-constrained countries, where a lack of sanitation and limited access to clean water maintains transmission. To reduce the STH-attributable morbidity (2 million disability-adjusted life-years were lost), World Health Organisation (WHO) recommends large-scale deworming programs during which at risk groups (children and women of reproductive age) in endemic areas are provided an anthelminthic drug. In 2021 alone, 411 million school-aged children (were dewormed, covering 62.9% of the children at risk for the morbidity attributable to STH infections. Although essential in reducing disease transmission, ensuring improved WASH in these areas often remains a challenge.

In recent years, there has been a growing interest in tiger worm toilets (TWT; sometimes known as vermifilter toilets). Eisenia fetida (the tiger worm) is one of the most widely used composting worms globally for consuming organic matter in human excreta (Samaranayake & Wijekoon, 2011). The TWT design features a superstructure (left side in Figure 1) with a toilet pan that directs waste into a biodigester (right side in Figure 1).

page3image166488848

Figure 1: Structural design of Tiger Worm Toilet (Sioné et al., 2023a)

Inside the biodigester, tiger worms reside within an organic layer of coconut husk or wood chips, which functions as a bedding layer to support the laying of worm eggs and as a filtration layer for capturing solid matter. Beneath this filtration layer is a drainage layer of gravel, which ensures that liquid effluent flows down into a soakaway and ensures that the worms do not become flooded in the biodigester.

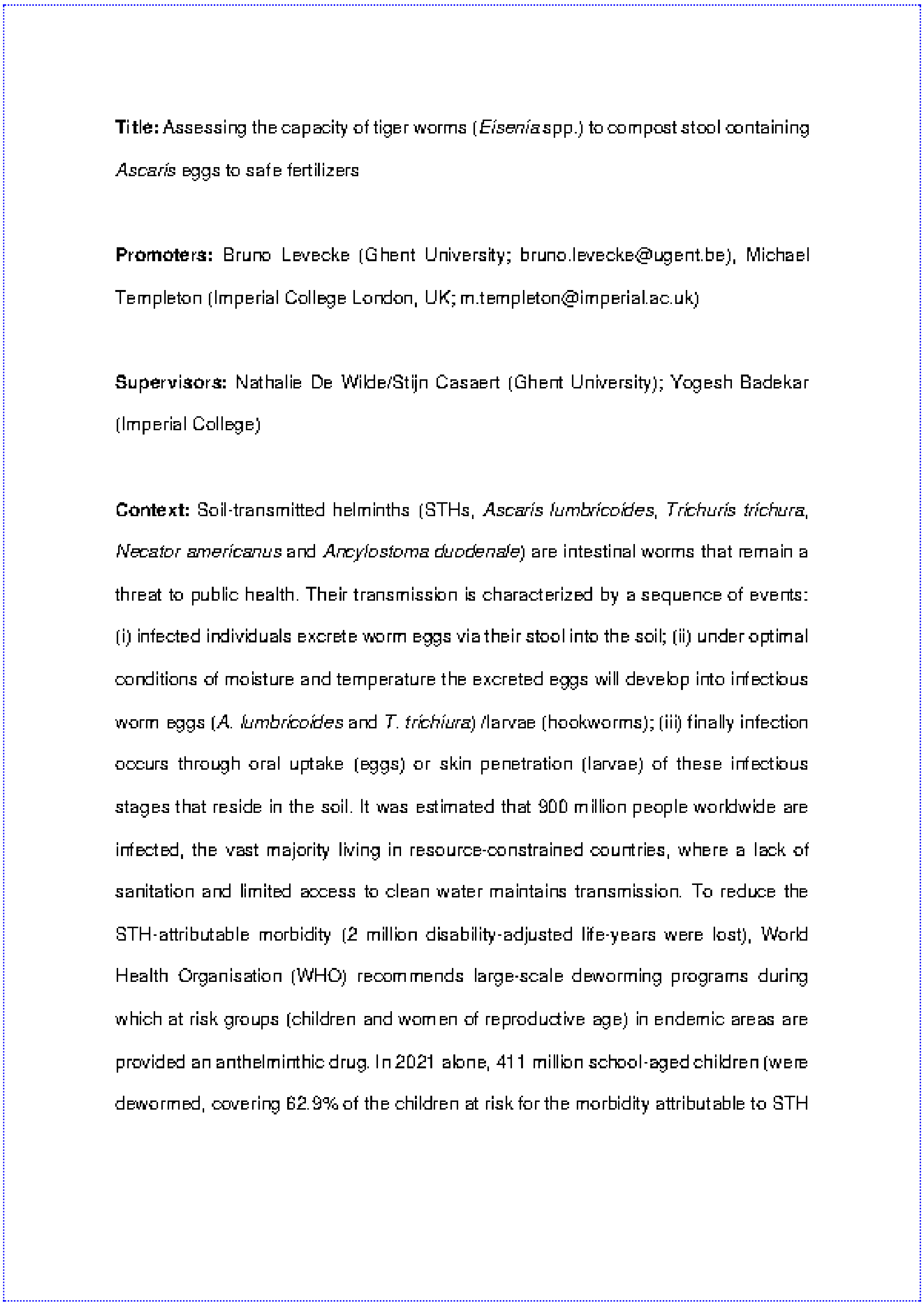
Charities and private companies have installed TWTs in rural and peri-urban areas across the globe, including countries such as Ethiopia, Liberia, Myanmar, India, Rwanda, and Uganda. By rapidly transforming human waste into vermicompost and carbon dioxide, TWTs dramatically reduce odours and flies and reduce the fill rate compared to a conventional pit latrine (Furlong et al., 2016). TWTs are more cost-effective than pit latrines in the long term because they eliminate the need for emptying costs (Sioné et al., 2023a). Emptying of TWTs is a much safer process compared to emptying pit latrines, as vermicompost has been shown to have a significantly lower content of faecal coliforms (98.6% reduction) compared to untreated faecal sludge (Furlong et al., 2016). However, there is limited research on TWT vermicompost in the context of soil-transmitted helminths (STHs).

Studies on vermicomposting sewage sludge show mixed results in reducing STHs. Some studies report significant reductions, while others find no effect. The outcomes depend on the species, sludge type, and conditions. Therefore, there is a need to provide robust evidence as to whether TWT vermicompost does or does not contain STHs. If TWT vermicompost is free of STHs, it can be effectively used in agriculture due to its nutrient-rich composition, containing essential nutrients like nitrogen (N), phosphorus (P), and potassium (K). These nutrients are vital for plant growth, and crops benefit from enhanced growth, yield, and quality when vermicompost is added to the soil.

Doelstelling:

The main objective of this thesis is to assess the capacity of tiger worms (Eisenia spp.) to compost stool containing Ascaris eggs to safe fertilizers. The specific objectives are (i) to establish a tiger worm colony on stool in a laboratory setting; (ii) validate a diagnostic method to detect parasites in worm compost; (iii) and to evaluate the capacity of tiger worms to compost stool containing Ascaris eggs to safe fertilizers. For these experiments, we will make use of pigs as an animal model. In other words, we will use porcine stool and eggs of the porcine Ascaris suum, which is prevalent in Belgium and closely related to the human A. lumbricoices. All the experiments will be conducted at the Laboratory of Parasitology, Faculty of Veterinary Medicine.

Eerste pagina van PDF:



Title: Assessing the capacity of tiger worms (*Eisenia* spp.) to compost stool containing *Ascaris* eggs to safe fertilizers

Promoters: Bruno Levecke (Ghent University; bruno.levecke@ugent.be), Michael Templeton (Imperial College London, UK; m.templeton@imperial.ac.uk)

Supervisors: Nathalie De Wilde/Stijn Casaert (Ghent University); Yogesh Badekar (Imperial College)

Context: Soil-transmitted helminths (STHs, *Ascaris lumbricoides*, *Trichuris trichura*, *Necator americanus* and *Ancylostoma duodenale*) are intestinal worms that remain a threat to public health. Their transmission is characterized by a sequence of events: (i) infected individuals excrete worm eggs via their stool into the soil; (ii) under optimal conditions of moisture and temperature the excreted eggs will develop into infectious worm eggs (*A. lumbricoides* and *T. trichiura*) /larvae (hookworms); (iii) finally infection occurs through oral uptake (eggs) or skin penetration (larvae) of these infectious stages that reside in the soil. It was estimated that 900 million people worldwide are infected, the vast majority living in resource-constrained countries, where a lack of sanitation and limited access to clean water maintains transmission. To reduce the STH-attributable morbidity (2 million disability-adjusted life-years were lost), World Health Organisation (WHO) recommends large-scale deworming programs during which at risk groups (children and women of reproductive age) in endemic areas are provided an anthelminthic drug. In 2021 alone, 411 million school-aged children (were dewormed, covering 62.9% of the children at risk for the morbidity attributable to STH

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Locatie:

Laboratory of Parasitology, Faculty of Veterinary Medicine

42658: Assessing the climatic variability hypothesis at a micro-scale: impacts on forest bird metabolic flexibility

Promotor(en):	Cesare Pacioni, Diederik Strubbe
Begeleider(s):	
Contactpersoon:	Cesare Pacioni
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

The climatic variability hypothesis posits that geographically separated populations inhabiting variable environments should exhibit greater physiological flexibility than populations from stable environments. This concept has been explored on larger scales, but little is known about whether it holds at finer scales. Heterogeneous environments produce a suite of microclimates that can influence energetic demands for species occupying such environments. For example, studies have shown that forest stands with higher structural complexity tend indeed to have more stable microclimates with less daily temperature variation. These differences in microclimate may influence how bird species adjust their physiology.

Doelstelling:

Hence the aim of the thesis is to determine if microclimatic variability drives differences in phenotypic flexibility in birds between forest plots with varying levels of structural complexity. As climate change intensifies, habitat structural complexity and associated microclimates are likely to shift, impacting species' physiological traits and survival strategies. Testing the climatic variability hypothesis at a microclimatic scale bridges a gap in ecological research and can reveal how localized habitat features influence metabolic flexibility. Such knowledge is essential for predicting the resilience of bird populations to habitat changes and for informing conservation strategies in forest ecosystems.

What will be the main tasks:

- Assist with and learn techniques for bird capture and handling
- Assist in setting up microclimate stations in forest plots.
- Assist with and, under supervision, conduct respirometry experiments to measure bird metabolism.

Eerste pagina van PDF:

Assessing the climatic variability hypothesis at a micro-scale: impacts on forest bird metabolic flexibility

The climatic variability hypothesis posits that geographically separated populations inhabiting variable environments should exhibit greater physiological flexibility than populations from stable environments. This concept has been explored on larger scales, but little is known about whether it holds at finer scales. Heterogeneous environments produce a suite of microclimates that can influence energetic demands for species occupying such environments. For example, studies have shown that forest stands with higher structural complexity tend indeed to have more stable microclimates with less daily temperature variation. These differences in microclimate may influence how bird species adjust their physiology.

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What will be the main tasks:

- Assist with and learn techniques for bird capture and handling
- Assist in setting up microclimate stations in forest plots.
- Assist with and, under supervision, conduct respirometry experiments to measure bird metabolism.

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Locatie:

Ledeganck campus

Onderwerp voorbehouden voor Pieter De Backer

42733: Biomimicry of bird structural colors using silica-melanin nanoparticles

Promotor(en):	Liliana D'Alba Altamirano, Matthew Shawkey
Begeleider(s):	Maria Boto Ordonez, Wanjie Xie
Contactpersoon:	Maria Boto Ordonez
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

The world of art and design has always looked to nature for inspiration and tried to replicate it, with color being one of the most fascinating aspects. The colors we see can be divided into pigmentary coloration and structural coloration. The latter is responsible for the blue of the Morpho butterfly, the metallic hues of hummingbirds, or the iridescence of jeweled beetles. In this case, color is due to light interaction with a nanostructure. These nanostructures are often built from simple biological building blocks, such as cellulose, chitin, keratin, and melanin, biomaterials highly abundant in nature, biodegradable, and non-toxic. Although these colors have always fascinated humans, knowledge of their formation and structure is relatively recent, as is their study within the field of biomimicry.

In this project, we want to answer the question: can we replicate nature's structural colors using natural, non-toxic materials? Can these colors be used as paint? We will recreate a color palette by creating silica nanoparticles of different sizes and coating them with synthetic melanin. After measuring the size and refractive index, we will mix them in painting media to test their color and applicability.

The student will produce and coat the different silica nanoparticles with synthetic melanin to facilitate the visualization of a color. She/he will measure the particles and refractive index using transmission electron microscopy. Then she/he will mix the particles in different painting media. The student will then perform comparative analyses of the data collected to answer the research question.

Doelstelling:

The goals are

1) To recreate a structural color palette due to the variation of silica particle sizes.

2) To test different painting media to value analyses of the applicability of paint.

Locatie:

campus Ledeganck, floor 9

42677: Characterization of benthic diatom microbiomes under abiotic stress

Promotor(en):	Anne Willems, Wim Vyverman
Begeleider(s):	Niranjana Roy
Contactpersoon:	Niranjana Roy
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Diatoms are eukaryotic microalgae responsible for almost 40% of marine primary production. Based on their cell shape, two main groups of diatoms are recognized: the radially symmetric centric diatoms and the bilateral pennate diatoms. Majority of the pennate diatoms have adopted a benthic lifestyle where they form biofilms on substrates. In these biofilms, diatoms form close relationships with heterotrophic bacteria. These interactions have major ecological implications as they affect food web structure and mediate biogeochemical cycling. Historically, diatom-bacteria interactions have been studied using planktonic model diatoms. Therefore, despite the global significance of benthic diatoms, little is known about diatom-bacteria interactions in benthic environments.

Global warming in ocean ecosystems alters temperature, acidification, oxygen content, and nutrient inputs. Given the importance of biofilm functioning for global biogeochemical cycling, understanding the susceptibility or resilience of the diatom-bacteria interactions to abiotic stresses are urgent questions that need to be addressed.

Doelstelling:

This project fits in the framework of a GOA project, aimed at identifying and functionally characterizing key adaptations that drive the extraordinary species diversity and ecological success of benthic diatoms. Focussing on a selection of ten model species, the specific aims of this thesis project include: 1) to characterize and compare bacterial community composition under normal growth conditions and abiotic stress, by means of 16S rRNA gene amplicon sequence analysis, 2) to perform co-inoculation experiments of diatoms and bacteria under normal and stress conditions to assess effects on diatom growth 3) to characterize bacteria of interest by whole genome sequencing and 4) to perform transcriptomic comparison of the selected co-inoculation experiments to assess genes and pathways involved in diatom-bacteria interactions under abiotic stress.

Locatie:

campus Ledeganck en Sterre

42667: Climate change and oil pollution effects on copepods feeding ecology

Promotor(en):	Marleen De Troch, Anna-Maria Vafeiadou
Begeleider(s):	Anna-Maria Vafeiadou
Contactpersoon:	Anna-Maria Vafeiadou
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Increasing oil pollution across the globe poses a growing concern for aquatic life and the function of marine ecosystems. This research topic will dive into the impact of crude oil, particularly its water-soluble fraction (WSF), on benthic habitats, which typically sustain highly productive ecosystems, in the framework of climatic changes. Copepods, a critical component of the meiobenthos, play a vital role in transferring energy from primary producers to higher trophic levels in marine food webs. Therefore, understanding how pollutants like crude oil may affect the survival and behavior of copepods and the marine food chain indirectly is of paramount importance. Previous research using the benthic copepod species Platychelipus littoralis has compared the effects of exposure to low oil (5% WSF) and high oil (10% WSF) concentration treatments over an 8-day period and resulted that the high oil treatment had a strong impact on feeding and mortality rates. The low oil treatment on the other hand showed a reduced feeding rate, but had no effect on the mortality rate. Despite the importance of oil pollution especially in coastal areas, the combined effects with climate change on marine invertebrates have not been well investigated.

Doelstelling:

Given the above, this research project aims to test the effects of temperature, as a proxy for climate change, and oil pollution in the ecology of marine coastal organisms. We will build a lab experiment with copepods collected from the field (coast of the North Sea) with a fully factorial design (temperature and oil exposure) and will measure mortality, feeding rates and fatty acids composition of copepods in this project framework. This is a pioneer study on toxicity effects and temperature for benthic copepods. Additionally, if the student is particularly interested in molecular analysis, there is potential for DNA extractions, PCR and lab analysis as well as sequence data analysis of the microbiome of copepods related to the experiments, as an additional aspect to test their response to exposure.

Locatie:

Sterre campus S8, potentially Ledeganck campus

Opmerkingen:

Partical information: Sediments will be collected from the intertidal zone of the Belgian part of the North Sea. This thesis topic involves field work, lab work and experiments (and potentially molecular techniques and bioinformatics, upon discussion with the student), giving an excellent opportunity to experience different paths of research work in the domain of marine biology. Experience with R and an independent working attitude are required. Good R knowledge and scientific writing skills are an asset.

42697: Comparative kinematics of seed eating in Finches: effect of seed properties

Promotor(en):	Dominique Adriaens
Begeleider(s):	Jana De Ridder
Contactpersoon:	
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Finches differ a lot in beak morphology: some have a very slender beak like the European goldfinch, others a very robust one like the hawfinch. These strong-biting species are able to feed on larger and stronger-shelled seeds. However, despite this morphological specialisation, they still feed on softer seeds. Birds can use different methods to open seeds, ranging from strong biting, to quick repeated beak movement. The question is if feeding beak kinematics differ for different seed types processed by the same species.

Doelstelling:

Kinematic characteristics of beak movement are studied for one finch species feeding on different seed types. For this, a few birds are video recorded while feeding on seeds differing gradually in either shape, surface structure, size or hardness. Beak tip is tracked over time, while positioning and cracking the seeds. With this data, frequency, amplitude, velocity and acceleration of the beak are calculated for the different seed properties. For this study, some of the practical work will be done at the Antwerp University, in the lab of Prof. Van Wassenbergh.

Locatie:

42747: Connectivity conservation by the design of Nature-based Solutions

Promotor(en):	Dries Bonte, Maxime Dahirel
Begeleider(s):	Dries Bonte, Maxime Dahirel
Contactpersoon:	Dries Bonte
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie, Master of Science in de geografie en de geomatica
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Coastlines along the North Sea are heavily urbanised. The rise of coastal cities has induced fragmentation of the remaining dune areas. With ongoing sea-level rise, beaches are nourished and new dunes designed in front of existing dikes and sea walls. These dune-in-front of dike Nature-based Solutions not only serve as a coastal protection service, they are also anticipated to restore ecological connectivity and to contribute to genetic diversity and metapopulation viability.

Doelstelling:

The student will use species parameterised models to quantify how these Nature-based Solutions contribute to coastal dune connectivity. Parameterisation of species life histories and dispersal capacities will be done based on existing literature, citizen-science data analysis and the collection of new data in the field during the summer season.

Locatie:

Website:

42603: Cultivating the future: searching for the best strategies to cultivate red algae to optimize biomass, chemical composition, and bioactive potential

Promotor(en):	Olivier De Clerck, Kris Audenaert
Begeleider(s):	Louka Noyen
Contactpersoon:	Louka Noyen
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Seaweed cultivation is becoming of foremost importance within the scope of climate change. Because the harvest of wild seaweed biomass is often unsustainable and unreliable, there is a growing body of research focused on cultivating seaweed for commercial applications in, for example, the food, feed, agriculture, and pharmaceutical industries.

Furcellaria lumbricalis is a red seaweed with a relatively large geographical distribution, ranging from the Atlantic Ocean to the hyposaline waters of the Baltic Sea. In the Baltic, where salinity can be as low as 3.6, Furcellaria is one of the few macroalgal species capable of surviving these extreme conditions. This resilience has sparked interest in extracting bioactive compounds from Furcellaria to enhance crop resilience during environmental stresses, such as drought. These extracts are commonly referred to as “plant biostimulants.”

More information on the different laboratories can be found on the following websites:

- https://lamp.ugent.be/
- https://phycology.ugent.be/

Doelstelling:

This thesis will focus on cultivating Furcellaria at lab-scale, where experiments will be conducted under varying external conditions, such as different salinity levels, to optimize growth rates, biochemical composition, and bioactive potential. The student will gain experience in extracting pigments, measuring total antioxidant activity, and performing biostimulant assays, using Furcellaria extracts added to Arabidopsis thaliana to estimate common plant health parameters such as: efficiency of photosynthesis (Fv/Fm), Chlorophyll Index (ChlIdx), and anthocyanin accumulation (mARI) using a multispectral imaging platform.

Additionally, the project offers flexibility for students to tailor the research to their specific interests within this broad field. In case the timing is right, the option to join field work during the summer holidays of 2025 can be discussed.

Locatie:

Campus Schoonmeersen and Sterre S8

42475: De innovatieve techniek Raman microscopie voor meer duurzame aquacultuur

Promotor(en):	Marleen De Troch, Nico Boon
Begeleider(s):	
Contactpersoon:	Bram Martin
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Vis die je koopt in de winkel komt ofwel van visvangst of van aquacultuur. Het kweken van vis is de snelst groeiende voedingssector wereldwijd. Gelukkig kweken we momenteel al meer vis dan er gevangen wordt en dit zal enkel nog stijgen in de toekomst. Maar aquacultuur heeft nog een lange weg af te leggen voor de productie duurzaam is. Momenteel wordt nog een redelijk deel van gevangen vis gebruikt om gekweekte vis te voeden. Klinkt dit heel bizar en onduurzaam? Dan is dit thesisproject iets voor jou.

In de huidige aquacultuur worden de larvale en juveniele fases van vissen vaak gevoed met een combinatie van rotiferen en Artemia. Echter hebben deze onnatuurlijke voedselbronnen voor vis, niet altijd de juiste vetzuursamenstelling. Daarom wordt gevangen vis gemalen en dit gevoederd aan de Artemia's, om daarna de verrijkte Artemia's te voeden aan de vissen. Duurzaam onderzoek focust op alternatieve bronnen voor de juiste vetzuren maar ook op het inzetten van copepoden, die al de juiste vetzuursamenstelling hebben en de natuurlijke voedselbron zijn voor vislarven. Echter is het heel tijdrovend en manueel werk om copepod culturen te optimaliseren.

Doelstelling:

In dit thesis onderwerp gaan we een nieuwe techniek, Raman microscopie, toepassen om aquacultuur te verduurzamen. Bij Raman microscopie wordt een laser gebruikt om een staal te exciteren. De moleculen van het staal gaan Raman vibraties vertonen, kleine bewegingen tussen moleculen. Deze zorgen ervoor dat het verstrooide licht een andere golflengte heeft voor elk type binding, vb. Een C-H binding geeft een andere piek in het Raman spectrum dan een C=C. Raman microscopie geeft de mogelijkheid om diverse stalen (vis-, copepodeneieren) snel en niet destructief te meten. Met deze techniek willen we incubaties van vis- en copepodeneieren opvolgen. Bij de viseieren gaan we aan de hand van het Raman spectrum een inschatting maken over de slaagkans tot uitkomen. Hierdoor zou bij het kweken van vis, je al op voorhand weten welke eieren effectief gaan uitkomen en verkwist je geen voedsel aan de vele eieren die het niet halen. Daarnaast kan Raman microscopie ook ingezet worden op de eieren van copepoden, hierbij gebruiken we het Raman spectrum als inschatting voor de kwaliteit van de copepod culturen. Hierdoor wordt het kweken van copepoden minder intensief en hopelijk breder inzetbaar in aquacultuur.

Niet duidelijk of heb je vragen, stuur me gerust een mailtje

Locatie:

campus Sterre

Opmerkingen:

Het onderwerp staat open voor eigen inbreng van de student

42680: De invloed van extreme droogtestress op bladverkleuring en radiale groei bij lijsterbes (Sorbus aucuparia)

Promotor(en):	Jan Van Uytvanck
Begeleider(s):	Kristine Vander Mijnsbrugge, Kristine Vander Mijnsbrugge
Contactpersoon:	Kristine Vander Mijnsbrugge
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Door klimaatverandering worden meer en extremere droogteperiodes voorspeld in de toekomst met mogelijk negatieve gevolgen voor inheemse bomen zoals de lijsterbes..

Doelstelling:

Deze studie onderzoekt het effect van een extreme droogteperiode op lijsterbes. Dit experiment wordt uitgevoerd in serrecondities. Er wordt gekeken naar de onmiddellijke recuperatie van de planten na de droogteperiode, de invloed op bladverkleuring in het najaar en naar de invloed op de radiale groei tijdens en na de droogteperiode.

Locatie:

Serres en gebouwen Instituut voor Natuur- en Bosonderzoek Geraardsbergen + UGent Campus Ledeganck

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42683: Deciphering the inhibitory effect of coumarin on germination: opening a century old black box

Promotor(en):	Bartel Vanholme
Begeleider(s):	Robin De Wulf
Contactpersoon:	Bartel Vanholme
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

200 years ago, coumarin was purified from extracts of different plants. Later was found that the newly identified compound affects many physiological plant processes including germination, hypocotyl elongation, respiration, and photosynthesis. For several of these processes coumarin was shown to act in a dose-dependent manner (stimulation or inhibition dependent on the concentration) characteristic for growth regulators. Its ubiquity over the plant kingdom combined with its bioactivity suggested for an unknown role in plant growth and development. However, coumarin never got the attention that was devoted to the classical phytohormones and as a consequence processes like biosynthesis, perception and signaling were never studied on a molecular level. This resulted in a complete lack of insight in the mode of coumarin action.

Doelstelling:

To get closer to the unravelling of coumarin's physiological relevance in plants we re-opened this research field, using the effect of coumarin on germination as model system. A breakthrough finding was the identification of a coumarin insensitive mutant (cic1; complete insensitive to coumarin 1). In this project CIC1 will be characterized in more detail to further decipher the molecular mechanism underlying the activity of coumarin during plant growth and development. For this, you will work with germinating seeds and 7-10-day-old seedlings grown in vitro under different light conditions (darkness and long-day photoperiods). Additionally, you will utilize coumarin analogs mutants in specific hormone signaling cascades. This approach will enable you to determine whether certain hormones are involved in the molecular mechanism underlying the activity of coumarin.

Locatie:

campus Zwijnaarde

Onderwerp voorbehouden voor Pauline Vandemoortele

42688: Diatom-based water quality analysis of Flemish surface waters: a comparison of DNA- and microscopy-based methods

Promotor(en):	Koen Sabbe, Bart Van de Vijver
Begeleider(s):	Dimitra-Ioli Skouroliakou
Contactpersoon:	Koen Sabbe
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Diatoms, microalgae with a siliceous cell wall, are widespread and common components of aquatic microbial communities. They are excellent indicators for assessing water quality, as they form highly diverse communities and show species-specific sensitivity to environmental variables, such as pH, nutrients and conductivity. For this reason, benthic diatoms are implemented as bioindicators for determining the ecological status of surface waters in the European Water Framework Directive. Traditionally, these bioassessments are based on microscopy-based identifications and counts, which require time and a high level of taxonomic expertise. For this reason, metabarcoding of environmental DNA (eDNA) is increasingly explored and applied for characterize diatom assemblages, which is faster, cheaper and has a higher taxonomic precision than microscopy. However, metabarcoding also has its shortcomings, such as a general lack of extensive DNA reference data bases. In Flanders, water quality assessment is at present still be carried out using microscopy.

Doelstelling:

The aim of this thesis is to explore the use of eDNA metabarcoding for water quality assessment in Flanders. To this end, in collaboration with VMM (Flanders Environment Agency), benthic diatom samples will be collected at about 50 freshwater sites in Flanders. These samples will then be processes using both microscopy (in collaboration with the Botanic Garden Meise) and DNA metabarcoding. The paired microscopy and metabarcoding data sets will then be used for comparative analyses of water quality status using commonly used water quality indices. The student will acquire skills in diatom sampling, microscopic identification and DNA metabarcoding, and the use of water quality indices.

Locatie:

campus Ledeganck, campus Sterre

Opmerkingen:

As this topic is under the supervision of someone who is not Dutch speaking, the supervision and writing of the thesis will be done in English.

Onderwerp voorbehouden voor Gauke Van den Abbeele

42720: Distribution and host range of zombie fungi along latitudinal gradients

Promotor(en):	Danny Haelewaters
Begeleider(s):	Frederik De Wint, Danny Haelewaters
Contactpersoon:	
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Background

Entomopathogenic fungi (EF) of the Hypocreales order, particularly those in the genera Cordyceps and Ophiocordyceps, play crucial roles in ecological systems by killing infected arthropods. Fungi in these genera are well known for striking interactions with their hosts, which includes manipulation of host behavior resulting in effective spore dispersal after death of the host. EF exhibit diverse host associations and show notable variations in species richness and host interactions across regions. Both species diversity and host specificity seem to change along latitudinal gradients for different organismal groups, but global patterns remain poorly understood for EF.

To address these questions, our team constructed EntomoFun, version 1.0 (https://datadryad.org/stash/dataset/doi:10.5061/dryad.1zcrjdg17). This global database compiles literature on EPF occurrences and host interactions, currently comprising 1791 records. This database will serve as an important data source to investigate global patterns in EF diversity and host relationships, focusing on how these patterns change along latitudinal gradients.

Different groups of macroorganisms typically follow a latitudinal gradient; their diversity decreases with increasing latitude. This is referred to as the latitudinal diversity gradient (LDG) in ecological studies. In contrast, the diversity of fungi, which produce propagules that are microscopic in size, is often thought of as cosmopolitan—although rigorous data are lacking. A huge study based on environmental DNA from soil samples around the world did find support for the LDG hypothesis for the diversity of fungi, with the exception of some ecological groups (e.g., ectomycorrhizal fungi).

Problems

While EF, particularly Cordyceps and Ophiocordyceps, are known for their diversity and ecological roles, several knowledge gaps exist:

- Latitudinal gradients in EPF diversity. The way in which EPF species richness changes along latitudinal gradients is poorly understood. The tropics are known for higher biodiversity in general, but it is unclear whether this holds true for EPF specifically. It has been suggested that the diversity of EPF is higher in tropical regions but empirical data are lacking.

- Host specialization along latitudinal gradients. It is unknown whether EPF host specialization—i.e., how host specific are fungal species to particular insect hosts—varies across different latitudes.

Doelstelling:

The primary goal of this research is to unravel the complex relationships between EPF diversity and host specialization along latitudinal gradients, focusing on the genera Cordyceps and Ophiocordyceps. Specifically, the following research questions will be addressed:

1. Examine latitudinal changes in EPF diversity. Is there a discernible increase in species richness in tropical areas compared to subtropical and temperate regions?

2. Estimate EPF diversity by climate zone. Are certain species or genera more abundant or unique to specific climatic zones?

3. Investigate host specialization along latitudinal gradients. Do EPF in tropical regions infect a broader range of insect hosts, or are they more specialized compared to those in temperate zones?

This Master thesis research will improve our understanding of global biodiversity patterns and the ecological drivers of species interactions between entomopathogenic fungi and their insect hosts. The results of this study will have implications for conservation strategies, particularly in biodiversity hotspots where these fungi and their hosts play key roles in ecosystem functioning. The student who will take on this project will become familiar with biogeography studies, fungal taxonomy and ecology, statistical analyses, hierarchical occurrence models, and databasing.

Locatie:

Campus Ledeganck

Opmerkingen:

References: Araújo JPM, Hughes DP. 2016. Diversity of entomopathogenic fungi: which groups conquered the insect body? Advances in Genetics 94: 1-39. https://doi.org/10.1016/bs.adgen.2016.01.001 de Bekker C, Beckerson WC, Elya C. 2021. Mechanisms behind the madness: How do zombie-making fungal entomopathogens affect host behavior to increase transmission? mBio 12(5): e01872-21. https://doi.org/10.1128/mbio.01872-21 De Wint FC, Nicholson S, Koid QQ, Zahra S, Chestney-Claasen G, Seelan JSS, Xie J, Xing S, Fayle TM, Haelewaters D. 2024. EntomoFun 1.0: A global database of entomopathogenic fungi and associations with their hosts. Dryad. https://doi.org/10.5061/dryad.1zcrjdg17 Hillebrand H. 2004. On the generality of the latitudinal diversity gradient. American Naturalist 163(2): 192-211. https://doi.org/10.1086/381004 Hughes DP, Araújo JPM, Loreto RG, Quevillon L, De Bekker C, Evans HC. 2016. From so simple a beginning: the evolution of behavioral manipulation by fungi. Advances in Genetics 94: 437-469. https://doi.org/10.1016/bs.adgen.2016.01.004 Iknayan KJ, Tingley MW, Furnas BJ, Beissinger SR. 2014. Detecting diversity: emerging methods to estimate species diversity. Trends in Ecology & Evolution 29(2): 97-106. https://doi.org/10.1016/j.tree.2013.10.012 Kinlock NL, Prowant L, Herstoff EM, Foley CM, Akin‐Fajiye M, Bender N, Umarani M, Ryu HY, Şen B, Gurevitch J. 2018. Explaining global variation in the latitudinal diversity gradient: Meta‐analysis confirms known patterns and uncovers new ones. Global Ecology and Biogeography 27(1): 125-141. https://doi.org/10.1111/geb.12665 Mannion PD, Upchurch P, Benson RBJ, Goswami A. 2014. The latitudinal biodiversity gradient through deep time. Trends in Ecology & Evolution 29(1): 42-50. https://doi.org/10.1016/j.tree.2013.09.012 Pinheiro RB, Felix GM, Bell JA, Fecchio A. 2023. The latitudinal specialization gradient of bird–malarial parasite networks in South America: lower connectance, but more evenly distributed interactions towards the equator. Ecography 2023: e06763. https://doi.org/10.1111/ecog.06763 Vega FE, Meyling NV, Luangsa-ard JJ, Blackwell M. 2012. Fungal entomopathogens. Insect Pathology 2: 171-220. https://doi.org/10.1016/B978-0-12-384984-7.00006-3

42669: Diversiteit van vliegende, bloembezoekende insecten in vegetatiestructuur-, beheerintensiteit- en bloemenrijkdomgradiënten.

Promotor(en):	Jan Van Uytvanck
Begeleider(s):	Jan Van Uytvanck
Contactpersoon:	
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Insecten en ongewervelden in het algemeen staan in het huidige Europese landschap onder zware druk. In Duitsland werd recent een terugval van 75% (biomassa) geregistreerd. Alternatieve en adaptieve maatregelen in het natuurbeheer -zoals extensief graasbeheer- kunnen van belang zijn om deze terugval te temperen.

Doelstelling:

Als onderdeel van procesonderzoek in open extensief begraasde ecosystemen wordt de relatie onderzocht tussen (functionele) biodiversiteit van ongewervelden, zich ontwikkelende vegetatiestructuren en vegetaties en de habitatvoorkeuren van grote herbivoren zoals runderen en paarden.

In deze thesis ligt de focus op het natuurherstel op voormalige landbouwgronden (akkers, graslanden) van drie gebieden in de (zand)leemstreek, Bos t' Ename, Moenebroek en Boelaremeersen. We onderzoeken de impact van de variatie in vegetatiestructuur, aanwezigheid van nectarbronnen en alternatieve beheervormen (extensieve begrazing vs. traditioneel hooibeheer) op de diversiteit van vliegende, bloembezoekende insecten (vlinders, hommels en bijen, zweefvliegen, kevers,...). Deze factoren worden onderzocht in gradiënten, m.a.w. van lage naar hoge structuurvariatie en bloemenrijkdom/nectaraanbod en van extensief naar intensief beheer. De variatie in vegetatiestructuur wordt afgeleid uit gedetailleerde vegetatie-hoogtemodellen die verkregen werden aan de hand van dronebeelden (fotogrammetrie). De beheerintensiteit wordt afgeleid uit de habitatvoorkeuren van grote herbivoren (GPS-data, verkregen via gps-collars bevestigd aan de dieren), met hooibeheer als (intensief) alternatief. Verder gaan we na in hoeverre de nutriëntenhuishouding in de onderzoeksterreinen (via N- en P-beschikbaarheid in de bodem en via N/P-verhoudingen in de vegetatie) een rol spelen in de ontwikkeling van vegetatie(structuur) en het bloemen/nectar-aanbod in permanente onderzoeksplots.

De voor natuurbehoud belangrijke responsvariabelen zijn diversiteit en aantallen van vliegende, bloembezoekende insecten. Veldwerk aan de hand van transecten en waarnemingen op de permanente plots over de diverse gradiënten vind plaats gedurende de zomermaanden van 2025 (juli-september).

Locatie:

campus ledeganck of labo inbo (Sint-Denijs Westrem)

Website:

Meer informatie op: https://sites.google.com/inbo.be/procesbeheer

Samenwerking met bedrijf of non-profit organisatie

Bedrijf: Instituut voor Natuur- en Bosonderzoek
Samenwerking: promotor + begeleider

Onderwerp voorbehouden voor Warre Buysse

42614: Does dispersal disrupt the geographic mosaics of coevolution?

Promotor(en):	Dries Bonte
Begeleider(s):	Siebe Van Wunnik
Contactpersoon:	Siebe Van Wunnik
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	

Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Dispersal plays a crucial role in driving gene flow and trait remixing, which significantly influences the evolution of a species. However, species interact with other species, and these ecological interactions can shape evolutionary pathways, leading to coevolution. As different species vary in their spatial distribution, this dynamic gives rise to the geographical mosaic theory of coevolution, which predicts regions of intense coevolutionary activity (hotspots) and regions where coevolution is minimal or absent (coldspots). How does the connectivity within a system, and hence the associated dispersal rates, influence the coevolutionary dynamics between species?

Doelstelling:

The student will use a plant-herbivore interaction between the two-spotted spider mite (Tetranychus urticae) and white clover (Trifolium repens) as a model system. Mesocosm experiments will be set up to monitor the population dynamics of both species over time. The effect of connectivity will be tested under different treatments, mimicking cold- and hotspots by varying genetic diversity within treatments.

Locatie:

campus Ledeganck

42625: Doet natuurbeleid genoeg? Impact-analyse van twee beleidsinstrumenten voor natuurontwikkeling

Promotor(en): Sander Jacobs
Begeleider(s):
Contactpersoon:
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

The IPBES assessment point to to the urgency and extent of the blobal biodiversity crisis, and the ongoing decline despite policy initiatives. The Transformative change assement provides clear pointers to which type of change and policies are needed. In Flanders, many policy intitiatives are being implmented, but it is unclear wether these are effective or efficient.

Using the framework of transformative change, structured interviews, content analysis and survey statistics, two instruments, Nature Management Plans and Nature Fabric Planning (Natuurbeheerplannen en Natuurweefselplanning) for the rural and urban context will be audited for effectiveness towards tranformative change.

Doelstelling:

Locatie:

Onderwerp voorbehouden voor Odile Roberfroid

42617: Dynamics and specificity of the interactions between Lasius fuliginosus and its associates across a habitat degradation gradient

Promotor(en): Dries Bonte
Begeleider(s): Thomas Parmenier
Contactpersoon: Thomas Parmenier

Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Habitat degradation places significant stress on populations, and the negative effects are often amplified when a keystone species is impacted. This environmental stress can cause shifts or even the collapse of entire species networks associated with the key stone species when negative effects cascade through ecological interactions in the network.

Different ant species are keystone species that play a central role in symbiotic networks. Previous research, primarily conducted in the tropics, has shown that these networks are highly responsive to environmental perturbations and therefore making them good models for assessing the impact on key stone species and ecological networks.

Doelstelling:

In this research we will first assess how the symbiotic network, consisting of parasitic beetles, commensalistic arthropods and mutualistic aphids, of the key stone species Lasius fuliginosus changes across a habitat degradation gradient in Belgium. Therefore we will map the symbiont community associated with L. fuliginosus at different sites using pitfalls, sieving nest material and hand counts.

Second, we will conduct controlled behavioral and chemical tests to test the behavioral specialization and specificity of different associates within this network.

Our ultimate goal is to link changes in species composition to the degree of specialization and specificity within the network. We hypothesize that networks experiencing higher levels of environmental stress will be the first to lose specialized, host-specific species, which may or may not be replaced by less specialized species.

Locatie:

Onderwerp voorbehouden voor Arnout De Clercq

42509: East Antarctic lakes as glacial refugia for micro-invertebrates and microbial eukaryotes: evidence from fossil DNA

Promotor(en): Elie Verleyen, Wim Vyverman
Begeleider(s): Bjorn Tytgat
Contactpersoon: Elie Verleyen
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Coupled climate and earth-system models predict increased temperatures and altered precipitation regimes in vast regions of Maritime and coastal Continental Antarctica. These climate perturbations will likely result in more extensive glacial melt, the expansion of ice-free areas and increasing connectivity between regions. In turn, this will potentially result in biotic homogenization between ice-free areas, as well as range expansions and the spread of invasive species. Combined with environmental changes, these exotic species might potentially affect the native Antarctic biota which are more biogeographically structured and globally distinct than previously believed. It is becoming increasingly clear that this uniqueness and biogeographic distinctness of Antarctic terrestrial and lacustrine food webs are underlain by the past climate and tectonic history of the continent. Indeed, the formation of the Antarctic Ice Sheets c. 35 million years ago resulted in the extinction of temperate taxa, followed by the disappearance of tundra biomes since the Mid Miocene cooling event c. 14 Ma. The formation of the Antarctic Ice Sheets not only resulted in increased fragmentation between ice-free regions, but also facilitated the evolution in geographic isolation of cold tolerant taxa in scattered glacial refugia. Identifying the location of these refugia is largely based on biodiversity data and molecular phylogenies of contemporary biota. The rationale behind this is that the presence of regional endemics suggests that the regions in which these biota occur remained ice-free during glacial maxima. However, in some cases, the available biological data are counter to reconstructions of the regional deglaciation history based on radiometric dating of landforms and lake sediments. It is evident that the observed disparity between geological and biological data regarding the exact location of potential glacial refugia needs to be solved by interdisciplinary research combining approaches from biological and earth sciences. In this context, the use of ancient DNA (aDNA) is a promising approach, allowing to reconstruct past communities from DNA that remains stored in sediments, thus allowing to track their assembly and temporal dynamics during glacial and interglacial periods.

Doelstelling:

This MSc project is aimed at studying the key processes that contributed to the present-day community structure in Antarctic lakes. These processes include long-term persistence of biota in glacial refugia, but also (regional) extinction, colonization, diversification and biological succession in response to past environmental changes. In this thesis, we will extract ancient DNA (aDNA) from a lake sediment core in the Larsemann Hills, which spans the Last Glacial Maximum (LGM) and the Holocene. The use of aDNA, in combination with fossil diatom and pigment analyses, will allow us to assess which organisms survived in the lake and by extension the region during the LGM, and which taxa colonized this ecosystem during the past 40,000 years.

Locatie:

Sterre S8, Ledeganck

42717: Environmental preferences of Laboulbeniales microfungi obligately associated with insects

Promotor(en):	Danny Haelewaters
Begeleider(s):	Warre Van Caenegem
Contactpersoon:	Danny Haelewaters
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Background

Laboulbeniales (Ascomycota) are obligate associates of arthropod hosts. Species in this order are microscopic in size and produce 3-dimensional structures—named thalli—instead of hyphae and mycelia. These fungi are dependent on a living host for the entire duration of their life cycle. With about 2325 described species in 145 genera, Laboulbeniales form the most diverse fungal assemblage associated with representatives of the phylum Arthropoda, predominantly insects. Laboulbeniales are a poorly studied group, with most research having focused on alpha taxonomy, which refers to species descriptions solely based on morphology. Our research group at Ghent University studies the Laboulbeniales using an integrative taxonomy approach (meaning that we also use evidence from ecology and molecular phylogeny). In addition, we focus on trophic interactions and community ecology.

Problems

To date, community ecology research of Laboulbeniales is in its infancy, with only three published studies. Szentiványi et al. (2019) investigated whether climatic variables (temperature, humidity) influenced the distribution of ant- and bat fly-associated Laboulbeniales. They found that both the presence and prevalence of Laboulbeniales on their hosts were positively associated with low annual mean temperature and humidity. Gippet et al. (2021), based on the study of more than 9,374 workers of the invasive ant Lasius neglectus in 66 colonies, found that the presence of Laboulbenia formicarum on the ants was positively linked to warmer and dryer conditions at lower elevations. Haelewaters et al. (2022) studied the prevalence of Hesperomyces harmoniae on Harmonia axyridis ladybirds in Europe considering biotic and abiotic factors. These authors found that elytral color had a significant effect on the parasite prevalence, whereas host sex, climate, and landscape composition did not.

These first community ecology studies do not give us a full picture of general patterns that are in play. On the contrary, the results from Szentiványi et al. (2019) and Gippet et al. (2021) are seemingly contrasting, while the data from Haelewaters et al. (2022) point at no influence by climate factors. Are our current datasets too small? Are ant-associated fungal patterns governed by ant nest-specific factors rather than outside climate factors? Do different study systems simply show different patterns? We do not know the answer to these questions at this time.

Doelstelling:

Laboulbeniales occur in many different ecosystems but we have currently no idea about their environmental preferences. Knowing how abiotic factors influence infection of Laboulbeniales on their host will help to improve our understanding of their global distribution. This master thesis will use multi-year specimen data from Zuid-Kennemerland National Park in The Netherlands to test the effect of selected climate and landscape variables. Insect specimens were collected using standardized pitfall traps between 2017 and 2022 and then screened for the presence of Laboulbeniales. Infected specimens were sent to the laboratory. The student that takes on this project will identify the Laboulbeniales based on available keys in combination with molecular methods (to confirm ID, if necessary). Parasite prevalence will be analyzed in light of selected characters: temperature, humidity, season, landscape composition. This will be done for the overall dataset as a whole but perhaps also at the species-level for the most frequently collected species—depending on sampling. The student will learn about statistical modeling and methods in community ecology. Finally, there will also be the opportunity for fieldwork in Zuid-Kennemerland National Park

Locatie:

Campus Ledeganck

Website:

Meer informatie op: www.dannyhaelewaters.com/research/student-research/environmental-preferences-laboulbeniales-microfungi-obligately-associated-with-insects/

Onderwerp voorbehouden voor Renars Guts

42634: Evaluating ecological management actions in het Zwin tidal lagoon

Promotor(en):	Carl Van Colen, Tom Moens
Begeleider(s):	Carl Van Colen
Contactpersoon:	
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Coastal lagoons are subject to sediment changes depending on interactions between geomorphological, hydrological and biological factors. In the Zwin coastal lagoon (Belgium and the Netherlands), sand deposits have led to the gradual filling up of the flood plain, causing loss of safe breeding opportunities and sleeping sites for the birds through increased access by ground predators. This 'sandification' has also led to the loss of tidal flats that provide a high biomass of intertidal prey organisms for wading birds and nektonic fish, such as crustaceans, polychaetes and molluscs. The deposited sands probably originate from the increased marine erosion of the sandy beach and fore-dunes, so that the loss of biodiversity can be considered an example of coastal squeeze as a consequence of climate change. Large-scale management works have been undertaken to restore the ecological dynamics in the Zwin lagoon aiming at increasing the biodiversity and food supply for wading birds and fish in this internationally important Natura 2000 site. This thesis investigates the macrobenthos and nekton communities in the lagoon to evaluate the restoration success by analysing samples collected before and after the completion of the restoration works. Optionally the habitat use by wading birds in relation to benthic prey can be evaluated. For this thesis topic sample collection (field work) is foreseen in October.

Doelstelling:

Locatie:

42621: Explaining the European phenology of the stag beetle (Lucanus cervus)

Promotor(en): Arno Thomaes, Sander Jacobs
Begeleider(s):
Contactpersoon:
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

The European stag beetle (Lucanus cervus) is a Habitats Directive species and the largest and one of the most emblematic beetles from Europe. Its phenology shows remarkable differences across Europe which cannot be simply explained by a north-south or climatic gradient. Furthermore, due to climate change a shift can be expected in the phenology of spring emerging insects. In this thesis, we will use the stag beetle as an example species to study both the local adaptation and shift in phenology across Europe.

Doelstelling:

Locatie:

42678: Exploring bacteria from underexplored habitats as novel sources of pigments for biotechnology

Promotor(en): Anne Willems
Begeleider(s):
Contactpersoon: Fleur Willekens
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Color is key in many products of various industries. Chemical dyes are suspected of inducing unwanted health effects. Therefore, there is a strong interest in natural pigments. These natural pigment have applications in the textile, plastic, pharmaceutical, food, nutraceutical and cosmetic industry.

A colorful diversity of pigments is produced by bacterial strains from diverse sources. Bacteria are promising pigment producers as a result of the relatively low cost for culturing, a rapid growth and easily scalable. Furthermore, bacteria are not influenced by season and are more eco-friendly than plants in terms of occupying less space and not competing with agriculture. These bacterial pigments have several beneficial features e.g. UV-protection, antimicrobial, antioxidant, antiparasitic and anticancer activities, which can be used for the discovery of novel drugs or in anti-aging creams and sunscreens. In contrast to synthetically produced dyes, natural dyes might even possess a health benefit.

While most researchers use well-studied bacteria in the search for natural pigments, this project focuses on pigmented bacteria from underexplored habitats including but not limited to Antarctica, parasitic worms in fish and the viscera of bees.

Doelstelling:

This project aims to discover new pigmented bacterial strains and their pigments by characterization of the pigments, purification of the pigments and revealing their interesting bioactive properties. As initial identification, pigments will be extracted from the bacteria and analyzed with a spectrophotometer. Interesting pigments will be purified using HPLC for further characterization. Pigment features such as acid, heat and light stability, solubility and hygroscopicity will be tested. In addition, some bioactive properties such as antioxidant and antimicrobial activity will be assessed. For strains of interest, the gene clusters associated with pigment production will be identified by using whole genome data.

Locatie:

Campus Ledeganck

42706: Exploring the role of marine nematodes in methane bioremediation within marine sediments

Promotor(en):	Rodgee Mae Guden, Tom Moens
Begeleider(s):	Rodgee Mae Guden
Contactpersoon:	Rodgee Mae Guden
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Methane (CH_4) is a potent greenhouse gas with a global warming potential approximately 25 times greater than that of carbon dioxide (CO_2) over a 100-year period. Marine sediments are known to be both sources and sinks of methane, with various microbial processes playing crucial roles in its production and consumption. While the role of bacteria and archaea in methane cycling is well-documented, the potential involvement of higher organisms, such as marine nematodes, in methane removal remains underexplored.

Marine nematodes are among the most abundant and diverse metazoans in marine sediments, playing essential roles in nutrient cycling, sediment structure, and organic matter decomposition. They are known to interact with microbial communities, potentially influencing microbial processes through grazing, bioturbation, and the release of organic compounds. Given their ecological significance, it is plausible that marine nematodes could also impact methane cycling in marine sediments, either directly or indirectly.

Doelstelling:

This research aims to investigate whether marine nematodes contribute to methane removal in marine sediments, thereby playing a role in bioremediation. Specifically, we will explore the presence and abundance of marine nematodes in methane-rich sediments, assess their potential to influence methane oxidation processes, identify specific nematode species involved in methane removal, and evaluate the interactions between marine nematodes and methane-oxidizing microorganisms. By elucidating these relationships, we hope to gain a deeper understanding of the ecological functions of marine nematodes and their potential role in mitigating methane emissions from marine sediments.

Locatie:

campus Sterre (S8) en campus Ledeganck

42675: Fantastic fungi from Indonesia

Promotor(en):	Annemieke Verbeken
Begeleider(s):	Bobby Sulistyo
Contactpersoon:	
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Indonesia is a megadiverse archipelagic country with 3 distinct biogeographical regions and various hotspots. Due to this, many species found there are endemic and undescribed, including macrofungi. Through 2 sampling trips in spring 2024 and 2025, we accumulated some interesting and potentially undescribed species of agaricoid fungi.

Doelstelling:

Aim

- Morphological study of agaricoid fungi from Indonesia
- DNA extraction and generation of some molecular markers
- Phylogenetic study of agaricoid from Indonesia

Locatie:

42656: Filling the gap in riboflavin (vitamin B2) metabolism

Promotor(en):	Dominique Van Der Straeten
Begeleider(s):	Kenzo De Coninck
Contactpersoon:	
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Today, more than two billion people suffer from micronutrient deficiencies, referred to as "hidden hunger". This condition results from inadequate intake or poor absorption of vitamins and essential minerals. It is particularly acute in lower-income countries, where it disproportionately affects children and women of reproductive age. Hidden hunger is closely linked to the consumption of monotonous diets. Biofortification of staple crops has been proposed as an efficient and sustainable away to combat hidden hunger. This involves the use of genetic engineering techniques to target the metabolic pathways of specific micronutrients to enhance their content in plant tissues. At the Laboratory of Functional Plant Biology, biofortified rice lines (Oryza sativa subsp. japonica) have been designed to enhance the content of two essential B-vitamins: thiamine (B1) and riboflavin (B2). We will screen the lines for their micronutrient content and the expression of the introduced transgenes. The impact of increased endogenous riboflavin production on plant growth, agronomic and physiological parameters, and vitamin metabolism will also be studied to understand the effects of biofortification on growth, metabolism, and physiology. Additionally, a new strategy is being developed to target a potential regulator of riboflavin biosynthesis. This will allow us to study riboflavin biofortification from a different angle, paving the way for future biofortification strategies to alleviate riboflavin deficiencies.

Doelstelling:

The aim of this project is to characterize transgenic biofortified rice lines. The phenotype of these plants will be assessed over a full growth cycle. Target (B1 and B2) and non-target (B3, B5, B6, B7, and B9) vitamins will be quantified. Transgene expression levels will be analyzed using real time quantitative PCR (qPCR). These data will be integrated to identify the best-performing lines, which will undergo further evaluation of their physiological parameters. Additionally, this project aims to characterize a potential regulator of riboflavin metabolism via mutant analysis and evaluate its use in a new biofortification strategy. This will involve vector construction using GoldenBraid cloning, followed by plant transformation, selection, and molecular analysis using qPCR on genomic DNA to obtain information regarding zygosity and T-DNA copy number.

Techniques used: Agrobacterium-mediated transformation of Arabidopsis and rice, GoldenBraid cloning, isolation of DNA and RNA, PCR, in vitro plant growth, phenotypic analyses, assessment of multiple physiological parameters.

Locatie:

Ledeganck Campus, Laboratory of Functional Plant Biology

42567: Functional Analysis of GLB-18 in Caenorhabditis elegans

Promotor(en):	Bart Braeckman
Begeleider(s):	Jingjing Luo
Contactpersoon:	Bart Braeckman
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Globins are proteins involved in oxygen transport/storage, redox reactions and signalling. GLB-18 of the nematode Caenorhabditis elegans is a globin-like protein that exists in two isoforms, both of which are predicted to be expressed in mitochondria. Mitochondria are essential organelles with critical roles in energy metabolism, apoptosis and various other cellular processes. Disruption of mitochondria can lead to excessive production of reactive oxygen species (ROS), which may result in disease and reduced lifespan. However, mild mitochondrial dysfunction, with limited ROS production, has been associated with increased lifespan. Among all C. elegans globins, GLB-18 is unique in that it is expressed in nearly all neurons. Neurons are essential for coordinating behavior, movement, sensory perception, and survival.

Doelstelling:

This thesis aims to investigate the role of GLB-18 in specific, well-studied neuronal pathways. As GLB-18 is expressed in oxygen-sensing neurons, we will test behavioral responses of glb-18 mutants to varying environmental oxygen levels (anoxia/hypoxia). To study its role in chemosensory neurons, the responses of glb-18 mutants to specific chemicals, such as diacetyl and isoamyl alcohol, will be assessed. These experiments will provide insight into whether GLB-18 plays a regulatory role in behavioral responses under different environmental conditions.

Locatie:

Campus Ledeganck

42668: Habitatgebruik van grote grazers in heide- en kustecosystemen

Promotor(en):	Jan Van Uytvanck
Begeleider(s):	Sam Provoost, Marijke Thoonen
Contactpersoon:	
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

In een hele reeks ecosystemen worden als vorm van natuurbeheer grote grazers ingezet. Ze zorgen voor structuurrijke vegetaties die voor een hoge biodiversiteit aan organismen kunnen instaan. Toch is niet steeds duidelijk hoe vegetatiestructuur en terreingebruik (en effectieve graasdruk) van grote grazers elkaar beïnvloeden.

Doelstelling:

Als onderdeel van onderzoek naar ecologische processen in open extensief begraasde ecosystemen werden in o.a. kustduin- en heide-ecosystemen grote grazers (runderen en paarden) uitgerust met een GPS-zender die om het half uur hun positie in het terrein registreert. Zo krijgen we voor de verschillende soorten grazers inzicht in hun habitatvoorkeuren, die we kunnen uitdrukken aan de hand van de aard (vegetatietypes, bodemvochtigheid) en de vegetatiestructuur (gedetailleerde vegetatiehoogtemodellen verkregen uit fotogrammetrie met drones).

In deze thesis ligt de focus dus op het verkrijgen van inzichten in de verschillen (of overeenkomsten) in het terreingebruik van verschillende soorten en in de verschillen (of overeenkomsten) van het terreingebruik van grote grazers in verschillende ecosystemen, hier kustduinen en heiden.

We proberen te begrijpen hoe de habitatvoorkeuren van grote herbivoren (maar ook bv. de aanwezigheid van drinkpoelen/vennen mee sturend kunnen zijn voor de ontwikkeling van vegetatie en structuurvariatie in de toekomst.

Locatie:

campus Ledeganck

Website:

Meer informatie op: https://sites.google.com/inbo.be/procesbeheer

Samenwerking met bedrijf of non-profit organisatie

Bedrijf: Instituut voor Natuur- en Bosonderzoek
Samenwerking: begeleider

Onderwerp voorbehouden voor Jobbe Vermandere

42671: Het belang van vegetatie, vegetatiestructuur en microklimaat voor de (functionele) biodiversiteit van ongewervelden (in het bijzonder kevers en wantsen) in extensief begraasde natuurgebieden

Promotor(en):	Jan Van Uytvanck
Begeleider(s):	Jan Van Uytvanck
Contactpersoon:	
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Insecten en ongewervelden in het algemeen staan in het huidige Europese landschap onder zware druk. In Duitsland werd recent een terugval van 75% (biomassa) geregistreerd. Alternatieve en adaptieve maatregelen in het natuurbeheer -zoals extensief graasbeheer- kunnen van belang zijn om deze terugval te temperen.

Doelstelling:

Als onderdeel van procesonderzoek in open extensief begraasde ecosystemen wordt de relatie onderzocht tussen (functionele) biodiversiteit van ongewervelden, zich ontwikkelende vegetatiestructuren en vegetaties en de habitatvoorkeuren van grote herbivoren zoals runderen en paarden.

In deze thesis ligt de focus op de diversiteit, aantal en biomassa van ongewervelden (in het bijzonder kevers en wantsen; via determinatie en met behulp van automatische beeldverwerking) die in nauwe relatie leven met vegetatie en vegetatiestructuur op verschillende schaalniveaus. Gedetailleerde, bestaande vegetatiekaarten en vegetatiehoogtemodellen die verkregen werden aan de hand van dronebeelden (fotogrammetrie) en de hier aan gerelateerde aard en variatie in microklimaten (aan de hand van warmtecamera-beelden en vochtloggers) worden gebruikt als verklarende factoren voor aantallen, diversiteit en biomassa van de bestudeerde ongewervelden. Het onderzoek wordt uitgevoerd in diverse ecosystemen waarin zich een vegetatiestructuurgradient ontwikkelde.

Bijkomend kan worden ingeschat hoe de habitatvoorkeuren van grote herbivoren (afgeleid uit GPS-data, verkregen via gps-collars bevestigd aan de dieren) mee sturend kunnen zijn voor de ontwikkeling van vegetatie en structuurvariatie in de proefgebieden.

Locatie:

campus ledeganck of labo inbo (Sint-Denijs Westrem)

Website:

Meer informatie op: https://sites.google.com/inbo.be/procesbeheer

Samenwerking met bedrijf of non-profit organisatie

Bedrijf: Instituut voor Natuur- en Bosonderzoek
Samenwerking: promotor + begeleider

Onderwerp voorbehouden voor Giulia Colazzo

42731: How do insect eggs survive opportunistic infections of micro-organisms

Promotor(en):	Nicky Wybouw, Gerben Debruyn
Begeleider(s):	
Contactpersoon:	Nicky Wybouw
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	Master of Science in Biochemistry and Biotechnology
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Various selective forces shape the size, shape, and colouration of insect eggs. One of these selective forces is the interaction of eggs with pathogenic and beneficial micro-organisms. Indeed, pathogenic fungi as well as (endo)symbiotic bacteria thrive inside and on insect eggs. Remarkably, a great diversity of egg morphology and colouration can be observed in stick insects, a speciose clade of herbivores. Interestingly, the yolk colouration of different stick insect species can vary from yellow to red. (Peruphasma schultei is just one example of a species with enigmatic red yolk.) At our lab, we currently breed a pigment mutant where yolk color shifted from red to yellow, creating interesting research avenues. In this master project, we study the ecological interaction of stick insect eggs with (endo)symbiotic bacteria and pathogenic fungi.

Doelstelling:

The student will use our collection of stick insect lab populations to determine whether different concentrations or types of pigments can inhibit growth of pathogenic fungi. These experiments include disc diffusion trials and growth inhibition assays. Furthermore, the student will also investigate the presence of endosymbiotic bacteria in the eggs by performing typical molecular biology experiments.

Locatie:

campus Ledeganck

42520: How do Messor ants make bread?

Promotor(en):	Nicky Wybouw, Jonathan Romiguier
Begeleider(s):	
Contactpersoon:	Nicky Wybouw
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

The evolution of herbivory, or feeding exclusively on plant material, is severely constrained in animals because plants are a highly unfavorable food source due to their nutritional and defensive qualities. As a result, herbivory is typically considered as an evolutionary key innovation in animals. For instance, of the ~25,000 species of ants, only few lineages have evolved a herbivorous lifestyle. Here, Messor ants are remarkable because this genus can survive on the highly imbalanced diet of plant seeds. Intriguingly, using plant seeds, workers make a bread-like substance to feed the whole colony.

To feed on plant leaves and sap, certain insect taxa rely on symbiotic bacteria for the digestion of complex sugars and the provision of essential amino acids and vitamins. Another well-known example of an insect/bacterial symbiosis promoting a remarkable plant-based diet is termites consuming wood. Our ongoing research has uncovered that the seed-harvesting Messor ants are intimately associated with a clade of lactic acid bacterial symbionts. Interestingly, lactic acid bacteria are also typically associated with bread making in human societies. We are currently drawn to the exciting hypothesis that the acquisition of these bacterial symbionts promoted the evolution of the seed-feeding and bread-making lifestyle of Messor.

Doelstelling:

The project will investigate whether lactic acid bacterial symbionts contribute to the feeding ecology of Messor ants. This is a highly multi-disciplinary master project, incorporating approaches from behavioural and feeding ecology, microbiology, and molecular biology. The project will use experimental colonies of the common seed-harvesting ant Messor barbarus. Depending on the student's interests, emphasis can be given to a certain discipline. This is in close collaboration with the University of Montpellier, where the co-supervisor is located.

Locatie:

Campus Ledeganck

Website:

Meer informatie op: www.nickywybouw.org

42539: How does temperature shape the spread and persistence of Wolbachia infection in haplodiploid mites

Promotor(en):	Nicky Wybouw
Begeleider(s):	Emma Van Reempts
Contactpersoon:	Nicky Wybouw
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Wolbachia are maternally transmitted bacterial symbionts that infect the reproductive organs of insects and mites. Wolbachia manipulate the reproduction of their arthropod host to spread within host populations. Cytoplasmic incompatibility (CI) is the most common manipulation strategy and disrupts the embryonal development when infected males mate with uninfected females.Previous studies have shown that temperature impacts the symbiotic interactions between Wolbachia and arthropods, suggesting that temperature might be a major determinant for Wolbachia spread and persistence.

Doelstelling:

The primary objective of this thesis is to contribute to unravelling the complex interactions between temperature and host/Wolbachia genotype. The student will focus on a three-species study system of sympatric and hybridizing Tetranychus species. The student will combine high-resolution phenotyping with classic population biology experiments.

Locatie:

campus Ledeganck

Onderwerp voorbehouden voor Milan De Corte

42493: How sturgeon becomes edentulous

Promotor(en):	Ann Huysseune, Adelbert De Clercq
Begeleider(s):	Ann Huysseune, Adelbert De Clercq
Contactpersoon:	Adelbert De Clercq
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

As a rule, all non-mammalian tooth-bearing vertebrates are capable of lifelong tooth replacement. This means that each tooth, after having exerted its function for a certain amount of time, is eventually lost and replaced by a new tooth, as a natural process (i.e., not induced by trauma or precocious loss of the tooth). There are nevertheless some exceptions to this rule. Certain taxa indeed develop a dentition in early life stages, but lose their teeth later in life. Examples can be found both in non-teleost actinopterygians as well as in teleost fish.

Sturgeons (Acipenser sp.) are non-teleost fish and representatives of one of the earliest branches after the divergence between actinopterygians and sarcopterygians. Although sturgeons possess a dentition in early post-embryonic and juvenile stages, adult sturgeons are edentulous. Hardly anything is known when and how teeth in sturgeons are eventually lost.

Doelstelling:

The aim of this study is to collect information on the loss of teeth in the sterlet sturgeon (Acipenser ruthenus). In particular, the following questions will be addressed: at what age/length does the sterlet sturgeon lose its teeth? Does it lose teeth simultaneously on all tooth-bearing elements? What is the underlying mechanism: precocious resorption of the functional tooth? Failure to form a replacement tooth? Another explanation? These questions will be addressed through whole mount staining, histological procedures and (immuno)histochemical methods.

This study is in collaboration with the Zoology Department of Charles University (Prague) from which the sterlet material will be obtained (and is already available to a large extent).

Locatie:

Campus Ledeganck

Onderwerp voorbehouden voor Raf Vanneste

42661: How Ulva blooms, genotyping mapping populations

Promotor(en):	Olivier De Clerck, Tom Jacobs
Begeleider(s):	Jonas Blomme, Emma Coulembier Vandelannoote
Contactpersoon:	Olivier De Clerck
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	Master of Science in Biochemistry and Biotechnology
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Coastal ecosystems are heavily impacted by human activity, resulting in habitat destruction and a large influx of nutrients. As a consequence, macroalgal populations belonging to the genus Ulva (Sea Lettuce) can bloom into so-called “green tides”. Green tides have intensified in tropical and temperate latitudes, including European coastlines. In the Yellow Sea of China, Ulva prolifera can cover up to 20,000 km² and negatively impacts ecosystems and local economies (aquaculture, clean-up, tourism). Various traits are associated with bloom formation such as faster colonization rates, larger tissue expansion, or more efficient utilization of nutrients. Still, the genetic regions and molecular mechanisms underlying green tide behavior are not known.

This master thesis is part of a larger research project aiming at studying the genetic factors of Ulva phenotypic traits such as growth, rhizoid formation and morphology. We have crossed two Ulva lab strains with contrasting phenotypes and have generated the first mapping population in a green seaweed. Phenotypes segregate in this mapping population, giving us the possibility to associate genetic variation to e.g. presence or absence of a rhizoid structure. In this master thesis, we want to develop high-throughput genotyping for the mapping population using known SNPs between both parental strains.

Ultimately, the research aims to identify and characterize genetic regions associated with green tide formation. Ulva is a model species for green seaweed research and currently the only seaweed for which a large set of genetic tools are available. Candidate genes underlying phenotypes will be strong candidates for future functional biology studies.

Doelstelling:

In this project, the student will identify SNPs between the parental strains by comparing their genomes, and later design primers to test if these SNPs can be amplified and verified by Sanger sequencing or short-read amplicon sequencing. The student will be involved in genotyping: DNA extraction, primer design, simplex & multiplex PCR, creating high-throughput genotyping methods. Genotyping outcomes will be analysed using Geneious software.

Growth characteristics will be tracked of the mapping population. Besides microscope observations, the semi-automated IGIS platform will be used to measure relative growth over time. These phenotypic traits can then be linked to the occurrence of SNPs (QTL-mapping).

In a next step, we will investigate if similar mutations are correlated to these phenotypes in natural populations, maintained in the host lab.

Locatie:

VIB - Center of Plant Systems Biology

42665: Identification and characterization of pesticide target site mutations associated with pesticide resistance in Apis mellifera

Promotor(en):	Dirk de Graaf
Begeleider(s):	Lina De Smet, Gilles Verbinnen
Contactpersoon:	
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Honey bees are important pollinators, both ecologically and in agriculture. However, bees and other pollinators face many threats such as disease, habitat loss, invasive species, climate change, exposure to pesticides… The combination of these threats causes worldwide colony losses. This topic is part of the Better-B project (https://www.better-b.eu/) which is trying to improve the resilience of beekeeping to abiotic stresses. More specifically, we will be looking at the resilience of honey bees against pesticides. Pesticides have many lethal and sub-lethal effects such as impaired learning, thereby contributing to colony losses.

Doelstelling:

Repeated exposure to pesticides can cause insects to develop resistance against those pesticides. This has only been described in pest species such as mosquitos, beetles and moths. However, we are interested whether beneficial insects such as honey bees also develop resistance against pesticides. Resistance at a genetic level happens either through mutations in the target sites of pesticides or in detoxification enzymes. We are screening large datasets of genetic information to identify target site mutations. These mutations will be then characterized to evaluate their impact on the resistance against pesticides. The overall goal is to develop a screening tool based on these mutations to identify honey bee populations historically burdened with pesticide exposure.

In this topic, you will be involved in the discovery of new mutations, by analysing large genetic datasets using different bioinformatic tools in Linux; the characterization of these mutations, through protein modelling, heterologous gene expression in oocytes from Xenopus laevis and enzymatic assays for functional characterization of voltage-gated sodium channels, the development of a quantitative TaqMan PCR test for mutations of interest and the usage of this screening tool to perform population studies. Expression profiling from some immunity and detoxification studies will be performed on exposed colonies in a gradient of landscape complexity in a European context.

Locatie:

campus Stere

Onderwerp voorbehouden voor Jonas Guidée

42569: Identifying molecular pathways related to the protein globin-3 in Caenorhabditis elegans

Promotor(en):	Bart Braeckman, Diana Naalden
Begeleider(s):	Diana Naalden
Contactpersoon:	Bart Braeckman
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Caenorhabditis elegans is a perfect model organism as it is small, easy to culture, has a high reproductive rate and genetic engineering is relatively easy. It has contributed greatly to the understanding of many complex cellular processes. In this simple worm, the nervous system consists of 302 neurons that are subdivided in a somatic nervous system (282 neurons) and a small pharyngeal nervous system (20 neurons). Our research group aims to understand the molecular mode of action of globins. The globin family in C. elegans is extensive (34 genes) compared to that of many other organisms (e.g. humans: 12 genes). The globin proteins vary strongly in size and sequence and demonstrate a distinct expression pattern in specific sets of neurons. Initially, it was assumed that the primary function of globins was confined to O2 storage and transport, but recent functional analysis has revealed involvement in a wide range of cellular processes. Nevertheless, for the majority of the globins expressed in C. elegans, the precise function remains unknown.

Doelstelling:

In this MSc thesis you will investigate GLB-3, a globin that is found in the reproductive organs and nervous system of C. elegans1. In agreement with this expression pattern, a knockout mutant shows severely reduced fertility and behavioural abnormalities. The glb-3 gene expresses two different isoforms suggesting isoform subfunctionalization in gonads and neurons. You will study the differences between the two GLB-3 isoforms by utilizing various mutant strains combined with phenotypic screening. Furthermore, you will explore the potential molecular mechanism and pathways in which glb-3 is involved. One of the approaches will be to utilize identified potential interactors and confirm this in the nematode by using co-immunoprecipitation, western blot and fluorescence microscopy.

1Hafideddine et al., 2023. GLB-3: A resilient, cysteine-rich, membrane-tethered globin expressed in the reproductive and nervous system of Caenorhabditis elegans. doi: 10.1016/j.jinorgbio.2022.112063.

Locatie:

Campus Ledeganck

Onderwerp voorbehouden voor Jules Tobback

42694: Impact of light and salinity stress on chytrid parasitism in estuarine diatom blooms

Promotor(en):	Wim Vyverman, Koen Sabbe
Begeleider(s):	Rik Debeer
Contactpersoon:	Wim Vyverman
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Among the many groups of phytoplankton, diatoms stand out as primary producers, contributing one fifth of global oxygen production, and often dominating seasonal phytoplankton blooms in all aquatic habitats. These blooms are shaped by interplaying drivers, of which parasitism is highly understudied. Chytrids (Fungi) are known to be important parasites for diatoms, potentially causing mass mortalities and impacting the timing, duration and succession of their blooms. The question remains however, to what extent abiotic stress affects the susceptibility of diatoms to chytrid parasitism, which is very relevant within the context of climate change and other human impacts. The prevalence of chytrid infections in diatom communities can be monitored microscopically allowing identification and quantification of infected diatom species, but this technique is labor-intensive, time-consuming and requires a certain level of taxonomic expertise. Instead, an innovative method combining fluorescent in situ hybridization of diatoms in suspension (FISH-IS) and chitin staining of chytrids enables automated and standardized quantification and identification of thousands of suspended diatom cells and their level of chytrid infections by Imaging Flow Cytometry (IFCM).

Doelstelling:

The main objective of this master thesis is to experimentally test whether diatoms are more susceptible to chytrid parasitism under light limitation and salinity stress. This will be done for diatoms isolated from samples of the Belgian part of the Schelde estuary, which is increasingly impacted by climate change-related discharge variability affecting salinity, and by dredging increasing turbidity. Dominant Schelde diatoms will be grown in microcosms under different light and salinity levels with or without chytrids. The prevalence of chytrid infections in each microcosm will be monitored by IMFC after combining FISH-IS of dominant Schelde diatoms with chitin staining of chytrids.

Locatie:

Campus Sterre

42664: Impacts of glacier retreat on the trophic niches of Greenlandic fjord communities

Promotor(en):	Jan Vanaverbeke
Begeleider(s):	Hannah Gaber
Contactpersoon:	Hannah Gaber
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Climate change is impacting marine ecosystems worldwide, with the Arctic facing some of the most obvious changes. Rising temperatures are causing glacier retreat in Arctic fjord systems, with marine-terminating glaciers eventually becoming land-terminating glaciers. This shift in glacier type alters the fjord’s hydrology, phytoplankton dynamics, and productivity (e.g., Meire et al., 2023, https://doi.org/10.1038/s41561-023-01218-y). Since phytoplankton is the primary energy source for Arctic fjord food webs, changes in phytoplankton dynamics and productivity are expected to alter the amount and quality of food available to species in these fjords, potentially shifting their resource use and trophic interactions. However, these impacts remain largely unknown.

Doelstelling:

This thesis will use stable isotope analysis to investigate how glacier retreat influences the trophic niches (resource use and trophic position) of Greenlandic fjord communities, based on a space-for-time approach. By comparing community trophic niches across three fjord systems covering a gradient from marine- to land-terminating glaciers, the study aims to understand how shifts in glacier type influence Arctic fjord food webs. The student will (1) process samples collected during a field campaign in June 2025 in Disko Bay, SW Greenland for stable isotope analysis; (2) integrate this new dataset with existing stable isotope data from other fjord systems in SW Greenland; and (3) model the isotopic niches of fjord communities, comparing niche characteristics using community-wide metrics (e.g., done in Mavraki et al., 2020, https://doi.org/10.1016/j.marenvres.2019.104868). Ultimately, this thesis will provide insights into the stability and resilience of Arctic fjord communities in the face of climate change, and will contribute to broader research on how glacier retreat affects the structure, functioning, and carbon flow in Arctic fjord food webs.

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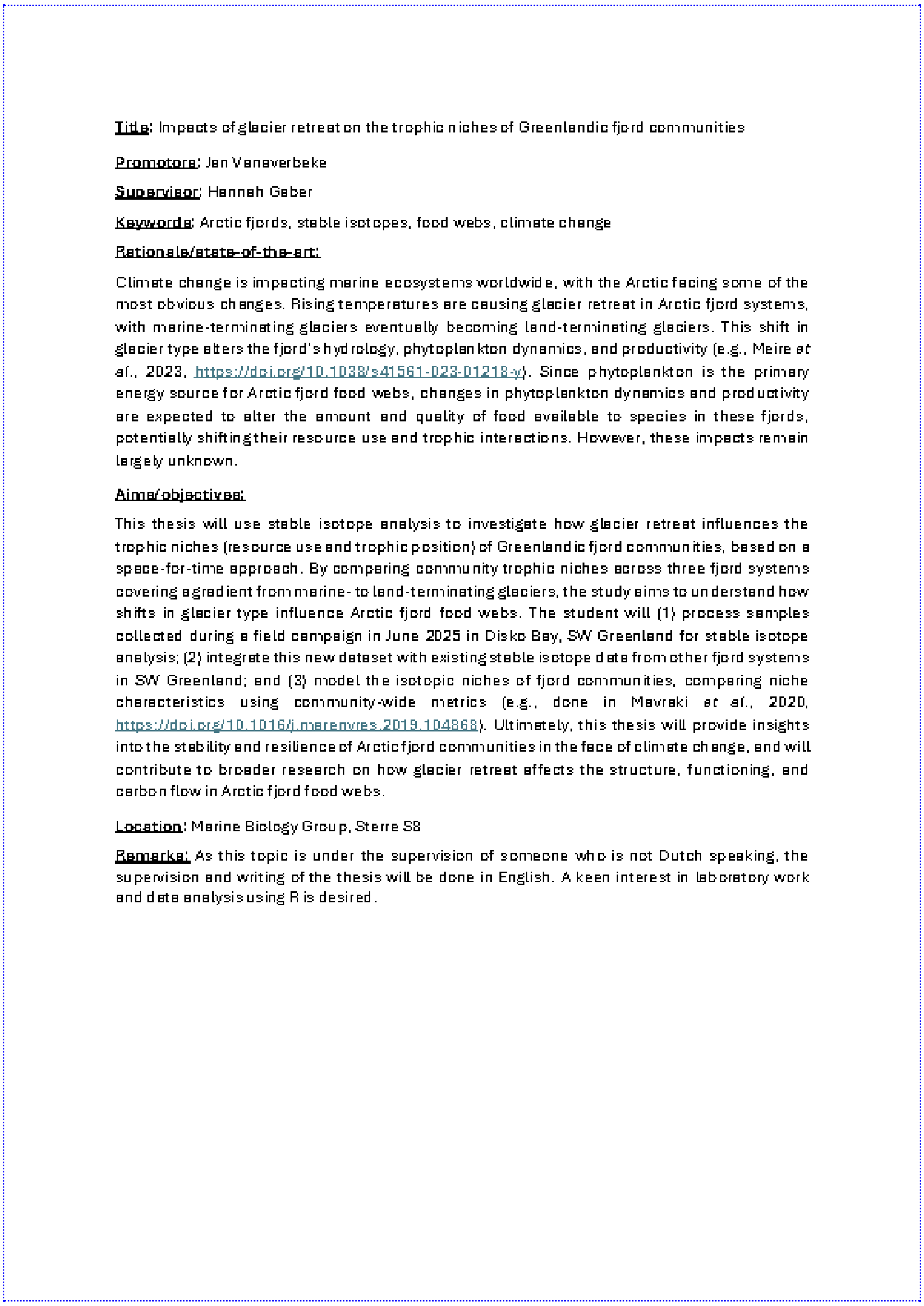

Title: Impacts of glacier retreat on the trophic niches of Greenlandic fjord communities

Promotors: Jan Vanaverbeke

Supervisor: Hannah Gaber

Keywords: Arctic fjords, stable isotopes, food webs, climate change

Rationale/state-of-the-art:

Climate change is impacting marine ecosystems worldwide, with the Arctic facing some of the most obvious changes. Rising temperatures are causing glacier retreat in Arctic fjord systems, with marine-terminating glaciers eventually becoming land-terminating glaciers. This shift in glacier type alters the fjord's hydrology, phytoplankton dynamics, and productivity (e.g., Meire *et al.*, 2023, https://doi.org/10.1038/s41561-023-01218-y). Since phytoplankton is the primary energy source for Arctic fjord food webs, changes in phytoplankton dynamics and productivity are expected to alter the amount and quality of food available to species in these fjords, potentially shifting their resource use and trophic interactions. However, these impacts remain largely unknown.

Aims/objectives:

This thesis will use stable isotope analysis to investigate how glacier retreat influences the trophic niches (resource use and trophic position) of Greenlandic fjord communities, based on a space-for-time approach. By comparing community trophic niches across three fjord systems covering a gradient from marine- to land-terminating glaciers, the study aims to understand how shifts in glacier type influence Arctic fjord food webs. The student will (1) process samples collected during a field campaign in June 2025 in Disko Bay, SW Greenland for stable isotope analysis; (2) integrate this new dataset with existing stable isotope data from other fjord systems in SW Greenland; and (3) model the isotopic niches of fjord communities, comparing niche characteristics using community-wide metrics (e.g., done in Mavraki *et al.*, 2020, https://doi.org/10.1016/j.marenvres.2019.104868). Ultimately, this thesis will provide insights into the stability and resilience of Arctic fjord communities in the face of climate change, and will contribute to broader research on how glacier retreat affects the structure, functioning, and carbon flow in Arctic fjord food webs.

Location: Marine Biology Group, Sterre S8

Remarks: As this topic is under the supervision of someone who is not Dutch speaking, the supervision and writing of the thesis will be done in English. A keen interest in laboratory work and data analysis using R is desired.

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Locatie:

Marine Biology Group, Campus Sterre S8

Opmerkingen:

As this topic is under the supervision of someone who is not Dutch speaking, the supervision and writing of the thesis will be done in English. A keen interest in laboratory work and data analysis using R is desired.

42662: Improving CRISPR/Cas efficiency for seaweed genome editing

Promotor(en): Jonas Blomme, Tom Jacobs
Begeleider(s): Olivier De Clerck, Alejandro Sebiani Calvo
Contactpersoon: Jonas Blomme
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor: Master of Science in Biochemistry and Biotechnology
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Green seaweeds of the Ulva genus are important primary producers in coastal ecosystems. Upon habitat disturbance, e.g. eutrophication, fast and massive blooms of Ulva can generate “green tides”. The increasing occurrence of such events causes ecosystem degradation and impacts coastal communities in many regions of the world. Our research group focuses on understanding the cellular process involved in carbon fixation and its relation to Ulva’s ability to grow so fast. This knowledge could also offer interesting applications in seaweed aquaculture.

Ulva mutabilis/compressa is a lab model organism for the study of green seaweed biology. We are able to activate the expression of genes (gain-of-function mutants), and recent developments allow us to generate loss-of-function mutants with a vector-based CRISPR/Cas systems. CRISPR efficiency is currently low, with mutation efficiencies of 6 E-07 – 5 E-05 for a single target. We need to improve the current vector-based CRISPR efficiency in order to design larger screenings of mutants (multiplex genome editing) and functionally characterize Ulva genes at scale.

Doelstelling:

The aim of this master thesis is to test which factors can boost vector-based CRISPR/Cas efficiency in Ulva. The student will evaluate the effect of different building blocks such as regulatory elements (e.g. promoters), protein domains (e.g.nuclear localization signals) but also culture conditions (e.g. nutrient starvation and light/dark cycle) on gene editing in Ulva. Targeted mutations will be evaluated using genotyping by Sanger sequencing and bioinformatic tools. In particular, this project will study the DNA repair mechanisms (HDR and NHEJ) favored in Ulva after the double-strand break induced by the CRISPR system. Our preliminary results point towards favoring HDR, a powerful mechanism in genome engineering that is rare in the green lineage.

The student will work with the following topics and/or techniques: Ulva cultivation and maintenance of lab strains, Golden Gate cloning, Gibson Assembly, E. coli and Ulva transformation, plasmid and genomic DNA extraction, PCR, CRISPR/Cas vector design, general molecular biology techniques, and bioinformatic analysis.

Locatie:

VIB - Center of Plant Systems Biology

42645: Improving kelp restoration efforts with probiotics - a case study of the golden kelp (Laminaria ochroleuca)

Promotor(en): Olivier De Clerck
Begeleider(s): Sofie Peeters
Contactpersoon: Sofie Peeters
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:

Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Kelps are large brown seaweeds that form vast underwater ‘rainforests’, referred to as kelp forests. Due to the high productivity of the kelps and the complex, three-dimensional habitats they create, kelp forests are one of the most diverse and productive marine habitats on Earth. Golden kelp (Laminaria ochroleuca) is a warm-water kelp species that has declined in southern Europe. Microbiome engineering is a rapidly evolving field with the goal to improve the function of an ecosystem by manipulating the composition of microbes. Within the framework of this thesis the student will investigate how to use bacteria to increase the survival of juvenile kelp (i.e. increase their resilience) under heat stress. We will study how kelp associated bacteria can reduce heat stress and increase kelp reproduction. The work will involve kelp and bacteria co-cultivation experiments, microscopy, molecular work and the analyses of bacterial and kelp (meta)genomic & transcriptomic data.

Doelstelling:

Locatie:

sterre s8

Website:

Meer informatie op: phycology.ugent.be

42618: Improving life cycle control of economically important seaweeds - a case study of European nori

Promotor(en): Olivier De Clerck, Jessica Knoop
Begeleider(s): Silke Bouckenooghe
Contactpersoon: Silke Bouckenooghe
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Eng: The genus Pyropia, belonging to the Bladed Bangiales, are globally known for nori production. The life cycle has been studied extensively in Asian species to optimize its cultivation as a food source. Interest is growing to cultivate the European counterparts (the genus Porphyra) for various applications. In addition to its use as food, Porphyra has value in the presence of bioactive compounds such as UV-protectants, biostimulants and pigments. However, its complex life cycle, which includes a diploid microscopic phase and a haploid thallus phase has not yet been fully clarified. Some bottlenecks in the life cycle control are hindering reliable production.

NL: Het genus Pyropia, dat behoort tot de groep van de bladed Bangiales, is wereldwijd gekend voor nori productie. De levencyclus is uitgebreid bestudeerd in de Aziatische soorten om de kweek als voedselbron te optimaliseren. Interesse groeit om ook de Europese tegenhanger (het genus Porphyra) in kweek te brengen. Bovenop het gebruik als voedselbron is Porphyra waardevol door de aanwezigheid van bioactieve componenten zoals UV-beschermers, biostimulanten en pigementen. De complexe levenscyclus van Porphyra, gekenmerkt door een diploide microscopische fase en haploide thallus fase is echter nog niet compleet ontrafeld. Enkele bottlenecks in het controleren van deze levenscyclus verhinderen betrouwbare productie. Deze thesis heeft als doel om de kweek te optimaliseren via life cycle control experimenten, kleinschalige Porphyra cultivatie en biochemische analyses. Deze masterhtesis kadert binnen het GAME project, gefinanceerd door Vlaanderen.

Doelstelling:

This thesis aims to optimize Porphyra cultivation through experiments focused on life cycle control, involving small scale cultivation and biochemical analysis. This research will be part of the GAME project, funded by Flanders.

Locatie:

sterre s8

Website:

Meer informatie op: phycology.ugent.be/

42674: Indonesian milkcaps inventory

Promotor(en):	Annemieke Verbeken
Begeleider(s):	Bobby Sulistyo
Contactpersoon:	
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Milkcaps are the common name of two closely related genera of fungi: Lactarius and Lactifluus. They are superficially very similar and used to be contained within one genus before molecular phylogeny revealed otherwise. Following the splitting, some patterns emerged that started to highlight their differences. One difference is their distribution pattern: Lactarius is worldwide while Lactifluus is mainly tropical. Thorough biogeographical study is needed to unravel the origin of the two genera. To conduct proper biogeographical study, a balanced sampling of the genera is needed. One region lacking in such sampling is Indonesia, a large archipelagic country in Southeast Asia. In addition to its size and status as an archipelago, it also harbors many ectomycorrhizal tree species that are known to associate with milkcaps. However, very few species have been described from Indonesia. We attempt to retrieve some samples from the region and their identity needs to be ascertained using molecular data and morphological study.

Doelstelling:

Aim

- Morphological study of milkcaps from Indonesia
- DNA extraction and generation of some molecular markers
- Phylogenetic study of milkcaps from Indonesia

Locatie:

42721: Interactions between endosymbiotic bacteria and ectoparastic microfungi in Harmonia axyridis

Promotor(en):	Danny Haelewaters
Begeleider(s):	Danny Haelewaters, Jie Xie
Contactpersoon:	
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Background

Harmonia axyridis (Pallas) (Coleoptera: Coccinellidae) has been introduced globally as a biological control agent against aphid pests. However, its release into the wild and subsequent rapid and unintended spread has posed significant threats to native ladybird species and other indigenous insect populations.

Hesperomyces virescens (Ascomycota: Laboulbeniales) is a complex of biotrophic fungal species that parasitize various ladybird hosts. A species within this complex, Hesperomyces harmoniae, is uniquely associated with Ha. axyridis and significantly increases ladybird mortality within 14 days in laboratory colonies.

Harmonia axyridis populations are also influenced by endosymbiotic bacteria. A recent paper reported infection rates up to 75% for Spiroplasma, and 2% for Wolbachia in ladybirds that survived in winter conditions. Spiroplasma is a male-killing bacterium, inducing female-biased populations in Ha. axyridis. Endosymbionts can influence insect immunity, potentially providing protection against pathogens. Studies in ants have demonstrated symbiont-mediated protection against entomopathogenic fungi. Understanding these interactions could inform integrated pest management strategies leveraging multiple pathogens and symbionts for biological control.

Problems

Many studies focus on the impact of entomopathogens on ladybirds, but the interactions among natural enemies of Ha. axyridis, especially between fungal parasites and endosymbiotic bacteria, remain elusive. How does the infection by He. harmoniae influence the presence and prevalence of endosymbiotic bacteria in Ha. axyridis? Specifically, do endosymbionts such as Spiroplasma or Wolbachia modulate the immune response of Ha. axyridis to resist fungal infection? This project will contribute to the broader understanding of host–pathogen–symbiont dynamics. Results from this project may inform strategies for integrated pest management using endosymbionts and fungal pathogens to regulate invasive ladybird populations.

Doelstelling:

First, this project will involve the rearing Ha. axyridis colonies in the laboratory and conducting transmission experiments of Hesperomyces harmoniae. The student undertaking this project will be responsible for maintaining the laboratory ladybird colonies, assisting PhD student Jie Xie. Second, bacterial screening will be performed on the same cohort of ladybirds, comparing ladybirds infected with the fungus to those uninfected. This will allow observation of changes in endosymbiotic bacterial presence within Ha. axyridis before and after fungal infection. The student will gain hands-on experience in insect feeding techniques and experimental ecology, become familiar with ectoparasitic microfungi, and use molecular methods such as DNA extraction and PCR amplification to detect endosymbiotic bacteria in ladybirds.

Locatie:

Campus Ledeganck

Opmerkingen:

References: Awad M, Piálková R, Haelewaters D, Nedvěd O. 2023. Infection patterns of ladybird Harmonia axyridis (Coleoptera: Coccinellidae) by ectoparasitic microfungi and endosymbiotic bacteria. Journal of Invertebrate Pathology 197: 107887. https://doi.org/10.1016/j.jip.2023.107887 Brown PMJ, Adriaens T, Bathon H, Cuppen J, Goldarazena A, Hägg T, Kenis M, Klausnitzer BEM, Kovář I, Loomans AJM, Majerus MEN, Nedvěd O, Pedersen J, Rabitsch W, Roy HE, Ternois V, Zakharov IA, Roy DB. 2008. Harmonia axyridis in Europe: Spread and distribution of a non-native coccinellid. BioControl 53(1): 5-21. https://doi.org/10.1007/s10526-007-9132-y Bruner-Montero G, Wood M, Horn HA, Gemperline E, Li L, Currie CR. 2021. Symbiont-mediated protection of Acromyrmex leaf-cutter ants from the entomopathogenic fungus Metarhizium anisopliae. MBio 12(6): e01885-21. https://doi.org/10.1128/mBio.01885-21 Eleftherianos I, Atri J, Accetta J, Castillo JC. 2013. Endosymbiotic bacteria in insects: guardians of the immune system? Frontiers in Physiology 4: 46. https://doi.org/10.3389/fphys.2013.00046 Haelewaters D, Hiller T, Kemp EA, van Wielink PS, Shapiro-Ilan DI, Aime MC, Nedvěd O, Pfister DH, Cottrell TE. 2020. Mortality of native and invasive ladybirds co-infected by ectoparasitic and entomopathogenic fungi. PeerJ 8: e10110. https://doi.org/10.7717/peerj.10110 Majerus TM, Majerus MEN, Knowles B, Wheeler J, Bertrand D, Kuznetzov VN, Ueno H, Hurst GD. 1998. Extreme variation in the prevalence of inherited male-killing microorganisms between three populations of Harmonia axyridis (Coleoptera: Coccinellidae). Heredity 81(6): 683-691. https://doi.org/10.1046/j.1365-2540.1998.00438.x

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42705: Investigating climate change impacts on meiofauna-microbial interactions and biogeochemical processes

Promotor(en):	Rodgee Mae Guden, Tom Moens
Begeleider(s):	Rodgee Mae Guden, Tom Moens, Carl Van Colen
Contactpersoon:	Rodgee Mae Guden

Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Climate change, driven by rising atmospheric CO2 levels, is causing ocean acidification and warming, which significantly impact marine ecosystems. These changes alter the physical and chemical properties of the oceans, affecting the biological communities within them. Meiofauna, small benthic invertebrates, play crucial roles in nutrient cycling, sediment stability, and as a food source for higher trophic levels. They interact closely with microbial communities, which drive biogeochemical processes such as organic matter decomposition and nutrient recycling. These interactions are vital for ecosystem health and stability. Ocean acidification and warming can disrupt meiofauna-microbial interactions, potentially leading to significant ecological consequences. Understanding these impacts is essential for predicting the future health of marine ecosystems.

Doelstelling:

In this research, we will investigate how ocean acidification and ocean warming affect the abundance and diversity of meiofauna and microbial communities. In addition, we will identify how meiofauna influence microbial-mediated biogeochemical processes under climate change scenarios. Meiofauna and microbial communities will be collected from the field from diverse marine locations with varying environmental conditions to capture a broad range of data. Microscopy and molecular techniques will be used to analyze meiofauna diversity and abundance. We will employ omics approaches to analyze microbial community composition and functional potential. In addition, we will conduct biogeochemical assays to measure nutrient cycling and organic matter decomposition rates. These findings will advance our understanding of the complex interactions between meiofauna and microbial communities and their responses to environmental stressors. This will help in predicting the future dynamics of marine ecosystems and for developing strategies to mitigate the adverse effects of climate change.

Locatie:

campus Sterre (S8) en campus Ledeganck

42660: Investigating seasonal adjustments in avian metabolic traits and their environmental drivers

Promotor(en): Cesare Pacioni, Diederik Strubbe
Begeleider(s):
Contactpersoon: Cesare Pacioni
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Basal metabolic rate (BMR) and summit metabolic rate (Msum) are key indicators of avian metabolic performance, each serving distinct physiological functions. BMR reflects the energy required for essential maintenance processes such as internal organ activity, while Msum represents the maximal capacity for heat production through shivering thermogenesis. Whether these traits are functionally linked or independently regulated remains an open question in ecophysiology.

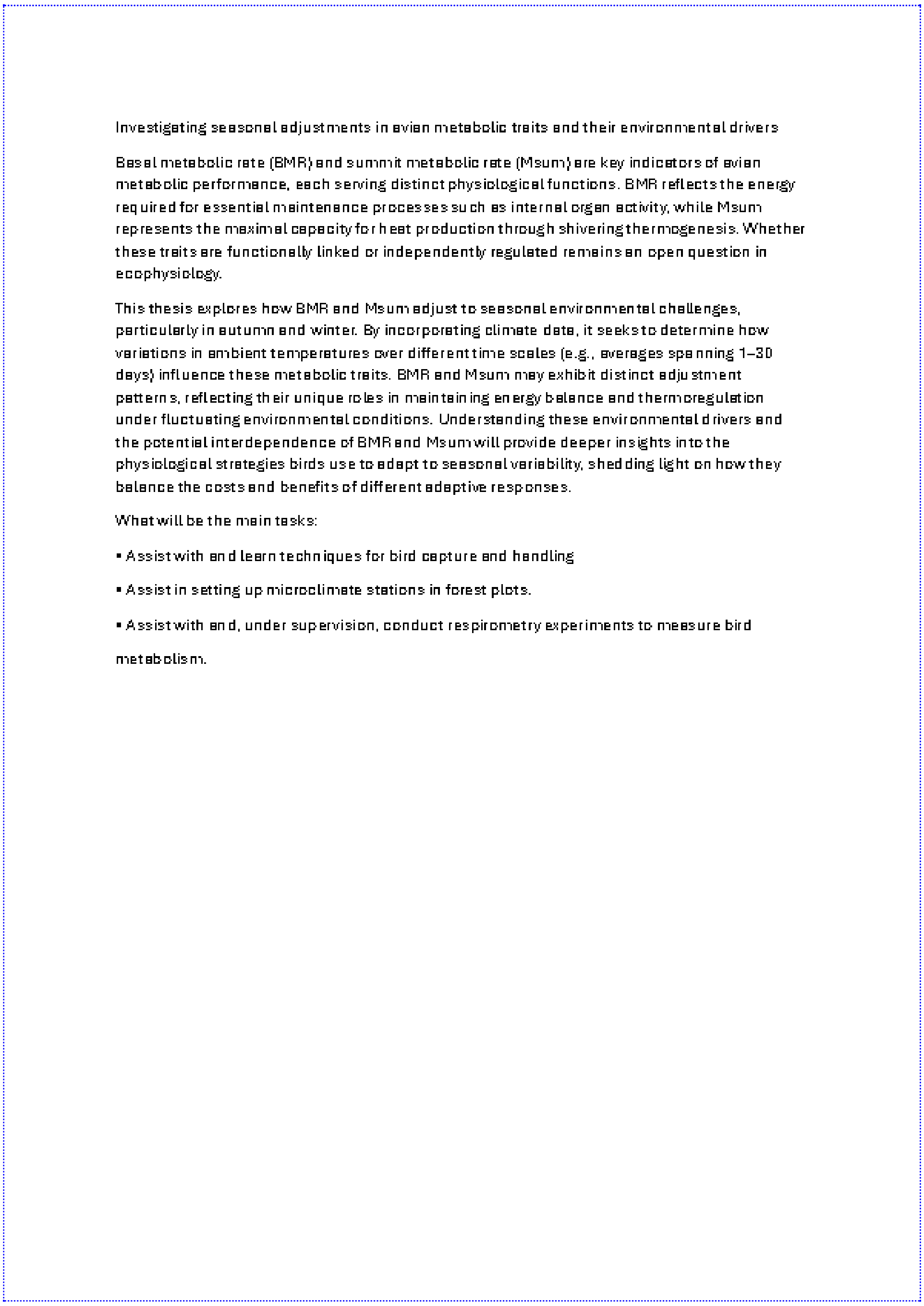
Doelstelling:

This thesis explores how BMR and Msum adjust to seasonal environmental challenges, particularly in autumn and winter. By incorporating climate data, it seeks to determine how variations in ambient temperatures over different time scales (e.g., averages spanning 1–30 days) influence these metabolic traits. BMR and Msum may exhibit distinct adjustment patterns, reflecting their unique roles in maintaining energy balance and thermoregulation under fluctuating environmental conditions. Understanding these environmental drivers and the potential interdependence of BMR and Msum will provide deeper insights into the physiological strategies birds use to adapt to seasonal variability, shedding light on how they balance the costs and benefits of different adaptive responses.

What will be the main tasks:

- Assist with and learn techniques for bird capture and handling
- Assist in setting up microclimate stations in forest plots.
- Assist with and, under supervision, conduct respirometry experiments to measure bird metabolism.

Eerste pagina van PDF:



Investigating seasonal adjustments in avian metabolic traits and their environmental drivers

Basal metabolic rate (BMR) and summit metabolic rate (Msum) are key indicators of avian metabolic performance, each serving distinct physiological functions. BMR reflects the energy required for essential maintenance processes such as internal organ activity, while Msum represents the maximal capacity for heat production through shivering thermogenesis. Whether these traits are functionally linked or independently regulated remains an open question in ecophysiology.

This thesis explores how BMR and Msum adjust to seasonal environmental challenges, particularly in autumn and winter. By incorporating climate data, it seeks to determine how variations in ambient temperatures over different time scales (e.g., averages spanning 1–30 days) influence these metabolic traits. BMR and Msum may exhibit distinct adjustment patterns, reflecting their unique roles in maintaining energy balance and thermoregulation under fluctuating environmental conditions. Understanding these environmental drivers and the potential interdependence of BMR and Msum will provide deeper insights into the physiological strategies birds use to adapt to seasonal variability, shedding light on how they balance the costs and benefits of different adaptive responses.

What will be the main tasks:

- Assist with and learn techniques for bird capture and handling
- Assist in setting up microclimate stations in forest plots.
- Assist with and, under supervision, conduct respirometry experiments to measure bird metabolism.

Download full PDF

Locatie:

Ledeganck campus

Onderwerp voorbehouden voor Laura Dutrieux

42663: Investigating the ecosystem functioning of natural hard substrates using food web models

Promotor(en):	Ulrike Braeckman, Jan Vanaverbeke
Begeleider(s):	Abril Reynés Cardona
Contactpersoon:	Abril Reynés Cardona
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

The seabed of the Belgian Part of the North Sea consists mainly of sandy substrate. Exceptions are the natural hard substrates, such as gravel beds, which foster greater habitat complexity and species richness compared to sandy areas, providing important ecosystem functions. However, these habitats are in a degraded state due to bottom fisheries, and little is known about their ecological functioning. On top, the new area planned for Offshore Wind Farm (OWF) development partly overlaps with the protected area of the Vlaamse Banken where natural gravel beds occur. Therefore, understanding the ecological relevance of the artificial hard substrates from a functional perspective is highly important to set conservation priorities.

Marine food web analysis offers an integrated approach to study changes in marine ecosystems by focusing on species interactions—essentially, identifying which species are present, who preys on whom, and at what rate. By constructing food web models, researchers can derive a variety of indices that can be related to ecosystem dynamics, resilience, and health.

Doelstelling:

In this master thesis the student will build a food web model for the gravel beds habitat. Food web models can be qualitative (topological), recording species presence/absence and feeding links from literature, or quantitative, capturing species densities and biomasses to model carbon flows using Linear Inverse Modelling (LIM) methodology. The professional practice would entail gathering species diets (from macrobenthic species up to fish), building a predator-prey matrix, and conducting network analysis (calculate network indices with different R packages, visualization of the network, etc). If working with LIM, the professional practice would also entail gathering biomass data of the species present and building LIM input files. The ultimate objective is to research how natural hard substrate differ from other habitats in terms of structure, functioning, carbon flows and nutrient cycling.

Locatie:

Marine Biology Research Group, Campus Sterre S8, Krijgslaan 281, 9000 Gent

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42704: Investigating the effects of noise pollution on marine microbial communities using omics approaches

Promotor(en):	Rodgee Mae Guden, Tom Moens
Begeleider(s):	Rodgee Mae Guden, Marie Cours
Contactpersoon:	Rodgee Mae Guden
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Marine ecosystems are increasingly subjected to a variety of anthropogenic stressors, with noise pollution emerging as a significant and pervasive concern. Noise pollution, primarily from shipping, industrial activities, and underwater construction, can disrupt marine life, affecting behavior, communication, and physiology. However, the impact of noise pollution on marine microbial communities, which form the foundation of marine ecosystems, remains largely unexplored. Microbial communities play crucial roles in nutrient cycling, primary production, and the overall functioning of marine ecosystems. They are involved in processes such as carbon fixation, nitrogen cycling, and the degradation of organic matter, making them essential for maintaining the health and stability of marine environments.

Recent advances in omics technologies, including metagenomics and metatranscriptomics, provide powerful tools to investigate the complex interactions within microbial communities and their responses to environmental stressors. These approaches allow for the comprehensive analysis of microbial diversity, functional potential, and gene expression profiles, offering insights into how microbial communities adapt to changing environmental conditions.

Doelstelling:

This research aims to investigate how noise pollution affect marine microbial communities using omics approaches. By examining both the taxonomic composition and functional dynamics of microbial communities, we seek to understand how noise pollution influences microbial diversity, metabolic pathways, and ecological functions. This study will not only enhance our understanding of the resilience and vulnerability of marine microbial communities to noise pollution but also provide valuable information for the development of conservation and management strategies to mitigate the impact of anthropogenic noise on marine ecosystems.

Locatie:

campus Sterre (S8) en campus Ledeganck

42701: Investigating the transgenerational effects of ocean warming on the microbiome of marine nematodes

Promotor(en):	Rodgee Mae Guden, Tom Moens
Begeleider(s):	Rodgee Mae Guden, Marie Cours
Contactpersoon:	Rodgee Mae Guden
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Climate change poses a major threat to marine ecosystems, with rising temperature driving widespread disruptions to marine life and ecosystem services. This phenomenon, referred to as ocean warming, is known to affect the abundance, distribution, life-history, and trophic interactions of marine organisms. Yet, the indirect consequences of ocean warming on microbiome of organisms are only beginning to be understood. The microbiome, consisting of bacteria, archaea, fungi, and viruses, play a crucial role in the health, functioning, and development of organisms. However, the stability and composition of these microbial communities are highly sensitive to environmental changes, including temperature fluctuations. Recent studies have highlighted the importance of understanding not only the immediate effects of environmental stressors but also their transgenerational impacts. Transgenerational effects refer to the influence of environmental changes on subsequent generations, which can have profound implications for species adaptation and survival. These effects can manifest through various mechanisms, including microbiome-mediated pathways.

In this study, we will investigate changes in the microbiome of marine nematodes after exposure to increased temperature across multiple generations. Nematodes are the most abundant and one of the most species-rich metazoan taxa in the marine realm. They form an essential link in marine food webs and mediate various ecosystem processes that are crucial for ecosystem functioning. By examining how elevated temperatures affect the microbiome of nematodes across multiple generations, we can gain insights into the long-term impacts of climate change on marine nematodes and their ecological roles.

Doelstelling:

Here, we will use the marine nematode species complex Litoditis marina as our model system, and expose the nematodes to different temperature conditions for multiple generations. Changes in the composition and function of nematode microbiome will be investigated using omics approaches. The findings of this research will contribute to our understanding of the ecological consequences of ocean warming and in developing strategies to mitigate the adverse effects of climate change on marine ecosystems.

Locatie:

campus Sterre (S8) en campus Ledeganck

42679: Invloed van temperatuur op reproductieve kenmerken bij spork (Rhamnus frangula)

Promotor(en):	Jan Van Uytvanck
Begeleider(s):	Kristine Vander Mijnsbrugge
Contactpersoon:	
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Klimaatverandering, waaronder wijzigende temperatuurregimes beïnvloedt mogelijk de reproductieve processen van planten zoals de spork.

Doelstelling:

Deze studie onderzoekt de impact van temperatuur op bloeitijd, vruchtvorming en zaadkwaliteit bij spork. Planten in pot worden blootgesteld aan twee verschillende temperatuurregimes in het voorjaar van 2025, in serrecondities. Reproductieve kenmerken worden geobserveerd en gemeten gedurende de zomer en het najaar van 2025. De proefopzet omvat een Italiaanse, een Vlaamse en een Zweedse herkomst van spork.

Locatie:

Serres en gebouwen Instituut voor Natuur- en Bosonderzoek Geraardsbergen + UGent Campus Ledeganck

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42644: Kelp Under Pressure: Exploring the Impacts of Industrial Harvesting on the Genetic Diversity and Connectivity of Two Commercially Exploited Kelp Species Across Europe

Promotor(en):	Olivier De Clerck, Sofie Vranken
Begeleider(s):	Lauren Elisa Vapillon
Contactpersoon:	Lauren Elisa Vapillon
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Climate change poses a significant threat to ecosystems globally, directly impacting species biodiversity and ecosystem functioning. Over the past 50 years, extensive research has highlighted the widespread decline of kelp forests, highlighting a serious risk to the genetic resources of these populations. Additionally, human-induced disturbances, such as intensive harvesting, are believed to reduce effective population sizes and drive habitat fragmentation—both recognized causes of genetic diversity loss—which, in turn, compromise the resilience of exploited populations. In Europe, natural populations of Laminaria digitata and Laminaria hyperborea are being industrially harvested, with Norway ranking as the world's second-largest harvester in terms of biomass extracted (FAO, 2021). However, the impacts of such practices on the genetic diversity of populations remain poorly understood, as current regulations primarily rely on inventories of distribution and abundance, taking little account of genetic aspects and resilience potential.

Doelstelling:

This Master's thesis aims to investigate the impact of industrial harvesting on the genetic diversity and connectivity of kelp populations across key exploited regions in Europe. Employing population genomic tools, this study will compare patterns of genetic diversity between harvested and non-harvested populations of the two main commercially exploited kelp species. Practical work will involve extracting DNA from samples collected in June 2024 across Europe. Low-coverage whole genome sequencing (lcWGS) will be used to identify single nucleotide polymorphisms (SNPs). We will estimate patterns of genetic diversity and connectivity between natural and exploited populations by performing population genomic analyses (e.g. calculating heterozygosity (He, Ho), allelic richness (Ar), fixation index (FST), inbreeding coefficient (FIS), effective population size (Ne), ...). This research will yield valuable insights into the impacts of harvesting on the ecosystem functioning and overall resilience of European kelp forests. Additionally, it will provide the student with practical experience in molecular techniques and valuable expertise in statistical tools for population genomics.

Locatie:

sterre s8

Website:

Meer informatie op: phycology.ugent.be

42511: Late Pleistocene and Holocene changes in relative sea level in Lützow-Holm Bay, East Antarctica

Promotor(en):	Elie Verleyen, Wim Vyverman
Begeleider(s):	
Contactpersoon:	Elie Verleyen
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

The East Antarctic Ice Sheet (EAIS) is probably the largest unknown in identifying regional contributions to global sea-level rise since the Last Glacial Maximum (LGM). This is because geological constraints on its past dynamics are still sparse, and the data that do exist indicate that the response of various sectors of the EAIS differs both in timing and rate of ice-mass changes. Given that the EAIS is by far the largest ice sheet on Earh and that recent observations suggest it may be more dynamic than previously assumed, understanding regional differences in its deglaciation history is crucial to predict the response of the EAIS to future changes. More in particular, it is key to get a better understanding of the response of the EAIS to various ocean/atmosphere forcing mechanisms since the LGM to test ice sheet models that seek to predict future ice sheet behaviour in a warmer world.

Information on the past response of ice sheets to external forcing such as changes in local climate and sea level can be inferred from studying regional relative sea-level (RSL) curves. RSL curves reflect changes in the regional dynamics of the ice sheet, as well as global sea level and earth crust processes. These RSL constraints can be subsequently combined with paleoclimate reconstructions and model-based estimates of sea level changes. This approach was proven to be successful in Antarctica and revealed that while some ice sheet models provide a reasonable fit with the geological data, others fail to correctly reproduce RSL changes in some regions and thus call for a revision of these models. In addition, because the vast majority of the existing RSL curves in East Antarctica are limited to the period following the regional Holocene RSL maximum (7000-9000 yr BP), there is an urgent need for RSL constraints on the rising limb of the post-LGM RSL curves that will allow to test the performance of ice sheet models during the transition from the Late Pleistocene to the Holocene (Termination 1; 18000 – 10500 yr BP). This is crucial because during Termination 1, atmospheric CO2 concentrations and temperature changed rapidly, and these boundary conditions might be similar to those the EAIS will experience in the near future (in terms of rates of change). However, in order to extend RSL curves into Termination 1, sedimentary archives preserved below the present-day sea level, such as sediments in basins in shallow marine waters and paleolakes that are now inundated by the sea, should be studied.

Doelstelling:

This MSc project is aimed at extending an existing relative sea level curve for Lützow-Holm Bay, East Antarctica towards the Late Pleistocene and the early Holocene by analysing fossil biological proxies (i.e., diatoms and pigments) in sediment cores taken in shallow marine basins. The fossil diatoms will be identified and enumerated using light microscopy. The fossil pigments will be analysed using high performance liquid chromatography. Based on these proxy data, transitions from marine to lacustrine conditions, and vice versa, will be identified and subsequently dated using radiocarbon dating.

Locatie:

42659: Leve de mestkever! Ecologie, rol in de landbouw en toekomst van de mestkever

Promotor(en):	Sander Jacobs, Mieke Lateir
Begeleider(s):	Tanja Milotic
Contactpersoon:	
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

In België leven er 2 groepen mestkevers: 'dwellers' en 'tunnelaars'. De 'rollers', een derde groep, komt in België niet voor.

Op het landbouwbedrijf spelen mestkevers een belangrijke rol voor een gezonde bodem: ze verwerken mest tot humus, ze zorgen voor waterinfiltratie en brengen lucht in de bodem. Daarnaast zorgen ze ervoor dat heel wat parasieten die schadelijk zijn voor het vee niet kunnen overleven of beperkt blijven. Zelf zijn de mestkevers weer een interessante prooi voor vogels, bv. voor zwaluwen bij aankomst na de trek.

Maar, mestkevers hebben het niet makkelijk. Zowel de aantallen als de diversiteit gaan achteruit. Koeien die vaker op stal staan bijvoorbeeld, ontwormingsmiddelen ook hebben een negatieve impact op mestkevers.

Met dit thesisonderwerp zorg je voor meer inzicht in de ecologie en de rol van de mestkever in de landbouw en verken je mogelijkheden om mestkevers meer kansen te bieden.

Doelstelling:

Locatie:

42619: Life-history-traits of a new invasive goby, Tridentiger bifasciatus, in Flanders

Promotor(en):	Hugo Verreycken, Sander Jacobs
Begeleider(s):	
Contactpersoon:	Sander Jacobs
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Recently (2022), a new non-native fish species, the shimofuri goby, was detected in the Canal Gent-Terneuzen. This goby is of Asian origin and probably arrived here by ballast water of transoceanic ships. Within two years, this species has managed to settle in the canal and the Scheldt and will probably become invasive in the near future. Little is known, however, about its life-history-traits or LHT (fecundity, longevity, growth, ...) in its invaded area. We sampled 100 shimofuri gobies from the Canal Gent-Terneuzen and will use these specimens to dissect them and learn more about its LHT.

Doelstelling:

Locatie:

42550: Mapping the reproductive barriers and habitats of a newly identified arthropod species

Promotor(en):	Nicky Wybouw
Begeleider(s):	Margarita Spirina
Contactpersoon:	Nicky Wybouw
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

The discovery of new species is an ongoing process, especially in an arthropod taxon as diverse as mites. Whereas many mite species have been documented, there are still countless species that remain unknown or poorly understood. Recently, a new species of Tetranychus was discovered by our French collaborators. However, beyond this initial identification, little is known about this novel species. Its ecological role, habitat preferences, potential as an agricultural pest, and ability to hybridize with other closely related Tetranychus species remain completely unknown. The lack of this fundamental information limits our ability to assess the significance of the species. Investigation of these factors is essential for understanding its role in ecosystems and, if necessary, for future pest management strategies.

Doelstelling:

The objective of this project is to conduct an in-depth study of the newly discovered Tetranychus species. First, the student will gain experience in the identification and taxonomy of the genus. Second, the student will investigate the ability of this new species to hybridize with other known species in the genus. This will involve controlled laboratory experiments and genetic analyses. The student will contribute to ongoing research on speciation and hybridization in spider mites.

Locatie:

campus Ledeganck

Website:

Meer informatie op: www.nickywybouw.org

42632: Mass-extinctions and misfits: Fossil teratologies as proxies to explore kill-mechanisms during the end-Ordovician extinction

Promotor(en):	Thijs Vandenbroucke
Begeleider(s):	Iris Vancoppenolle
Contactpersoon:	
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	Master of Science in Geology
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Until recently, teratological (malformed) palynomorphs (organic walled microfossils) have been widely viewed as miscellaneous specimens with little scientific value. However, a number of recent high-profile studies are leading to a seed change in how we view these biological aberrations, abnormalities and misfits. Emerging data suggest that teratological palynomorphs are a ubiquitous feature of mass-extinction intervals and may be widespread during these upheavals in both the marine and terrestrial realm.

Teratological palynomorphs provide the potential of linking the marine and terrestrial realms as recorders of changing paleo-environmental conditions during the onset of mass extinctions. The supervisor's international HFSP project brings together international researchers (from Ghent, Nottingham, Utrecht and Berkeley) working on multiple aspects of teratologies in palynomorphs (including their morphology, geochemistry and modern analogues) to explore what information can be recovered from these X-files. This master's project will integrate with the research efforts of this consortium.

As such, this MSc project is part of an interdisciplinary research programme that tests a set of related hypotheses linking malformed palynomorphs to either: (i) metal toxicity related to marine anoxia (Hg, Cd, Ni, Pb), (ii) increased UV-B radiation due to ozone loss, or (iii) environmental stress related to climate change. We use these microfossils and their modern analogues in experimental and field settings to explore the true potential of teratology as a proxy to test, integrate, and refine the many existing models for biotic crises across time and space.

Doelstelling:

Within the wider context explained above, the student choosing this particular project will focus on teratologies of chitinozoans, Ordovician fossil micro-zooplankton, thought to be indicative of major perturbations of the paleo-marine environments during their life and growth. Specifically, the focus here will be on multiple occurrences of the intruiging deformities within the chitinozoan species *Ancyrochitina spongiosa.* These malformations have been observed during the Katian Waynesville geobiological event (c. 449 Ma), during pilot analysis, in two drillcores in the USA Midwest: the Garner Kiln core from Wisconsin and the IGWS 440 core from Indiana. However, formal detailed countings and rigorous analysis of the various teratologies remain an urgent priority and will be at the core of this project. The findings are of particular interest, as they potentially occur within the initial onset (?) towards the End-Ordovician (Hirnantian, 445 Ma) Mass Extinction Event, one of the 'big 5' mass extinctions documented in the evolution of Life on our Planet. The data produced will be benchmarked against existing geochemical data collected from those cores, which will help explore the mechanisms behind the teratology and, eventually, the root causes of extinction. The student will be able to further tailor the project to their particular interests. For instance, and optionally, it will be possible to generate additional geochemical data on the fossils specimens themselves (e.g., La-ICP-MS or ToF-SIMS).

Outcomes of this work are expected to be publishable, and as a student, you will be trained how to best present your data in the form of a scientific paper or a presentation at an international meeting.

Locatie:

Campus Sterre: Research Group Palaeontology and Palaeo-environments (Dept. of Geology, UGent)

Website:

Meer informatie op: www.nature.com/articles/ncomms8966

Opmerkingen:

(International) promotors/supervisors will be added in accordance with the expertise required once the student has identified their preferred angle to the topic

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42690: Microbial community dynamics in a Greenlandic fjord influenced by marine-terminating glaciers

Promotor(en):	Koen Sabbe, Dimitra-Ioli Skouroliakou
Begeleider(s):	Hannah Gaber
Contactpersoon:	Koen Sabbe
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Arctic fjords are highly productive and biodiverse ecosystems, with marine-terminating glaciers (MTGs) playing a key role in sustaining their productivity (e.g., Meire et al., 2017, https://doi.org/10.1111/gcb.13801). MTGs release meltwater below the surface, promoting nutrient upwelling into the photic zone, which supports the growth of large phytoplankton, the primary energy source for the fjord's food web. However, climate change is causing rapid retreat of MTGs out of the fjords. As these glaciers retreat, they will eventually end on land and become land-terminating (LTGs), altering the hydrology, phytoplankton community dynamics, and productivity in Greenlandic fjords. While research suggests such shifts in glacier type could have significant downstream effects on Arctic fjord food webs (see Meire et al., 2023, https://doi.org/10.1038/s41561-023-01218-y), the extent and mechanisms of these impacts remain poorly understood.

Doelstelling:

The aim of this thesis is to resolve the microbial diversity and community structure in a marine-terminating glacier (MTG)-influenced fjord, providing detailed insights into the microbial compartment within the broader Arctic fjord food web. The student will analyse pelagic samples collected in June 2025 from Disko Bay, Southwest Greenland, using metabarcoding, FlowCam, and Imaging Flow Cytometry, to investigate how MTG presence and environmental factors shape microbial community dynamics. This work will generate a comprehensive dataset on pelagic microbial food web components, contributing to broader research on how glacier retreat impacts the structure, functioning, and carbon flow in Arctic fjord food webs.

Locatie:

campus Sterre

Opmerkingen:

As this topic is under the supervision of someone who is not Dutch speaking, the supervision and writing of the thesis will be done in English. A keen interest in laboratory work and bioinformatics using R is desired.

42654: Molecular analysis of a conserved transcription factor in lateral root stem cell specification in the fern Ceratopteris

Promotor(en):	Tom Beeckman
Begeleider(s):	Abdellah Lakehal
Contactpersoon:	Abdellah Lakehal
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

During evolution, plants have developed the remarkable ability to form new organs post-embryonically, such as lateral roots (LR). LR organogenesis begins with the specification of a subset of stem cells. However, the molecular mechanisms governing LR stem cell specification remain largely unknown. To investigate this, we performed single-cell RNA sequencing on the roots of the model fern Ceratopteris richardii, a member of the sister clade to seed plants. Our data revealed that an evolutionarily conserved transcription factor (TF), is specifically expressed in LR stem cells. However, its role in LR stem cell specification has not been studied to date.

The student will contribute to characterizing the evolution and function of this gene in LR stem cell specification in Ceratopteris richardii. The project will be conducted in the lab of prof. dr. Tom Beeckman at PSB/VIB.

Doelstelling:

The main objective of the thesis is to contribute to the functional analysis of a candidate transcription factor in the context of lateral root stem cell specification in Ceratopteris. To achieve this, the student will perform the following tasks:

1. Generate inducible overexpression and dominant-negative transgenic lines.
2. Generate knock-down mutants using RNA interference (RNAi) and knock-out mutants using CRISPR-Cas9 technologies.
3. Perform live-cell imaging of promoter activity during lateral root (LR) stem cell specification using confocal microscopy.
4. Generate transcriptional and translational fusion lines.
5. Phenotypic characterization of the coresponding mutants

Locatie:

VIB-UGent Center for Plant Systems Biology

Website:

Meer informatie op: https://www.beeckmanlab.be/

Onderwerp voorbehouden voor Lucas Cool

42605: Molecular Complexity in a Simple Organism: Functional Analysis of C. elegans Globin Genes.

Promotor(en):	Bart Braeckman
Begeleider(s):	Giuliano Lecompte
Contactpersoon:	Bart Braeckman
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Globins are a superfamily of proteins characterized by a tertiary protein structure known as the globin-fold. Historically, these proteins were primarily associated with oxygen transport (e.g. myo- and hemoglobin). However, with the rise of high-throughput genome sequencing, it became evident that this view merely scratched the surface of globin functionality. The ancient roots of globins extend to the earliest stages of life, 4 billion years ago, where they are hypothesized to have emerged among the basic proteins required for life. Throughout Earth's evolutionary history, globins have evolved and radiated within every kingdom of life, giving rise to the multitude of functions we observe today: NO production and scavenging, reactive oxygen species (ROS) detoxification and signalling, sulfide transport, peroxidation and oxygen sensing, transport, and storage. Despite their remarkable (biochemical) functional diversity and widespread occurrence in nature, the biological role of many globins, including some human globins, remains poorly understood. A promising model to explore this mystery lies within Caenorhabditis elegans, which impressively encodes for 34 globin genes (cfr. 6-8 glb genes within vertebrates currently ununderstood, yet functionally important,). These genes display exceptional diversity in structure, expression pattern, and subcellular localization, while some also share significant similarities with human globin genes (e.g. cyto- and neuroglobin). Why would such a simple organism require such a large and diverse globin repertoire? What are the physiological roles of these globins? Are they comparable with vertebrate globins or do they serve unique roles? These questions remain open for discovery.

Doelstelling:

In this master project, we will functionally analyze C. elegans glb mutant(s). Depending on the status of the ongoing research and the student's preferences, the thesis can focus on either previously studied glb mutants or entirely unstudied ones. To determine the levels and tissue-specific localization of the selected globin(s), existing translational glb reporters or scRNA-seq databases will be used. The expression pattern will allow us to design specific experiments. As most C. elegans globins are expressed in neurons, it is highly likely that these experiments will focus on behavioral analyses, such as specific aspects of locomotion (TIERPSY video-analysis), chemotaxis (e.g. smell or taste), mechanosensation, or oxygen sensing. Additional experiments may involve studying stress-resistance, reproduction or development. Given that many C. elegans glb genes are implicated in hypoxia and/or anoxia, most of these biological processes will be studied in response to such conditions.

Locatie:

Campus Ledeganck

42732: Morphological variation in hair in relation to phylogeny and ecology across mammals

Promotor(en):	Liliana D̀Alba Altamirano, Matthew Shawkey
Begeleider(s):	Jessica Leigh Dobson
Contactpersoon:	Jessica Leigh Dobson
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	

Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Hair is a uniquely mammalian characteristic, and like the diversity we see in the overall appearance of mammals, we also see on a microscale, with the morphology of individual hair structures (i.e. cuticle patterns and hair thickness) differing greatly between species. In this project, the goal is to determine the degree of variation in hair morphology that is explained by the phylogenetic relatedness between species, testing the hypothesis that hair morphology may not be phylogenetically constrained and therefore other factors (i.e. related to the ecology of each species) might explain the remarkable diversity of cuticle patterns. Specifically, they will look at how hair morphology differs between species which are terrestrial, fossorial, and (semi)aquatic, looking at whether hairs of these species show any morphological adaptions. The student will take electron micrographs of hair, and combine them with a preexisting set of images to categorize scale morphology patterns of different body regions on multiple species, and take measurements from hair images, including total number of scales, and hair thickness, as well as collating SEM images from already published studies on hair morphology.

Doelstelling:

The specific opbjectives of the project are:

To produce a dataset of hair morphology using electron micrographs and published data

To perform phylogenetically controlled analyses to test the associations between hair morphology and species ecology

Locatie:

campus Ledeganck, floor 9

42623: Natural Capital Accounting: are we saving or selling nature?

Promotor(en): Sander Jacobs
Begeleider(s):
Contactpersoon:
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Two main international policy developments regarding sustainability are (A) the development of the UN system of environmental economic accounts - ecosystem accounting (SEEA-EA) and the (B) IPBES methodological report on diverse values and valuation of nature. A deploys an economic-valuation based accounting system to internalize damages to natire and ecosystem services in the national economic accounts, and as such aims to correct economic decisions which damage natural capital. B proposes a plural vauation, and points ot that values of natiure should be considered from different viewpoints, especially when complex and impactful decisions are considered.

While A certainly aims to diversify national accounts (which now are not considering nature at all), it certainly is holding the risks of any valuation based on a specific type of valyation method (in this case exchange values in (pseudo)markets. B, on the contrary, has no concrete proposals to convey sustainability messages to natioanl economic decisions.

Doelstelling:

The mission is to rite a scientific paper, together with some main authors from within the SEEA and IPBES-VA field, which confronts SEEA with the procipIes of plural valutaion, and critically discusses opportunities and risks of this acccounting, and poroposing things that work better. English writing skills required. Main method will be document review, content analysis and coding.

Locatie:

42700: Ontwikkeling van mitochondriale primers voor fylogenetica en een taxonomische herziening van Schizorhynchia (Platyhelminthes)

Promotor(en): Marlies Monnens, Tom Moens
Begeleider(s): Jhoe Reyes, Rodgee Mae Guden, Marlies Monnens
Contactpersoon:
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

De fylogenetische relaties binnen platwormen blijven tot op heden onduidelijk voor diverse taxa. Dit is deels een gevolg van de grote genetische diversiteit van deze dieren, wat de toepasbaarheid van zogenaamd 'universele' primers sterk beperkt. Zo is Schizorhynchia (Rhabdocoela, Kalyptorhynchia) een soortenrijk taxon binnen de platwormen waarvan de huidige fylogenie verdere verduidelijking vereist Het doel van deze masterthesis is het ontwikkelen van nieuwe, mitochondriale primers voor deze groep. Hiervoor zullen nieuwe specimens verzameld worden door middel van (inter)nationaal veldwerk, waarna gebruikgemaakt zal worden van shotgun sequencing (Illumina) om de eerste mitogenomen van deze dieren te assembleren. De verkregen sequenties dienen als template voor de ontwikkeling van nieuwe barcoding primers, die ingezet kunnen worden voor de analyse van zowel nieuw verzamelde als reeds bestaande stalen van Schizorhynchia. Dit onderzoek heeft als doel om de fylogenetische relaties binnen dit taxon beter te begrijpen en de huidige (morfologische) classificatie te herzien.

Aan het einde van dit biologisch onderzoek, zullen ook 9 studiepunten worden toegewijd aan de pedagogische kant van deze masterthesis. Wat dit precies wordt hangt af van hoe het biologische onderzoek loopt en wat de huidige leerkrachten missen als leermiddel (voor in de klas). Het pedagogische werk kan gaan over:

- DNA, PCR en sequencing
- Classificatie
- Soortconcept (en evolutie)
- Microscopie
- ...

21 studiepunten worden dus gewijd aan het puur biologisch onderzoek en 9 aan het uitwerken van een pedagogisch(e) onderzoek/tool.

Doelstelling:

Leerdoelen voor de student:

- academisch schrijven
- moleculaire technieken zoals: shotgun sequencing, primers maken...

- fylogenetische analyse
- correcte soortbeschrijvingen (inclusief morfologische tekeningen)
- (professioneel werken in een labo, met de nadruk op communicatie)

Locatie:

UHasselt en campus Ledeganck

Onderwerp voorbehouden voor Myrthe De Puydt

42686: Parallel Paths: Convergent Evolution in Algal Genomes

Promotor(en):	Kenny Bogaert, Olivier De Clerck
Begeleider(s):	Kenny Bogaert
Contactpersoon:	Kenny Bogaert
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

The rapid increase in available genomes from diverse protist and algal evolutionary clades opens up exciting opportunities to address key evo-devo questions. One area of exploration is the role of convergent evolution in shaping similar genomic adaptations across different evolutionary lineages exhibiting traits such as clonality, multicellularity, specific habitat preferences, or trophic strategies.

Doelstelling:

This project aims to extend and refine a pipeline for analyzing enrichment and depletion in conserved eukaryotic protein domains and gene families (using InterPro/EggNOG), as well as protein domain combinations (InterPro). The focus will be on uncovering associations between these features and key traits like multicellularity, environmental adaptation, and trophic mode. The project will integrate phylogenetically explicit and implicit approaches to explore hypotheses regarding the evolutionary mechanisms driving these patterns.

The student will apply data analysis methods, leveraging Python and R programming to handle large genomic datasets, and using multivariate statistical approaches and existing tools and packages (such as CAFE and packages ape, phyloglm, pglmm). Training and support will be provided in computational biology techniques, but a strong motivation to work with Python, R, and statistical analysis is essential. The outcomes of this project will provide novel insights into how similar ecological or functional pressures drive convergent genomic adaptations in multicellular evolution and the ecological specialization of marine organisms.

Locatie:

campus Sterre, home office

42793: Plant species diversity on the monastic ruins of Orval, with a special focus on the wall flora

Promotor(en):	Lars Chatrou, Kenneth Bauters
Begeleider(s):	Chantal Dugardin
Contactpersoon:	
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Walls, and other exposed historic stonework, are often colonised by plants and other wildlife in a similar way to cliffs and scree. These historic structures are providing additional habitats that are often scarce in the natural environment. They are natural examples of green or living walls.

The long association between these plant species and walls is reflected in names such as wallflower (Erysimum cheiri, Brassicaceae), eastern Pellitory-of-the-wall (Parietaria officinalis, Urticaceae) or in their scientific names. The ivy-leaved toadflax's scientific name is Cymbalaria muralis.

Walls provide demanding conditions for plants because of exposure, drought and sparse amounts of soil development. True wall plants are able to withstand extremes of temperature and drought. These specialised conditions allow uncommon plants to grow which would be displaced by more vigorous, common species on less hostile sites. The mortar is usually more alkaline than the stonework so a wall built of acid stone may still support lime-loving plants. Historic sites are especially important because the structure and age of their walls provide a range of opportunities for plants, such as weathered stonework and lime-rich mortar.

The Orval Abbey (Villers-devant-Orval, Florenville) offers such a historic site. Next to the contemporary abbey with a monastic community of the Order of Cistercians, the ruins of the old abbey are located which was burnt to the ground in 1793. The ruins provide many opportunities for wall plants, and thus provide both a cultural and a floristic heritage.

The inventory of the flora of the ruins of the Orval Abbey, with particular focus on the wall plants, is of interest to the community of Villers-devant-Orval. Moreover, knowledge of the wall flora of the ruins of Orval Abbey provides indispensable data that improve our understanding of wall flora in Belgium, several species of which are in decline.

Doelstelling:

In this project, you will make an inventory of the flora of the ruins of the Orval Abbey, with a special focus on the wall flora. To ensure that the flora is sampled year-round, your project will be a collaboration with staff of the Botanic Gardens of Ghent University, who will sample during the months before the start of this MSc project.

The project will consist of the following elements:

- sampling of wall plants following the protocol developed by FLORON (Floristisch Onderzoek Nederland, an organisation dedicated to the research and conservation of plants), identification, and deposition of voucher specimens in the herbarium of Ghent University.
- Evaluation of ecological parameters (e.g. exposition, acidity / alkalinity of substrate, moisture content etc.)
- Occurrence data will be added to the database at www.waarnemingen.be, to address the research question to what extent walls support rare plant species.

This project will suit a student who is a true plants woman or a plants man. You like to work in a team, and you enjoy thinking in an original and creative way. You appreciate the historic and cultural aspects of this project, and care about the conservation of rare wall plants. The output will be written in the form of a scientific article aiming to submit it to a peer-reviewed journal for publishing.

Locatie:

campus Ledeganck; Orval Abbey (Florenville)

42643: Population Genomics and Hybridization Potential in Porphyra umbilicalis

Promotor(en):	Olivier De Clerck, Sofie Vranken
Begeleider(s):	Jordi Morcillo Baeza
Contactpersoon:	Jordi Morcillo Baeza
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

The red alga Porphyra umbilicalis belongs to the bladed Bangiales, a group of seaweeds with significant economic and cultural value as the basis for nori production, an essential ingredient in sushi.

Like other members of the bladed Bangiales, P. umbilicalis exhibits a complex heteromorphic life cycle, alternating between a macroscopic gametophyte (blade phase) and a microscopic sporophyte (conchocelis phase). Interestingly, P. umbilicalis can bypass the sporophyte phase through asexual reproduction, where spores from the blade develop directly into new blades. While both sexual and asexual reproduction have been observed in wild populations from Northern Europe (including France, Belgium, and the Netherlands), laboratory crossings between these life history stages have not yet been successful.

The complexity of studying Porphyra species is further compounded by difficulties in delineating species boundaries within the genus. This is due to factors such as simple morphology, significant morphological plasticity, the presence of cryptic species, chimerism, polyploidy, and potential hybridization.

This thesis project aims to use population genomics to characterize patterns of genomic variation and investigate whether crossing between sexual and asexual strains occurs in natural populations. To achieve this, different populations of P. umbilicalis will be genotyped using whole-genome resequencing, and genomic patterns will be compared both within and between populations. The research will primarily involve molecular lab work and genomic data analysis.

Doelstelling:

The goals of the project consist of setting hybridisation experiments and examining the effect of hybridisation on the phenotype and the genotype (e.g. poly- or aneuploidy).

Locatie:

sterre s8

Website:

Meer informatie op: phycology.ugent.be

42655: Predicting the arrival of migratory moth species based on weather conditions

Promotor(en):	Luc Lens
Begeleider(s):	Reinoud Allaert
Contactpersoon:	Reinoud Allaert
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Bird migration has been extensively studied, leading to a thorough understanding of how meteorological conditions such as wind direction, temperature, and atmospheric pressure influence their journeys. However, much less is known about how these same weather patterns affect the migratory behaviour of invertebrates, particularly moths. Despite the rich datasets collected by citizen scientists through moth trapping, the role of both local and global weather conditions in moth migration remains largely unexplored. Citizen science efforts have provided extensive data on moth arrivals, which, when combined with meteorological records, offer the potential to uncover the environmental drivers behind moth migration.

Doelstelling:

The aim of this Master's thesis is to investigate how local and global weather conditions influence the arrival of migratory moths. Using five years of moth trap data collected by citizen scientists, the student will integrate these observations with meteorological data to determine which weather conditions facilitate moth migration. The goal is to develop predictive models that can forecast the likelihood of moth migration on specific nights, offering insights into the environmental triggers behind invertebrate movements.

Locatie:

campus Ledeganck

42699: Priority effects and the dynamics of competition among closely related species

Promotor(en): Tom Moens, Rodgee Mae Guden
Begeleider(s): Rodgee Mae Guden, Marie Cours, Tom Moens
Contactpersoon: Tom Moens
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Interference - one species interferes with the ability of another species to obtain resources - and exploitation competition – the superior species depletes the resource faster or better, not leaving enough resources available for inferior species - are the two main types of competitive interactions between species. These types of competition mostly increase with relatedness between species, according to classical competition theory (Darwin, 1859). As a consequence, competition is predicted to be high in cryptic species –closely related species that are morphologically indistinguishable, but show consistent genetic differences. Cryptic diversity is prominently present in coastal nematodes, and the best studied model 'species' in this context is Litoditis marina, which is mostly found associated with decomposing macroalgae. Both competition and facilitation between these cryptic species have been reported in closed, homogeneous microcosms. Changing the composition of the cryptic species changes the interactions between them and abiotic factors - temperature and salinity- also have an influence on the interactions between the species. The nature of this competition, however, is not clear yet. Moreover, species that start a new population early in a certain patch may have a greater chance of becoming dominant than later arriving species (priority effects) and this may help to explain why the species are able to co-occur in different species compositions in the field .

Doelstelling:

In this master thesis, we will test whether priority effects affect the outcome of competitive interactions among cryptic species of the Litoditis marina species complex. The competitive interactions among these species have been well-studied in situations where they arrive simultaneously and in equal abundances, and the dynamics of these interactions have been modelled using individual-based modelling. Here, we will test whether competitively inferior species may be able to remain abundant in a certain patch if they have a larger starting population and/or an earlier arrival compared with a competitively superior species. Depending on the student's interest, this thesis will consist mainly of laboratory experiments (setting-up experiments, molecular identification and quantification of nematode species using quantitative PCR , …), of a combination of laboratory experiments and modelling, or mostly of individual-based modelling of population and community dynamics.

Locatie:

campus Sterre, S8 en (afhankelijk van bijdrage modellering) campus Coupure

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42692: Proportional Analysis of Syngnathid Tail Segments for Parametric Bioinspired Robotic Models

Promotor(en): Dominique Adriaens, Francis wyffels
Begeleider(s):
Contactpersoon: Dominique Adriaens
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:

Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

The prehensile tails of syngnathid fishes, such as seahorses, exhibit a conical structure with segments that taper distally. This unique morphology has significant potential to inspire the design of robotic manipulators. However, to create a functional parametric model, understanding the proportional relationships between the sizes of tail segments is crucial. Analyzing these proportions across species ensures the findings are broadly applicable and not restricted to a single species. Statistical analysis is needed to uncover consistent relationships between segments and across species.

Doelstelling:

The objective of this study is to quantify and analyze the inter- and intraspecific patterns in the proportional relationships between tail segments in syngnathid fishes (seahorses, pipehorses, and pipefish). Using reconstructed 3D µCT models, the student will manually measure segment dimensions and perform multivariate statistical analyses to identify significant relationships and trends. This process will highlight critical dimensions and their interrelationships, ensuring a robust understanding of syngnathid tail morphology. The results will be used in the development of parametric models for bioinspired robotic designs.

Locatie:

Ledeganck campuscampus Ledeganck, Research Group Evolutionary Morphology of Vertebrates

Website:

Meer informatie op: https://www.ugent.be/we/biology/evo-morph/en

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42622: Re-wilding van de Vlaamse heide: tussen droom en daad.

Promotor(en):	Marijke Thoonen
Begeleider(s):	
Contactpersoon:	
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Rewilding is een populair concept in het hedendaags natuurbeheer dat zich richt op het herstellen van ecosystemen door inheemse soorten terug te brengen en natuurlijke processen zonder menselijke interventie hun gang te laten gaan. Heidegebieden bieden potentieel voor de implementatie van verschillende rewilding-principes. In deze thesis wordt het beheer van de afgelopen jaren in kaart gebracht via de analyse van remote-sensing beelden enerzijds en wordt anderzijds onderzocht in welke mate rewilding-principes reeds geïntegreerd zijn in het beheer van een selectie van heidegebieden via document-analyse of gestructureerde bevraging van heidebeheerders.

Doelstelling:

Locatie:

42673: Red velvet: confirming the identity of edible Heimioporus sp. from Indonesia

Promotor(en):	Annemieke Verbeken
Begeleider(s):	Bobby Sulistyo
Contactpersoon:	
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

The Bangka-Belitung islands are situated on the east of Sumatera, Indonesia. Within the island lies the Pelawan forest which is dominated by Tristaniopsis merguensis (Myrtaceae). One interesting ectomycorrhizal associate of this tree is a species of Heimioporus sp. or locally known as kulat pelawan (pelawan mushroom). Kulat pelawan is an attractive looking bolete with red velvety cap, yellow pore surface, and reticulated stipe. This mushroom is locally harvested and fetch a high price on the market. However, its true identity remains hidden. It is said to be closely associated with H. retisporus but recent studies are inconclusive. More data is needed to ascertain its association.

Doelstelling:

Aim

- Morphological study of pelawan mushrooms
- DNA extraction and generation of some molecular markers
- Phylogenetic study of pelawan mushrooms
- Determination of real identity of pelawan mushrooms and potential description of new species

Locatie:

42631: Reducing nitrogen pollution through the identification of biological nitrification inhibitors

Promotor(en):	Tom Beeckman, Hans Motte
Begeleider(s):	Fabian Beeckman, Laure Annetta
Contactpersoon:	Fabian Beeckman
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	Master of Science in Biochemistry and Biotechnology
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Fertilizers are highly applied in agriculture leading to major environmental issues, including nitrogen (N) pollution and greenhouse gas emissions. These issues are caused by a microbial process called nitrification, which is the transformation of ammonia ($NH3$) into nitrite ($NO2-$) and nitrate ($NO3-$). Nitrate and nitrite easily leach through the soil, leading to a loss of N available for plant growth, and possible conversion of these N-forms into the strong greenhouse gas nitrous oxide ($N2O$). In the Root Development group of Prof. Dr. Tom Beeckman, an ongoing research project aims to identify new types of nitrification inhibitors using a drug-discovery based approach. Therefore, a high-throughput soil assay was recently developed to simultaneously test the effect of thousands of compounds on nitrification in diverse soils.

Doelstelling:

The goal of this master thesis will be the identification of biological nitrification inhibitors (BNI) by using this new screening method. In principle, a collection of natural products will be collected (extraction and fractionation from plants or microbes) or acquired. Identified inhibitors will be further characterized by testing their effect on nitrifying bacteria and on nitrifying archaea, either directly in culture, or in soil via qPCR and/or microbiome analysis. Moreover, the effect of the microbiome and the physicochemical soil characteristics on the inhibitor efficacy will be tested by applying different soils in the new soil assay. This project might result in the finding of new fertilizer additives with increased efficiency and reduced side-effects on the environment.

Techniques that might be applied in this master thesis:

- Microbial culture work, both bacteria and archaea
- High-throughput robotic liquid handling
- HPLC fractionation
- Ammonium and nitrate measurements (spectrophotometry)
- DNA/RNA extraction from soil
- (RT-)-qPCR
- 16S-sequencing

Locatie:

42689: Reproductive barriers and genomic divergence in the cryptic diatom species complex Cylindrotheca closterium

Promotor(en):	Eveline Pinseel, Wim Vyverman
Begeleider(s):	Anne-Laura Monten
Contactpersoon:	Eveline Pinseel
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

The huge population sizes and high passive dispersal potential of marine planktonic microorganisms, together with the lack of apparent dispersal barriers in the ocean, made researchers hypothesize that marine environments only sustain a limited number of cosmopolitan planktonic, microbial species. However, an increasing amount of evidence is suggesting that many cryptic species exist, resulting in extensive, previously unrecognized, genetic diversity within the planktonic microbial community. One such clade of potentially highly diverse marine microbes are diatoms. Diatoms are unicellular stramenopile algae, and represent one of the most diverse and ecologically important phytoplankton groups, contributing around 20% of global net primary productivity. Nevertheless, little is known about what drives diatom diversity and speciation in the global oceans, including the genomic basis of reproductive barriers between species.

Doelstelling:

The objective of this master thesis is to unravel the global species-level diversity and reproductive barriers in the cryptic, marine diatom species complex Cylindrotheca closterium. To this end, the student will combine laboratory crossing experiments with phylogenetic analysis of marker genes (from Sanger and/or whole-genome sequencing). The focus lays on various C. closterium strains obtained from different geographic regions (polar, temperate, tropic). If feasible, environmental DNA data will be integrated to gain deeper insights into the biogeography of C. closterium. The student will gain experience with laboratory work (microscopy, diatom culturing, molecular lab work) and bioinformatic analyses of sequence data. The expertise of the promotors, together with the lab experience of the supervisor will ensure that the student has the guidance that is needed to successfully complete the thesis.

Locatie:

campus Ledeganck, campus Sterre

42809: SealMeal: Can we estimate natural mortality rates to improve commercial fish stocks assessments based on seal diet?

Promotor(en):	Marleen De Troch, Lies Vansteenbrugge
Begeleider(s):	
Contactpersoon:	Lies Vansteenbrugge
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1 of 2
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Understanding the interactions between marine mammals and fish populations is crucial for sustainable ecosystem management. Over the last 15 years, the harbour seal (Phoca vitulina) and grey seal (Halichoerus grypus), two common seal species in the North Sea,have shown significant increases in population size. The ecological impacts of these growing populations on commercially important fish stocks, however, is poorly understood.

Doelstelling:

In fisheries stock assessments, estimates of natural mortality (e.g., predation, senescence, disease) are often based on old or limited datasets and maintain a degree of uncertainty. This uncertainty is reflected in the stock assessment models (i.e., larger process errors) and could eventually result in less accurate catch advice for commercial fish stocks. To address this issue, we propose using the unique resources of two institutes.

The Royal Belgian Institute of Natural Sciences (RBINS) has a valuable collection of seal stomachs obtained from strandings over the past years. The analysis of stomach contents can provide critical insights into the prey composition of seals, including temporal and spatial variations. Comparisons with stomach content data from harbour porpoises (Phocoena phocoena) could offer additional context on trophic interactions within the ecosystem.

The Flanders Research Institute for Agriculture, Fisheries, and Food (ILVO) has extensive expertise in otolith (calcified structure in the inner ear of fish) analysis, which is critical for determining the age of fish. Extracting otoliths from seal stomach contents will enable a detailed understanding of the age structure of prey populations, shedding light on the mortality pressure seals exert on commercially important flatfish species, such as sole (Solea solea) and plaice (Pleuronectes platessa).

This study aims to 1) review the current knowledge on seal diets in the North Sea, with a focus on the southern North Sea; 2) analyse seal stomachs obtained from strandings to determine the diet composition and extract fish otoliths for age determination; 3) investigate spatial and temporal trends in seal diet and compare with diet of harbour porpoises and 4) calculate age-specific mortality rates for sole and plaice, contributing to more accurate stock assessments and sustainable fisheries management.

Number of students: max. 2

Locatie:

ILVO (Oostende)

42602: Seaweed secrets: uncovering a red algae's adaptive potential to thrive (or survive) in low salinity environments

Promotor(en):	Olivier De Clerck, Sofie Vranken
Begeleider(s):	Louka Noyen
Contactpersoon:	Louka Noyen
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Furcellaria lumbricalis is a red seaweed with a relatively large geographical distribution, inhabiting both the Atlantic Ocean as well as the hyposaline waters of the Baltic Sea. Furcellaria is one of the only macroalgal species that is able to thrive in the Baltic Sea, where it faces salinities as low as 3.6. Yet, our understanding of this species' genetic adaptations to such low salinity conditions, as well as any potential local adaptations, remains limited. As Furcellaria is an important commercial seaweed in the Baltic region, knowledge of its various genetic adaptations, and its remaining adaptive potential will be of crucial importance for the conservation of the species within the scope of climate change.

Doelstelling:

This thesis aims to uncover the genetic basis of Furcellaria's tolerance to extremely low salinities through whole genome sequencing, comparative analysis of populations from the Atlantic and Baltic Sea, RNA sequencing, and population genomics. Currently, the species' life cycle dynamics remain unexplored, yet understanding and manipulating these cycles is essential for sustainable seaweed cultivation. This research will investigate the life cycle of various Furcellaria populations to determine whether salinity influences the mode of reproduction—sexual or asexual. Adopting an integrated approach, this study integrates population genomics with hands-on laboratory techniques, providing a comprehensive understanding of both genetic and environmental factors that drive Furcellaria resilience and reproduction.

The subject is wide and can be directed towards the student's interests. In case the timing is right, the option to join fieldwork during the summer holidays of 2025 can be discussed.

Locatie:

sterre s8

Website:

Meer informatie op: www.phycology.ugent.be

42640: Sociality in the Anthropocene: an experimental study of (pre)dispersal strategies in a cooperative-breeding bird

Promotor(en):	Lucy Mitchell, Luc Lens
Begeleider(s):	
Contactpersoon:	Lucy Mitchell
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

The impact of habitat degradation on sociality and (pre)dispersal strategies in tropical cooperatively breeding birds remains poorly understood. This is partly due to a lack of appropriate tracking technologies capable of simultaneously monitoring large numbers of individuals over extended periods with high spatial and temporal resolution. However, recent advances in semi-automated radio telemetry systems represent a significant breakthrough in understanding how environmental conditions influence the evolution and maintenance of social systems. Moreover, an experimental approach is essential to separate the effects of habitat quality on dispersal from those of landscape configuration and social factors. This approach is especially important for studying tropical cooperative species, which tend to be long-lived and may delay dispersal for many years. While manipulating habitat quality directly in tropical rainforests is difficult, CORT implants provide an indirect means of simulating the physiological responses of individuals to degraded habitat conditions.

Doelstelling:

In this thesis, the student will (i) examine the effect of simulated habitat quality on natal dispersal decisions by quantifying the natal dispersal behavior of subordinate Placid greenbuls, using state-of-the-art animal tracking techniques and experimentally manipulated baseline CORT levels; and (ii) develop models to explore the various pathways through which habitat degradation can influence dispersal strategies in tropical cooperative breeders

Locatie:

campus Ledeganck

Onderwerp voorbehouden voor Seppe Deprez

42685: Spatial and temporal dynamics of coccolithophore blooms in the North Sea

Promotor(en):	Griet Neukermans
Begeleider(s):	
Contactpersoon:	

Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie, Master of Science in de geografie en de geomatica
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Coccolithophores are a group of phytoplankton that build a calcite armour. They are major contributors to pelagic calcification and play a crucial role in ocean biogeochemistry and various climate feedback mechanisms. Among coccolithophores, the species Emiliania huxleyi, forms extensive quasi-monospecific annual blooms in the North Sea. E. huxleyi is unique in the sense that it overproduces coccoliths, the calcite platelets that make up its armour, which are released into the water at the final stages of a bloom. E. huxleyi cells and their detached coccoliths accumulate in surface waters, scattering light so intensely they colour seawater bright milky-turquoise. Owing to their characteristic light backscattering features, these blooms can thus be differentiated from blooms of non-calcifying phytoplankton and are easily detectable from space by ocean colour satellites, which give daily near-surface observations since 1998.

Despite a long standing research interest in E. huxleyi as a representative species for coccolithophores, the environmental conditions for E. huxleyi's bloom formation and termination are poorly understood, particularly in the North Sea. The proposed master thesis will address those knowledge gaps by analysing ocean colour satellite data, as well as in situ observations collected on board RV Simon Stevin early summer 2025.

Doelstelling:

The specific objective of this master thesis is to examine the spatial and temporal characteristics of E. huxleyi blooms (spatial extent, peak magnitude and timing) and the conditions that trigger their onset and decline. This requires the analyses of ocean colour (1998-present) satellite data of E. huxleyi blooms in conjunction with remotely sensed or model-derived environmental conditions that likely impact these blooms (such as sea surface temperature, mixed-layer depth, wind stress, net heat flux, and light availability). Such integrative approaches combining synoptic biological and environmental observations have already revealed important findings on the environmental controls on phytoplankton blooms.

Locatie:

campus Sterre

Website:

Meer informatie op: marsensugent.wixsite.com/marsens

Opmerkingen:

good programming skills required

42642: Studying the underlying mechanisms of 'Suppressed in ovo virus infection ' in honeybees

Promotor(en):	Dirk de Graaf
Begeleider(s):	Lina De Smet
Contactpersoon:	Lina De Smet
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Honeybees together with wild bees play essential roles in the pollination of flowering plants. Unfortunately during the last decade, bee depopulation events and loss of honeybee colonies have been reported worldwide. Several parasites and pathogens contributed to this decline. Viruses, and in particular the deformed wing virus (DWV), are considered as one of the main antagonists of honey bee health. In 2012, Belgian beekeepers started screening breeding queens for the presence of viruses in eggs deposited in worker brood cells and found 75% to be infected with at least one virus and 40% to be infected with DWV. These high results led to the start of a yearly sanitary control of the breeding queens and eventually to the discovery of the 'Suppressed in ovo virus infection' trait (SOV). This trait is described by the absence of virus infections in 10 pooled drone eggs and was the first study to show that the potential of honey bees to suppress virus infections is heritable ($R \approx 0.25$). In addition, colonies headed by a SOV-positive queen have fewer and less severe DWV infections in almost all developmental phases of both worker bees and drones indicating the beneficial implications for the health status of the colony. The underlying mechanisms of the SOV trait are yet to be discovered; possible hypotheses could be an increase in the expression or effectivity of the RNA interference pathway, transgenerational effects or increased expression levels of Toll-6 which has been linked with survival after artificial infection with Israeli acute paralysis virus (IAPV).

Doelstelling:

Currently, we are in the stage of identifying the genetic markers associated with SOV. After identifiation of the markers, a TaqMan assay should be developed to screen for the presence of the markers. First, the allel frequencies of the identified markers in the Belgian bee population should be determined. This study will be followed by a nation wide association study in which the association of the phenotype (=virus load) with the genotype (=identified markers) will have to be confirmed.

In addition, we also want to identify the underlying mechanismes of the SOV trait. DNA polymorphisms are genetic variations among individuals, including single nucleotide polymorphisms (SNPs). They may affect some key cellular functions, resulting in severe phenotypic consequences in the growth and development of organisms. The identified markers are associated with the trait but are not necessarily the causal mutation. This means that once the markers have been identified, we need to design and perform expession profyling studies of the genes in the vicinity of the marker(s) (=mutation).

Locatie:

campus Stere

Onderwerp voorbehouden voor Nathan Heirbaut

42696: Syrinx variation within the songbird families

Promotor(en):	Dominique Adriaens
Begeleider(s):	Jana De Ridder
Contactpersoon:	
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

As the name suggests, are songbirds characterised by the song they produce. Song quality is an important factor in mate selection. Females prefer males with higher song performance. However, not every songbird species produces equally complex songs. In general, the strong biting species produce less complicated songs, with for example lower trill rates and lower frequency bandwidth.

Song is influenced by the complete distance the sound travels, from the beak through the trachea to the syrinx. The syrinx is a complex organ responsible for sound production in birds. Many studies looked into the function of this organ, also describing morphological differences. As songbirds differ a lot in song capacities, the question is to what extent does the syrinx morphology differ within a family.

Doelstelling:

Possible differences in syrinx musculature are being studied for a few finch species (Estrildidae, Fringillidae and Darwin finches). This is done using µCT-scans of stained specimens or dissections, and where needed combined with histology. Additionally, several functional characteristics, like muscle volume, architecture (pennation) and angle in which the muscle functions, are compared between the species in function of song performance.

Locatie:

42726: Testing the efficiency of Berlese Tullgren funnels to assess abundance of terrestrial isopods

Promotor(en): Pallieter De Smedt
Begeleider(s):
Contactpersoon: Pallieter De Smedt
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Berlese Tullgren funnels are frequently used to assess soil fauna abundance. Leaf litter or topsoil from a fixed-size plot is placed in the funnels, and soil fauna are driven downward by a light and heat source at the top. At the bottom, soil fauna falls into a small vial containing alcohol, which preserves them. This process continues until all the soil is dry and all the animals have moved into the vial. However, there have been few assessments of the efficiency of these funnels for different soil fauna taxa.

Doelstelling:

This research will investigate how well different species of terrestrial isopods are extracted by the funnels. Terrestrial isopods will be collected from the field and placed in standardized soil to evaluate their extraction efficiency. The results will be linked to the species' morphological and ecological traits. This study will provide valuable insights into a commonly used method for soil fauna research.

Locatie:

Campus Gontrode, Universiteit Gent

42522: The evolution of silent flight

Promotor(en): Michaël Nicolaï, Gerben Debruyn
Begeleider(s):
Contactpersoon: Michaël Nicolaï
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Birds have evolved a wide range of adaptation to improve flight. However, few birds such as owls, nightjars and few other raptors, seem to have evolve a set of adaptation for silent flight. These adaptations include fringes, comb-like serrations and others that influence the air stream near the wing, resulting in the absence of fluttering. These adaptations differ in length and dimensions, but to what extent and why they do so is not clear. Similarly, it is unclear why these adaptations did not evolve in all (predatory) birds even though they potentially benefit too.

Doelstelling:

The student will collect morphological data of all silent-flight-traits and this from all birds of prey present in the collection at RBINS (Brussels), the Africa Museum (Tervuren) and Naturalis (Leiden). This data will be coupled to biotic, behavioural and environmental variables in a phylogenetic comparative framework to try and identify why differences exist in the presence/absence and size of these traits.

Locatie:

campus Ledeganck, RBINS, Africa Museum, Naturalis

Opmerkingen:

While the student will be accompanied to each first visit to the natural history collections, some independence is expected afterwards.

42500: The fish scale: towards developing a minimal-invasive tool to read age and life-history of fishes

Promotor(en): Adelbert De Clercq, Karen Bekaert
Begeleider(s): Adelbert De Clercq, Karen Bekaert, Jade Maes
Contactpersoon: Adelbert De Clercq
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Age reading on marine fish in the current context of stock assessment (estimating the population size of fish species in order to know stock biomass and health) happens on ear bones or otoliths. These ear bones need to be extracted from the auditory capsule in the skull of the fish. Ear bones are embedded, and sections are polished and sometimes stained to help visualise the growth lines within the ear bones. It is these growth lines, similar to growth lines in a tree stump, that can be counted to determine the age of the animal. Although this technique works well for age determination of fishes, the animals needs to be killed. Age reading via otoliths, although accurate, only gives a single time point and thus life history of a single animal cannot be tracked. An alternative to otoliths for age and life history reading are the scales of fish. Scales also show growth lines, called circuli and annuli, and although well-established life history reading protocols exist especially for salmonids, the validity of these protocols has not been investigated for many marine fish species. Using scales for life history reading is advantageous as they regenerate quickly and thus do not kill the animal when several scales are sampled. Moreover, scales can be sampled from the same individual over time thus representing an opportunity to track the life history of an individual fish. Importantly, avoiding to kill the animal to take age and life history measurement is an improvement for fish animal ethics and can help to asses stock of protected fish, rare fish and fish in marine protected areas where fishing is not allowed.

Doelstelling:

The aim of the project is to eventually develop the scale as a minimal invasive age and life history reading tool. However, initial exploration of the scales of many marine fish species has to happen first. You will take part in activities of the sclerochronology group at the Flemish Institute for Agriculture, Fisheries and Food (ILVO). You will sample scales of fishes, visualise the growth rings via staining, describe the scale morphology and visualised pattern, and count growth rings if clear patterns can be observed. Also, specific disturbances of patterns will be described as well as the proportion between ontogenetic (originally developed) and regenerating scales. Deeper histological investigation of the scales will happen in the Evolutionary Developmental Biology group in the Biology Department (UGent). To validate possible age and life history readings on scales, otoliths of the corresponding fish will be analysed in parallel to the scales. Comparative analyses of the scales and otoliths will help to determine if close correlation between age and life history reading on otoliths and scales exit. Such, analyses will help to understand if the fish scales can be used to study age and life history patterns and therefore be used in the future as a minimal invasive data platform tool to help stock assessment.

Locatie:

Campus Ledeganck, ILVO-MARIEN (Oostende)

42672: The formation of lateral roots in Equisetum arvense

Promotor(en):	Tom Beeckman
Begeleider(s):	Xilan Yang
Contactpersoon:	Xilan Yang
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

The formation of lateral roots (LR) is crucial for the survival of plants in dry land conditions. Throughout plant evolution, the branching of root systems has become increasingly more efficient enabling the plants to mine for water and nutrients. While LR formation in flowering plants has drawn significant attention, relatively less focus has been placed on LR development in ferns, despite their potentially interesting anatomical and morphological differences from flowering plants. What is more, to understand this important developmental process, it is instructive to try to understand how plants achieved this skill which can be done by studying representative plant species belonging to early diverging clades that have an alternative and mostly more simple root system.

In the model plant Arabidopsis thaliana, LRs originate from a single concentric layer of pericycle cells within the root. It is generally assumed that LRs in ferns are originally formed from the endodermal cell layer, based on the sparse literature on LR formation in early diverging vascular plants. This idea is primarily based on studies of the leptosporangiate group, while the eusporangiate ferns are less well studied or even omitted. Within the eusporangiate ferns, the Equisetaceae represent an early-diverging lineage, having diverged from leptosporangiate ferns about 350 million years ago (Mya) and from seed plants about 380 Mya. As representatives of the early diverging ferns, it could be hypothesized that these plants have maintained the most original mode of LR formation which would be LRs with an endodermal origin. Intriguingly, few studies have reported the development of LRs from the pericycle instead of the endodermis in these species. This apparent contradiction led to the suggestion that Equisetaceae might lack a pericycle but would have a double endodermis, attempting to keep the central idea of endodermis-derived LR initiation as the most primitive state. Without the availability of tissue-specific markers such hypotheses are hard to prove, and more in-depth studies are required to solve this mystery.

It is now generally accepted that roots originated at least twice during evolution, once in the lycophyte clade, and once in the euphyllophyte clade encompassing ferns and seed plants. The lycophytes form roots by dichotomous branching, while ferns and seed plants branch laterally. As an early diverging fern species, Equisetum (Equisetum arvense), serves as a good model system to study the evolution of LR specification. Many common features in root morphology are shared between ferns and seed plants. The common structure of underlying transcriptional networks points to a highly convergent evolution, where a similar program was already present in both lineages or a similar genetic program was recruited.

Doelstelling:

In this project, we aim to identify the LR founder cell and reveal the process of LR formation. Importantly, we will employ whole mount RNA-FISH using the hybridization chain reaction (HCR RNA-FISH) to visualize the expression of key genes expression in Equisetum arvense. This technique is crucial given the absence of a transformation protocol for this plant.

Our first objective is to understand the identity of the inner endodermis. In Arabidopsis, the pericycle is initiated in the stele, whereas this process differs in Equisetum. The root meristem of Equisetum exhibits a distinct pattern (Figure 1A). Stem cells of the endodermis divide and form two cell layers (Figure 1B), which maintain a typical cell pattern reflecting their common origin (Figure 1C). To figure out whether the second layer has acquired a pericycle identity or remains as an inner endodermis, we will use HCR RNA-FISH to check the expression of homologs of key marker genes for endodermis identity, such as the SCARECROW (SCR) transcription factor used to demonstrate endodermis identity in seed plants. This technique is used in Selaginella roots, showing clear signals (Figure 2).

Importantly, we will select candidate genes to facilitate the understanding of LR founder cell specification (Figure 3). Given the lack of available transcriptome and genome data of Equisetum arvense, we have recently sequenced its huge genome and transcriptome. Roots are well-studied in Arabidopsis and some ferns, so we can select conserved genes in Euphyllophyte. We will then search for these genes in Equisetum transcriptome data and construct phylogenetic tree for candidate genes. Approximately 4 genes will be selected for probes synthesis for HCR RNA-FISH. After this, the HCR RNA-FISH will be conducted in Equisetum roots, which will be examined using confocal microscopy. Varies parts of the root will be imaged, and based on all images, we may identify the LR founder cells and elucidate the process of lateral root formation.

Furthermore, due to the lack of a transformation protocol for Equisetum, we will test some peptide treatment. The application peptide can be designed to target specific pathways or processes without genetically transformation. Small peptides are crucial signaling molecules in varies aspects of developmental processes in plant roots, such as CLAVATA3 (CLV3)/EMBRYO SURROUNDING REGION peptide (CLE), which is associated with stem cell maintenance; ROOT MERISTEM GROWTH FACTOR (RGF) which is required for maintenance of the root stem cell niche and transit-amplifying cell proliferation.

Eerste pagina van PDF:

The formation of lateral roots in *Equisetum arvense*

Introduction

The formation of lateral roots (LR) is crucial for the survival of plants in dry land conditions. Throughout plant evolution, the branching of root systems has become increasingly more efficient enabling the plants to mine for water and nutrients. While LR formation in flowering plants has drawn significant attention, relatively less focus has been placed on LR development in ferns, despite their potentially interesting anatomical and morphological differences from flowering plants. What is more, to understand this important developmental process, it is instructive to try to understand how plants achieved this skill which can be done by studying representative plant species belonging to early diverging clades that have an alternative and mostly more simple root system.

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It is now generally accepted that roots originated at least twice during evolution, once in the lycophyte clade, and once in the euphyllophyte clade encompassing ferns and seed plants. The lycophytes form roots by dichotomous branching, while ferns and seed plants branch laterally. As an early diverging fern species, Equisetum (*Equisetum arvense*), serves as a good model system to study the evolution of LR specification. Many common features in root morphology are shared between ferns and seed plants. The common structure of underlying transcriptional networks points to a highly convergent evolution, where a similar program was already present in both lineages or a similar genetic program was recruited.

objective

In this project, we aim to identify the LR founder cell and reveal the process of LR formation. Importantly, we will employ whole mount RNA-FISH using the hybridization chain reaction (HCR RNA-FISH) to visualize the expression of key genes expression in Equisetum arvense. This technique is crucial given the absence of a transformation protocol for this plant.

Our first objective is to understand the identity of the inner endodermis. In Arabidopsis, the pericycle is initiated in the stele, whereas this process differs in Equisetum. The root meristem of Equisetum exhibits a distinct pattern (Figure 1A). Stem cells of the endodermis divide and form two cell layers (Figure 1B), which maintain a typical cell pattern reflecting their common origin (Figure 1C). To figure out whether the second layer has acquired a pericycle identity or remains as an inner endodermis,

Download full PDF

Locatie:

VIB-PSB

Website:

Meer informatie op: www.beeckmanlab.be/research/horsetails-elucidate-evolution-lateral-root-branching

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42676: The Fungarium of Ghent University: a valuable source of information hidden in boxes

Promotor(en):	Annemieke Verbeken
Begeleider(s):	
Contactpersoon:	
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Mycologists are now routinely analyzing fungal communities directly from the soil using metagenomics. In order to link these environmental sequences to actual species, a solid taxonomical framework is needed with which sequence data can be compared. As most ecosystems worldwide, tropical and subtropical African forests are depending on ectomycorrhizal associations, often with fungi that form mushrooms. This project wants to contribute to the knowledge of the diversity in these ecosystems by constructing a reference framework for the African ectomycorrhizal fungal genera, making use of a wealth of hidden information: the fungal herbarium of Ghent University. The Fungarium of our research group contains over 35000 collections, of which at least 5000 are African. The majority of specimens and their associated data is not digitized and hence hidden for research. We aim to digitize the African collections and their associated data.

Doelstelling:

The Fungarium of Ghent University: a valuable source of information hidden in boxesAim of this thesis

Meanwhile we have DNA barcodes for the 1000 most important collections. These data need to be analyzed and processed. This information will be combined with existing data and phylogenies, to construct a comprehensive taxonomical framework on African ectomycorrhizal genera (Lactarius, Lactifluus, Russula, Cantharellus, Amanita, boletes).

Locatie:

42568: The impact of induced plant defences on plant-herbivore interactions

Promotor(en):	Nicky Wybouw
Begeleider(s):	Lennert Beele
Contactpersoon:	Nicky Wybouw
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

For 400 million years plants have been coevolving with arthropod herbivores. In response to herbivore feeding, plants evolved defence mechanisms, which subsequently selected for herbivores that able to cope with these plant defences. There are a multitude of plant defences that comprise both constitutive and induced physiological pathways. An induced plant defence is activated by signals emitted by herbivores, allowing the plant to alter either their morphology and physiology upon herbivore attack.

White clover (Trifolium repens) produces cyanide as a powerful toxin to deter arthropod herbivores, a process triggered by cell damage caused by herbivore feeding. White clover exhibits a polymorphism for cyanide production, with plants being either cyanogenic or acyanogenic. Research whether cyanide production can be induced and how this could affect herbivore fitness is scarce. This line of research could provide valuable insights into plant-herbivore interactions as well as other antagonistic interactions, such as parasitism.

Doelstelling:

This thesis will investigate whether cyanide production can be induced in white clover and how this could shape herbivore communities. The project integrates approaches from both molecular biology and ecology. The student will use lab populations of clover, aphids, flies, and mites. The research focus of the project can be tailored according to the student's preference for a certain research field.

Locatie:

campus Ledeganck

Website:

Meer informatie op: www.nickywybouw.org/

42510: The response of microbial and micro-invertebrate communities to increased snow cover in Antarctic polar desert soils

Promotor(en):	Elie Verleyen, Bjorn Tytgat
Begeleider(s):	Ruben Van Daele
Contactpersoon:	Elie Verleyen
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Antarctic polar deserts are among the driest regions on Earth. Terrestrial life in these biomes is dominated by microorganisms with micro-invertebrates such mites, springtails and tardigrades forming the top of the food-web. Water availability is one of the key factors in structuring these biological communities, with food-webs in the wet soils being largely different compared with those in the drier habitats. In relatively wet soils, microbial mats or biocrusts consisting of cyanobacteria, green algae, lichens, and mosses form the base of the food-web. In hyper-arid 'soils', green algae as well as the bacterial phyla Actinomycetota and Acidobacteriota appear to be the main primary producers. Indeed, members of these bacterial phyla were recently shown to be able to scavenge molecular hydrogen (H2), CO2 and CO from the atmosphere and use these molecules as energy and carbon sources.

Climate models predict that the amount of precipitation and snow cover in Antarctic deserts will increase during the coming decades. Increasing snow cover is expected to result in increased water availability in these polar desert soils during the short summer season. How these changes will affect the soil food-webs and their biodiversity remains poorly understood.

Doelstelling:

In the Austral summer of 2017-2018 a long-term field experiment was initiated in hyper-arid soils in Widerøefjellet (Sør Rondane Mountains, East Antarctica) using snow fences which experimentally increase snow cover. Control and snow fence plots were sampled at the very start of the experiment and during the Austral summer of 2023-2024. Loggers measuring changes in soil temperature and relative humidity were also installed, as well as time-lapse cameras to monitor changes in snow cover. In this MSc project, we will analyse changes in the biodiversity and community structure of different taxonomic groups over this 6 year's time period based on high-throughput sequencing of the 16S rRNA and 18S rRNA genes for bacteria and micro-eukaryotes, respectively. These biological data will be subsequently combined in a food-web network analysis and linked with the temperature, humidity and snow cover monitoring data. The student will be involved in the DNA extraction and library preparation for sequencing, and the bioinformatics and statistical downstream analyses.

Locatie:

42666: The role of microbiomes in thermal stress response and meiofaunal interactions

Promotor(en):	Marleen De Troch, Anna-Maria Vafeiadou
Begeleider(s):	Anna-Maria Vafeiadou, Bram Martin
Contactpersoon:	Anna-Maria Vafeiadou
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	2
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Global warming is one of the main consequences of climate change threatening the fitness and functioning in marine ecosystems. The combination of temperature fluctuations and episodically elevated water temperature may exceed the tolerance of some organisms, whereas some others may develop plasticity towards the changing environmental conditions. Different species show different tolerances to thermal stress, but there is evidence that species response alters with the presence of other species and their interactions (e.g. direct or indirect species interactions). Microbiomes comprise genetic diversity of all microorganisms associated with a host, including symbiotic microbiota. Microbiome characterisation of all organisms on earth is an ongoing research task of biologists worldwide and it has the potential to explain some traits, such as responses to stress. For example, species-specific microbiomes have been associated with the overall performance and fitness of their hosts. Disentangling the role of microbiomes of marine animals is a growing research path of marine science. To date only few studies have investigated the microbiome of marine copepods, including only pelagic species, while little is known about the interactions of microbiomes and benthic invertebrates in response to stress.

Doelstelling:

In this project we will question whether microbiomes are associated with species tolerance to thermal stress and whether they change with species interactions. Benthic copepods collected from the field will be subjected to normal and elevated temperature regimes representing warming effects, in the presence and absence of other meiofauna, to assess how species and trophic interactions are affected by thermal stress conditions and explore if any particular patterns of microbiomes are reflected on population responses. The present project will focus on the effects of temperature on benthic copepod species under the presence and absence of species interactions within the meiofauna (eg. nematodes, other copepods). Analysing the microbiomes of benthic copepods, we aim at gaining insight on the indirect trophic interactions within meiofauna (for instance if higher microbial diversity in the copepod microbiomes could be linked with nematode presence), as well as on the microbiome-host interactions (for instance benefit from symbiotic microbiome taxa for tolerance to stress). The microbiome of individual copepods will be analysed using Next Generation Sequencing before and after exposure to experimental treatments, in the presence or absence of interactions. We aim to investigate shifts in microbiome that may be correlated with resilience of populations and to understand the role of microbiomes on temperature resilience of the selected species and their interspecific interactions.

Locatie:

campus Sterre, campus Ledeganck

Opmerkingen:

Sediments will be collected from the intertidal zone of the Belgian part of the North Sea. This thesis topic involves field work, lab work and experiments, molecular techniques and bioinformatics, giving an excellent opportunity to the student to experience different paths of research work in the marine biology domain. Experience with R and an independent working attitude is required. Previous experience with molecular techniques (eg. PCR) is an asset but not a requirement. Good R knowledge and scientific writing skills is an asset.

42601: This tiny mistake costs individuals their ploidy: modeling whole genome duplication events

Promotor(en):	Dries Bonte

Begeleider(s): Silvija Milosavljević
Contactpersoon: Silvija Milosavljević
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor: Master of Science in Biochemistry and Biotechnology
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Whole genome duplication (polyploidization) is the increase in chromosomal set size, arising mostly due to the fusion of unreduced gametes. Polyploid plants are widespread and extensively explored due to their common occurrence and benefits to the agriculture, but polyploidy is also found in animals, fungi and prokaryotes. Upon polyploidization, most commonly found change is the change in cell size and/or body size as most polyploids are larger than their diploid parents. This gives rise to the question of how metabolism must adapt to the new cellular conditions and how can newly formed polyploids survive and reproduce successfully while being surrounded by diploids.

Doelstelling:

We try to answer these questions on polyploid establishment and invasion using ecological modeling approach. This master thesis will include learning how to make and document individual-based models, with focus on coding in Python and formulating hypotheses that can be answered by model modification and simulation. Althought the focus of an existing model is plant asexual polyploids, during this thesis adapting the model to answer question about animal polyploidy is very welcome. In addition, including sexual reproduction, higher level ploidies (triploids etc), environmental disturbances and similar processes is expected to be done.

Locatie:

Ledeganck campus and/or VIB Plant Systems Biology in Technology park

Website:

Meer informatie op: vandepeerlab.org/?q=research/genome-duplication-polyploidy

Opmerkingen:

We encourage students with interest in computational biology, but extensive experience with programming is not a necessary prerequisite.

42620: Towards a red list for saproxylic beetles

Promotor(en): Arno Thomaes, Sander Jacobs
Begeleider(s):
Contactpersoon:
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

In Flanders, a few hundred saproxylic (dead-wood depending) beetles are present, a group which is very relevant for nutrient cycling and carbon storage in forests. A first red list was made in 2015 but for only 19 rather large and emblematic saproxylic scarab beetles. In this thesis we will compile a list of all saproxylic beetles present in Flanders and explore for which beetle families a red list would be feasible, how the data would be best compiled and analysed and how the preliminary result would end.

Doelstelling:

Locatie:

42521: Trait-based biogeographic models in dinosaurs

Promotor(en):	Michaël Nicolaï
Begeleider(s):	
Contactpersoon:	Michaël Nicolaï
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	Master of Science in de geologie
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

In a span of 50my years dinosaurs managed to obtain a circumglobal distribution. Yet, how they did so remains an open question. Vicariance, trans-oceanic dispersal and potentially trait-based dispersal (i.e. where specific traits, such as aquatic lifestyle and/or big size influence dispersal potential) undoubtably played a role but so far this has not been shown. Recent advances in both modelling (i.e. BioGeoBEARS) and availability of large datasets enable us to reconstruct how dinosaurs spread across the world.

Doelstelling:

The goal of this project is to concatenate all available data to reconstruct the biogeography of dinosaurs. In particular, the model will include:

-stratigraphic information: paleoreconstructions of different landmasses and potentially oceanic currents will have to be estimated for different periods of time

-distributions for as many dinosaurs have to be collected

-traits that potentially influence dispersal have to be collected

-BioGeoBEARS will be used to estimate the biogeography of dinosaurs.

Locatie:

campus Ledeganck

42616: Understanding plant-herbivore eco-evolutionary interactions: a pattern-based approach using individual-based modelling

Promotor(en):	Dries Bonte
Begeleider(s):	Dries Bonte
Contactpersoon:	Dries Bonte
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Plants and their herbivores are continuously involved in an armsrace, but they are also on the move. Mosaic co-evolution theory predicts these interactions to depend on their dispersal and their reciprocal impact. But to what extent does this theory hold in nature?

Doelstelling:

The student will develop a paramerised individual-based model to simulate the interactions between hondstongue and its herbivore Curciliod beetle. Based on time-serie data from the Belgian coastal dunes, the model will allow the estimation of size-dependent gene-flow and selection pressures acting on the plant, and to test to which degree rewilding by large grazers promote or constrain co-evolutionary dynamics. Pending on the student's interest, field work can be organised to quantify the plant's stage structured demography.

Locatie:

Onderwerp voorbehouden voor Amke De Cleer

42512: Understanding vulture hotspot and habitat use through movement ecology

Promotor(en): Lucy Mitchell
Begeleider(s):
Contactpersoon: Lucy Mitchell
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Background:

Long lived birds develop in their foraging strategies over time, once they have fledged and are independent. As adults, they may be better able to judge where good quality, profitable foraging resources are located. Particularly for avian scavengers, appropriate food resources are likely to be widely dispersed and unpredictable. But, we might expect repeated use of predictable, profitable resources where these are located, particularly by adult birds who have experience of these profitable locations.

We have a wealth of high resolution tracking data, and although it is often not clear why, and with what frequency, these sites are revisited, we should be able to identify the basis of these 'hotspot' areas, potentially identifying repeatable predictable resource locations.

Doelstelling:

Aim:

This study will use high resolution GPS tracking data of vulture spp. in Spain, alongside environmental covariates such as land use and weather data, taken from external data sources. We can identify profitable areas, what these consist of, and with what frequency they are used. This will concentrate on adult birds, but can be contrasted with sub-adult birds to observe any differences among age groups, and thus experience. This is a data based project, with heavy use of R and QGIS, with data capture from a number of external sources.

Locatie:

Ledeganck

Onderwerp voorbehouden voor Thibo Bracke

42515: Unravelling ecological networks of the Asian hornet: pollination capabilities

Promotor(en): Dries Bonte, Jasmijn Hillaert

Begeleider(s): Heleen Van Ransbeeck, Jasmijn Hillaert
Contactpersoon: Heleen Van Ransbeeck
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Pollination, one of nature's contributions to people, is crucial for sustaining terrestrial ecosystems and global food security. This service faces significant threats on a broad scale, including habitat loss and homogenization, pesticide use, the proliferation of parasites and pathogens, and the overarching impact of climate change. Besides diseases, also invasive species put such services at risk by their direct ecological impact on pollinator abundances and diversity. One invasive alien species forming a threat to pollination services is the Asian hornet (*Vespa velutina*). Originating from Asia, this species was accidentally introduced via a pottery import in France in 2004.

The Asian hornet has an impact on biodiversity through competition for food with native wasps, predation on native insects, but also by affecting the behaviour of pollinators. Its presence chases away native pollinators from foraging sites, either because of direct interactions (competition and predation) or from the induction of "a landscape of fear". This can affect the resulting flower pollination, where seed production decreased in areas where the Asian hornet was present. Apart from being a predator, the invasive hornet might also act as a pollinator itself, but this remains understudied.

Doelstelling:

In this thesis the student will study the ecological interactions of *V. velutina* through a pollen analysis. The pollen attached to workers will be with metabarcoding to unravel the diversity of plants potentially pollinated by *V. velutina*.

Locatie:

Onderwerp voorbehouden voor Maud Vanhoecke

42794: Unravelling species complexes and cryptic species in African rain forests, using genomic data

Promotor(en): Lars Chatrou, Luiz Fonseca
Begeleider(s):
Contactpersoon:
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Rain forests are most species-rich terrestrial ecosystems. Interestingly, tree species abundance in rain forests is not evenly distributed, and most areas are inhabited by a few, highly abundant species, termed oligarchic or hyperdominant. It is hypothesized that in some species, hyperdominance can be a result of species complexes and poorly defined species.

The determination of hyperdominant species status relies on correct botanical identification of tree species in rain forests. While defining a species is potentially one of the most difficult tasks in biology and highly dependent on the species concept applied, it is a fundamental unit of biological science. In tropical rain forests, the species concept applied in almost all cases is the morphological species concept, as other species concepts effectively cannot be applied due to logistic difficulties. Increasingly, we find that widespread species are harbouring multiple species, which may only be discernible using genetic techniques as the morphology of the genetic clusters is similar.

In this project, you will be looking at some widespread species of Annonaceae in the Congo basin, and test whether they contain distinct genetic clusters. The Congo Basin contains the second largest extent of continuous tropical rain forest after the Amazon.

The Annonaceae are a pantropical family of rain forest trees and lianas. African Annonaceae are trees and lianas, and often belong to genera that have all been revised by taxonomists in the past 20 years. In other words, the morphological species concept has been applied and can be taken as a hypothesis for species circumscription. Some of the species are widespread and may represent cryptic species.

The resources to be used in this project are within reach: the herbarium at the Meise Botanic Garden (Belgium) contains one of the largest collections worldwide of African Annonaceae. A number of specimens of widespread species will be sampled from across the distribution area, for which a number of genetic markers will be sequenced. Geographic patterns of genetic variation will be inferred, testing the hypothesis of the presence of cryptic species in widespread African species of Annonaceae.

Doelstelling:

In this project, you will test hypotheses on the presence of cryptic species in widespread African species of Annonaceae. These species will be identified based on taxonomic monographs and revisions that have been published in the past ca 20 years. The markers that will be sequenced for each individual in a species complex will have to be decided, evaluating cost-effectiveness and resolution.

Specifically, we will test the following hypotheses:

- Widespread species of Annonaceae in the African rain forests harbour cryptic species.
- Cryptic species in African Annonaceae follow well-established biogeographic boundaries.

This project will suit a student with an analytical mindset and a strong interest in evolution, ecology and taxonomy. The student will learn how to use a variety of lab techniques and analytical tools and concepts. The output will be written in the form of a scientific article aiming to submit it to a peer-reviewed journal for publishing.

Locatie:

Ledeganck

42624: Urban Green Projects in Flanders: Windowdressing or Nature-based Solutions?

Promotor(en):	Sander Jacobs, Ewaut Van Wambeke
Begeleider(s):	
Contactpersoon:	
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie, Master of Science in de geografie en de geomatica
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

n Vlaanderen worden heel wat terreinrealisaties uit de grond gestampt met het oog op het verhogen van de klimaatrobuustheid en leefbaarheid van onze omgeving. Deze ingrepen gebeuren op verschillende schaalniveaus, in uiteenlopende gebiedstypes en door diverse actoren. Ook de aanpak/strategieën en visies hierachter zijn zeer uiteenlopend.

De Atlas Groenblauwe Oplossingen brengt terreinrealisaties in kaart die inzetten op de optimalisatie van de stedelijke waterhuishouding en het vergroenen van de bebouwde omgeving, en ook hierin is deze diversiteit aan ingrepen/strategieën terug te vinden. Met deze thesis gaan we op zoek naar antwoorden op volgende vragen:

- Welke ingrepen en maatregelen worden het vaakst geïmplementeerd en hoe? (Welke visies/strategieën zitten hier achter?)

- Wat is de "state of the art" van deze terreinrealisaties? Wat zijn de succesfactoren?

- Hoe kunnen we de kosten-baten van deze terreinrealisaties opmaken op het vlak van o.a. biodiversiteit, bodemverzet, spontane ontwikkeling vegetatie of aanplant, ontwerpen of meer "organisch" ontwikkelen, ...

Doelstelling:

This thesis will deploy a critical evaluation on a number of case studies in Flanders, sampling from the Flanders' Nature Based Solution Atlas, which is under construction. The thesis might focus either on effectiveness of (a few) subsidy instruments, or on a range of different NBS types, or on effectiveness to 'solve' certain problems. It will entail data work, field visits with observations as well as interviews, and potentially questionnaires. Apart from this NBS-assessment, this thesis will also develop/test an assessment procedure for NBS.

Locatie:

42695: Using DNA metabarcoding to monitor phytoplankton dynamics in the Schelde estuary

Promotor(en):	Wim Vyverman, Koen Sabbe
Begeleider(s):	Rik Debeer
Contactpersoon:	Wim Vyverman
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Phytoplankton, due to their small size, short generation times and large population sizes, are excellent bioindicators of environmental change. Changes in phytoplankton abundance and species composition inform us about the health of aquatic ecosystems, and can resonate through aquatic food webs, with important ecological and economic repercussions. Traditionally, phytoplankton is monitored using microscopy, which allows the identification and quantification of phytoplankton species. However, this technique is labor-intensive, time-consuming, and requires a certain level of taxonomic expertise. Moreover, it is usually not possible to distinguish morphologically similar (but often ecologically different) species using this approach. Metabarcoding is a novel DNA-based approach to monitor phytoplankton. Short DNA sequences of all phytoplankton species present in a water sample, and which are species-specific (hence 'barcodes'), are sequenced using high-throughput next-generation sequencing (NGS) techniques. This approach provides a rapid and cost-effective alternative to microscopy, and has a higher taxonomic resolution. However, metabarcoding itself also has its shortcomings, and it is therefore important that both approaches are compared.

Doelstelling:

The main objective of this MSc thesis is to compare the results of phytoplankton community composition analyses based on metabarcoding and microscopy, to evaluate the applicability of metabarcoding for phytoplankton monitoring in the Schelde estuary (Belgium). This estuary has gone through significant changes in the last decades, characterized by a marked improvement in water quality but also a pronounced increase in turbidity, that has affected phytoplankton assemblages (Amadei Martinez et al, 2023, http://dx.doi.org/10.1016/j.scitotenv.2022.160402). The student will take part in field sampling (monthly monitoring), microscopic and metabarcoding analyses, and will compare and evaluate the results of both approaches.

Locatie:

campus Ledeganck, campus Sterre

42687: Using metabarcoding to assess patterns of microbial diversity in intertidal habitats in relation to coastal rewilding

Promotor(en):	Koen Sabbe, Dimitra-Ioli Skouroliakou
Begeleider(s):	Yeseren Kayacan

Contactpersoon:	Koen Sabbe
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

Intertidal zones are highly productive environments at the interface between land and sea, covering over 10,000 km² along Europe's coastline. These zones consist of diverse habitats, including tidal mud- and sandflats, salt marshes, and seagrass beds, which are very important as they deliver essential ecosystem services, such as carbon sequestration, coastal protection, climate resilience, and biodiversity enhancement. For this reason, coastal habitats are increasingly being rewilded, by returning land to the sea (depoldering) or discontinuing human exploitation (e.g. salt pans).

Although tidal environments are highly dynamic and stressful environments, they support unique, highly productive microbial communities. Microphytobenthos, a collective term for benthic microalgae, builds benthic biofilms and plays a vital role in primary production, enhancing sediment stability and supporting higher trophic levels. Prokaryotes, another essential component of these biofilms, process organic matter and influence the availability of carbon and nutrients within the community. Despite their importance, the diversity patterns of these microbial communities remain underexplored, and little is known about what regulates their diversity at regional and global scales. In addition, it is not known how these organisms respond to rewilding efforts.

Doelstelling:

The main objective of this work is to investigate diversity patterns and ecological processes (e.g., environmental filtering, stochastic processes) in microbial communities in intertidal habitats (i.e., salt marsh, seagrass, intertidal flats). To this end, new data on eukaryotic and prokaryotic microbial diversity will be obtained using DNA metabarcoding in different European natural and rewilded sites in the framework of the EU REWRITE project (Rewilding and Restoration of Intertidal Sediment Ecosystems for Carbon Sequestration, Climate Adaptation, and Biodiversity Support; https://rewriteproject.eu/). In addition, data from publicly available regional and global sources will be collected from the same habitats. The student will be involved in gaining hands-on experience in DNA extraction, library preparation, and bioinformatics analyses of microbial samples.

Locatie:

campus Ledeganck, campus Sterre

Opmerkingen:

As this topic is under the supervision of someone who is not Dutch speaking, the supervision and writing of the thesis will be done in English.

42638: Vangst-hervangst en populatiemodellering van Vuursalamander in Vlaanderen

Promotor(en):	Femke Batsleer
Begeleider(s):	Jeroen Speybroeck
Contactpersoon:	Jeroen Speybroeck
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

De vuursalamander Salamandra salamandra is een habitattypische soort van bronbossen en een prioritaire soort voor het Vlaamse natuurbeleid. De soort komt in Vlaanderen verspreid voor in sterk gefragmenteerde boshabitats, met haar zwaartepunt in de zuidelijk helft van Oost-Vlaanderen. Een uit Azië afkomstige schimmelziekte roeide verschillende Nederlandse, Duitse en Vlaamse populaties nagenoeg volledig uit. Het INBO onderzoekt de Vlaamse populaties onder meer door middel van vangsthervangstonderzoek en populatiemodellering en zoekt een student om hieraan bij te dragen. Daarnaast liet eerder onderzoek verschillen in vlekkenpatroon tussen verschillende populaties opmerken, die we willen ontrafelen en in verband brengen met habitatkenmerken en beschikbare genetische diversiteitsgegevens.

Doelstelling:

De student zal 's nachts veldwerk uitvoeren in de herfstperiode om langsheen vaste routes individuele salamanders te fotografen in functie van vangst-hervangst-onderzoek, gecombineerd met veldwerk overdag om habitatkenmerken te bepalen. Deze data, in combinatie met oudere gegevens, zullen gebruikt worden voor vangst-hervangst analyses en populatiemodellering. Dit wordt gecombineerd met statistische analyses om de vlekkenpatronen in de verschillende populaties in verband te brengen met habitatkenmerken en reeds beschikbare genetische data.

Locatie:

42682: Vegetatie en flora in extensief begraasde natuurgebieden: linken met vegetatiestructuur en begrazingsintensiteit

Promotor(en):	Jan Van Uytvanck
Begeleider(s):	Jan Van Uytvanck, Sam Provoost
Contactpersoon:	Jan Van Uytvanck
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

In een hele reeks ecosystemen worden -als vorm van natuurbeheer- grote grazers op een extensieve manier ingezet. Ze zorgen voor structuurrijke vegetaties die voor een hoge biodiversiteit aan organismen kunnen instaan. Toch is niet steeds duidelijk hoe vegetatiestructuur en terreingebruik (en effectieve graasdruk) van grote grazers een invloed uit oefenen op de diversiteit en de verspreiding van plantensoorten. In diverse vegetaties is er risico voor verruiging, anderzijds kunnen structuurrijkdom en variatie aan microhabitats en -klimaten instaan voor meer plantendiversiteit.

Doelstelling:

Als onderdeel van onderzoek (aan het Instituut voor Natuur- en Bosonderzoek (INBO)) naar ecologische processen in open extensief begraasde ecosystemen, werden aan de hand van dronebeelden (en fotogrammetrie) gedetailleerde vegetatiehoogtemodellen gemaakt die de vegetatiestructuur in een selectie van natuurgebieden in kaart brengt. In deze gebieden werden grote grazers (runderen en paarden) uitgerust met een GPS-zender die om het uur hun positie in het terrein registreert. Zo krijgen we voor de verschillende soorten grazers inzicht in hun voorkeuren voor vegtetatietypen en -structuren. Op verschillende schalen werden data van flora en vegetatie opgenomen: (1) gebiedsdekkende puntwaarnemingen van aandachtssoorten (zeldzame en/of ecologisch belangrijke soorten) en vegetatiekaarten, (2) plotwaarnemigen van bloeiende planten, (3) subplotwaarnemingen: vegetatie-opnamen.

In deze thesis ligt de focus dus op het verkrijgen van inzichten in het voorkomen, de abundantie en de bloei van verschillende plantensoorten in relatie tot de vegetatiestructuur en het terreingebruik van verschillende soorten grazers in een een set van verschillende ecosystemen en/of gebieden (nog nader vast te leggen, in overeenstemming met de student).

Afhankelijk van de gekozen proefterreinen kan dit onderwerp ook veldwerk inhouden, goede GIS- en R-skills zijn belangrijk voor dit onderwerp.

Locatie:

campus ledeganck of labo inbo (Sint-Denijs Westrem)

Website:

Meer informatie op: https://sites.google.com/inbo.be/procesbeheer

42714: What factors drive the carrying capacity of landscapes for invasive ring-necked parakeets (Psittacula krameri)?

Promotor(en):	Diederik Strubbe
Begeleider(s):	
Contactpersoon:	
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

In Flanders and surrounding regions, the ring-necked parakeet (Psittacula krameri) is an increasing concern due to the ecological and economic impacts of this invasive species. Beyond potential competition with native cavity-dwelling species such as bats and birds, there is growing apprehension about damage to agricultural crops and the risk of further expansion into non-urban areas. Despite the substantial body of research on the species, fundamental knowledge about the carrying capacity of different habitats remains lacking. Determining this carrying capacity—the maximum density of individuals that a specific area can sustain—is essential for modeling population dynamics and assessing the feasibility of management measures. Without such information, it is challenging to develop effective strategies to mitigate the negative impacts of parakeet populations and curb further spread. This project aims to address this knowledge gap by investigating which habitat characteristics influence the carrying capacity for ring-necked parakeets.

Doelstelling:

The objective of this research is to develop a statistical model that quantifies the carrying capacity of Flanders for ring-necked parakeets and identifies the habitat factors underpinning it. This model will be based on a combination of newly collected and existing data. Fieldwork may include breeding surveys to estimate local population sizes and densities, potentially using techniques like passive acoustic monitoring for improved efficiency. Additionally, existing information from previously published studies, breeding bird atlases, and data from neighboring countries will be analyzed. The final model will estimate carrying capacity using habitat and land use maps, producing density maps (e.g., the number of breeding pairs per km^2). This approach will not only provide concrete information about where parakeet populations could establish but also support the design of effective management strategies. Furthermore, the model will offer insights into how habitat factors, such as food availability and nesting opportunities, contribute to carrying capacity and identify key landscape elements critical for managing this invasive species.

Locatie:

Opmerkingen:

in samenwerking met INBO

42681: Your new best PAL: a new player at the interface between primary and secondary metabolism in plants

Promotor(en):	Bartel Vanholme
Begeleider(s):	, Caroline Van Beirs
Contactpersoon:	Bartel Vanholme
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

The enzyme PHENYLALANINE AMMONIA LYASE (PAL) is the entry point of the plant specific phenylpropanoid pathway, which is crucial for plant growth, development, and defense. PAL catalyzes the deamination of phenylalanine to cinnamic acid, a precursor for a diverse array of secondary metabolites. By modulating phenylpropanoid production, PAL contributes to lignin biosynthesis, a critical process for cell wall strengthening and vascular integrity. Additionally, the enzyme supports the synthesis of flavonoids and other phenolic compounds, which function in antioxidative defense and stress adaptation. Arabidopsis has four PALs (PAL1-4), of which PAL1, 2 and 4 are involved in lignification and/or suberization of the cell wall. Surprisingly little is known about the function of PAL3, but most likely it is not involved in cell wall synthesis.

Doelstelling:

The general objective of this project is to gain insight into the physiological role of PAL3 in the plant. You will investigate (i) the enzymatic reaction catalyzed by PAL3 through metabolomics and enzyme assays, (ii) uncover the role of PAL3 in the plant by phenotyping pal3 knockout and overexpression lines, and (iii) analyze the expression pattern of PAL3 by using novel transcriptional and translational reporter lines.

Locatie:

campus Zwijnaarde