# Master of Science Biology, incl. Educatieve Master Biologie - AJ 2026-2027

# Goedgekeurde onderwerpen

*Lijst gegenereerd op: Wed, 24 Dec 2025 04:04:21 +0100.* *Laatst ingediende onderwerp: 48571*

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## 48485: In welke mate bepalen fysico-chemische parameters en verschralingsbeheer het herstel van laagveenvegeaties in de paleomeander van de Schelde in Berlare (Oost-Vlaanderen)?

| | |
|---|---|
| Promotor(en): | Jan Van Uytvanck |
| Begeleider(s): | michaël Crapoen, Michaël Crapoen |
| Contactpersoon: | Michaël Crapoen |
| 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 de paleomeander van de Schelde in Berlare werden de afgelopen jaren grote inspanningen gedaan om laagveenvegetaties te herstellen

Dat gaat gepaard met hydrologisch herstel, verandering van het landgebruik, inrichtingsmaatregelen (bv. eenmalige kappingen) en ontwikkelingsbeheer (vnl. maaibeheer).

Dit leidt niet altijd tot de gewenste resultaten omdat vaak de abiotische of biotische drempels niet zijn of kunnen weggewerkt worden.

**Doelstelling:**

In deze theisis wordt onderzocht hoe specifieke fysico-chemische parameters (Olsen P, Fe, Al, %C, %N, (Fe-S)/P-ratio) de effectiviteit van verschralingsbeheer in habitattypes rond het Donkmeer bepalen en hoe kan de kennis hiervan bijdragen tot het realiseren van doelhabitats?

Door het analyseren van specifieke fysico-chemische parameters (Olsen P, Fe, Al, %C, %N, (Fe-S)/P-ratio) kan de effectiviteit van verschralingsbeheer in de habitattypes rond het Donkmeer nauwkeuriger worden beoordeeld. Volgens het natuurbeheerplan Berlare Broek-Donkmeer gaat het hierbij om Natura2000-habitattypes, meer bepaald de Europees beschermde habitats (3150: water met waterplanten, 6410: blauwgraslanden, 7410: laagveen (met rietland of mesotroof broekbos), 91E0_vn: ruigte elzenbos en 91E0_vm: mesotroof broekbos) en de regionaal belangrijke biotopen (=rbb) (rbbhf: moerasspirearuigte, rbbhc: dotterbloemgrasland, rbbmc: grote zeggenvegetatie en rbbmr: rietland).

Door middel van bodemanalyses en vegetatieopnames wordt nagegaan hoe ver percelen verwijderd zijn van hun natuurdoeltype en in welke mate nutriëntenoverschotten nog moeten worden weggewerkt. Het onderzoek evalueert aan de hand van verschillende beheertrajecten of regulier maaibeheer volstaat om de Natura2000-doelhabitats te realiseren, of dat bijkomende herstelmaatregelen (bv. aangepast maaibeheer, plaggen of uitmijnen) noodzakelijk zijn. Op basis van de resultaten worden concrete adviezen geformuleerd die het toekomstig beheer van deze habitats kan sturen.

**Locatie:**

vedwerk Berlare, Labowerk Ugent campus Ledeganck

**Samenwerking met bedrijf of non-profit organisatie**

Bedrijf: vzw Durme
Samenwerking: begeleider

**Onderwerp voorbehouden voor Ruth Vergalle**

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## 48282: (How) Does Grazing Management Shape Invertebrate Communities in Coastal Saltwater Marshes?

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:

Vegetation and its structural complexity in saltwater marshes such as the Zwin and the IJzermonding are primarily governed by tidal dynamics. However, grazing by cattle (Zwin) and/or sheep (Zwin/IJzermonding) is often applied as an additional management strategy to prevent overgrowth by species such as Sea Couch. Grazing further creates heterogeneity in vegetation structure, which likely plays a key role in shaping both plant composition and invertebrate communities.

### Doelstelling:

This study aims to assess how the diversity, abundance, and biomass of invertebrate fauna, as well as plant communities, are influenced by the interplay of grazing, tidal dynamics, and vegetation structure. The findings are expected to provide practical insights for the effective management of coastal saltwater marshes.

Particular attention will be given to rare or protected species, such as the Narrow-mouthed Whorl Snail (Vertigo angustior) in the Zwin, whose ecological requirements remain poorly understood, as well as flower-visiting insects.

The study will combine existing data (vegetation maps, species surveys, hydrological maps, and habitat preferences of grazers) with fieldwork conducted in July, August, and September 2026, including sampling and mapping flower-visiting insects. Laboratory analyses will involve processing samples through sorting, measuring, and species identification.

### Locatie:

Zwin, Ijzermonding, Campus Ledeganck Gent (ev. labo INBO Gent (nabij Gent Expo), thuis

### Samenwerking met bedrijf of non-profit organisatie

Bedrijf: Instituut voor Natuur- en Bosonderzoek (INBO)
Samenwerking: begeleider

### Onderwerp voorbehouden voor Hanne Van Biervliet

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## 48428: A checklist of Laboulbeniales in Norway

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:

Although our knowledge of the fungal kingdom (Fungi) has significantly increased over the past decades, many taxa remain understudied. A clear example is the order Laboulbeniales (Ascomycota), a group of obligate ectoparasites associated with various hosts within Arthropoda. Currently, 2,454 species of Laboulbeniales have been described worldwide, distributed across 164 genera. Their hosts belong to different subphyla, but they are most commonly found on beetles (Coleoptera), particularly within the families Carabidae (ground beetles) and Staphylinidae (rove beetles).

Problem statement

In Norway, only 17 species of Laboulbeniales have been found so far, whereas in neighboring countries a considerably higher diversity is reported, e.g., Denmark (n = 195) and Sweden (n = 102). This discrepancy is most likely not due to a genuinely lower diversity in Norway but rather a result of insufficient research in the region.

**Doelstelling:**

The aim of this master's thesis is to compile a catalogue that provides an overview of the diversity of Laboulbeniales in Norway. Through this project, the student will gain experience in applying DNA-based methods to distinguish species. The study builds upon a previous bachelor's thesis with the same objective, which did not incorporate molecular techniques. The master student will become familiar with curation and management of biodiversity records, and integrative taxonomy approaches in mycology. The results of this project will be submitted to a peer-reviewed journal, in collaboration with our international partners.

**Locatie:**

Campus Ledeganck

**Onderwerp voorbehouden voor Emile Vanderbeck**

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## 48268: A chemical genetics screen for highly specific inhibitors of nematode feeding site establishment

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|---|---|
| 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 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

**Onderwerp voorbehouden voor Klara Vastmans**

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## 48379: A fungal monitoring project in Honduras: diversity, communication, and ethnomycology

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|---|---|
| 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. 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. Additionally, 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. Finally, traditional knowledge is indispensible to better understand how different species are used by local communities. This kind of knowledge is lacking from northwestern Honduras.

**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 2026 summer field season, learning fungal collection, identification, and processing skills in a remote location (pending funding). Second, data from the 2022, 2023, 2024, and 2025 field seasons will be used to map the fungal diversity in Cusuco National Park and to analyze whether species have distributions along an altitudinal gradient. The student will have the opportunity to describe new species found during their fieldwork. Second, an information campaign will be set up for visitors to Cusuco National Park, with posters and simple identification guides, both in English and in Spanish. This part of the project will gap the bridge between the science and the broader audience, including locals. Third, interviews will be conducted with local communities to gain a better understanding of how different species of fungi are used locally. This ethnomycological aspect of the study could provide valuable information spanning generations and give a sense of how mycophile the region is. 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, educate peoplee about fungi in English and Spanish, and interact with local communities in Honduras. This project will be a collaborative effort with researchers from Operation Wallacea, the Biology Centre of the Czech Academy of Sciences, and the Universidad Autónoma de Honduras.

**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 Lisa Van Cutsem**

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## 48510: Advancing Sustainable Fertilization: Agronomic and Environmental Assessment of New Nitrification Inhibitors

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|---|---|
| Promotor(en): | Tom Beeckman, Hans Motte |
| Begeleider(s): | Cedric Thierens, Hannelore De Hooghe |
| Contactpersoon: | Hans Motte |
| 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 widely applied in agriculture to sustain crop productivity, but their use often leads to major environmental challenges, including nitrogen (N) pollution and emissions of nitrous oxide ($N_2O$), a potent greenhouse gas. A key driver of these issues is nitrification, a microbial process that converts ammonium or ammonia into nitrite and nitrate. In contrast to ammonium, nitrate and nitrite are highly mobile in soil, resulting in significant nitrogen losses through leaching and denitrification. These losses reduce nitrogen use efficiency (NUE) for crops and contribute to groundwater contamination and greenhouse gas emissions.

Nitrification inhibitors are able to significantly reduce these N losses. However, current commercial nitrification inhibitors face economic, biological, and regulatory uncertainties. This creates an urgent need for alternative nitrification inhibitors that are effective, affordable, and environmentally safe.

In an ongoing project in the Beeckman lab, several promising new nitrification inhibitors have been or are being discovered. To fully assess their potential, it is essential to characterize their impact on the microbial nitrogen cycle, evaluate possible off-target effects, and demonstrate their agronomic benefits and pollution-reducing capacity.

**Doelstelling:**

The main goal of this thesis is to evaluate the agronomic and environmental potential of newly discovered nitrification inhibitors. Specifically, the project aims to characterize how these inhibitors influence the microbial nitrogen cycle in soil, including their effect on nitrification rates and possible off-target processes. It will also assess their ability to reduce nitrogen losses and nitrous oxide emissions under different soil conditions. Furthermore, the study will investigate the impact of these inhibitors on crop performance and nitrogen use efficiency, while validating their environmental safety. Together, these objectives will provide a comprehensive understanding of the effectiveness and sustainability of novel nitrification inhibitors.

Possible techniques include:

- Soil microcosm assays: Measurement of different nitrogen forms (ammonium, nitrite, nitrate) using spectrophotometric methods, combined with continuous monitoring of nitrous oxide emissions via a trace gas analyzer.
- High-throughput soil assays: Automated liquid handling and robotics for efficient compound testing in soil-based assays.
- Pot experiments: Evaluation of plant growth, nitrogen use efficiency (NUE), and yield-related parameters under controlled conditions.
- Molecular analyses: DNA extraction from soil followed by microbiome profiling and/or qPCR to assess the impact on nitrogen-cycle microorganisms.
- Microbial cultivation: Growth assays using nitrifying microorganisms to confirm inhibitor activity and specificity.
- Ecotoxicological tests: Microtox assays and EcoPlates (Biolog) to evaluate ecological safety and potential off-target effects.

Impact
This project offers hands-on experience in soil microbiology, greenhouse gas mitigation, and agronomic testing. The student will directly contribute to the development of next-generation nitrification inhibitors, helping to reduce nitrogen losses and improve sustainability in agriculture.

**Locatie:**

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## 48571: African Indigenous Perspectives on Flanders' Nature Conservation

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|---|---|
| Promotor(en): | Sander Jacobs, Charlotte Noël |
| 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:**

In vele regio's in Afrika bestaan uitgebreide ervaringen met community-based conservation, waarbij natuurbeheer sterk verweven is met lokale cultuur, landgebruiksrechten en collectieve waarden. Deze gemeenschappen bieden inzichten, zowel uit successen als uit failures, die relevant kunnen zijn voor de ontwikkeling van natuurbeleid in Vlaanderen. Hier is natuurbehoud historisch gericht op soorten- en habitatbescherming binnen afgebakende zones, met de nadruk op intrinsieke natuurwaarden. Recente internationale conclusies (onder meer IPBES) wijzen op de beperkingen van dergelijke klassieke benadering beperkingen heeft, onder meer wat betreft maatschappelijk draagvlak en sociaal-ecologische rechtvaardigheid. Innovatieve Vlaamse initiatieven zoals natuurweefselplanning en landschapsparken zijn community-gerichte projecten in stedelijke en rurale context, die vragen om nieuwe kennis en vergelijkende perspectieven.

**Doelstelling:**

Dit onderzoek gaat na welke inzichten uit Afrikaanse indigenous natuurbeschermingspraktijken relevant zijn voor Vlaanderen en hoe deze kunnen bijdragen aan een meer inclusieve, sociaal gedragen vorm van natuurbeheer.

Onderzoeksvragen

- Welke principes en praktijken kenmerken Afrikaanse community-based conservation vanuit het perspectief van lokale en inheemse gemeenschappen?
- Welke onderliggende visies en historiek bepalen het Vlaamse natuurbehoud en beleidsstrategieën?
- Welke lessen uit deze Afrikaanse context zijn relevant voor nieuwe en meer sociaal bewuste en effectieve Vlaamse natuurbeleid- en beheerpraktijken?

**Locatie:**

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## 48474: AI-assisted analysis of seasonal foraging ecology in urban ring-necked parakeets using citizen-science photographs

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|---|---|
| Promotor(en): | Diederik Strubbe |
| Begeleider(s): | Frouke De Witte |
| 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 ring-necked parakeet (Psittacula krameri) has become a successful urban invader across Europe, establishing large populations in cities across Europe. Although their broad ecological success is often linked to behavioral flexibility and generalist foraging, it remains poorly understood how their diet composition changes across seasons and geographic contexts, and whether these shifts reflect systematic reliance on anthropogenic or non-native plant resources. At the same time, citizen science platforms such as iNaturalist, eBird and waarnemingen.be generate vast numbers of photographs that offer rich ecological information. These images capture behaviors such as foraging, feeding from artificial feeders, nest provisioning, or roosting near cavity sites, yet extracting such information requires an integrated workflow combining AI-based image recognition, behavioral classification, and background plant identification. Developing and testing such a workflow offers an opportunity to quantify how invasive parakeets use urban habitats, whether resource use varies geographically, and how specific plant species or resource types support population persistence. The findings will contribute to our understanding of invasion success mechanisms, including the possibility that dependence on human-provided food sources or exotic ornamental plants buffers parakeets against seasonal deficits in natural resources.

**Doelstelling:**

The central objective of this thesis is to develop and operationalize a reproducible workflow that leverages citizen-science photographs to study how ring-necked parakeets allocate their foraging effort across seasons, plant types, and urban habitats. The student will combine automated image recognition, behavioral classification, and plant identification tools to extract ecological information from large visual datasets. Specifically, the project aims to: (1) reliably detect the presence of parakeets in photographs and assign behavioral categories (foraging, breeding/roosting, other), (2) isolate the environmental context of relevant images through parakeet masking, and (3) identify the plant species and resource types being used, distinguishing native vegetation from ornamental, non-native plants and anthropogenic food sources. Using the metadata associated with each image (location, time, season, habitat), the student will quantify spatial and temporal patterns in resource use, assess how these patterns differ across European regions, and test whether dependence on human-provided or non-native resources buffers parakeets against seasonal food scarcity.

**Locatie:**

desk-based thesis (no fieldwork)

**Opmerkingen:**

This is a fully desk-based thesis with no fieldwork component. All work consists of downloading, organizing, and analysing photographic data from citizen-science platforms, and applying AI-based tools for species detection, behavioural classification, and plant identification. The project is suitable for students who are interested in ecological data exploration and are either familiar with (or motivated to) learn—software and workflows involving image recognition. No bird handling, site visits, or field sampling are involved.

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## 48478: All white but not the same: describing species in Russula

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|---|---|
| Promotor(en): | Annemieke Verbeken |
| Begeleider(s): | Ruben De Lange |

Contactpersoon: Ruben De Lange
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:**

Russula is a genus of ectomycorrhizal fungi with a worldwide distribution. Although being a popular genus among mycologists, its diversity is still not fully discovered – even in a well-explored region as Europe. Within the genus, R. subg. Brevipedum – also known as the “big white russulas – is a rather extraordinary group. Despite not being as colourful as most species in the genus, they are morphologically challenging. Recent studies on the subgenus have unravelled a much higher diversity as previously known, with up to 15 (or more?) new species in Europe.

**Doelstelling:**

The aim of this thesis is to describe new species within Russula subgenus Brevipedum. The student will go through the all the steps of the taxonomic journey: field work, lab work, microscopy, illustration and phylogenetic analysis. And last but not least, deciding on a well-suited name for the newly described species.

**Locatie:**

campus Ledeganck

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## 48519: Aquatic community dynamics in an African crater lake during the glacial-to-Holocene transition (17,800-10,000 years ago): tracing the influences of salinity tolerance and dispersal limitation

Promotor(en): Dirk Verschuren
Begeleider(s): Dirk Verschuren
Contactpersoon: Dirk Verschuren
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:**

Large natural climate variability at time scales from decades to multiple millennia play a major role in the long-term ecological dynamics of the large Rift lakes and other water bodies in tropical East Africa. Lake-sediment records are an important tool to assess the sensitivity of these aquatic systems to the impact of ongoing anthropogenic climate change on water resources. This thesis project aims to assess this sensitivity to climate variability by reconstructing changes in the aquatic community of Lake Ntambi, a deep isolated crater lake in western Uganda, during the transition from the last ice age to the current interglacial period (the Holocene), through analysis of fossil remains of chironomid and phantom midge larvae, aquatic snails and fish preserved in its sedimentary record.

**Doelstelling:**

Adult chironomids are non-biting mosquitoes which can easily disperse between isolated water bodies, and thus can be assumed to have been present from the base of the record dated to 17,800 years ago. Moreover different species have different tolerance for elevated salinity, which allows to reconstruct when the lake was either fresh or saline from the composition of fossil chironomid assemblages. Adult phantom midges can also easily disperse between lakes, but can colonize it successfully only when the lake is fresh. Moreover local population abundance is also controlled by the intensity of fish predation. For aquatic snails, colonizing an isolated lake depends on hitching a ride in the plumage of water birds without drying out along the way, and on finding freshwater conditions upon arrival. Therefore it may take several decades or even centuries after the lake became fresh for the first snails to establish a local population, and even more time before all snail habitat niches are filled with the best-adapted species. The only native fish inhabiting the Ugandan crater lakes are mouthbrooding cichlids. Although new colonizations have never been documented they are thought to be introduced when a fish eagle, pelican or cormorant brings a brooding female fish from another lake to its nest, such that young fish can fall from their dead mom's mouth into the water and survive. Needless to say, also this must be a rare event, and can only be successful when the lake is fresh. Thus, this thesis project will determine when phantom midges, snails and fish first arrived in Lake Ntambi, and trace changes in population abundance and community composition through a period of ca 8000 years punctuated by climate-driven salinity fluctuations; a period of high salinity after a first colonization may have caused local extinction, followed by another long period of absence before a new event of successful introduction.

The practical work for this thesis involves chemical preparation and sieving of sediment samples from the oldest portion of a 8.3-meter long sediment core, followed by scanning of the sieved residues under a binocular microscope (25-100x) to identify and count the fossil remains of chironomid and phantom midge larvae, fossil snails, and the scales and teeth of cichlid fishes with the help of photo atlases, identification guides and reference collections. The obtained data set is then analyzed using univariate and multivariate statistics to support the ecological interpretation of trends in abundance through time, both at the level of individual species and that of the aquatic community as a whole.

Eerste pagina van PDF:

**Aquatic community dynamics in an African crater lake during the glacial-to-Holocene transition (17,800-10,000 years ago): tracing the influences of salinity tolerance and dispersal limitation**

PROBLEEMSTELLING

Large natural climate variability at time scales from decades to multiple millennia play a major role in the long-term ecological dynamics of the large Rift lakes and other water bodies in tropical East Africa. Lake-sediment records are an important tool to assess the sensitivity of these aquatic systems to the impact of ongoing anthropogenic climate change on water resources. This thesis project aims to assess this sensitivity to climate variability by reconstructing changes in the aquatic community of Lake Ntambi, a deep isolated crater lake in western Uganda, during the transition from the last ice age to the current interglacial period (the Holocene), through analysis of fossil remains of chironomid and phantom midge larvae, aquatic snails and fish preserved in its sedimentary record.

DOELSTELLING

Adult chironomids are non-biting mosquitoes which can easily disperse between isolated water bodies, and thus can be assumed to have been present from the base of the record dated to 17,800 years ago. Moreover different species have different tolerance for elevated salinity, which allows to reconstruct when the lake was either fresh or saline from the composition of fossil chironomid assemblages. Adult phantom midges can also easily disperse between lakes, but can colonize it successfully only when the lake is fresh. Moreover local population abundance is also controlled by the intensity of fish predation. For aquatic snails, colonizing an isolated lake depends on hitching a ride in the plumage of water birds without drying out along the way, and on finding freshwater conditions upon arrival. Therefore it may take several decades or even centuries after the lake became fresh for the first snails to establish a local population, and even more time before all snail habitat niches are filled with the best-adapted species. The only native fish inhabiting the Ugandan crater lakes are mouthbrooding cichlids. Although new colonizations have never been documented they are thought to be introduced when a fish eagle, pelican or cormorant brings a brooding female fish from another lake to its nest, such that young fish can fall from their dead mom's mouth into the water and survive. Needless to say, also this must be a rare event, and can only be successful when the lake is fresh. Thus, this thesis project will determine when phantom midges, snails and fish first arrived in Lake Ntambi, and trace changes in population abundance and community composition through a period of ca 8000 years punctuated by climate-driven salinity fluctuations; a period of high salinity after a first colonization may have caused local extinction, followed by another long period of absence before a new event of successful introduction.

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Download full PDF

**Locatie:**

campus Ledeganck

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## 48476: Biochemical and transcriptional control of pennate diatom sex-inducing pheromones

| | |
|---|---|
| Promotor(en): | Lieven De Veylder |
| Begeleider(s): | Mirna Sekulić |
| Contactpersoon: | Mirna Sekulić |
| 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:**

Diatoms are extraordinary siliceous micro-algae that are among the world's most prolific primary producers. They play an essential role in global nutrient cycling, carbon sequestration and contribute about one-fifth of global oxygen production. Furthermore, they have diverse metabolic capabilities and an immense potential for biotechnological applications, including the production of biofuels, nutritional compounds, and various heterologous molecules. These unicellular eukaryotes are characterized by a tremendous biodiversity and an almost ubiquitous presence in the biosphere, inhabiting freshwater, marine and terrestrial environments. Consequently, multiple lifestyles and survival strategies have evolved to fit a wide variety of ecological niches. Sexual reproduction is the main driver of speciation, but in pennate diatoms it is also the main mechanism for restoring cell size. As a result of their characteristic silica cell wall, repeated mitotic divisions cause a gradual decrease in the cell size of diatom populations, resulting in cell death. However, sexual reproduction can be initiated below a species-specific size threshold (SST) to restore the initial cell size. Pennate diatoms have a heterothallic mating system, where sexual reproduction can only occur between cells of opposite mating types (Figure 1). The two mating types - type plus (MT+) and type minus (MT-), find each other through the production of sex-inducing pheromones (SIPs): SIP+ and SIP-. These SIPs arrest the cell cycle in the G1 phase to synchronize the cells and commit to sexual reproduction.

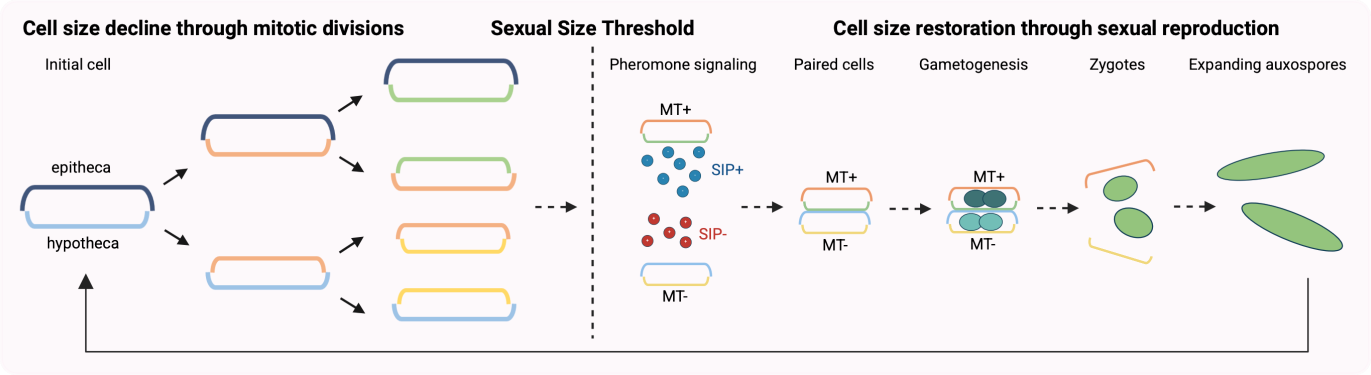


Figure 1. Typical diplontic life cycle of a pennate diatom. Vegetative cell divisions lead to an average cell size decrease in a diatom population. When a (species-specific) sexual sizethreshold is reached, sexual reproduction can occur. Most pennate diatoms are heterothallic and fertilization can only occur between gametes produced by cells of the opposite mating type (MT+/-).MT+ and MT- start producing sex-inducing pheromones (SIP+ and SIP-), which will induce changes in the opposite MT, preparing them for mating. The MTs will produce gametes that fuse to produce zygotes that expand into auxospores. These will form an initial cell once maximal cell size is reached. In this manner, the initial cell size is restored through sexual reproduction. Cleyman and Sekulić, 2024.

Recently, the chemical structures of SIP pheromones of the diatom Seminavis robusta have been determined, revealing peptides with unusual amino acid modifications. The authors hypothesized that a non-ribosomal peptide synthetase is involved in SIP biosynthesis. However, we have identified two proteins in the proteome of S. robusta: 1) containing 3 internal repeats that correspond to the unmodified SIP+ pheromone and 2) containing 2 internal repeats that correspond to the unmodified SIP-pheromone; both bearing signal peptides for secretion. Furthermore, genes encoding these proteins appear to be expressed exclusively in cells bellow SST, in the corresponding mating type and are upregulated during mating. They also appear to be conserved in several pennate diatom species. These observations support the existence of a genetically encoded preprotein that is targeted to the secretory system for post-transcriptional modification and eventually secreted as a mature pheromone.

**Doelstelling:**

The overall aims of the project are to:

1. prove that SIP peptides originate from the putative protein precursor genes.
2. identify enzymes involved in the processing of the preprotein into bioactive pheromones.
3. understand transcriptional regulation of SIP-encoding genes.
4. identify SIP peptide receptors.

The master thesis can be embedded in any of the objectives, depending on the student's interests and the progress of the project. E.g., for objectives 1) and 2): The student will generate overexpression and knock-out lines of SIP precursor genes and/or processing enzymes. The generated lines will be tested in physiological assays for their (lack of) ability to induce a cell cycle arrest in the opposite mating type and gametogenesis, through flow cytometric and microscopic analysis respectively (Figure 2). The work will be done in the marine benthic diatom Cylindrotheca closterium, due to the existence of a molecular toolbox.

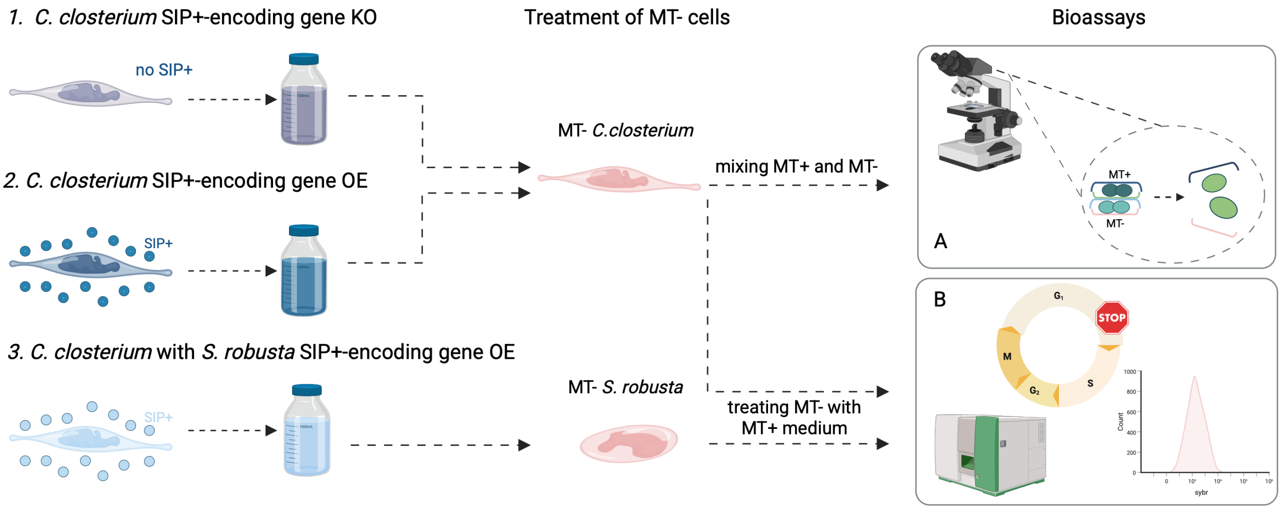
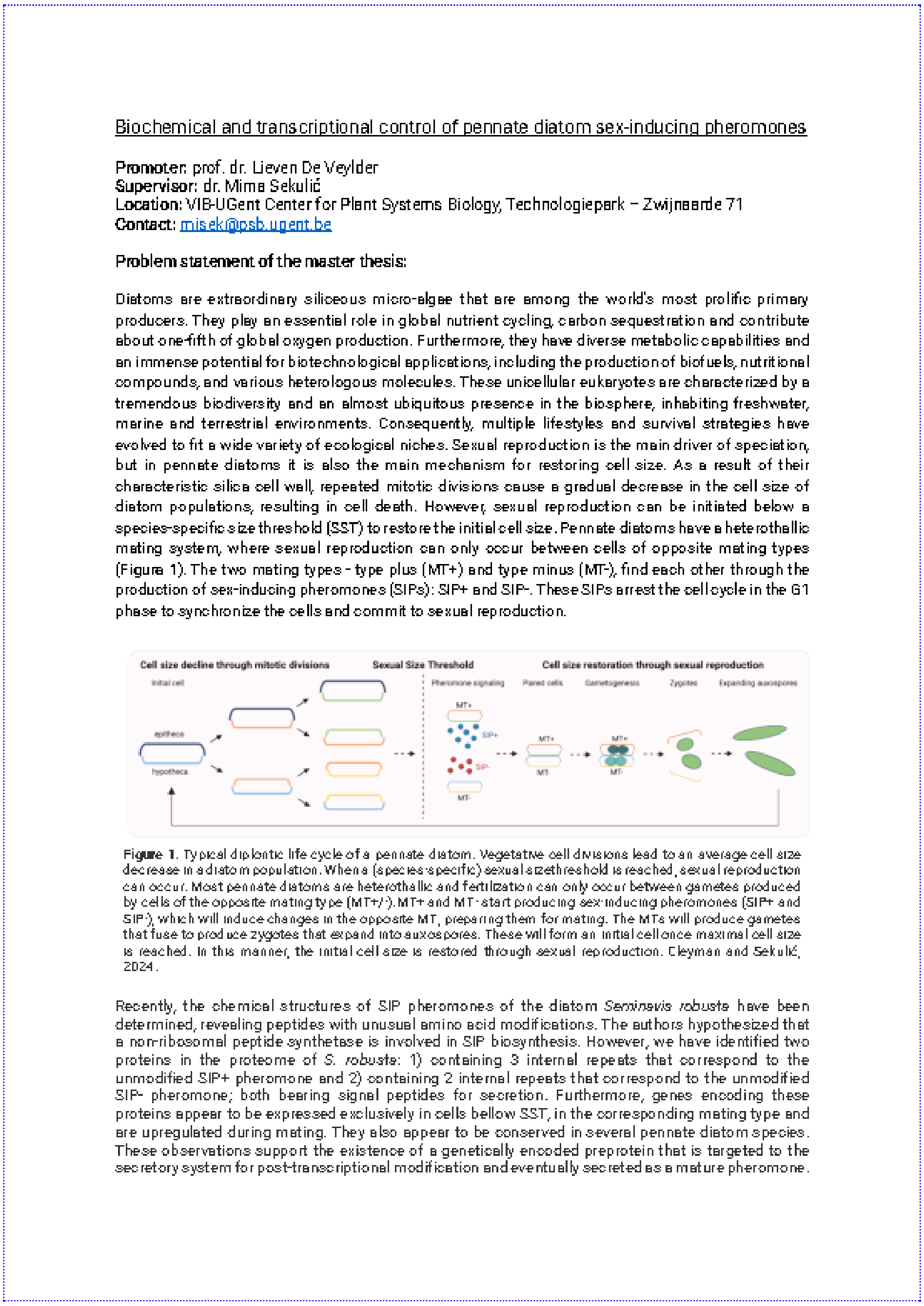


Figure 2. Transgenic strains and bioassays. Selected C. closterium SIP+ encoding gene knock-out lines (1.), overexpression lines (2.) and lines expressing the S. robusta SIP+ encoding gene (3.) will be tested in bioassays. A. The 1. and 2. MT+ lines will be mixed with C. closterium MT- and microscopically analyzed to see if gametogenesis and mating occurs. B. Next, the medium of the same lines will be collected to treat the MT- cells. DNA of treated MT- cells will be stained with SYBR Green and analyzed using flow cytometry, which will show if a G1 cell cycle arrest was induced. The medium of lines 3. will be used to treat S. robusta MT- cells that will be analyzed using flow cytometry in the same manner.

Techniques that could be used in the project:

- diatom culturing
- molecular biology techniques (DNA and RNA extraction, PCR, cloning, qPCR etc)
- diatom transformation: biolistics and bacterial conjugation
- CRISPR/Cas9 gene editing
- flow cytometry
- confocal microscopy
- RNA sequencing
- targeted metabolomics
- protein modeling

**Eerste pagina van PDF:**



Biochemical and transcriptional control of pennate diatom sex-inducing pheromones

**Promoter:** prof. dr. Lieven De Veylder
**Supervisor:** dr. Mirna Sekulić
**Location:** VIB-UGent Center for Plant Systems Biology, Technologiepark – Zwijnaarde 71
**Contact:** misek@psb.ugent.be

**Problem statement of the master thesis:**

Diatoms are extraordinary siliceous micro-algae that are among the world's most prolific primary producers. They play an essential role in global nutrient cycling, carbon sequestration and contribute about one-fifth of global oxygen production. Furthermore, they have diverse metabolic capabilities and an immense potential for biotechnological applications, including the production of biofuels, nutritional compounds, and various heterologous molecules. These unicellular eukaryotes are characterized by a tremendous biodiversity and an almost ubiquitous presence in the biosphere, inhabiting freshwater, marine and terrestrial environments. Consequently, multiple lifestyles and survival strategies have evolved to fit a wide variety of ecological niches. Sexual reproduction is the main driver of speciation, but in pennate diatoms it is also the main mechanism for restoring cell size. As a result of their characteristic silica cell wall, repeated mitotic divisions cause a gradual decrease in the cell size of diatom populations, resulting in cell death. However, sexual reproduction can be initiated below a species-specific size threshold (SST) to restore the initial cell size. Pennate diatoms have a heterothallic mating system, where sexual reproduction can only occur between cells of opposite mating types (Figure 1). The two mating types - type plus (MT+) and type minus (MT-), find each other through the production of sex-inducing pheromones (SIPs): SIP+ and SIP-. These SIPs arrest the cell cycle in the G1 phase to synchronize the cells and commit to sexual reproduction.

**Figure 1.** Typical diplontic life cycle of a pennate diatom. Vegetative cell divisions lead to an average cell size decrease in a diatom population. When a (species-specific) sexual size threshold is reached, sexual reproduction can occur. Most pennate diatoms are heterothallic and fertilization can only occur between gametes produced by cells of the opposite mating type (MT+/-). MT+ and MT- start producing sex-inducing pheromones (SIP+ and SIP-), which will induce changes in the opposite MT, preparing them for mating. The MTs will produce gametes that fuse to produce zygotes that expand into auxospores. These will form an initial cell once maximal cell size is reached. In this manner, the initial cell size is restored through sexual reproduction. Cleyman and Sekulić, 2024.

Recently, the chemical structures of SIP pheromones of the diatom *Seminavis robusta* have been determined, revealing peptides with unusual amino acid modifications. The authors hypothesized that a non-ribosomal peptide synthetase is involved in SIP biosynthesis. However, we have identified two proteins in the proteome of *S. robusta*: 1) containing 3 internal repeats that correspond to the unmodified SIP+ pheromone and 2) containing 2 internal repeats that correspond to the unmodified SIP- pheromone; both bearing signal peptides for secretion. Furthermore, genes encoding these proteins appear to be expressed exclusively in cells bellow SST, in the corresponding mating type and are upregulated during mating. They also appear to be conserved in several pennate diatom species. These observations support the existence of a genetically encoded preprotein that is targeted to the secretory system for post-transcriptional modification and eventually secreted as a mature pheromone.

*Download full PDF*

**Locatie:**

VIB-UGent Center for Plant Systems Biology, Technologiepark – Zwijnaarde 71

**Website:**

Meer informatie op: www.deveylderlab.be/research/diatom-cell-division

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## 48461: Blueprints of Adaptation: Genomic Processes Driving Climate Adaptation in Diatoms

| | |
|---|---|
| Promotor(en): | Eveline Pinseel, Wim Vyverman |
| Begeleider(s): | Daan Deleu |
| 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:**

Diatoms are a group of unicellular algae that play an important role in global carbon fixation and biogeochemical cycles. With an estimated 100,000 to 200,000 extant species, they are among the most diverse and successful groups of microbial eukaryotes. As a result, understanding how diatoms adapt to different environmental conditions has become a major research focus. However, while the phenotypic responses to environmental change have been studied extensively, the genomic variation associated with these adaptations has received much less attention. Therefore, the genomic processes that enable diatoms to respond and adapt to environmental shifts are still poorly understood. Investigating these processes is essential for improving our understanding of how diatoms evolve and cope with changing climates.

**Doelstelling:**

In this thesis, the roles of different genomic processes in adaptation to climate shifts by diatoms will be investigated. The focal taxon is the marine, tychoplanktonic Cylindrotheca closterium species complex, which colonized polar, temperate, and tropical regions repeatedly throughout its evolutionary history. Here, we will leverage these repeated colonizations of different climate zones as a model to understand climate adaptation. To this end, the student will analyse already existing diatom genomes, and if needed, grow additional diatom strains in the lab for whole-genome (re)sequencing, assembly, and annotation. Next, phylogenomic and comparative genomic analyses will allow to interrogate the assembled genomes for signals of climate adaptation. To this end, the student will apply three or more of the following techniques: genome assembly and annotation, ortholog/paralog detection, phylogeny-building using genome-scale data, tests for signals of positive selection and introgression, and/or reconstruction of gene duplication/loss dynamics.

The main focus of this thesis are bioinformatic analyses of diatom genomes, if needed complemented with culture work to obtain additional diatom genomes. The student will gain broad experience in genome-scale bioinformatic analyses and the use of a High Performance Computing (HPC) environment. The supervisor will provide sufficient training in bioinformatic methods as well as guidance in troubleshooting computational workflows.

**Locatie:**

campus Sterre, S8

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## 48484: Breaking bottlenecks in seagrass restoration: seed germination and seedling establishment in Zostera marina

| | |
|---|---|
| Promotor(en): | Riccardo Pieraccini, Olivier De Clerck |
| Begeleider(s): | |
| Contactpersoon: | Riccardo Pieraccini |
| 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:**

Seagrasses are widespread underwater flowering plants that play a crucial role in coastal ecosystems. They support biodiversity, stabilize sediments, store blue carbon, and contribute to coastal protection. However, in Europe we have lost an estimated ~60% of the historical areal extent of Zostera marina over the past two centuries. Restoring seagrass meadows is therefore a major conservation priority.

Seed-based restoration methods are increasingly being adopted to restore Z. marina meadows, because they can enhance genetic diversity, are logistically flexible, and can be scaled up more easily than sod-transplantation methods. Although seed viability in Z. marina can be high, typically only a small fraction of seeds germinate and successfully develop into established seedlings. Germination failure and early seedling mortality are thus key bottlenecks limiting seed-based restoration success and sustainable use of seed stock.

**Doelstelling:**

This thesis directly addresses some of the major bottlenecks in Z. marina seed-based restoration. The student will participate in experiments aimed at improving seed germination and early seedling establishment under controlled conditions, working with a seagrass nursery and in vitro plant propagation.

The project will specifically:

1. Test how combinations of hormones, nutrients, and slow-release seed coatings influence seed germination and early seedling growth under controlled light and temperature regimes.
2. Develop and evaluate hormone- and nutrient-enriched slow-release seed coatings as a tool to improve germination success, reduce early seedling mortality, and enhance seedling performance relative to uncoated seeds.
3. Link treatment-specific physiological and biochemical traits (photosynthetic performance, pigment composition, elemental/isotopic signatures) to seedling growth and survival, to identify the most promising coating formulations and culture conditions for restoration application

Experimental treatments will focus on environmental and physiological germination triggers (e.g. hormones, nutrients) that are delivered via newly developed slow-release seed coatings, designed to provide a gradual and sustained release to the seed and emerging seedling.

The student will be involved in:

- Handling and culturing Z. marina seeds in controlled germination and seedling growth experiments.
- Preparing, and testing hormone- and nutrient-enriched slow-release seed coatings, and comparing coated vs. uncoated seeds.
- Setting up and monitoring germination cultures under different light, coating, hormone, and nutrient regimes.
- Monitoring seed and seedling quality, e.g. using elemental or isotopic analyses (IRMS).
- Measuring and modeling seedling growth and photosynthetic performance using Pulse Amplitude Modulated (PAM) fluorometry.
- Quantifying seedling pigment composition using High-Performance Liquid Chromatography (HPLC).
- Analyzing germination dynamics and growth responses to identify coating formulations and culture conditions that are most promising for seed-based restoration

Fieldwork: if permitting allows, some of the results will be also tested in field setting in Belgium.

**Locatie:**

Campus Sterre

**Samenwerking met bedrijf of non-profit organisatie**

Bedrijf: Sea Rangers The Netherlands
Samenwerking: fieldwork

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## 48481: Characterization of the Carbon Concentrating Mechanisms in the green seaweed Ulva

| | |
|---|---|
| Promotor(en): | Jonas Blomme, Tom Jacobs |
| Begeleider(s): | 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.

The carbon concentrating mechanism (CCM) evolved in many photosynthetic organisms as an adaptation to low CO2conditions. Ulva uses a pyrenoid-based biophysical mechanism to pump and concentrate CO2 sources (mainly as HCO3-) into a condensate, the pyrenoid, that contains Rubisco proteins. We have identified the intracellular localization of many CCM-related proteins, and have an insight into the structure of the carbon acquisition mechanism in Ulva including a proposed structure for the pyrenoid and the assembly of Rubisco proteins within the chloroplast.

The next step is to study the function of these protein encoding genes to better understand their role in carbon capture and Ulva development. To do so, we will leverage novel molecular tools developed in the research group over the past years. We use genetic transformation for stable integration and generate overexpression lines (gain-of-function) and targeted mutagenesis using CRISPR (loss-of-function).

**Doelstelling:**

The aim of this master thesis is to study the function of genes involved in the carbon concentrating mechanisms of Ulva. The student will generate mutant lines for the overexpression/disruption of genes, screening of phenotypes under differential CO2 conditions, and perform molecular analysis, e.g. gene expression (qPCR, western blot) and protein interaction (co-immunoprecipitation).

The student will work with the following topics and/or techniques: Ulva cultivation and maintenance of lab strains, Ulvagenetic transformation, phenotyping, molecular cloning and molecular analysis (DNA/RNA/protein extraction, PCR, qPCR, sanger sequencing), bioinformatic analysis.

**Locatie:**

VIB-PSB. Technologiepark 71, 9052 Gent

**Website:**

Meer informatie op: jacobslab.sites.vib.be/en/ulva

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## 48514: Climate change and the fate of Belgium's insectivorous flora

| | |
|---|---|
| Promotor(en): | Lars Chatrou, Wesley Tack |
| 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:**

Climate change is expected to have substantial impacts on the distribution and survival of insectivorous plants in Europe. Most European insectivorous plant species - such as Drosera, Pinguicula, and Utricularia -are adapted to nutrient-poor, water-saturated, and typically cool habitats including bogs, fens, wet heathlands, and alpine wetlands. Rising temperatures, more frequent summer droughts, and altered precipitation patterns are projected to accelerate peatland drying, lower water tables, and increase competition from faster-growing non-carnivorous plants. Because these specialised species depend on high humidity, stable hydrology, and low nutrient availability, many populations are expected to shift northward or upward in elevation, with southern and lowland populations at the greatest risk. Habitat fragmentation and ongoing wetland loss may further limit their ability to track suitable climates. Overall, climate change is likely to lead to range contractions, local extinctions, and reduced population viability for insectivorous plants across much of Europe, unless hydrological conditions are actively conserved or restored.

Modelling approaches can help us understand how species may respond to future climatic changes. Species distribution models (SDMs) are a particularly useful tool: they use the current distribution of a species, combined with climate variables from the locations where it occurs, to estimate its potential geographic range. SDMs can be applied to infer past distribution shifts as well as to project future distributions under different climate scenarios.

Species distribution data can be extracted from large online databases such as the Global Biodiversity Information Facility (GBIF) or from digital databases of major herbaria that hold extensive collections of insectivorous plants. These occurrence records can be combined with high-resolution climate layers from WorldClim, which provide data on temperature, precipitation, solar radiation, and related variables. Together, these datasets form the basis for modelling both current and future species ranges.

Hypothesis

In this MSc project, you will test the hypothesis that climate change will alter the distribution of insectivorous plant species currently occurring in Belgium, driving their ranges northward and causing overall contractions in suitable habitat.

**Doelstelling:**

The goal of this project is to investigate the impact of climate change on the future distribution of insectivorous plant species occurring in Belgium.

Techniques and analysis methods include:

- Data mining of virtual herbarium specimens: databasing and georeferencing of taxonomically verified botanical collections from herbaria such as Meise, Leiden, Kew, and Aarhus, as well as GBIF and waarnemingen.be; this may be supplemented with field observations in Belgium.

- Species distribution modelling: using WorldClim bioclimatic variables, Maxent software, and R scripts to predict current and future species ranges.

This project is suitable for students with a strong interest in ecology, climate change, and computational biology. The results will be written in the form of a scientific article, with the aim of publication in a peer-reviewed journal.

**Locatie:**

**Onderwerp voorbehouden voor Alice Cesar**

*Deze masterproef werd reeds 1-maal toegekend!*

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## 48480: Comparative genomics in Ulva compressa natural populations

| | |
|---|---|
| Promotor(en): | Olivier De Clerck, Jonas Blomme |
| Begeleider(s): | 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:**

The green seaweed Ulva compressa is an important primary producer in coastal ecosystems worldwide. Its growth potential can cause nuisance (blooms), but is also interesting from an economic viewpoint (aquaculture). Ulva compressa has a large geographic distribution, occurs from hyper- to hyposaline conditions, and shows large intraspecific morphological diversity. The genetic diversity possibly underlying this phenotypic variation is unknown. It is the ambition of the Phycology Research Group to better understand the genetic diversity within Ulva. To this end, we have collected a large culture collection containing diverse strains of Ulva compressa containing European and Asian populations.

**Doelstelling:**

In this master thesis, strains from differentiating habitats will be selected to compare the genetic variation. The genetic variation (SNPs, indels, large structural variation) will be analyzed through comparative genomics. The student will associate genetic variation to variation in phenotypes (e.g. salinity or temperature preference, habitat, or growth speed).

The student will culture several different strains of Ulva compressa. These strains will be subject to experiments to document phenotypes such as growth rate, morphology and rhizoid formation. The student will also examine environmental stresses, e.g. salinity and temperature tolerance. To understand the genomic variation, the student will perform high-molecular weight DNA-extractions and long-read sequencing (Nanopore technology), perform genome assemblies and genome annotation with established bioinformatics pipelines on the selected strains. The genome assemblies will be compared to each other to identify genetic variation. This variation will the be linked to the phenotypic data gathered to perform comparative genomics.

**Locatie:**

VIB Center of Plant Systems Biology (Technologiepark) en Phycology Research Group (campus Sterre S8)

**Website:**

Meer informatie op: jacobslab.sites.vib.be/en/ulva

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## 48508: Comparative genomics of bacterial isolates from Antarctic cold desert soils

| | |
|---|---|
| Promotor(en): | Anne Willems, Elie Verleyen |
| Begeleider(s): | Yemma Verbeek |
| 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 inland regions of the Western Sør Rondane Mountains in East Antarctica harbour unique terrestrial communities, which are dominated by microorganisms. The food webs in the region are structurally simple, and composed of only a limited number of trophic levels. Recent taxonomic inventories using DNA markers revealed that the different substrate and bedrock types present in the region (marble, gneiss, granite and moraines) support significantly different microbial communities. Cyanobacteria and green algae form the base of the food webs on substrates composed of weathered bedrock, while on the drier moraine substrates, green algae are the main primary producers possibly in combination with chemosynthetic members belonging to the Actinomycetota. The success of the latter group in moraine samples may be related to chemoautotrophic metabolic properties such as oxidation of H2 or CO. A wide range of taxa belonging to the Acidobacteriota and Actinomycetota are the main heterotrophic bacteria. Despite the high incidence of endemism and the presence of potentially unique adaptations to the extreme conditions in these polar desert soils, surprisingly few Antarctic bacteria were brought into culture.

**Doelstelling:**

In this MSc-project, a targeted isolation campaign will be carried out on samples from different ice-free regions in the Sør Rondane Mountains. New bacterial isolates will first be dereplicated and initially identified using MALDI TOF mass spectrometry to select taxa for whole genome sequencing. Genome sequencing will be performed using Nanopore and/or Illumina sequencing for improved quality and coverage. Comparative genome analysis will be used to study adaptations of Antarctic strains in contrast to taxonomically related non-Antarctic strains that are present in the UGent research collection and literature data. This will shed light on the metabolic adaptations that ensure survival of polar strains in extreme polar desert environments.

**Locatie:**

K.L. Ledeganckstraat

**Onderwerp voorbehouden voor Lune Carton**

*Deze masterproef werd reeds 1-maal toegekend!*

---

## 48506: Comparison of fouling communities in Belgian ports, with a focus on introduced non-indigenous species

| | |
|---|---|
| Promotor(en): | Thomas Kerkhove, Ulrike Braeckman |
| Begeleider(s): | Danae Kapasakali |
| Contactpersoon: | Thomas Kerkhove |
| 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:**

Ports are hotspot for the introduction of non-indigenous species, mainly through ballast water and hull fouling. To keep track of these introductions, standardised monitoring using settlements plates is conducted in several countries worldwide. The Marine Ecology and Management (MARECO, https://mareco-odnature.naturalsciences.be/) team of the Institute of Natural Sciences monitors fouling assemblages on a variety of natural and artificial hard substrates, including in port environments. One of its focusses thereby is on introduced non-indigenous species.

**Doelstelling:**

For this topic, the student will explore the macroinvertebrate fouling fauna (> 1 mm) of settlement plates deployed in several Belgian ports. A comparison will be made of the fouling communities of different Belgian ports using settlement plates, with a focus on non-indigenous species. Community patters will be linked to factors such as size of the port, number of vessels, and environmental factors such as salinity. A seasonal aspect might also be included in the research.

The student will get acquainted with standard lab practices of processing benthic/fouling samples and improve their taxonomic identification skills. Depending on the period of the work, the opportunity might exist to join a research campaign with the RV Belgica during spring/summer and get familiar with various sampling procedures and overall working experience on board a research vessel.

**Locatie:**

**Opmerkingen:**

Location: Royal Belgian Institute of Natural Sciences Operational Directorate Natural Environment Marine Ecology and Management 3de en 23ste Linieregimentsplein 8400 Oostende

**Onderwerp voorbehouden voor Inez Lentrebecq**

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## 48488: Cool Spots in a Warming Heath: Spiders, Microclimate and Climate-Adaptive Management

| | |
|---|---|
| Promotor(en): | Jan Van Uytvanck |
| Begeleider(s): | Marijke Thoonen |

Contactpersoon: Marijke Thoonen
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 driving substantial declines in arthropods, including spiders, which serve as key predators and sensitive indicators of ecosystem functioning. Open heathlands are characterised by fine-scale heterogeneity in moisture, microtopography and vegetation structure. Dwarf shrubs may buffer thermal and hydric extremes by shading the soil and reducing air movement, potentially creating microclimatic refuges for spider communities. However, the extent to which these factors mitigate climatic stress and alter spider community composition remains insufficiently understood. In addition, heathland management interventions such as mowing, choppering and sod-cutting substantially modify vegetation structure and may strongly alter microclimatic conditions, yet their ecological consequences under climate change remain poorly quantified.

**Doelstelling:**

This thesis investigates how soil moisture, microtopography and vegetation structure shape microclimates in open heathlands and assesses whether dwarf shrubs act as microclimatic refuges for spiders. The study is based on spider assemblages sampled at 46 locations in the Kalmthoutse Heide between 2023 and 2025. Community composition is compared across a multifactorial design incorporating topography (slope and aspect) and management history (managed vs. unmanaged). The aim is to determine how shrub-associated microhabitats influence spider diversity, abundance and thermal preferences, and to translate these findings into actionable insights for climate-adaptive heathland management.

**Locatie:**

veldwerk kalmthoutse heide; labowerk UGent campus Ledeganck

**Samenwerking met bedrijf of non-profit organisatie**

Bedrijf: Instituut voor Natuur- en Bosonderzoek (INBO)
Samenwerking: begeleider

---

## 48552: Correlatie tussen populatiedensiteit en habitatkenmerken van de Kamsalamander in Vlaanderen

Promotor(en): Dries Bonte
Begeleider(s): Jeroen Speybroeck
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 Kamsalamander is een kwetsbare soort in Vlaanderen. Het is belangrijk dat beleid en beheersmaatregelen voor deze soort ondersteund worden door wetenschappelijke gegevens. Deze thesis zal de link tussen populatiedensiteiten en habitatkenmerken onderzoeken binnen verschillende Vlaamse populaties.

**Doelstelling:**

Tijdens de vroege zomermaanden zullen waterplassen verspreid over Vlaanderen bezocht worden voor staalnames. Hierbij zullen verschillende biotische en abiotische variabelen genoteerd worden voor elke plas en de omringende omgeving (pH, aanwezigheid van vissen, diepte van de waterplassen, eutrofiëring,...) om habitatkenmerken te onderzoeken. Dit zal gebeuren op een zo kort mogelijke tijdspanne om seizoenale verschillen tussen poelen te vermijden. Deze data

**Locatie:**

**Opmerkingen:**

De student is in bezit van een rijbewijs en is op de hoogte van de hoge verplaatsingsvereisten van deze thesis. De verantwoordelijkheid voor de verplaatsing ligt bij de student zelf. Om seizoenale variatie te voorkomen zal het merendeel van het veldwerk buiten het academiejaar plaatsvinden (begin juli).

**Onderwerp voorbehouden voor Robbe Depraetere**

---

## 48074: Creating a Digital Twin of the Schipgatduinen: Inverse Modeling and Validation of a Biogeomorphological Model using High-Resolution Remote Sensing Data

| | |
|---|---|
| Promotor(en): | Frederik Van Daele, Dries Bonte |
| Begeleider(s): | |
| Contactpersoon: | Frederik Van Daele |
| 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 climate change intensifies, our coastlines face increasing threats from sea-level rise and more powerful storms. In response, we are shifting away from hard infrastructure, like concrete sea walls, towards Nature-Based Solutions (NbS). These solutions, such as restoring or building coastal dunes, are designed to work with nature. They are "living" defences that are more sustainable, adaptable, and cost-effective than concrete.

However, the success of a "living" defence is not guaranteed. A concrete wall is predictable; we know exactly how tall it is and when it will fail. A coastal dune, by contrast, is a dynamic ecosystem. Its ability to protect our coast depends entirely on a continuous biological process: the biomorphogenic feedback loop. This is the critical, two-way interaction between the plants (the "bio") and the landform (the "morpho"). In simple terms:

1. Bio -> Morpho: Pioneer plants, like marram grass, act as ecosystem engineers. Their stems and leaves trap wind-blown sand, actively building the dune and increasing its height.
2. Morpho -> Bio: The new dune shape, in turn, changes the local environment (e.g., wind speed, sand burial rates, salt spray). This new environment then determines which plants can survive and how well they can grow.

This feedback loop is the "engine" that builds and maintains the dune as a coastal defence. If this engine runs well, the dune can grow with sea-level rise and repair itself after storms. But if this engine breaks—for example, if a severe drought (a climate change impact) kills the marram grass—the feedback loop collapses. Sand is no longer trapped, the dune erodes, and the "Nature-Based Solution" fails, leaving the coastline vulnerable.

This creates an urgent problem for coastal managers: we need to be able to predict if these NbS will work in the future. We cannot afford to wait 50 years to see if our living dikes hold, nor can we run large-scale experiments on the entire coast.

This is precisely why we must model biomorphogenic feedbacks. By using process-based models—computer simulations built on the physical and biological rules of these feedbacks—we can create virtual laboratories. This thesis will use Living Dunes, a specific model developed at UGent, to simulate this engine. Modelling allows us to forecast how the dune system (our NbS) will respond to future climate scenarios. More importantly, it allows us to identify the system's "tipping points" and vulnerabilities before they lead to failure in the real world. This project will test and refine this model against high-resolution, real-world drone data from the Schipgatduinen, ensuring our forecasts are as accurate as possible.

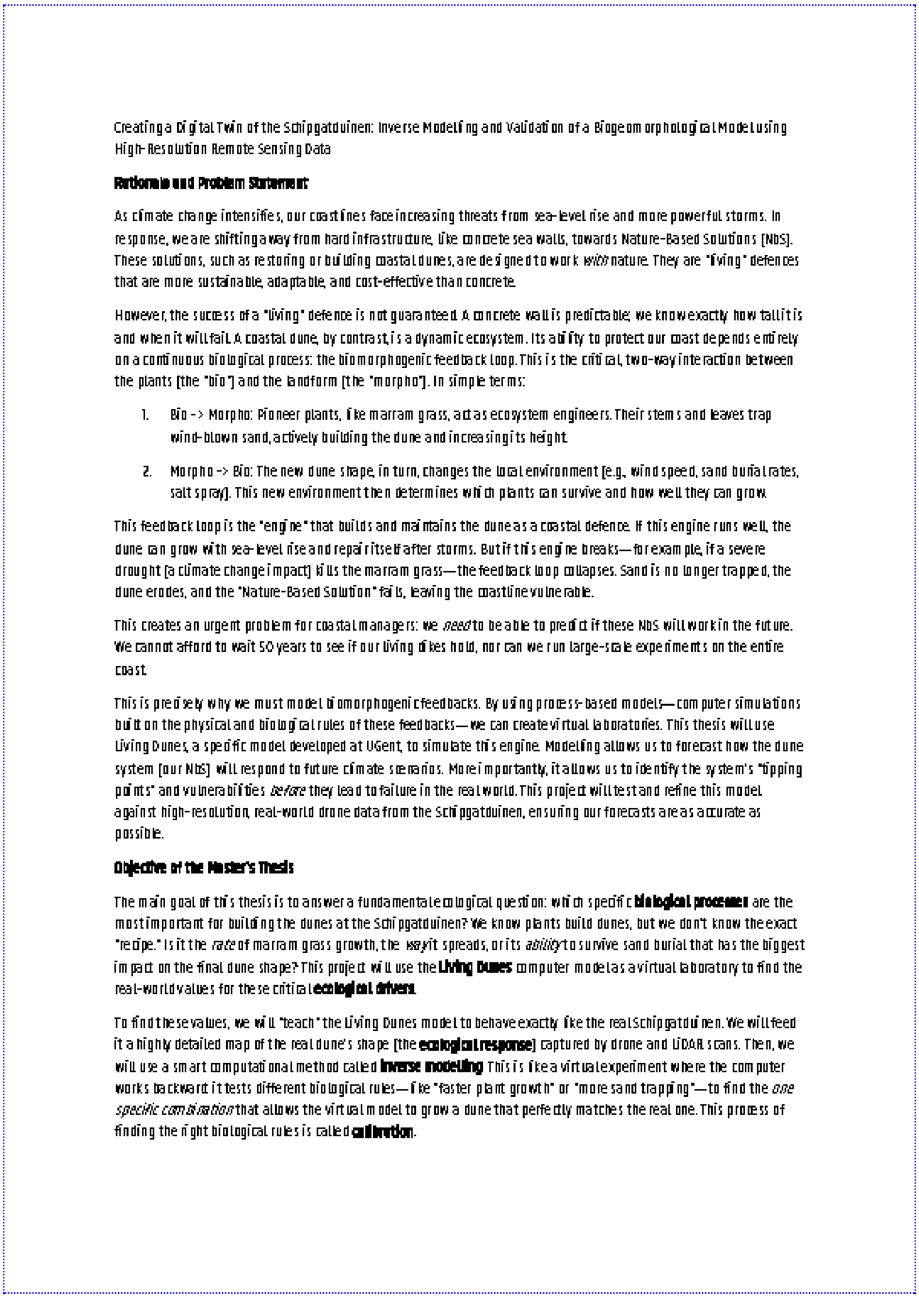
**Doelstelling:**

The main goal of this thesis is to answer a fundamental ecological question: which specific biological processes are the most important for building the dunes at the Schipgatduinen? We know plants build dunes, but we don't know the exact "recipe." Is it the rate of marram grass growth, the way it spreads, or its ability to survive sand burial that has the biggest impact on the final dune shape? This project will use the Living Dunes computer model as a virtual laboratory to find the real-world values for these critical ecological drivers.

To find these values, we will "teach" the Living Dunes model to behave exactly like the real Schipgatduinen. We will feed it a highly detailed map of the real dune's shape (the ecological response) captured by drone and LiDAR scans. Then, we will use a smart computational method called inverse modelling. This is like a virtual experiment where the computer works backward: it tests different biological rules—like "faster plant growth" or "more sand trapping"—to find the one specific combination that allows the virtual model to grow a dune that perfectly matches the real one. This process of finding the right biological rules is called calibration.

This is a cutting-edge computational challenge, and a primary objective for the student will be to design an intelligent and efficient way to run this virtual experiment. But the true scientific discovery comes from finding the "bottlenecks." These are the moments where the model, even with the best-tuned rules, still fails to match what we see in the real world. This is the most exciting part, because it gives us insights when our biological understanding is wrong or incomplete. The final objective is to investigate these failures. For example, does the model fail because it misjudges how plants allocate resources to roots versus shoots when they are buried by sand? Or because it doesn't correctly simulate how plants respond to drought? By finding these gaps, the student will make a crucial discovery about dune ecology that we could never find just by looking at the dunes themselves.

Eerste pagina van PDF:



Creating a Digital Twin of the Schipgatduinen: Inverse Modeling and Validation of a Biogeomorphological Model using High-Resolution Remote Sensing Data

**Rationale and Problem Statement**

As climate change intensifies, our coastlines face increasing threats from sea-level rise and more powerful storms. In response, we are shifting away from hard infrastructure, like concrete sea walls, towards Nature-Based Solutions (NbS). These solutions, such as restoring or building coastal dunes, are designed to work *with* nature. They are "living" defences that are more sustainable, adaptable, and cost-effective than concrete.

However, the success of a "living" defence is not guaranteed. A concrete wall is predictable; we know exactly how tall it is and when it will fail. A coastal dune, by contrast, is a dynamic ecosystem. Its ability to protect our coast depends entirely on a continuous biological process: the biomorphogenic feedback loop. This is the critical, two-way interaction between the plants (the "bio") and the landform (the "morpho"). In simple terms:

1. Bio -> Morpho: Pioneer plants, like marram grass, act as ecosystem engineers. Their stems and leaves trap wind-blown sand, actively building the dune and increasing its height.
2. Morpho -> Bio: The new dune shape, in turn, changes the local environment (e.g., wind speed, sand burial rates, salt spray). This new environment then determines which plants can survive and how well they can grow.

This feedback loop is the "engine" that builds and maintains the dune as a coastal defence. If this engine runs well, the dune can grow with sea-level rise and repair itself after storms. But if this engine breaks—for example, if a severe drought (a climate change impact) kills the marram grass—the feedback loop collapses. Sand is no longer trapped, the dune erodes, and the "Nature-Based Solution" fails, leaving the coastline vulnerable.

This creates an urgent problem for coastal managers: we *need* to be able to predict if these NbS will work in the future. We cannot afford to wait 50 years to see if our living dikes hold, nor can we run large-scale experiments on the entire coast.

This is precisely why we must model biomorphogenic feedbacks. By using process-based models—computer simulations built on the physical and biological rules of these feedbacks—we can create virtual laboratories. This thesis will use Living Dunes, a specific model developed at UGent, to simulate this engine. Modeling allows us to forecast how the dune system (our NbS) will respond to future climate scenarios. More importantly, it allows us to identify the system's "tipping points" and vulnerabilities *before* they lead to failure in the real world. This project will test and refine this model against high-resolution, real-world drone data from the Schipgatduinen, ensuring our forecasts are as accurate as possible.

**Objective of the Master's Thesis**

The main goal of this thesis is to answer a fundamental ecological question: which specific **biological processes** are the most important for building the dunes at the Schipgatduinen? We know plants build dunes, but we don't know the exact "recipe." Is it the *rate* of marram grass growth, the *way* it spreads, or its *ability* to survive sand burial that has the biggest impact on the final dune shape? This project will use the **Living Dunes** computer model as a virtual laboratory to find the real-world values for these critical **ecological drivers**.

To find these values, we will "teach" the Living Dunes model to behave exactly like the real Schipgatduinen. We will feed it a highly detailed map of the real dune's shape (the **ecological response**) captured by drone and LiDAR scans. Then, we will use a smart computational method called **inverse modelling**. This is like a virtual experiment where the computer works backward: it tests different biological rules—like "faster plant growth" or "more sand trapping"—to find the *one specific combination* that allows the virtual model to grow a dune that perfectly matches the real one. This process of finding the right biological rules is called **calibration**.

*Download full PDF*

**Locatie:**

campus Ledeganck

**Website:**

Meer informatie op: frederikvand.github.io/living_dunes/

**Onderwerp voorbehouden voor Nina De Block**

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## 48459: Determine the origin of unknown hominin skulls

| | |
|---|---|
| Promotor(en): | Dominique Adriaens, Tara Chapman |
| Begeleider(s): | Tara Chapman |
| 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:**

There is a large interest in provenance research in Belgium on human remains in both public and private collections. This is particularly the case with human remains which may be from the colonial era, which are often skulls and where requests for repatriation of human remains have been made to Belgium from several countries. Unfortunately, human remains which were collected many years ago often have no accompanying information. Therefore, it is difficult to know where these remains came from. One avenue is to analyse the skulls themselves. The aim of this research is to take a sample of over 50 skulls from a collection to find out more about them. The analyses that will be performed will include age, sex, trauma analysis and origin determination. It can also include further provenance research. Measurements will be taken on the skull and the programme AncesTrees will be used to determine the origin of the human remains. Part of the research question will be how accurate AncesTrees is and whether it should be used. The student will be taught different techniques at the Royal Belgian Institute of Natural Sciences such as such as Ancestrees, Age, Sex and Trauma determination methods.  They may need to travel to a different location to analyse the skulls and travel expenses can be covered if necessary. The skulls may be from a colonial era and therefore this is a topic which requires sensitivity and confidentiality.

**Doelstelling:**

The aim of this Masters research topic is to determine as much as possible from a collection of skulls which will include age sex and trauma diagnosis. Ancestrees will be used and the student will question if this is a good system to determine origin on unknown skulls.

**Locatie:**

KBIN, Vautierstraat Brussel

**Onderwerp voorbehouden voor Jana De Bie**

*Deze masterproef werd reeds 1-maal toegekend!*

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## 48507: Development of a food web model of an offshore windfarm ecosystem

| | |
|---|---|
| Promotor(en): | Jan Vanaverbeke, Ulrike Braeckman |
| Begeleider(s): | Ee Zin Ong |
| Contactpersoon: | Ulrike 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:**

Addressing climate change and achieving energy independence are major global priorities. Offshore renewable energy, particularly offshore wind farms (OWFs), plays a central role in these goals. The installation of wind turbines adds extensive hard substrates—such as foundations and scour protection layers—to naturally soft-bottom environments. These artificial structures are quickly colonized by dense fouling communities that attract higher trophic levels like fish and crustaceans, potentially altering local food webs.
Research around the oldest Belgian OWF (installed in 2008) has indeed revealed such changes as large densities of suspension feeders on turbine foundations act as important biofilters on the hand (removing organic matter from the water column) and biodepositors of organic carbon to the sediment on the other hand (De Borger et al. 2025), hence acting as a carbon pump.

Reference:

De Borger E, van Oevelen D, Mavraki N, De Backer A, Braeckman U, Soetaert K, Vanaverbeke J. Offshore wind farms modify coastal food web dynamics by enhancing suspension feeder pathways. Commun Earth Environ. 2025;6(1):330. doi: 10.1038/s43247-025-02253-w

**Doelstelling:**

This thesis aims to further develop a comprehensive food web model describing trophic structure and energy flow near a wind turbine located further offshore. Fieldwork will involve sampling food web components from the turbine foundation, scour protection, sediments, and mobile fauna (fish, crustaceans). In the lab, species will be identified, biomass quantified, and stable isotopes ($\delta^{13}$C, $\delta^{15}$N) analyzed to infer trophic relationships.

The study may focus on qualitative (topological) analysis to map species interactions or quantitative modelling to estimate energy flows based on biomass and isotopic data. Comparing results with the nearshore turbine model will reveal spatial patterns in OWF effects on marine food webs.

This project offers hands-on experience across all stages of food web research—from field sampling and lab analysis to data interpretation and ecological modelling—within the context of offshore renewable energy habitats.

**Locatie:**

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## 48487: Diatom-chytrid interactions: parasitism and host response under changing conditions

Promotor(en): Wim Vyverman, Koen Sabbe
Begeleider(s): Rik Debeer
Contactpersoon: Rik Debeer
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. The dynamics of these blooms – their wax, wane and species successions – are shaped by the interaction of multiple drivers, of which parasitism is highly understudied. Yet, recent studies revealed that parasites are important components of aquatic food webs, forming an intermediate link between phytoplankton and higher trophic levels and impacting carbon transfer.

Chytridiomycota (chytrids) are important parasitic fungi that infect diatoms. Their uniflagellate zoospores actively search for suitable diatom hosts and encyst on their frustule. From these cysts, rhizoids grow into the diatom cell for nutrient extraction, supporting the development of a zoosporangium that ultimately releases new zoospores. Chytrid infections can cause mass mortalities in diatoms, impacting their blooms and aquatic ecosystems in general. Yet, while very relevant within the context of climate change and other human impacts, the question remains to what extent abiotic stress affects the susceptibility of diatoms to chytrid parasitism.

**Doelstelling:**

In this thesis, the progression of chytrid infections and the diatom response will be investigated under laboratory conditions and across different environmental treatments. To this end, diatom cultures established from single-cell isolates from the Schelde estuary will be inoculated with a chytrid zoospore suspension. From the moment of inoculation until culture collapse, infected and uninfected cultures will be monitored by microscopy, imaging flow cytometry and Pulse Amplitude Modulated (PAM) fluorometry. In addition, RNA sequencing will be conducted to reveal molecular responses of diatoms to chytrid infections and environmental stress.

**Locatie:**

campus Sterre S8

**Opmerkingen:**

Supervision of this thesis can be in Dutch or English. Writing will be done in English.

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## 48304: Differences in migration patterns of Eurasian Blackcaps in Europe

| | |
|---|---|
| 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:**

There are many changes to bird migration patterns globally, because of alterations to habitat amounts and quality, as well as climate change. This includes shifting range extents, wintering and breeding locations, and can result in altered population distributions, as well as the routes themselves. One of the best known examples of this is the European blackcap Sylvia atricapilla which breeds in northern Europe and winters in southern Europe/ northern Africa. Because of milder winters and extensive garden bird feeding, this species is now able to winter in the UK. A new migration route in this direction developed in the last 30 years, and now breeding birds from across Central Europe migrate a shorter distance to a sufficiently mild overwintering area in the UK.

Because this species is so small, routes have not been extensively tracked, and those birds that have been tracked are studied using geolocators, which cannot pick up precise patterns and locations. However, with the advent of Motus VHF tracking technology we are now able to follow these birds as they depart on migration at a finer spatial and temporal scale. This thesis project will use already collected Motus tracking data from across Europe to study departure directions and flight patterns of migrating blackcaps, to identify differences within and between years and locations, as well as with age to quantify the movements of this fascinating example of micro evolution. This thesis requires skills in R, and will also develop some skills in QGIS.

**Doelstelling:**

**Locatie:**

Ledeganck/ thuis

**Onderwerp voorbehouden voor Maxime Everaert**

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## 48504: Discovery of Novel Denitrification Inhibitors to Reduce N₂O Emissions

| | |
|---|---|
| Promotor(en): | Tom Beeckman, Hans Motte |
| Begeleider(s): | Hannelore De Hooghe, Laure Annetta |
| Contactpersoon: | Hans Motte |
| 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:**

Nitrous oxide (N2O) is a potent greenhouse gas and a major contributor to climate change, primarily emitted from agricultural soils through microbial processes in the nitrogen cycle. The first step in this cycle, nitrification or the conversion of ammonium to nitrate, can be inhibited by nitrification inhibitors, which strongly reduce N2O emissions. However, this inhibition is never complete, while many fertilizers are applied as ammonium-nitrate blends, meaning that nitrate is present. Nitrate will be further converted into N2O via a process called denitrification, which remains an important source of N2O emissions. In contrast to nitrification inhibitors, there are no efficient inhibitors targeting denitrification steps in soil. Developing such inhibitors could revolutionize sustainable agriculture and drastically reduce N2O emissions.

**Doelstelling:**

This project aims to identify novel small molecules with denitrification-inhibiting activity directly in soil, using an innovative screening approach: the Beeckman lab recently developed a soil-based screening assay to identify novel soil-efficient nitrification inhibitors using innovative approaches to extract and measure ammonium and as such ammonium consumption in the soil. A similar assay is available to measure nitrate consumption and could be applied to test and identify denitrification inhibitors.

Practically, the project aims to optimize and use the existing soil-based screening assay to identify denitrification inhibitors by screening a small molecule library. The most promising inhibitors will then be validated via nitrous oxide measurements. To understand the microbial targets, the project will quantify the effect on key nitrogen-cycle microorganisms via qPCR of nirK, nirS, norB and nosZ genes, while potential off-target effects will be evaluated on plants and non-target microorganisms. Finally, in vitro culture assays will be performed on representative denitrifying microorganisms to confirm inhibitory activity and explore potential mechanisms of action.

Techniques & Tools

- High-throughput screening using adapted soil-based assay (including use of liquid handling robotics).
- Soil microcosm assays for nitrate (spectrophotometrically) and N2O (trace gas analyzer) quantification.
- DNA extraction from soil and qPCR for N-cycle functional genes (nirK, nirS, norB, nosZ).
- Microbial work, culture-based inhibition tests.
- In vitro plant growth assays.

Expected Impact

This project will pioneer the search for practical denitrification inhibitors, offering a new strategy to mitigate N2O emissions and improve agricultural sustainability.

**Locatie:**

VIB-UGent Center for Plant Systems Biology

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## 48262: Dissecting the mechanistic basis of 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:**

Within animals, evolutionary transitions toward herbivory are severely constrained by the hostile characteristics of plants. Arthropods have nonetheless counteracted many defensive and nutritional barriers imposed by plants and are considered as the most successful animal herbivores. Many arthropod herbivores rely on endosymbionts or genes of endosymbiotic origin to survive on plant diets.

**Doelstelling:**

WIth this thesis, we want to advance our mechanistic understanding of herbivory using the clover-mite system. We will combine population and molecular biology.

**Locatie:**

Campus Ledeganck

**Opmerkingen:**

Dit onderwerp is gereserveerd voor Heleen Haesen.

**Onderwerp voorbehouden voor Heleen Haesen**

---

## 48499: East Antarctic lakes as glacial refugia for micro-invertebrates and microbial eukaryotes: evidence from fossil DNA

Promotor(en): Elie Verleyen, Wim Vyverman
Begeleider(s): Rune Lagaisse
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) and K.L. Ledeganckstraat

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## 48432: Ecological and functional approaches to sustainable copepod cultures as live-feed in aquaculture

| | |
|---|---|
| Promotor(en): | Marleen De Troch, Annelies Declercq |
| Begeleider(s): | |
| Contactpersoon: | Sara Degrande |
| 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:**

Currently, the most frequently used live fish feed in larviculture are rotifers (Brachionus sp.) and brine shrimp (Artemia sp.). However, these are nutritionally deficient in essential fatty acids. Being natural food to juvenile fish and naturally rich in polyunsaturated fatty acids (PUFA), copepods are known to enhance the survival, growth and development of fish larvae compared to rotifers and brine shrimp. Benthic copepods specifically are of interest for larviculture due to their ability to bioconvert short chain fatty acids into long-chain PUFA.  However, scaling of copepod cultures to commercial volumes and densities remains a complex task.

**Doelstelling:**

The aim of this MSc thesis research is to contribute to a larger project investigating optimal culturing techniques for benthic copepods.

This research topic allows the MSc student to explore innovative techniques to improve culturing of (benthic) copepods. Key areas of this research include:

- Copepods as a qualitative food source: fatty acid content/profiling of copepods under changing environmental conditions (food, temperature, and salinity) can be evaluated. Fatty acid profiles can be analysed using GC-MS.
- Culturing success: Testing and optimizing culture techniques of copepod cultures by evaluating population dynamics, yield and reproduction.

The student will have the flexibility to define or refine their individual research topic in agreements with the tutor and promotors, ensuring feasibility.c

**Locatie:**

campus Sterre, S8, Ostend Science Park

**Opmerkingen:**

Dit onderwerp wordt toegewezen aan Emma Pylyser.

**Onderwerp voorbehouden voor Emma Pylyser**

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## 48341: Effectiveness of Wolf-Proof Fencing for Protecting (Small) Livestock

Promotor(en): Jan Van Uytvanck
Begeleider(s): Joachim Mergaey
Contactpersoon: Joachim Mergaey
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:**

Wolf-proof fences are generally known to be effective, yet there is a lack of robust, field-based evaluation of their efficiency. In Limburg, damage incidents fluctuate seasonally but have decreased over the years due to wolf protection measures. Notably, no damage has occurred among owners assisted by the Wolf Fencing Team.

**Doelstelling:**

This study aims to assess the effectiveness of wolf-proof fencing in reducing predation risk for livestock. Key questions include: How many pastures are protected versus unprotected? Which species and herd sizes are involved? What is the actual risk of wolf attacks with and without proper fencing? Public data per municipality are limited, and field-based evaluation is needed to determine the fraction of livestock effectively protected, including ponies.

Additionally, for each predation event, rough estimates of meat consumed will be collected to evaluate the contribution of small livestock to wolves' energy intake in Flanders.

Fieldwork will involve sampling pastures in Limburg, and potentially in the Noorderkempen region (Kalmthout, Brecht, Essen, Wuustwezel, Hoogstraten), to assess whether they are wolf-proof. Prior training with the Wolf Fencing Team and contact with pasture owners will be required for site visits.

**Locatie:**

Veldwerk in Limburg, dataverwerking UGent en/of INBO

**Samenwerking met bedrijf of non-profit organisatie**

Bedrijf: Instituut voor Natuur- en Bosonderzoek (INBO)
Samenwerking: begeleider

**Onderwerp voorbehouden voor Johannes De Clercq**

*Deze masterproef werd reeds 1-maal toegekend!*

---

## 48220: Engineering Programmed Cell Death in Maize Kernels to Improve Yield Stability

Promotor(en): Moritz Nowack
Begeleider(s): Jie Zhang, Geng Sun
Contactpersoon: Moritz Nowack

| | |
|---|---|
| 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:**

Our research aims to genetically engineer maize plants to improve yield stability and stress resilience in collaboration with a major international agricultural chemical and seed company.

Cereal grains are the major source of nutrients for humankind. In developing maize kernels, maternal tissues nourish the growing embryo and endosperm. Maternal kernel tissues undergo programmed cell death (PCD) in a highly coordinated manner, facilitating embryo and endosperm growth.

We hypothesize that modulating specific PCD processes in maternal kernel tissues will enhance embryo growth and endosperm filling, leading to larger and more nutrient-rich kernels, especially under adverse environmental conditions.

Developing this agricultural trait can decisively contribute to stabilizing future crop yields under more and more extreme weather conditions as are expected to happen due to climate change.

**Doelstelling:**

As a Master student, you will be part of the international PCD team (https://www.nowacklab.be/) at the VIB-UGent Center for Plant Systems Biology (https://www.psb.ugent.be/).

In our lab, we have screened candidate transcription factors involved in the PCD of maize kernel maternal tissues. Using bulk RNA-seq and spatial transcriptome data from maize kernels, we have identified a set of transcription factors implicated in cell death through heterologous and transient expression systems. One of them, DeathEater1, is expressed in a specific part of the maternally derived kernel tissues. We hypothesize that DeathEater1 regulates cell death in this region by modulating dPCD-related executive genes.

To further validate the function of the DeathEater1 gene regulatory network, we have identified several transcription factors that are putatively downstream of DeathEater1. We tested these candidates and identified several factors capable of inducing cell death and activating PCD marker genes in rapid heterologous systems. You will employ CRISPR/Cas9-mediated mutagenesis to generate knockout lines for these candidate genes, enabling functional characterization of their roles in regulating PCD in maize kernels. This work will provide a foundation for developing maize varieties with optimized kernel development and improved grain yield.

If you are interested in participating in this project, please contact Prof. Moritz Nowack (moritz.nowack@ugent.be; moritz.nowack@vib.be) to arrange a visit of the lab and to discuss project options in detail. We are looking forward to meeting you!

**Locatie:**

Campus Ardoyen / Tech Lane Ghent Science Park

**Website:**

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

**Samenwerking met bedrijf of non-profit organisatie**

Bedrijf: CORTEVA
Samenwerking: use case

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## 48426: Evolutionary ecology of ant-associated and free-living rove beetles

Promotor(en): Nicky Wybouw, Thomas Parmentier
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:**

Symbiosis, a close association between distinct organisms, is a pervasive ecological interaction in insects. Certain insect taxa engage in symbiosis with ants to obtain nutrients and to reproduce in a stable and predator-free environment. Many questions remain regarding the behavioural, chemical, and morphological adaptations of myrmecophiles to interact with ant hosts. This project will focus on the evolutionary ecology of myrmecophilous rove beetles.

**Doelstelling:**

This project will advance our understanding of the ecology, behaviour, reproduction, and dispersal of free-living and myrmecophilous rove beetles.

**Locatie:**

**Website:**

Meer informatie op: www.nickywybouw.org/

**Opmerkingen:**

Dit onderwerp is gereserveerd voor Aaron Van de Woestijne.

**Onderwerp voorbehouden voor Aaron Van de Woestijne**

*Deze masterproef werd reeds 1-maal toegekend!*

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## 48255: Evolutionary lineage and species variety among the ursids at La Belle-Roche cave

Promotor(en): Dominique Adriaens, Daniel Charters
Begeleider(s): Tristan Dedrie
Contactpersoon: Tristan Dedrie
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:**

La Belle-Roche is mogelijks de oudste archeologische site in België, met een unieke faunale populatie binnen de paleontologische geschiedenis van de regio. Contextuele problemen houden echter aan. Momenteel is een nieuw onderzoeksproject aan de gang om de context op te klaren en het materiaal uit de site te valoriseren. Paleontologische studies en studies op de fauna worden door T. Dedrie en D. Charters uitgevoerd. Resten van beren vormen meer dan 80 procent van de gevonden specimens. Aangezien deze soortfamilie doorheen de laatste miljoen jaar een complexe evolutie doormaakte, is een studie van dit materiaal zeer waardevol binnen de context.

**Doelstelling:**

De student voert een analyse uit op een steekproef van de dentale specimens uit de collectie La Belle-Roche, aan de hand van 2D geometrische morphometrie. Aan de hand van de resultaten zal tijdens de data-analyse een onderscheid gemaakt worden tussen verschillende populaties of soorten. De student wordt verwacht om de resultaten, in samenwerking met D. Charters en T. Dedrie binnen de archeologische, sedimentologische, geomorfologische, geologische en paleontologische context binnen de site te interpreteren. Het onderzoek valt binnen lopend onderzoek onder D. Charters (aanwezigheid van Ursus deningeri sensu stricto in La Belle-Roche, met betrekking tot de evolutie van beren in België) en T. Dedrie (Biostratigrafische implicaties van de faunale populatie in La Belle-Roche, met betrekking tot de vroegste menselijke aanwezigheid en midden-pleistocene contexten in België). Een publicatie in een peer-reviewed journal met de student als hoofd- of co-auteur is het uiteindelijke doel na het volbrengen van de masterthesis.

**Locatie:**

campus Ledeganck, Onderzoeksgroepen Evomorf en Osteolab/Paleolab ArcheoZOOs

**Opmerkingen:**

Embargo op publiek maken van de masterthesis tot de uiteindelijke officiële publicatie van de resultaten in peer-reviewed journal (Student als hoofd- of co-auteur).

**Onderwerp voorbehouden voor Nikolas Deschacht**

*Deze masterproef werd reeds 1-maal toegekend!*

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## 48098: Experimental Evolution of a Major Evolutionary Transition: Investigating the Role of Whole Genome Duplication in Multicellularity

| | |
|---|---|
| Promotor(en): | Olivier De Clerck, Yves Van de Peer |
| Begeleider(s): | Quinten Bafort |
| Contactpersoon: | Quinten Bafort |
| 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 their seminal 1995 work The Major Transitions in Evolution, Eörs Szathmáry and John Maynard Smith explored the origins of organismal complexity through a series of key evolutionary transitions. One such transition is the emergence of multicellularity—a pivotal step in the evolution of complex life forms.

Recent studies have demonstrated that whole genome duplication (WGD) can facilitate the transition to multicellularity in the brewer's yeast Saccharomyces cerevisiae. This raises the question: is genome duplication a universal catalyst for the evolution of multicellularity across diverse lineages? To address this, comparative evidence from other branches of the tree of life is essential.

**Doelstelling:**

This master thesis aims to experimentally test whether whole genome duplication can promote the evolutionary transition to multicellularity in volvocine green algae. Specifically, the project will focus on the unicellular volvocine alga Chlamydomonas reinhardtii. You will: (1) Culture haploid and synthetic diploid strains of C. reinhardtii under controlled laboratory conditions. (2) Subject these cultures to selective pressures known to induce multicellularity: centrifugation and predation. (3) Monitor and quantify the emergence of multicellular traits over time. (4) Compare the rate and extent of multicellular transition between haploid and diploid populations.

By analyzing whether diploid strains exhibit a faster transition to multicellularity, this study will contribute to our understanding of genome duplication as a potential driver of multicellularity and evolutionary innovations.

**Locatie:**

campus Ledeganck, campus Sterre & campus Ardoyen

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## 48439: Exploring the undocumented diversity of Lactarius and Lactifluus in Burkina Faso

| | |
|---|---|
| Promotor(en): | Annemieke Verbeken |
| Begeleider(s): | Bobby Sulistyo |
| Contactpersoon: | Annemieke Verbeken |
| 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:**

Lactarius and Lactifluus are among the best-studied ectomycorrhizal (ECM) mushroom genera in Africa and are key components of tropical woodland and savanna ecosystems.

Their diversity has been relatively well documented in several regions across Central and West Africa. However, despite their ecological importance and the progress made in African mycology, virtually no data exist for Burkina Faso. As a result, the true species richness and distribution of Lactarius and Lactifluus in the country remain almost completely unknown. This gap not only limits our understanding of fungal diversity in the Sudanian zone of West Africa but also constrains ecological and conservation-oriented research that depends on accurate fungal identification.

**Doelstelling:**

This thesis aims to help fill these knowledge gaps by documenting the diversity of Lactarius and Lactifluus in Burkina Faso and improving the taxonomic framework necessary for reliable species identification.

You will study dried specimens and annotate and document microscopical characters.

A selection of specimens will be sequenced to obtain ITS barcodes or other relevant markers in order to fit it in our milkcap phylogeny, enabling molecular confirmation of morphological species hypotheses. Reference material is available in the fungaria of Ghent and Meise.

**Locatie:**

campus Ledeganck

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## 48464: Food or Fear? Risk-Reward Tradeoffs in Foraging Shorebirds

| | |
|---|---|
| Promotor(en): | Luc Lens, Frederick Verbruggen |
| Begeleider(s): | Sophia Knoch |
| Contactpersoon: | Sophia Knoch |
| 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 mudflats are dynamic and patchy environments where prey availability and potential risks, such as human disturbance, predators, or competition, vary spatially and temporally. Wading birds, such as oystercatchers, foraging in these landscapes face fundamental trade-offs between energy gain and safety. According to optimal foraging theory, animals are expected to make decisions that maximise net energy intake, but in real-world settings, foraging efficiency can be influenced by risk perception.

**Doelstelling:**

The central question could be whether different types of risk influences not only where birds feed and how they allocate their time among activities but also what they eat and how they handle prey. Do birds in risky patches only invest in high-quality prey that justify the danger? Or do they retreat to safer sites, even when food quality is lower, thereby trading energetic gain for safety? And does disturbance reduce foraging efficiency by increasing handling errors or vigilance interruptions? By combining prey sampling with behavioural observations of time-activity budgets, prey choice, handling time, and vigilance across risk gradients and resource availability, this study will test how risk-reward tradeoffs shapes shorebird foraging.

This project offers a great opportunity to explore principles of animal behaviour, risk perception, and ecology in the wild and collect data beyond the city of Ghent, in (semi) natural areas, and mudflats along the coast.

**Locatie:**

campus Ledeganck, campus Dunant, coastal fieldwork

**Opmerkingen:**

There is some scope for the student to shape the specific direction of the research depending on their interest. The student must be able to travel to field sites (limited public transport) and work outdoors in all kinds of weather.

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## 48505: From classroom to greenhouse: Evaluating the impact of botanical garden visits on plant awareness in secondary-school students?

| | |
|---|---|
| Promotor(en): | Kenneth Bauters, Lander Blommaert |
| 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:**

Plants sustain all live on earth, yet are often unnoticed. The term “plant blindness” was first introduced more than 25 years ago to describe the inability of people to notice plants in their environment. Since then, many studies have been devoted to the topic, and the focus has shifted from “plant blindness” to “plant awareness.”

This phenomenon consists of three components:

- Attention to plants (the extend to which people consciously notice, recognize, and distinguish plants from their surroundings)
- Understanding of plants (covering knowledge of plant needs and life cycles, their contribution to ecosystems, and their interactions with animals, humans, and cultures)
- Attitude towards plants (affective response to plants, general appreciation of plants)

Although botanical gardens are expected to play an active role in enhancing visitors’ plant awareness, this topic has not yet been studied within the Belgian context. Our botanical garden hosts more than 1,000 pupils each year for guided tours, workshops, and art classes, and during the Ghent Floralies in spring 2026 we expect a large influx of visitors. This event provides an excellent opportunity to measure plant awareness both among general visitors and among participating school groups.

**Doelstelling:**

The aim of this master's thesis is to examine the effectiveness of a visit to the Botanical Garden in increasing plant awareness among secondary-school pupils. The research is based on questionnaires completed by the public and by pupils before and after participating in an activity in the Botanical Garden. The activities include a guided tour, a workshop, and an art assignment in the garden.

The following sub-questions are investigated:

- What is the level of plant awareness among secondary-school pupils compared to regular visitors?
- Does age play a role in the level of plant awareness?
- Does a visit to the botanical garden increases the plant awareness of secondary-school pupils? And to what extent?
- Which type of activity (guided tour, workshop, art assignment) has the greatest effect on plant awareness?
- Is this effect still visible after, for example, 6 weeks?
- Which aspect(s) of plant awareness (attention, understanding, attitude) are most affected?
- Which aspects are missing in the current educational program of the botanical garden? (question for teachers and pupils)

**Locatie:**

GUM&Plantentuin (Ledeganck)

**Onderwerp voorbehouden voor Janne Stevens**

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## 48427: From hosts to fungi: tritrophic dynamics and novel fungal diversity in Honduran bat communities

| | |
|---|---|
| Promotor(en): | Danny Haelewaters |
| Begeleider(s): | Danny Haelewaters, Aimée Blondelle |
| 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:**

Tropical Montane Cloud Forests (TMCFs) cover only a fraction of the Earth's land surface (0.26%), yet they harbor disproportionately high levels of biodiversity and endemism. One of the key groups within TMCFs are bats (Chiroptera), which account for 40% of mammal species in these ecosystems. They play essential roles as pollinators, seed dispersers, insect suppressors, and nutrient cyclers. Bats also serve as hosts for diverse ectoparasites, including bat flies (Diptera: Nycteribiidae and Streblidae). These are obligate, host-specific, blood-feeding parasites that are exclusively associated with bats. Bat flies, in turn, can be parasitized by Laboulbeniales (Ascomycota), obligate ectoparasitic fungi. This unique system forms a tritrophic interaction: bats (primary hosts) – bat flies (primary parasites, secondary hosts) – Laboulbeniales (hyperparasites, secondary parasites).

Problems

While the effects of habitat alteration on bats are relatively well documented, far less is known about how such changes impact their associated parasites and hyperparasites. This gap is particularly pronounced for Laboulbeniales fungi, of which only a small fraction of the global diversity has been described, and for which virtually no baseline data exist in Honduras. As a result, parasitic interactions within TMCFs remain understudied, limiting our ability to monitor changes in parasite communities over time and restricting opportunities to track parasite community dynamics and to evaluate their role within broader biodiversity patterns.

**Doelstelling:**

This project aims to investigate the ecological and taxonomic dimensions of the bat–fly–fungus system in Honduras.

- Ecological analyses: Examine how habitat structure, particularly canopy cover, influences the prevalence of bat flies and Laboulbeniales on their respective hosts, and assess whether bat sex, age, or reproductive state affects infection dynamics.
- Tritrophic interaction network analyses: Analyze host specificity, potential host shifts, and infection prevalence in both bat

flies and Laboulbeniales, evaluating their contribution to the stability of the hyperparasitic system.
- Taxonomic contributions: Describe novel species of Laboulbeniales associated with bat flies in Honduras, integrating morphological and molecular data.
- Biodiversity monitoring: Provide baseline data for long-term monitoring and conservation of cloud forest ecosystems and their unique parasitic networks.

**Locatie:**

Campus Ledeganck

**Onderwerp voorbehouden voor Tine Cornelis**

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## 48300: Game of whole genome duplications: modeling animal polyploidy establishment

| | |
|---|---|
| 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: | |
| 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. In addition, most animals have intricate development and differentiated sex chromosomes, which makes whole genome duplication complex and potentially incompatible with life. These are the main hypotheses to explain why polyploidy is rare in animals, but these remain to be tested.

**Doelstelling:**

We try to answer these questions on polyploid establishment and invasion using ecological and evolutionary 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 a theoretical polyploid species, during this thesis the goal is adapting the model to answer questions about animal polyploidy and sex chromosome differentiation. In addition, including higher level ploidies (triploids etc), and environmental disturbances and similar processes is welcome.

**Locatie:**

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

**Website:**

Meer informatie op: www.vandepeerlab.be/research/theoretical-methods-polyploid-research

**Opmerkingen:**

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

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## 48557: Herinventarisatie van holtebewonende dood-houtkevers in een halfopen landschap

| | |
|---|---|
| Promotor(en): | Dries Bonte |

Begeleider(s): Arno Thomaes
Contactpersoon: Arno Thomaes
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 2013 werden in Voeren 51 pitfalls geplaatst in boomholtes in 10 deelgebieden en gedurende 3 maanden opgevolgd. Het gaat om appelbomen, knotwilgen, -essen en -eiken. Alle kevers uit die pitfalls werden gedetermineerd. Hieruit bleek dat Voeren nog een grote soortenrijkdom kende van deze sterk gespecialiseerde gemeenschap. Halfopen landschappen staan echter sterk onder druk en gaan nog steeds verder achteruit. Ook in Voeren zien we het landschap achteruit gaan voornamelijk door verdere intensivering van de landbouw

**Doelstelling:**

Doelstelling binnen deze thesis is dan ook om het aantal holle bomen in de 10 deelgebieden opnieuw te inventariseren en de 51 pitfalls opnieuw te installeren (in dezelfde boom indien nog aanwezig, mei-jul 2026). Nadat de kevers gedetermineerd zijn (aug-dec 2026), kan er gekeken worden hoe de huidige kevergemeenschap en soortenrijkdom veranderd is ten opzichte van 13 jaar geleden. Verder kunnen veranderingen op landschapsniveau gerelateerd worden aan de veranderingen in soorten samenstelling.

**Locatie:**

**Onderwerp voorbehouden voor Kaat Rasson**

*Deze masterproef werd reeds 1-maal toegekend!*

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## 48284: 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**

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## 48440: Hidden life in fallen logs: mapping deadwood fungi in Meerdaalwoud

| | |
|---|---|
| Promotor(en): | Annemieke Verbeken |
| Begeleider(s): | Glen Dierickx |
| Contactpersoon: | Glen Dierickx |
| 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:**

Deadwood is essential for forest biodiversity, especially for fungi that break down wood and drive nutrient cycling. Meerdaalwoud, one of Flanders' most natural beech forests, contains a rich but largely undocumented community of deadwood-inhabiting fungi. Traditional fruitbody surveys only reveal a small part of this diversity, while new molecular techniques using environmental DNA (eDNA) can detect the many species that do not or rarely produce visible fruiting bodies. The results will support better biodiversity monitoring and forest management strategies.

**Doelstelling:**

This thesis explores how both approaches can be combined to better understand fungal diversity in this forest.

You will survey fungal fruitbodies on logs, snags, and finer woody debris in Meerdaalwoud, collect wood and/or soil samples and perform eDNA metabarcoding (ITS), compare the fungal communities detected by fruitbodies versus eDNA and analyse how diversity varies with deadwood type and decay stage.

**Locatie:**

campus Ledeganck

**Onderwerp voorbehouden voor Kaat Mols**

## 48545: Historische Ecologie Mollusca van België

| | |
|---|---|
| Promotor(en): | Dominick Verschelde, Sander Govaerts |
| Begeleider(s): | Dominick Verschelde, Greet Vanderhaegen |
| Contactpersoon: | Dominick Verschelde |
| 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:**

Voor deze masterthesis is het de bedoeling om de historische ecologie van een reeks Bivalven en Gastropoden uit verschillende regio's in België (collectie Emiel Hostie) in kaart te brengen en in te schatten hoe deze veranderd is tegenover het heden. Hiervoor worden verschillende collecties geraadpleegd

**Doelstelling:**

1. Collectie Emile Hostie (GUM)

Dit is een collectie uit het GUM, nagelaten door E. Hostie met voornamelijk Bivalven en Gastropoden uit de jaren 1920 en 1930.

Deze collectie wordt gedigitaliseerd (Access) door de student. Hiermee wordt bedoeld dat de collectie eerst in kaart wordt gebracht met geupdatete taxonomie. Uit de wetenschappelijk relevante stukken worden specimens geselecteerd die in aanmerking komen voor dit onderzoek.

1. Collectie KBIN (to be confirmed)
   In samenwerking met het KBIN worden Bivalven en Gastropoden uit de jaren 1920 en 1930 geselecteerd. Ook recente specimens en recente populatiegroottes van gekende plaatsen worden mee verwerkt in de thesis.

Hierbij is het de bedoeling om voornamelijk zoetwatersoorten te uit het verleden en heden in kaart te brengen, maar ook mariene collecties komen in aanmerking.

1. Collectie VLIZ (to be confirmed)
   In samenwerking met het VLIZ wordt er geprobeerd om huidige mariene populaties in kaart te brengen. Eventuele bevindingen of collectiestukken uit vroegere tijden zijn ook nuttig.
2. Onderzoek prof. Sander Govaerts

Bij archeologische opgravingen (Middeleeuwen) worden vaak schelpen van Molluscen teruggevonden.Bij recentere studies worden die ook telkens gedetermineerd en kunnen zo een nuttig beeld vormen over deze sites in vroegere periodes. Het geeft tevens ook een beeld over het eetgedrag van mensen doorheen de tijd, die op die manier een predatiedruk meebrengt.

Professor Sander Govaerts is bezig met een onderzoek, waarvoor hij dergelijk opgravingsrapporten doorneemt en heeft op die manier een beeld op de hoeveelheid beschikbare informatie.

Professor Govaerts staat open voor een samenwerking voor deze thesis.

Met behulp van deze collecties zal er worden getracht om een beeld te geven van bepaalde soorten Molluscen doorheen de tijd. Hierbij hopen we bepaalde patronen te zien, zoals soorten die het steeds moeilijker of net gemakkelijker hebben. Hierbij kan het zijn dat er wordt opgemerkt dat soorten dicht bij steden het over het algemeen moeilijker hebben. Afhankelijk van de historische gegevens, zou predatie door mensen hier een grote invloed op gehad kunnen hebben.

**Locatie:**

**Onderwerp voorbehouden voor Tibo Desmet**

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## 48465: Holding their Breath: Ecological Drivers of Diving Behaviour in Cormorants

| | |
|---|---|
| Promotor(en): | Luc Lens, Frederick Verbruggen |
| Begeleider(s): | Sophia Knoch |
| Contactpersoon: | Sophia Knoch |
| 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:**

Cormorants are pursuit-diving seabirds that forage mainly inshore, preying on benthic and demersal fish as well as invertebrates. Their ecology offers an excellent system to investigate how diving birds balance physiological constraints with ecological opportunities. Previous work on diving birds has shown that species differ in the way they allocate time underwater and on the surface, with dive duration and recovery intervals reflecting both oxygen limitation and behavioural strategy. In addition, variation in prey ecology, such as prey type and distribution, can strongly influence diving effort and tactics. Cormorants are particularly interesting in this respect, as they exploit both shallow and deeper waters, potentially requiring flexibility in their foraging tactics.

**Doelstelling:**

This thesis could explore the ecological drivers of diving behaviour in cormorants along the Dutch, Belgian, and French coast, but also within city areas (e.g. Ghent). The project will focus on finescale behavioural observations (from shore-based observation points) of diving sequences, recording for example dive duration, frequency, and surface intervals, as well as environmental parameters such as weather, tidal stage, and habitat type. Key questions could include whether cormorants show consistent differences in diving strategy between habitats, how environmental conditions shape their behaviour, and whether dive–surface time trade-offs are context-dependent. For example, do cormorants shorten recovery intervals in order to increase foraging time under certain conditions, or do they adjust surface pauses depending on whether a dive was successful or not?

By combining behavioural observations with environmental data, this project offers a great opportunity to understand the flexibility and constraints of cormorant diving strategies.

**Locatie:**

campus Ledeganck, campus Dunant, fieldwork in coastal areas (Belgium, Northern France, The Netherlands), potentially also city areas (e.g. Ghent)

**Opmerkingen:**

There is some scope for the student to shape the specific direction of the research depending on their interest. The student must be able to travel to field sites (limited public transport) and work outdoors in all kinds of weather.

**Onderwerp voorbehouden voor Jelle De Brauwer**

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## 48473: Home-range dynamics and fine-scale habitat preferences of invasive ring-necked parakeets across urban gradients

| | |
|---|---|
| Promotor(en): | Diederik Strubbe |
| Begeleider(s): | Frouke De Witte |
| 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 invasive ring-necked parakeet (Psittacula krameri) has established stable and expanding populations in Flanders, yet the mechanisms shaping its spatial ecology in human-dominated environments remain insufficiently understood. Although parakeets are often associated with urban parks, gardens, and green infrastructure, evidence about how they organize their movements, how far they travel on a daily basis, and which environmental features they prioritize is still limited. Most existing knowledge is based on sightings or broad-scale distribution data, which do not capture the fine-scale movement decisions that determine resource use, foraging patterns, and breeding behaviour. This gap is particularly relevant in urban and peri-urban contexts, where resource availability is highly heterogeneous and vegetation is embedded within a matrix of built-up structures. Without high-resolution telemetry data, it is difficult to understand whether invasive parakeets reduce their space use in cities due to abundant anthropogenic resources or whether they maintain large ranges to exploit scattered green patches. Moreover, the lack of integrated habitat metrics prevents a mechanistic understanding of how vegetation structure, canopy cover, and other landscape features shape their movement ecology. Addressing these knowledge gaps is crucial for advancing ecological understanding of invasion processes and for informing evidence-based management strategies in regions where parakeets are becoming increasingly common.

**Doelstelling:**

This Master thesis aims to investigate how ring-necked parakeets structure their space use and habitat selection across contrasting environments in Flanders, with a focus on urban versus non-urban landscapes. The first objective is to quantify home-range size using high-resolution GPS telemetry and assess whether parakeets in urban areas maintain smaller ranges due to higher resource concentration and predictability compared to individuals in more natural or rural settings. The second objective is to identify the environmental features that shape habitat selection within these home ranges, focusing on vegetation cover, structural complexity, and other landscape characteristics relevant to foraging and nesting opportunities. To achieve this, the study will integrate movement analyses with high-resolution spatial datasets, including remotely sensed products derived from sources such as Copernicus and Google Earth Engine. These will provide quantitative measures of habitat traits such as NDVI, canopy density, vegetation height, and impervious surface cover. Finally, the thesis will include the development of R-based analytical workflows for processing telemetry data, estimating home-range metrics, and testing habitat selection patterns using established packages in movement ecology and GIS. By combining fieldwork, animal tracking, and spatial analysis, the research will generate new insights into how invasive parakeets adapt their spatial behaviour to different landscape contexts and will contribute to a broader ecological understanding of invasion success in human-modified environments.

**Locatie:**

Gent/Antwerpen/Brussel + nog te kiezen rurale locaties

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## 48211: Hopping through habitats, studying Common Toad movement.

Promotor(en): Dries Bonte
Begeleider(s): Henri Rommel
Contactpersoon: Henri Rommel
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:**

Movement, defined as the change of an individual's spatial location in time, plays a major role in the life of an organism. Organisms need to move in order to find food, shelter and in case of amphibians, reach breeding ponds for reproduction, while, on a population-level, it structures gene flow and metapopulation dynamics. In amphibians movement depends a lot on the environmental conditions the animal experiences.

**Doelstelling:**

The aim of this thesis is to measure and study how movement parameters such as distance, direction and tortuosity differ between different habitats the Common Toad might experience and evaluate different tracking techniques for this species. Being nocturnal and water-dependent animals fieldwork for this project will mainly be conducted during the rainy/humid nights in the summer to autumn months. Furthermore, it will involve modelling and statistical analysis of these movement parameters.

**Locatie:**

**Onderwerp voorbehouden voor Lander Van Maele**

*Deze masterproef werd reeds 1-maal toegekend!*

## 48460: How diatoms conquered the climate gradient: reconstructing the thermal niche of diatom species complexes

Promotor(en): Eveline Pinseel, Willem Stock
Begeleider(s): Eléonore Pottier
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:**

Temperature is an important environmental barrier to dispersal because of the temperature-dependence of many different physiological processes. Nevertheless, certain lineages, such as diatoms, have managed to colonise the entire planet and can now be found living at a large range of temperatures. Both the terrestrial Pinnularia borealis species complex and the marine Cylindrotheca closterium species complex have, for example, repeatedly colonized and adapted to different climate zones, from the poles to the tropics, since their origin about 30 million years ago. This makes them a perfect study system to gain insight into climate adaptation. Additionally, diatoms play an essential role in global biogeochemical cycling and primary production. Therefore, unravelling their capacity for climate adaptation might help understand the potential impact of climate change on the ecosystem services that diatoms provide.

**Doelstelling:**

The main objective of this master thesis is to gain a better understanding of thermal adaptation in diatoms by reconstructing and comparing the temperature response of closely related species found in different climate zones. To achieve this, the student will be working with one or two diatom species complexes (terrestrial Pinnularia borealis and/or marine Cylindrotheca closterium). The student will collect data on the thermal response (most likely in the form of a growth response curve, but potentially also in terms of gene expression) of diatom strains that originate from different climate zones (polar, temperate, tropical), reconstruct growth curves, and assess thermal niche width. This will allow to test to what extent strains that inhabit similar climate conditions show niche conservation and will allow to assess which populations and species are most sensitive to climate warming. The student will learn how to work with unicellular eukaryotes (diatom culturing and microscopy) in a common garden environment, as well as how to gather and analyse thermal response data (growth curve reconstruction, statistics in R).

**Locatie:**

campus Sterre, S8

## 48342: How genetic diversity drives 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:**

Genetic diversity provides the raw material for evolution, and its distribution across populations can strongly shape coevolutionary dynamics. When interacting species possess high genetic variation, they are better able to respond to each other's adaptations, allowing coevolutionary arms races to intensify and persist. Conversely, low genetic diversity can limit adaptive potential, weakening reciprocal selection and potentially collapsing coevolutionary feedbacks. According to the geographical mosaic theory of coevolution, differences in genetic diversity across landscapes contribute to the formation of coevolutionary hotspots, where abundant genetic variation fuels rapid reciprocal adaptation and population dynamics are stable, and coldspots, where limited diversity constrains evolutionary responses. Thus, the spatial patterns of genetic diversity within and between species play a critical role in determining where coevolution is strong, where it is weak, and how evolutionary trajectories unfold across ecological landscapes.

**Doelstelling:**

This study will examine the stabilizing role of genetic diversity in an experimental system, and quantify which elements influence these dynamics. For this, the student will use a plant-herbivore model system consisting of the two-spotted spider mite (Tetranychus urticae) and white clover (Trifolium repens). Mesocosm experiments will be set up to monitor the population dynamics of both species over time, as well as certain traits of the two species.

**Locatie:**

campus Ledeganck

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## 48221: How to meet the deadline: The molecular regulation of programmed cell death in plants

Promotor(en): Moritz Nowack
Begeleider(s): Eugenia Pitsili
Contactpersoon: Moritz Nowack
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:**

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 a pioneering field. 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 the international PCD team (https://www.nowacklab.be/) performing cutting-edge research in plant developmental biology. We are using advanced technologies (e.g. CRISPR-based genome editing, tissue-specific genome engineering, advanced light-and electron-microscopy, live-cell imaging, protein biochemistry, protein interactomics, (single-cell) RNA sequencing, low-input proteomics, and many more) to answer the big biological question on how PCD is molecularly controlled 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 / Tech Lane Ghent Science Park

**Website:**

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

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## 48467: Identifying molecular protein interactors of the neuronal globin 23 in Caenorhabditis elegans

| | |
|---|---|
| Promotor(en): | Bart Braeckman |
| Begeleider(s): | Diana Naalden |
| 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:**

Caenorhabditis elegans is an excellent 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 cellular processes. Despite the simplicity of the small worm, the nervous system is rather complex with 302 neurons that are subdivided into 118 distinct classes based on position and synaptic connectivity. It is well characterized and considered as structurally and functionally similar to that of mammals. The C. elegans globin family is a large group of proteins encoded by 34 genes, predicted to produce a total of 55 distinct globin isoforms. The proteins structurally exhibit a globin domain, yet vary strongly in size and sequence. They each display a distinct expression pattern in specific sets of neurons. Although there is a general understanding that some of these proteins are involved in cellular processes like signaling and gas binding, the exact function remains unknown for the majority of the globins.

**Doelstelling:**

In this MSc thesis you will investigate GLB-23, one of the very underexplored globins. glb-23 is expressed in neurons located in the head region as well as in motor neurons along the ventral nerve cord of the nematode. In previous studies, it was demonstrated that glb-23 expression in adult worms is upregulated under stress conditions such as anoxia and chronic heat stress. C. elegans serves as a model organism for studying tau toxicity in tauopathies (Natale et al., 2020). In tau-expressing nematodes, knockout of glb-23 results in a more severe phenotype, an effect that is also observed in specific neuron-related mutants (Kraemer, 2006). This hints at a direct or indirect role of GLB-23 in protein stability in the neurons. Our recent results indicate that GLB-23 plays a role in food attraction as well. Altogether, these findings indicate that this globin has diverse roles in neuronal signaling in the nematode.

The GLB-23 protein possesses a large N-terminal disordered extension, suggesting this part of the protein plays a role in interaction with other proteins. In this thesis you will identify and/or screen for potential interactors. The thesis may involve (molecular) techniques such as cloning, co-immunoprecipitation, yeast two-hybrid screening, and C. elegans bioassays.

References

*Kraemer BC, Burgess JK, Chen JH, Thomas JH, Schellenberg GD. Molecular pathways that influence human tau-induced pathology in Caenorhabditis elegans. Hum Mol Genet. 2006 May 1;15(9):1483-96. doi: 10.1093/hmg/ddl067. Epub 2006 Apr 6. PMID: 16600994.

*Natale C, Barzago MM, Diomede L. Caenorhabditis elegans Models to Investigate the Mechanisms Underlying Tau Toxicity in

Tauopathies. Brain Sci. 2020 Nov 11;10(11):838. doi: 10.3390/brainsci10110838. PMID: 33187241; PMCID: PMC7697895.

**Locatie:**

Campus Ledeganck

**Onderwerp voorbehouden voor Iene Lotte Huysentruyt**

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## 48245: Impact of glacier retreat on trophic flow and functioning of Greenlandic fjord food webs: an ecosystem modelling approach

| | |
|---|---|
| Promotor(en): | Ulrike Braeckman |
| 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:**

Global warming causes glacier retreat in Arctic fjords, with potentially cascading effects on these highly productive ecosystems. Marine-terminating glaciers (MTGs) create local upwelling zones through subglacial meltwater release, supplying nutrients that support large phytoplankton at the base of fjord food webs. As Arctic temperatures rise, MTGs are retreating out of fjords and will eventually become land-terminating glaciers (LTGs), altering fjord hydrodynamics. The loss of MTG-induced upwelling and increasing surface inflows from LTGs make fjords more stratified, reducing primary production and phytoplankton cell size, thus possibly the amount and quality of food available to fjord species (e.g., Meire et al., 2023, https://doi.org/10.1038/s41561-023-01218-y). How shifts from MTG to LTG—and the associated changes in phytoplankton dynamics—will affect Arctic fjord food webs, from benthic to pelagic, trophic flow and overall ecosystem functioning, remains poorly understood.

**Doelstelling:**

The aim of this thesis is to develop carbon flow networks for two Greenlandic fjord systems with contrasting glacial influence—one influenced solely by land-terminating glaciers (LTGs) and one influenced by both marine-terminating (MTGs) and LTGs. These networks will quantitatively estimate carbon flows between food web compartments, including living (species) and non-living (detritus) organic carbon pools, to compare food web functioning (e.g., secondary production, food web efficiency, carbon burial) across fjord systems. The approach is modelling-based (using linear inverse modelling), integrating extensive field data collected in summer 2023 from Greenlandic fjords. This includes measurements of carbon stocks in food web compartments (species biomass and organic matter pools), trophic interactions (derived from stable isotopes), and ecological rates (e.g., primary production, respiration). The student will learn how to develop and analyze food web models—compiling data and food web topology, coding and running the model in R, performing model diagnostics, and applying analysis tools to address their research questions. Ultimately, the results of this thesis will contribute to a broader understanding of how glacier retreat may affect Arctic fjord food webs in the future.

**Locatie:**

Marine Biology Lab, Sterre S8

**Website:**

Meer informatie op: canoe.marinetraining.eu/

**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 programming using R is desired.

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## 48385: Impact of pesticides on interspecific interactions with social insects

Promotor(en): Nicky Wybouw, Thomas Parmentier
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:**

Pesticides can harm non-target organisms. These effects can be acute and induce high levels of mortality. Sub-lethal effects, such as increased susceptibility to parasites, have also been observed in non-target organisms. Unfortunately, there has been a historical bias toward studying pollinators such as bees. How synthetic and plant-derived pesticides modulate the behaviour of ants is still poorly understood.

**Doelstelling:**

This project will investigate how different pesticides influence the interspecific interactions between ants and associated myrmecophiles.

**Locatie:**

**Website:**

Meer informatie op: www.nickywybouw.org/

**Opmerkingen:**

Dit onderwerp is gereserveerd voor Iebe Gigante.

**Onderwerp voorbehouden voor Iebe Gigante**

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## 48498: Impact of temperature rise during spring on soil microbial and invertebrate communities in High Arctic tundra

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:**

High Arctic soils are undergoing rapid environmental change due to accelerated climate warming. While most ecological studies in the region focus on the late summer growing season, the early spring thaw represents a highly dynamic but understudied period during which freeze–thaw cycles, snowmelt, and moisture pulses strongly influence soil ecosystem functioning. These early-season dynamics initiate the first major carbon and nutrient fluxes of the year and may play a disproportionate role in driving greenhouse gas (GHG) emissions. Despite their importance, the responses of bacterial and (micro-) eukaryotic communities—including fungi, protists, and small metazoans—to warming in early spring remain poorly understood. Understanding how warming modifies these early spring soil communities is essential for predicting year-round ecosystem trajectories, particularly given the strong links between microbial processes, soil moisture, and GHG emissions.

**Doelstelling:**

This MSC thesis will investigate how an experimental increase in soil temperature induced by open-top chambers (OTCs) alters bacterial and eukaryotic community structure at two soil depths during the early spring thaw period in a High Arctic tundra ecosystem near Ny-Ålesund (Svalbard). Soil samples were collected in June 2025. The community structure of bacteria, fungi, protists, and other eukaryotes will be studied under ambient and warmed conditions using DNA-based 16S and 18S rRNA amplicon sequencing. The student will gain hands-on experience with DNA extraction and amplification, as well as bioinformatics pipelines and downstream analysis techniques to study these soil communities. These results will be integrated with soil physical and chemical conditions as well as GHG flux measurements, to determine how warming modifies these communities during spring. Finally, these results will be compared with a late-summer dataset to evaluate whether warming effects differ fundamentally between early spring and late summer. This seasonal comparison will contribute to a broader understanding of how warming alters High Arctic ecosystem functioning across different time windows of the growing season.

**Locatie:**

Sterre (S8) and K.L. Ledeganckstraat

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## 48429: Impact of the Princess Elisabeth Island on soft-sediment communities in the Belgian part of the North Sea

| | |
|---|---|
| Promotor(en): | Ulrike Braeckman |
| Begeleider(s): | Christelle Jammar |
| Contactpersoon: | Christelle Jammar |
| 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:**

Since 2024, an artificial energy island is being built in the Belgian Part of the North Sea that connects wind farms at the sea to the mainland and creates new connections with neighboring countries. The energy island, which is a world first, is located adjacent to an area designated for marine protection under the EU Natura2000 Habitat Directive for its high biodiversity of soft-sediment benthic communities and the presence of gravel beds that are important spawning and nursing areas for fish. Installing the energy island can alter several aspects of the benthic ecosystem, both in the positive and negative sense. The (pseudo)faeces of the fouling fauna growing on the concrete island structures can enrich the sediments with organic matter. This may in the first instance lead to increased food availability for detritivores, but on the long term, it can also lead to hypoxia when organic matter accumulates. Shellfish growing on the side walls of the Island may drop down to the soft-sediment seabed and form small patches of biogenic reefs, which can increase habitat heterogeneity and potentially increase local biodiversity.

**Doelstelling:**

By law, the effect of anthropogenic activities on the local marine ecosystem needs to be monitored. As part of a larger monitoring programme, the Marine Biology Research Group at Ghent University monitors the effect of the construction and operation of the energy island on the macrobenthos community and the sediment habitat. For this thesis topic macrobenthos samples will be processed in the lab, involving sorting and identification at species level. Statistical analysis involves relating temporal patterns in macrobenthic biodiversity to environmental variables and position with respect to the location of the Island. Potentially the student can take part in the sample collection in October 2026.

**Locatie:**

**Onderwerp voorbehouden voor Noah Rawoens**

*Deze masterproef werd reeds 1-maal toegekend!*

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## 48430: Impact of the Westdiep seafarm on soft-sediment communities in the Belgian part of the North Sea

Promotor(en): Ulrike Braeckman
Begeleider(s): Christelle Jammar
Contactpersoon: Christelle Jammar
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:**

Since 2022, a seafarm is built about 5 km offshore of Nieuwpoort. The farm focuses on cultivating blue mussels Mytilus edulis using continuous capture lines or single dropper lines to capture mussel spat from the environment and harvest them to a size suitable for human consumption. Alongside mussels, the farm plans to cultivate native oysters and seaweed in the future. Mussel farming can have broad ecological effects, e.g. mussels serve as a food source for larger predators, such as starfish, and hard-bottom communities can emerge as shells drop off, creating microhabitats on the ambient soft-sediment seafloor. However, the decomposition of mussels and accumulated organic matter can create anoxic conditions and release of free sulphides which can reduce abundance, species richness, diversity, and biomass of benthos. The extent of mussel farming's impact is influenced by factors such as the age and size of the farm, species density, and local environmental conditions. Detecting and monitoring these effects is complex, as impacts vary spatially and temporally, with differences between areas directly beneath the farm and those further away.

**Doelstelling:**

This thesis will evaluate the spatio-temporal variability of macrobenthic communities near the Westdiep sea farm four years post-installation. Therefore macrobenthos samples will be processed in the lab, involving sorting and identification at species level. Statistical analysis involves relating temporal patterns in macrobenthic biodiversity to environmental variables and position with R.

**Locatie:**

**Onderwerp voorbehouden voor Matthias De Weerdt**

*Deze masterproef werd reeds 1-maal toegekend!*

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## 48471: In-silico Analysis of Muscle-tendon-bone Architecture of Seahorse Tail

Promotor(en): Dominique Adriaens, Francis wyffels
Begeleider(s): Danial Forouhar
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 seahorse tail possesses a highly unusual muscle–tendon architecture, with long hypaxial muscle-tendon sheets system that span many vertebrae. This arrangement underlies its remarkable grasping performance. A validated biomechanical model has already demonstrated the functional value of long muscle spans, yet new dissections have revealed additional structural details, especially regarding the precise routing and attachment of myosepta. These recent insights raise new questions about how variation in tendon routing, tendon attachment points on bone, or potential helical organisation of the tendon sheet would influence grasping force, torque generation, and tail shape during bending. Testing these alternative configurations may help explain why the current muscle–tendon–bone arrangement evolved in seahorses and whether it represents an optimal or constrained solution.

**Doelstelling:**

The aim of this MSc project is to use the existing validated musculoskeletal model of the seahorse tail to test a set of alternative hypotheses about tendon–bone attachment strategies, informed by updated knowledge of tendon–muscle arrangements from new dissections or 3D reconstructions. The student will quantify how changes in tendon routing, the number and distribution of attachment points, possible helical tendon geometries, and different spanning configurations affect bending mechanics, torque production, grasping efficiency, and the resulting shape morphology.

**Locatie:**

Ledeganck campuscampus Ledeganck, Research Group Evolutionary Morphology of Vertebrates

**Website:**

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

**Opmerkingen:**

Main Tasks in the topic and interconnections Become familiar with the validated MuJoCo model and reproduce baseline simulations. Translate new anatomical observations/3D reconstructions into model parameters, such as tendon routing and attachment locations. (=>iodine staining) Implement alternative tendon configurations, including variations in the number of attachments, routing paths and potential helical arrangements. (Insights from Marionette Method)

**Onderwerp voorbehouden voor Joppe Bettens**

*Deze masterproef werd reeds 1-maal toegekend!*

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## 48501: 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:**

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## 48305: Initial movement and dispersal patterns of juvenile released and wild born Cinereous vultures in Spain

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:**

We know very little about the dispersal phase of most bird species, often because they range very far and make unpredictable movements. However, in the last few decades high quality, low weight, high resolution GPS units have been developed that can be deployed onto species that are of sufficient body weight such as large waterfowl, or raptors. These are also equipped with solar panels so that the battery can be recharge for an almost indefinite period, allowing researchers to follow birds for multiple months. This period of time can cover the entire dispersal period in detail; for raptors, such as vultures, this can be an extended period starting around August/September of the year they are born in, and increasing at arouind 6 months old, as they live for many years and do not start to breed until they are around 5 years old.

This project will investigate the movement and dispersal patterns of Cinereous vultures Aegypius monachus, one of four European vulture species. It has been subject to large scale reintroduction programmes due to many years of decline and near extinction from hunting, poisoning, and mortality upon interaction with human infrastructure. The project is data based, and will use ˜60 individuals GPS tracked for minimum of 1 month after fledging, to investigate differences in initial movements, dispersal distances and directions, as well as comparisons over time for birds that live long enough. The project will mostly use R, but will also map data in QGIS.

**Doelstelling:**

**Locatie:**

Ledeganck/ thuis

**Onderwerp voorbehouden voor Renzo De Mayere**

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## 48531: Insects and their associated Laboulbeniales microfungi from decomposing carcasses

Promotor(en): Danny Haelewaters, Menno Schilthuizen
Begeleider(s): Danny Haelewaters, Menno Schilthuizen
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:**

Dead and decaying wood are rich sources for insect species. The knowledge about carrion ecology, however, is scarce. This includes the succession of insects on different species of cadavers. Yet, faunal inventory data are desirably linked to the ecological coherence of the system studied. Also understudied in this microhabitat are associates of insects attracted by carrion, for example

Laboulbeniales microfungi. Thus far, 13 species of Laboulbeniales have been reported from insects attracted by cadavers of roe deer, pigeon, crayfish, badger, and hedgehog. These are: Appendiculina entomophila, Asaphomyces tubanticus, Corethromyces henrotii, Diphymyces kaaistoepi, Laboulbenia algerina, Laboulbenia calathi, Laboulbenia eubradycelli, Laboulbenia notiophili, Peyritschiella princeps, Rhachomyces furcatus, Rhachomyces philonthinus, Stigmatomyces crassicollis, Stigmatomyces limosinae. However, it remains unclear if these species are typical for this microhabitat or rather represent incidental inhabitants.

**Doelstelling:**

The goal of this Master's thesis is to analyze the succession of insects attracted by decomposing carcasses as well as their associated Laboulbeniales microfungi. This will based on literature study, the analysis of previously collected data from hedgehog, and the collection of insects from carcasses. Carcasses will be located through our contacts with wildlife shelters and collaborators in Belgium and the Netherlands. Insects will be collected via pitfall traps and by hand at different stages of decomposition (fresh, bloated, active decay, advanced decay, dry). Identification of insects will take place in Leiden, under supervision by Dr. Menno Schilthuizen (Taxon Expeditions, Leiden University). Insects will be screened for Laboulbeniales ectoparasitic microfungi. Fungi will be analyzed via integrative taxonomy. The student who takes on this project will perform fieldwork, become familiar with fungal and insect taxonomy, and receive hands-on training in specimen preparation and curation, microscopy, and DNA barcoding. He/she will gain experience in ecological analysis and contribute to a better understanding of insect–fungus associations during carrion decomposition. The project is suitable for students interested in entomology, mycology, forensic ecology, and biodiversity research.

**Locatie:**

Campus Ledeganck

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## 48431: Invasive species alert in the Zeeschelde estuary: ecological effects of the Amur river clam Potamocorbula amurensis

| | |
|---|---|
| Promotor(en): | Carl Van Colen |
| Begeleider(s): | Gunther Van Ryckegem, Merlijn Jocqué |
| Contactpersoon: | Gunther Van Ryckegem |
| 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:**

Potamocorbula amurensis is an invasive bivalve that is listed by the IUCN among the 100 most invasive species worldwide. This species is originally an Asian bivalve with a very broad tolerance for temperature and salinity. For a long time, observations outside its native range were limited to San Francisco Bay (North America), but in 2019 the first specimens for Europe were reported in the Zeeschelde and Westerschelde, followed by an explosive increase in the estuary. This invasion has most likely strongly disrupted the local food web. In this thesis, you will complement field research (monitoring) on the distribution of this species along the Scheldt estuary with experimental studies on the ecological impact of this bivalve, such as its interactions with phytoplankton and zooplankton, other benthos, and waterbirds.

**Doelstelling:**

**Locatie:**

labo INBO - VMM Gent en campus Sterre - Onderzoeksgroep Mariene Biology

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## 48306: Investigation of White Stork Ciconia ciconia migratory patterns

| | |
|---|---|
| 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:**

Climate change is driving changes in bird migration globally. In addition, human infrastructure and behaviours are driving concurrant shifts in abundance, distribution and bird behaviour. Birds are now wintering in new areas and using new routes because of milder conditions, and they are deciding not to migrate because they can rely on human infrastructure to survive overwinter. One of the main examples of this short-stopping behaviour is the white stork Ciconia ciconia, which now migrates to southern Europe, or even stays in central Europe overwinter, instead of travelling to its traditional wintering grounds in Africa. They are social, long lived species, and large groups of storks now rely instead of anthropogenic waste dumps to sustain them for their non breeding period, as well as agricultural lands continent wide. We also see changes in adults, compared to juveniles, reflecting experienced gained as a result of living longer.

This project will use GPS tracking data from birds tagged at De Zwin natuur park on the Belgian coast. We will look at differences in migration routes and stopover locations, between adults and juveniles and look at specific behaviours such as site revisiting to see if there are age related differences here. We can also use weather data to support the GPS data, by identifying potential causes of specific behaviours.This project is data based and relies on the use of R and QGIS.

**Doelstelling:**

**Locatie:**

**Onderwerp voorbehouden voor Lars Vandenhaute**

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## 48280: Invloed van droogtestress op de radiale groei bij Sorbus aucuparia (gewone lijsterbes)

Promotor(en): Jan Van Uytvanck
Begeleider(s): 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:**

De huidige klimaatverandering zal meer droogteperiodes met zich meebrengen, mogelijks met negatieve gevolgen voor bomen en struiken.

**Doelstelling:**

De studie heeft tot doem om de reacties van houtige planten op hevige droogteperiodes bete rte begrijpen.

Als modelsoort wordt hier de gewone lijsterbes gebruikt. Driejarige planten in pot worden in gecontroleerde serrecondities aan een eenmalige droogteperiode (geen watergift) onderworpen.

De droogteperiode duurt tot verschillende niveaus van zichtbare droogtestress symptomen ontwikkeld zijn. Planten worden uit de droogte gehaald en recuperatie wordt gemonitord. Met dendrometers wordt de diameter van de stammetjes tijdens en na het volledige proces opgevolgd.

Ook chlorophylgehalte in de (overlevende) bladeren wordt opgevolgd.

Het praktische werk (serreproef) gaat door in Geraardsbergen (gebouwen INBO) in juli, met opvolging van augustus tot oktober.

### Locatie:

INBO Geraardsbergen / thuis

### Samenwerking met bedrijf of non-profit organisatie

Bedrijf: Instituut voor Natuur- en Bosonderzoek (INBO)
Samenwerking: begeleider

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## 48475: Kan jarenlang regulier maaibeheer leiden tot een afname van de biodiversiteit?

| | |
|---|---|
| Promotor(en): | Jan Van Uytvanck |
| Begeleider(s): | Jan Wouters |
| Contactpersoon: | Jan Wouters |
| 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:

Voor het instandhouden van soortenrijke vegetaties van open milieus is het een standaardpraktijk om de vegetatie jaarlijks te maaien gecombineerd met het afvoeren van het maaisel. Deze beheervorm beïnvloedt niet alleen de concurrentieverhoudingen tussen planten, maar zorgt ook voor het verwijderen van allerlei stoffen, waaronder nutriënten, uit het milieu. In een milieu dat onder druk staat van eutrofiëring (historisch landgebruik, atmosferische depositie, voedselrijk water) is dat een bewuste keuze en meestal ook een nodige voorwaarde om de soortenrijkdom van deze vegetaties te behouden.

### Doelstelling:

De te onderzoeken hypothese is dat onder bepaalde voorwaarden op lange termijn deze beheervorm nadelig kan zijn t.a.v. de botanische soortenrijkdom.

We willen bestuderen welke factoren hierin een rol spelen en hoe ze dat doen. Aangezien verschillende factoren de soortenrijkdom beïnvloeden, waaronder ook factoren die onafhankelijk zijn van het maaibeheer, zoals dispersie en hydrologie, zal het onderzoek deze externe factoren zoveel mogelijk onder controle moeten houden.

Men kan opteren voor een experimenteel onderzoek waarbij potexperimenten worden toegepast op enkele kenmerkende plantensoorten: men controleert alle omgevingsvariabelen, waardoor de factoren die gekoppeld zijn aan maaibeheer, namelijk een fysische beschadiging en een export van stoffen kunnen bestudeerd worden.

Een andere optie is de behandeling van één of meer concrete gevalstudies.

In het Torfbroek, een gebied met zeer goed ontwikkelde schraalland-vegetaties, neemt men op een van de langst beheerde percelen sinds +/- 2020 een stelselmatige achteruitgang waar. Dit vertaalt zich in het verdwijnen of vegetatief blijven van kenmerkende soorten (zoals orchideeën, blauwe knoop, karwijselie, schubzegge, ...). Aan het beheer, een jaarlijkse maaibeurt met afvoer, is in de loop der jaren niets veranderd. In terreindelen die iets droger gelegen zijn, in de rand van struiken of die minder frequent gemaaid worden, is dat verarmingsproces zichtbaar minder uitgesproken.

In het gebied kunnen verarmde en nog goed ontwikkelde zones met een vergelijkbare hydrologie vergeleken worden op bodemchemisch vlak. Hierbij zal de beschikbaarheid van nutriënten (stikstof, fosfor, kalium), buffering, zuurtegraad, redoxpotentiaal en aanwezigheid van sulfiden onder de loupe genomen worden.

De student zal vegetatie-opnamen maken en water- en bodemstalen nemen. Op kantoor zal de student ervaring opdoen met software voor databeheer, -verwerking en statistiek. Literatuurstudie zal zich toespitsen op de abiotiek van het habitattype en kenmerkende soorten. Begeleiding wordt voorzien bij het terreinwerk, de verwerking en interpretatie van de gegevens.

**Locatie:**

Veldwerk: Torfbroek (Kampenhout); Labowerk : UGent en/of INBO (Brussel)

**Samenwerking met bedrijf of non-profit organisatie**

Bedrijf: Instituut voor Natuur- en Bosonderzoek (INBO)
Samenwerking:

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## 48435: Life history of thornback ray (Raja clavata) and blonde ray (Raja brachyura) in the western waters and English Channel

| | |
|---|---|
| Promotor(en): | Marleen De Troch |
| Begeleider(s): | Damian Villagra, Laura Lemey |
| Contactpersoon: | Damian Villagra |
| 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:**

Rays are mainly caught as bycatch in the Belgian beam trawl fisheries targeting sole. Although these species do have commercial value, their total catch represents a rather small economic value compared with key species such as sole and plaice. As a result, skates have not been a priority in fisheries management. Unlike other fish stocks, several skate stocks are grouped under a single Total Allowable Catch for a given area, despite having distinct life-history traits that require species- specific management approaches.

Since 2020, ILVO has collected detailed catch, length, weight, age and maturity data for thornback ray in blonde ray in the western waters, the North Sea and the English Channel.

**Doelstelling:**

This research aims to provide the most up-to-date, species- specific life-history trait parameters for these two ray species and if data allows it model across time. Also stock assessment methods could be explored considering the above acquired knowledge.

Key activities include:

- Performing dataset wrangling and quality control in R
- Producing spatial maps using various shapefiles in R
- Constructing of Length – Weight keys, Growth models (i.e. Von Bertalanffy), maturity ogives, longevity and other if possible, in R.
- Statistical analysis in R
- Conducting a comprehensive literature review

**Locatie:**

Instituut voor Landbouw-, Visserij- en Voedingsonderzoek (ILVO) - Flanders Research Institute for Agriculture, Fisheries and Food

**Opmerkingen:**

Language requirements: English Specific competences required: Some knowledge of R (dplyr, tidyr, ggplot2 packages). The location where the thesis research will take place: ILVO Oostende, Jacobsenstraat 1, 8400 Oostende, but also possible to work remotely. Accommodation possibilities No accommodation is available at the host institute. Housing costs vary depending on location and type of accommodation but typically amount to around 500 euro per month for a single room. Any additional costs to be covered by the student If student is not housed in Ostend, train costs should be covered by the student.

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## 48437: Life-History Insights and Ecosystem Implications of the Common Cuttlefish in Belgian Fishing Grounds

| | |
|---|---|
| Promotor(en): | Marleen De Troch, Sarah Maes |
| Begeleider(s): | |
| Contactpersoon: | Sarah Maes |
| 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 student will support exploratory research on the common cuttlefish (Sepia officinalis) to improve our understanding of the ecosystem changes associated with the increasing presence of cephalopods in Belgian fishing grounds.

**Doelstelling:**

This work aims to clarify the ecological impact of cuttlefish and to generate insights into key life-history parameters that can inform the sustainable management of the species.

Key activities will include:

- Stomach content analysis of cuttlefish
- Age determination of cuttlefish based on different structures (beak, cuttlebone or statoliths)
- Age analysis with the SmartDots software
- Data analysis using software such as R

**Locatie:**

Instituut voor Landbouw-, Visserij- en Voedingsonderzoek (ILVO) - Flanders Research Institute for Agriculture, Fisheries and Food

**Opmerkingen:**

Language requirements: English Specific competences required: Some knowledge of R (dplyr, tidyr, ggplot2 packages). Student should be willing to actively participate in laboratory activities. The location where the thesis research will take place: ILVO Oostende, Jacobsenstraat 1, 8400 Oostende. Accommodation possibilities No accommodation is available at the host institute. Housing costs vary depending on location and type of accommodation but typically amount to around 500 euro per month for a single room. Any additional costs to be covered by the student If student is not housed in Ostend, train costs should be covered by the student.

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## 48436: Life-history traits of brill (Scolphtalmus rombus) and turbot (Scolphtalmus maximus) caught in Belgian fisheries and international demersal surveys.

| | |
|---|---|
| Promotor(en): | Marleen De Troch |
| Begeleider(s): | Damian Villagra |
| Contactpersoon: | Damian Villagra |
| 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:**

Life-history traits such as growth rate, size at maturity, and weight–length relationships are essential for understanding the productivity, resilience, and vulnerability of fish stocks. Although long-term biological data for brill and turbot have been routinely collected through Belgian commercial sampling and international survey programs, these rich datasets have not yet been fully explored or incorporated into formal stock assessments (specially for brill).

**Doelstelling:**

This thesis will investigate long-term and spatial (if feasible) variability in key life-history traits for these species across the Northeastern Atlantic, assess potential drivers and potentially how these could be implemented into stock assessment methods.

Key activities include:

- Extracting data on brill and turbot biological variables.
- Performing dataset wrangling, quality control and analysis in R.
- Construction of Length-Weight keys, Growth models (i.e. Von Bertalanffy), maturity ogives, longevity, and others, if possible, in R.
- Conducting a comprehensive literature review and comparison
- Explore how the estimated parameters can be included into assessment methods (if feasible) and/or spatial-temporal modelling.

**Locatie:**

Instituut voor Landbouw-, Visserij- en Voedingsonderzoek (ILVO) - Flanders Research Institute for Agriculture, Fisheries and Food

**Opmerkingen:**

Language requirements: English Specific competences required: Confident knowledge of R (dplyr, tidyr, ggplot2 packages) and statistical regression (i.e. linear and non-linear regressions). The location where the thesis research will take place: ILVO Oostende, Jacobsenstraat 1, 8400 Oostende, but also possible to work remotely. Accommodation possibilities No accommodation is available at the host institute. Housing costs vary depending on location and type of accommodation but typically amount to around 500 euro per month for a single room. Any additional costs to be covered by the student If student is not housed in Ostend, train costs should be covered by the student.

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## 48512: Life-history-traits of a new invasive goby, Tridentiger bifasciatus, in Flanders

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|---|---|
| Promotor(en): | Rhea Maesele, Sander Jacobs |
| Begeleider(s): | Hugo Verreycken |
| Contactpersoon: | Rhea Maesele |
| 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 northern oriental weatherfish (M. bipartitus) was first recorded in the spring of 2019 in the nature reserve Smeethof near Bocholt (northeast Flanders). Originating from a rapidly expanding source population across the Dutch border, the species has now occupied nearly all brook valleys between Bocholt and the Netherlands, and has also found its way into the river Lossing. This river harbours one of the last remaining relic populations of the critically endangered native European weatherfish (M. fossilis) in Belgium.
The establishment of M. bipartitus poses potential threats to native aquatic fauna through mechanisms such as competitive exclusion, hybridization, and the transmission of non-native diseases. Initial sampling with small double fyke nets revealed high catches of M. bipartitus (&gt;100 individuals per fyke) and a specific fishery campaign by volunteers on strategic locations was launched in 2021 as an Early Detection Rapid Response (EDRR) measure to repress their numbers and further spread. Ecological and life-history data of this rarely studied fish is however largely lacking.

**Doelstelling:**

This thesis aims to characterize key life history traits of M. bipartitus in Flanders, including growth patterns, diet composition, reproductive biology, and population structure. The obtained data will improve our understanding of its invasive success and potential ecological impact with the native M. fossilis.

The practical work implies biometric measurements, dissections, (stereo)microscopic analyses, identification/quantification of different food items, fecundity analysis and occasionally contributing to fieldwork.

**Locatie:**

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## 48254: Linking microbiome and physicochemical soil parameters to optimize nitrification inhibition

| | |
|---|---|
| Promotor(en): | Tom Beeckman, Caroline De Tender |
| Begeleider(s): | Hans Motte, Fabian Beeckman |
| Contactpersoon: | |
| 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:**

Nitrification (the conversion of ammonium into nitrate) is an undesirable microbial process in soil: unlike ammonium, nitrate easily leaches through the soil, making it unavailable for plant uptake and contributing to environmental eutrophication. Nitrate can also be converted into nitrous oxide ($N_2O$), a potent greenhouse gas. Therefore, inhibiting nitrification could be beneficial on multiple levels, including reducing the frequency and/or dosage of fertilizer applications. However, the efficacy of nitrification inhibitors is highly dependent on various physicochemical soil parameters. It is hypothesized that these parameters influence the composition of the soil microbial community, which in turn affects the efficacy of different inhibitors. Previous studies often used a limited number of soils and inhibitors to estimate which soil parameters are the main determinants of nitrification (and inhibition) efficacy.

**Doelstelling:**

In this project, we aim to elucidate these determinants using a miniaturized, high-throughput soil assay developed in the VIB-UGent lab of Prof. Tom Beeckman, along with more than 100 agricultural soils whose microbiomes and physicochemical parameters were analyzed by the lab of Prof. Caroline De Tender. By testing different nitrification inhibitors, including both novel and benchmark inhibitors, across all these soils, we aim to gain deeper insights and establish stronger correlations between nitrification (and inhibition) efficacy, soil physicochemical properties, and the soil microbiome. Furthermore, a metagenomics experiment was conducted on two different agricultural soils treated with several nitrification inhibitors, either individually or in combination. Bioinformatic analysis of the resulting data will be used to uncover the effects on key functional genes involved in the complete nitrogen cycle. These results could finally be validated through growth experiments and RT-qPCR analysis on bacterial cultures, as well as through greenhouse gas measurements from soil.

**Locatie:**

VIB-UGent Center for Plant Systems Biology, Technologiepark 71, 9052 Zwijnaarde

**Website:**

Meer informatie op: www.beeckmanlab.be/research/nutrients-and-small-molecule-screening

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## 48340: Linking Models and Ecosystems: A Comparative Study of Quantitative Food Webs in the Belgian North Sea

| | |
|---|---|
| Promotor(en): | Ulrike Braeckman |
| Begeleider(s): | Martha Stevens, 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:**

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. Two of the most widely used approaches to study food webs are Ecopath with Ecosim (EwE) and Linear Inverse Models (LIM). Both methods combine limited field data with ecological principles to quantify the flow of energy or matter throughout the food web, but there are some differences in methodology and application. In this thesis topic, the student will do a comparative study of the two methods using the same dataset, originating from the Belgian part of the North Sea.

The seabed of the Belgian Part of the North Sea consists mainly of sandy substrates, with exceptions such as artificial hard substrates created by offshore wind farms and natural hard substrates like gravel beds. Hard substrates enhance habitat complexity and species richness, providing important ecosystem functions.

**Doelstelling:**

In this master thesis at Ghent University's Marine Biology Research Group (MarBiol), the student will explore the complementarities between EwE and LIM. The project involves building an Ecopath food web model for either an artificial or natural hard substrate habitat in the Belgian Part of the North Sea and comparing it to an existing LIM model from the same area. This comparison will provide new insights into how the two approaches differ and what these differences imply for ecosystem functioning. The work will include data compilation, model construction in Ecopath, and network analysis, offering valuable experience in ecological modelling and ecosystem assessment.

**Locatie:**

Campus Sterre

**Opmerkingen:**

Knowledge of R software is important and experience in network or modelling techniques is an asset. Depending on ongoing field campaigns, there may be an opportunity to participate in a research cruise aboard the RV Simon Stevin during the summer months to sample a wind turbine site in the Belgian Part of the North Sea.

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## 48006: Local Adaptation and Phenotypic Plasticity in Coastal Defence: A European Reciprocal Transplant Experiment with Marram Grass (Ammophila arenaria)

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|---|---|
| Promotor(en): | Frederik Van Daele, Dries Bonte |
| Begeleider(s): | Jiayue Yan |
| Contactpersoon: | Frederik Van Daele |
| 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 dunes are critical Nature-based Solutions that provide essential coastal protection services. This function is largely driven by ecosystem engineering plants, particularly marram grass (Ammophila arenaria), which trap sand and stabilize the coastline through a process known as biomorphogenic feedback. However, these vital ecosystems are under increasing threat from climate change, including rising sea levels, altered precipitation patterns, and more intense storms.

These climate-driven pressures can trigger ecological and evolutionary mismatches when the pace of environmental change exceeds a plant population's ability to adapt. For example, a plant's adaptive response to increased drought might involve shifting resources from shoots (critical for sand capture) to roots (for water uptake), which could inadvertently weaken its dune-building capacity and compromise the entire ecosystem's resilience. This potential for maladaptation can disrupt the delicate biomorphogenic feedbacks, creating a negative loop that degrades coastal protection.

While we know these processes are critical, our understanding of these geo-evolutionary dynamics and their potential tipping points remains incomplete. This knowledge gap is a significant barrier to predicting how our coastal defenses will fare and to implementing effective climate adaptation strategies like assisted migration. This Master's thesis directly addresses this gap by contributing to the DUNELIFE project. By monitoring a key site within a large-scale European reciprocal transplant experiment, this research will provide crucial empirical data on how different marram grass populations perform outside their native environment, offering direct insight into their local adaptation and potential for maladaptation under novel climatic and disturbance conditions.

**Doelstelling:**

The overarching objective of this Master's thesis is to address the critical uncertainty in predicting coastal ecosystem responses to climate change by providing a mechanistic understanding of plant-driven dune dynamics. This research will specifically aim to disentangle the interplay between local adaptation, phenotypic plasticity, and ecosystem engineering in the keystone species, Ammophila arenaria. To achieve this, the student will assume responsibility for the comprehensive data collection at a key European reciprocal transplant site. The goal is to generate a unique, high-resolution dataset that empirically connects plant biological responses to their geomorphological consequences.

The core of the investigation will involve a detailed assessment of plant performance and functional traits. The student will rigorously quantify fitness differentials among populations by measuring key proxies such as survival rates, biomass accumulation, and reproductive output. Concurrently, the project will characterize the plasticity of functional 'engineering' traits, documenting how plant architecture and resource allocation patterns shift in response to novel environmental pressures. This component is designed to reveal the fundamental biological mechanisms that govern a population's capacity to cope with environmental change.

A primary innovation of this thesis is the integration of plant-level measurements with landscape-scale processes. The student will leverage high-resolution topographic data, derived from periodic drone surveys, to quantify the expression of the plant's extended phenotype. This involves precise volumetric analysis of sand accretion and erosion at the scale of individual plants, thereby translating the concept of ecosystem engineering into a measurable geomorphological impact. This methodological approach provides a direct link between a plant's genetic origin, its expressed phenotype, and its functional role in dune formation.

The synthesis of these integrated datasets, comprising fitness metrics, trait plasticity, and geomorphological impact, will culminate in a robust and direct test of the local adaptation hypothesis. The findings will contribute significantly to the fields of evolutionary ecology and biogeomorphology. Furthermore, the results are expected to yield actionable knowledge to inform evidence-based coastal management, particularly regarding the viability of strategies such as assisted migration for enhancing the climate resilience of coastal defense systems.

**Eerste pagina van PDF:**

# Local Adaptation and Phenotypic Plasticity in Coastal Defence: A European Reciprocal Transplant Experiment with Marram Grass (*Ammophila arenaria*)

## Rationale and Problem Statement

Coastal dunes are critical Nature-based Solutions that provide essential coastal protection services. This function is largely driven by ecosystem engineering plants, particularly marram grass (*Ammophila arenaria*), which trap sand and stabilize the coastline through a process known as biomorphogenic feedback. However, these vital ecosystems are under increasing threat from climate change, including rising sea levels, altered precipitation patterns, and more intense storms.

These climate-driven pressures can trigger **ecological and evolutionary mismatches** when the pace of environmental change exceeds a plant population's ability to adapt. For example, a plant's adaptive response to increased drought might involve shifting resources from shoots (critical for sand capture) to roots (for water uptake), which could inadvertently weaken its dune-building capacity and compromise the entire ecosystem's resilience. This potential for **maladaptation** can disrupt the delicate biomorphogenic feedbacks, creating a negative loop that degrades coastal protection.

While we know these processes are critical, our understanding of these geo-evolutionary dynamics and their potential tipping points remains incomplete. This knowledge gap is a significant barrier to predicting how our coastal defenses will fare and to implementing effective climate adaptation strategies like assisted migration. This Master's thesis directly addresses this gap by contributing to the DUNELIFE project. By monitoring a key site within a large-scale European reciprocal transplant experiment, this research will provide crucial empirical data on how different marram grass populations perform outside their native environment, offering direct insight into their local adaptation and potential for maladaptation under novel climatic and disturbance conditions.

## Goal

The overarching objective of this Master's thesis is to address the critical uncertainty in predicting coastal ecosystem responses to climate change by providing a mechanistic understanding of plant-driven dune dynamics. This research will specifically aim to disentangle the interplay between local adaptation, phenotypic plasticity, and ecosystem engineering in the keystone species, *Ammophila arenaria*. To achieve this, the student will assume responsibility for the comprehensive data collection at a key European reciprocal transplant site. The goal is to generate a unique, high-resolution dataset that empirically connects plant biological responses to their geomorphological consequences.

The core of the investigation will involve a detailed assessment of plant performance and functional traits. The student will rigorously quantify fitness differentials among populations by measuring key proxies such as survival rates, biomass accumulation, and reproductive output. Concurrently, the project will characterize the plasticity of functional 'engineering' traits, documenting how plant architecture and resource allocation patterns shift in response to novel

*Download full PDF*

**Locatie:**

campus Ledeganck, coastal transplant site

**Opmerkingen:**

This Master 's thesis will contribute to a long-term, multi-year reciprocal transplant experiment. The student 's role will be to manage one of the experimental sites and conduct a comprehensive analysis of the plant responses throughout the first full growing season. The methodology integrates non-destructive monitoring with a strategically limited destructive sampling campaign to ensure the long-term integrity of the core experiment. Throughout the growing season, the student will perform regular non-destructive monitoring. This involves measuring key fitness proxies (survival, height, tiller count) and physiological indicators. A central component of this monitoring is the analysis of high-resolution topographic data from periodic drone surveys. The student will process this data using Structure-from-Motion (SfM) techniques to generate sequential Digital Elevation Models (DEMs). From these DEMs, they will calculate volumetric sand changes around each plant, providing a direct, non-invasive metric of its ecosystem engineering performance. At the conclusion of the first year 's growing season, a partial and targeted destructive harvest will be conducted. This harvest will be limited to a specific, pre-determined subset of replicate plants designated for annual sampling. This approach allows for the collection of critical data on above- and below-ground biomass and root-to-shoot allocation without compromising the continuation of the overall experiment. The final stage will involve the integrated statistical analysis of all field, remote sensing, and laboratory data to provide a comprehensive assessment of the first-year adaptation and performance of the transplanted populations.

Onderwerp voorbehouden voor Jacob Cogen

*Deze masterproef werd reeds 1-maal toegekend!*

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## 48434: Long-term changes in reproductive dynamics of commercial flatfish.

| | |
|---|---|
| Promotor(en): | Marleen De Troch |
| Begeleider(s): | Karen Bekaert |
| Contactpersoon: | Karen Bekaert |
| 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:

Understanding how reproductive traits shift over time is essential for assessing the resilience and productivity of fish stocks. One key indicator of fecundity is the gonadosomatic index, which captures how reproductive investment varies seasonally and across years. ILVO has built a valuable long-term dataset by regularly collecting life-history parameters of commercially important flatfish species.

### Doelstelling:

This research line investigates changes in the peak gonadosomatic index, shifts in maturity onset, and seasonal distribution patterns. Using two decades of data, it examines how reproductive characteristics have evolved over time, with a particular focus on plaice (Pleuronectes platessa).

Key activities include:

- Compiling historical data.
- Performing dataset wrangling and quality control in R
- Statistical analysis in in R
- Conducting a comprehensive literature review

### Locatie:

Instituut voor Landbouw-, Visserij- en Voedingsonderzoek (ILVO) - Flanders Research Institute for Agriculture, Fisheries and Food

### Opmerkingen:

Language requirements: English Specific competences required: Some knowledge of R (dplyr, tidyr, ggplot2 packages). The location where the thesis research will take place: ILVO Oostende, Jacobsenstraat 1, 8400 Oostende, but also possible to work partly remotely. Accommodation possibilities No accommodation is available at the host institute. Housing costs vary depending on location and type of accommodation but typically amount to around 500 euro per month for a single room. Any additional costs to be covered by the student If student is not housed in Ostend, train costs should be covered by the student.

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## 48433: Long-term changes in the demersal community of the southern North Sea.

| | |
|---|---|
| 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 |

Aantal masterproeven: 1
Motivering voor deze opleiding:

**Probleemstelling:**

The shallow southern North Sea has undergone a series of rapid ecological and environmental changes over the past decade, driven both by increasingly evident climate-change effects and the accelerated development of offshore wind farms. Since 1993, ILVO Belgium has conducted a fisheries-independent beam-trawl survey, monitoring 62 fixed stations across the southern North Sea. These stations, situated along the eastern UK coastline, encompass key spawning and nursery areas for sole (Solea solea). While fish populations are well monitored, considerably less attention has been directed toward understanding long-term dynamics within the epibenthic community.

**Doelstelling:**

This research line focuses on analysing a long time of survey data to investigate long-term ecological changes in the region and to identify the key drivers underlying these patterns.

Key activities include:

- Compiling historical data on offshore wind farms and relevant abiotic parameters
- Performing dataset wrangling and quality control in R
- Producing spatial maps using various shapefiles in R
- Conducting a comprehensive literature review

**Locatie:**

Instituut voor Landbouw-, Visserij- en Voedingsonderzoek (ILVO) - Flanders Research Institute for Agriculture, Fisheries and Food

**Opmerkingen:**

Specific competences required: Some knowledge of R (dplyr, tidyr, ggplot2 packages). Accommodation possibilities No accommodation is available at the host institute. Housing costs vary depending on location and type of accommodation but typically amount to around 500 euro per month for a single room. Any additional costs to be covered by the student If student is not housed in Ostend, train costs should be covered by the student.

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## 48244: Microbial community dynamics in Greenlandic fjords with contrasting glacial influence

| | |
|---|---|
| Promotor(en): | Koen Sabbe, Lorenz Meire |
| Begeleider(s): | Willem Stock, 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:**

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). Direct subsurface meltwater release by MTGs into a fjord promotes nutrient upwelling, 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. 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 on the pelagic microbial ecosystem remain poorly understood.

**Doelstelling:**

The aim of this thesis is to resolve the microbial diversity and community structure in Greenlandic fjords with contrasting glacial influence: one fjord with marine-terminating glaciers (MTGs) and one with land-terminating glaciers (LTGs), 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 DNA metabarcoding and Imaging Flow Cytometry to investigate how the impact of MTGs vs. LTGs shapes 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:**

Lab. Protistology & Aquatic Ecology, Sterre S8; Campus Ledeganck

**Website:**

Meer informatie op: canoe.marinetraining.eu/

**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. Since the samples have already been collected, this thesis will not involve any fieldwork. Some laboratory work will be required for processing the samples; however, the majority of the thesis will focus on computational analyses, including bioinformatics and modelling, and interpretation of the data in an environmental framework. An interest in programming is therefore desirable.

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## 48287: Mind your fossils: integrating ancient morphology in phylogenetics and biogeography of a pantropical plant family

| | |
|---|---|
| Promotor(en): | Lars Chatrou |
| 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:**

Dated phylogenetic trees (chronograms) are essential tools for reconstructing the past natural history of organisms. They are central to biogeographical and evolutionary research because they allow us to infer when key events - such as speciation, dispersal, or adaptive radiations - took place.

A critical step in molecular dating is the use of calibration points, typically derived from fossils or well-dated geological events (e.g., continental break-ups or island emergence). In most studies, fossil calibrations rely on expert interpretation, which inevitably introduces some degree of subjectivity. Different interpretations of the same fossils or geological events can lead to markedly different age estimates for evolutionary events. As a result, downstream analyses - such as ancestral area reconstruction or estimates of evolutionary rates - may inherit these uncertainties and potentially become biased.

One way to understand this uncertainty is to compare different molecular-dating models. Another, equally important aspect is to improve the quality and justification of fossil calibration points themselves. In the pantropical plant family Annonaceae, fossilized seeds provide crucial calibration data. However, determining which morphological characters are truly homologous between fossil seeds and extant species or clades is challenging.

This MSc project will use state-of-the-art techniques, including high-resolution CT scanning of seeds, to compare fossil and modern Annonaceae and identify reliable morphological characters for total-evidence dating.

The Annonaceae (ca. 2500 species) are a diverse family of basal angiosperms with a pantropical distribution and play a major ecological role in tropical rain forests. Several studies have explored how and when the family attained its modern distribution, but none has yet applied a total-evidence framework combining molecular and fossil morphological data. The availability of well-documented Eocene fossil seeds and extensive molecular datasets makes this an ideal system for such an approach.

**Doelstelling:**

In this project, the student will:

- Study seed morphology of fossil and extant Annonaceae and identify homologous characters.
- Generate a dated phylogeny of Annonaceae, integrating the studied fossils and existing molecular data sets, while using a total-evidence approach.
- Reconstruct the biogeographical history (ancestral areas) of the family.

This project suits a student with a strong interest in evolution, phylogenetics, and plant morphology. The student will gain hands-on experience with modern methods for integrating fossil morphology into phylogenetic analyses, including CT-based imaging and a range of computational tools and software.

The results will be written in the format of a scientific article, with the goal of submitting it to a peer-reviewed journal.

**Locatie:**

**Onderwerp voorbehouden voor Alex Saniz Balderrama**

*Deze masterproef werd reeds 1-maal toegekend!*

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## 48289: Modifying demersal trawls to mitigate impacts on unwanted catches and improve product quality

| | |
|---|---|
| Promotor(en): | Sebastian Uhlmann, Adelbert De Clercq |
| Begeleider(s): | Mattias Van Opstal |
| Contactpersoon: | Sebastian Uhlmann |
| 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 Belgian beam trawl sector is a socio-economic important part of the Belgian fisheries. This type of fisheries focusses on demersal and benthic sepcies such as flatfish. Plaice and brill are two economically important species the Belgian beam trawlers target. However, undersized fish as well as untargeted fish species (called bycatch) are caught during beam trawl fishing. When fish come on board of the fishing vessels, they are sorted. Although undersized fish are sorted out, and thrown back into the water together with some bycatch (fish that do not fall under the landing obligation laws), survivablity of fish that enter the water may be low. In addiition, classing beam trawl fishing with on board sorting my impact the fish freshness and quality before it can be processed and brought unto the marked. Summarised, bycatch, survivability of fish the re-enter the water and product quality are challenges that the Belgian beam trawl fleet faces.

**Doelstelling:**

The VivaVis project aims to advance sustainable fisheries by investigating the survival and product quality of undersized flatfish—specifically tongschar (plaice) and griet (brill)—within the Belgian beam trawl sector. Central to this research is the evaluation of modified fishing gear and operational practices designed to minimize unwanted bycatch (protected elasmobranch species) and enhance the quality of marketable catches.

The conservation importance of this work lies in its dual approach: first, by quantifying the survival rates of discarded undersized fish, the project provides scientific evidence to support exemptions from the EU landing obligation, which otherwise mandates the landing of all catches, including non-target and undersized species. High survival rates, achieved through gear modifications and improved handling, can justify such exemptions, reducing unnecessary mortality and supporting healthier fish stocks.

Second, the project assesses how changes in gear and sorting processes affect the freshness and quality of landed fish. By correlating product quality indicators (such as KIM score, TVB analysis, and pH) with operational parameters (depth, water temperature, tow duration, sorting time), the research demonstrates that conservation-oriented practices can also deliver economic benefits—higher quality fish fetch better market prices and reduce waste.

Innovative data collection, including onboard sensors and AI-driven image analysis, enables precise monitoring of fish welfare and injury. The project's outcomes will inform policy advice, promote selective fishing practices, and contribute to the ecological, social, and economic sustainability of the sector. Ultimately, VivaVis exemplifies how targeted gear modifications can reconcile conservation goals with industry needs, fostering resilient marine ecosystems and responsible seafood production.

**Locatie:**

InnovOcean campus (ILVO-MARIEN, Oostende)

**Samenwerking met bedrijf of non-profit organisatie**

Bedrijf: Research Institute for Agriculture, Fisheries and Food (ILVO)
Samenwerking: promotor

**Onderwerp voorbehouden voor Monia Meerpoel**

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## 48333: Mussel reefs on sandy sediments: carbon sinks or sources?

| | |
|---|---|
| Promotor(en): | Ulrike Braeckman |
| Begeleider(s): | Martha Stevens |
| Contactpersoon: | Martha Stevens |
| 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 presence of mussel reefs on soft sediments affects carbon cycling through a variety of counteracting processes, which has made the assessment of their potential as a carbon sink or source heavily debated. Respiration and shell formation release $CO_2$ into the water column, whereas shell dissolution decreases $pCO_2$ and biodeposition can enable carbon burial in the sediment. By combining data from in situ samples with laboratory experiments, we aim to quantify the impact of these processes on the carbon cycle and determine whether mussel reefs act as a carbon source or sink.

**Doelstelling:**

During this master thesis at Ghent University's Marine Biology Research Group (MarBiol), the student will investigate the impact of subtidal mussel reefs on benthic carbon cycling in the Belgian North Sea. The project will include laboratory work (e.g. DIC flux measurements, carbon content of sediment…) and data analysis. Depending on field campaign timing, there may also be the opportunity to participate in a research cruise aboard the RV Abbé Mann.

**Locatie:**

campus Sterre - S8

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## 48482: Optimalisatie van Europese nori kweek (1): maturatieprocessen

| | |
|---|---|
| Promotor(en): | Olivier De Clerck |
| 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:**

(NL) Nori, wereldwijd bekend als voedsingproduct, wordt momenteel geproduceerd met Aziatische roodwieren uit het geslacht Pyropia. De Europese zeewierteelt staat echter nog in haar kinderschoenen. Voor de nori productie in Europa vooruit te helpen is het doorgronden van de kweekomstandigheden die de sporofytfase (ook wel conchocelis genoemd) aanzetten tot het produceren van fertiele structuren (conchosporangia) van belang.

(EN) Nori, known worldwide as a food product, is currently produced using Asian red seaweeds from the genus Pyropia. European seaweed cultivation, however, is still in an early developmental stage. To advance nori production in Europe, it is important to understand the cultivation conditions that trigger the sporophyte phase (the conchocelis) to produce fertile structures (conchosporangia).

**Doelstelling:**

(NL) Deze masterproef richt zich op de beschrijving van de maturatie van de conchocelis fase van Europese Porphyra soorten, met het ook op het verbeteren van de Europese teelt. Dit project omvat zowel microscopisch werk (het verkrijgen van duidelijke microscopische beelden van de verschillende maturatiestadia van de conchocelis) en experimenteel werk (het fotoperiodische effect op de vorming van de fertiele structuren en de biochemische karakterisatie van deze structuren). Afhankelijk van de interesse van de student kan de experimentele insteek flexibel worden ingevuld.

(EN) This thesis focuses on describing the maturation of the conchocelis phase in European Porphyra species, with the aim of supporting and improving European cultivation efforts. The project includes both microscopy (obtaining clear images of the different maturation stages of the conchocelis) and experimental work (studying the effect of photoperiod on the formation of fertile structures and carrying out biochemical characterisation of these structures). The experimental component can be adapted depending on the student’s interests.

**Locatie:**

Sterre S8

**Website:**

Meer informatie op: https://phycology.ugent.be/

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## 48483: Optimalisatie van Europese nori kweek (2): kruisingen

| | |
|---|---|
| Promotor(en): | Olivier De Clerck |
| 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:**

(NL) Nori, wereldwijd bekend als voedingsprduct, wordt momenteel geproduceerd met Aziatische roodwieren uit het geslacht Pyropia. De strains gebruikt in de commerciale kweek zijn het resultaat van decennialange (on)bewuste selectie op groei, smaak en kleur kenmerken. De Europese zeewierteelt staat echter nog in haar kinderschoenen. Hoewel we steeds meer inzicht krijgen in de levenscyclus, biochemische samenstelling en optimale kweekomstandigheden van Europese Porphyra soorten, ontbreekt één cruciale stap: het doelgericht selecteren en verbeteren van strains. Een potentieel veelbelovende strategie hiervoor is het uitvoeren van gecontroleerde kruisingen.

(EN) Nori, known worldwide as a food product, is currently produced using Asian red seaweeds from the genus Pyropia. The strains used in commercial production are the result of decades of (un)intentional selection for traits such as growth, flavour and colour. European seaweed cultivation, however, is still developing. Although progress has been made in understanding the life cycle, biochemical composition and cultivation requirements of European Porphyra species, one crucial step is still missing: the targeted selection and improvement of strains. Controlled hybridisation is a promising approach to achieve this.

**Doelstelling:**

(NL)Deze masterproef onderzoekt de haalbaarheid van kruisingen om Europese Porphyra strains te verbeteren voor toepassingen in de voeding, nutraceuticals en biostimulanten. De student gaat in de literatuur op zoek naar de meest geschikte kruisingsmethode. Het experimentele werkt omvat het opkweken van verschillende strains en het uitvoeren en evalueren van gecontroleerde kruisingen in het labo. Bij succesvolle kruisingen kan er aanvullend genetisch onderzoek worden uitgevoerd, waarbij moleculaire merkers worden ingezet om de kruisingen te bevestigen. Daarnaast is er mogelijkheid om de ontwikkeling, groei en biochemische kenmerken (zoals pigment concentraties en antioxidant activiteit) van ouderlijke en gekruiste lijnen met elkaar te vergelijken.

(EN) This thesis examines the feasibility of using controlled crosses to improve European Porphyra strains for applications in food, nutraceuticals and biostimulants. The student will review the literature to identify suitable crossing methods. The experimental work involves cultivating different strains and carrying out controlled crosses in the laboratory. If crosses are successful, additional genetic analyses can be performed using molecular markers to confirm hybrid status. There is also the option to compare development, growth and biochemical characteristics (such as pigment concentrations and antioxidant activity) between parental strains and newly obtained hybrids.

**Locatie:**

Sterre S8

**Website:**

Meer informatie op: https://phycology.ugent.be/

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## 48490: 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

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## 48443: 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

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## 48283: Potential Impacts of European Beavers on the Spread of Invasive Plant Species

| | |
|---|---|
| Promotor(en): | Jan Van Uytvanck |
| Begeleider(s): | Frank Huysentruyt |
| Contactpersoon: | Frank Huysentruyt |

| | |
|---|---|
| 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:**

European beavers (Castor fiber), as ecosystem engineers, are well known for their generally positive effects on biodiversity. However, their potential role in facilitating or inhibiting the spread of non-native invasive plant species remains poorly understood. Both positive and negative impacts are plausible, depending on species interactions and habitat modifications.

**Doelstelling:**

This study aims to assess how beavers influence populations of invasive plant species, focusing on water pennywort (Hydrocotyle ranunculoides) and Large flower primrose-willow (Ludwigia grandiflora), within current beaver territories.

The analysis will consider the recent colonization history of beavers in Flanders, as well as field observations including territory mapping, population estimates, and browsing impacts. Comparisons will be made between territories with and without dams to evaluate the role of beaver engineering activities in shaping invasive plant dynamics.

Fieldwork will be conducted in July, August, and September 2026, in selected river valleys of East Flanders. Data collection will include mapping of invasive plant populations, recording beaver activity and dam presence, and assessing potential correlations between beaver-induced habitat modifications and plant spread.

**Locatie:**

veldwerk Oost-Vlaanderen, nog verder af te spreken

**Onderwerp voorbehouden voor Noa Vanholst**

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## 48076: Quantifying the Functional Traits and Environmental Responses of Sea Rocket (Cakile maritima) for Coastal Models

| | |
|---|---|
| Promotor(en): | Frederik Van Daele, Dries Bonte |
| Begeleider(s): | |
| Contactpersoon: | Frederik Van Daele |
| 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:**

Our living dune coastal defences (Nature-Based Solutions) are complex ecosystems. To predict how they will behave, computer models, like Living Dunes, must simulate the biomorphogenic feedback loop. This is the critical, two-way cycle where the plants ("bio") actively build the dune's shape ("morpho"), and that new dune shape, in turn, "feeds back" by creating new conditions that determine how and where the plants can grow. This continuous interaction is the "engine" that builds dunes, and this engine is powered by plants.

So far, our models have focused heavily on the main "builder" species, marram grass (Ammophila arenaria). We have a detailed "character sheet" (a config file) for it, defining all its rules for growth, sand capture, and survival. But Ammophila doesn't start the dune-building process. It needs an "embryo dune" to establish itself on.

That embryo dune is often created by annual pioneer plants. The most important of these is Sea Rocket (Cakile maritima). This tough, succulent plant is the "first responder." It can germinate and survive on the bare beach, trapping the first grains of sand and adding organic matter to the soil. It creates the stable patch that allows the key "ecosystem engineer" to move in.

Here is the problem: We are missing the first chapter of our story. Our models are simulating a dune system without its critical first responder. We have no "character sheet" for Cakile maritima. We don't know its "rules of life."

- What are its key functional traits (e.g., its shape, its root-to-shoot ratio)?
- What are the exact environmental cues that make its seeds germinate?
- How much sand burial can it survive?
- How does it respond to drought or heat?

Without this data, our models are scientifically incomplete. This Master's thesis will solve this problem. It is a biological detective story to find these missing rules.

**Doelstelling:**

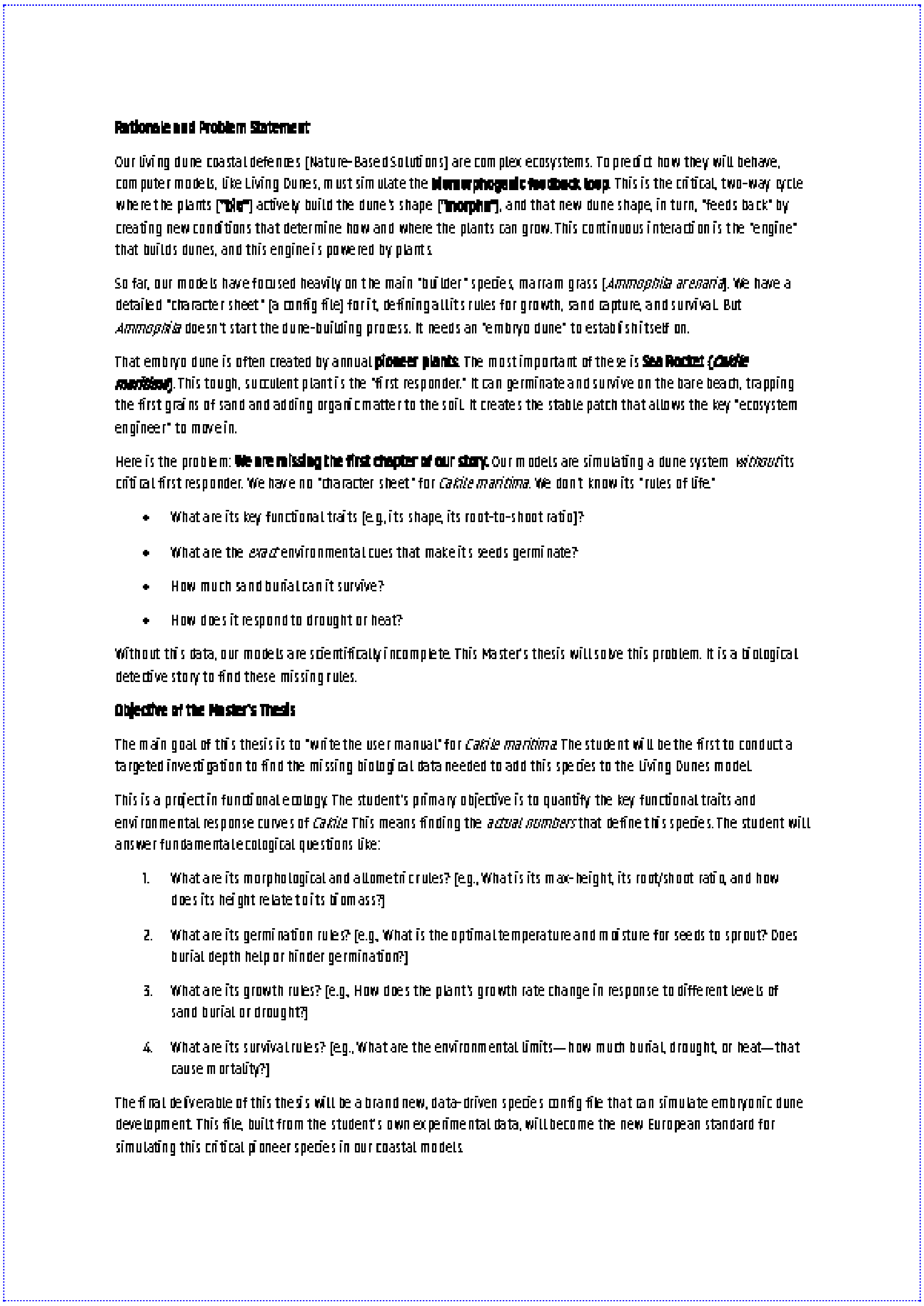
The main goal of this thesis is to "write the user manual" for Cakile maritima. The student will be the first to conduct a targeted investigation to find the missing biological data needed to add this species to the Living Dunes model.

This is a project in functional ecology. The student's primary objective is to quantify the key functional traits and environmental response curves of Cakile. This means finding the actual numbers that define this species. The student will answer fundamental ecological questions like:

1. What are its morphological and allometric rules? (e.g., What is its max-height, its root/shoot ratio, and how does its height relate to its biomass?)
2. What are its germination rules? (e.g., What is the optimal temperature and moisture for seeds to sprout? Does burial depth help or hinder germination?)
3. What are its growth rules? (e.g., How does the plant's growth rate change in response to different levels of sand burial or drought?)
4. What are its survival rules? (e.g., What are the environmental limits—how much burial, drought, or heat—that cause mortality?)

The final deliverable of this thesis will be a brand new, data-driven species config file that can simulate embryonic dune development. This file, built from the student's own experimental data, will become the new European standard for simulating this critical pioneer species in our coastal models.

**Eerste pagina van PDF:**



### Rationale and Problem Statement

Our living dune coastal defences (Nature-Based Solutions) are complex ecosystems. To predict how they will behave, computer models, like Living Dunes, must simulate the **biomorphogenic feedback loop**. This is the critical, two-way cycle where the plants (**"bio"**) actively build the dune's shape (**"morpho"**), and that new dune shape, in turn, "feeds back" by creating new conditions that determine how and where the plants can grow. This continuous interaction is the "engine" that builds dunes, and this engine is powered by plants.

So far, our models have focused heavily on the main "builder" species, marram grass (*Ammophila arenaria*). We have a detailed "character sheet" (a config file) for it, defining all its rules for growth, sand capture, and survival. But *Ammophila* doesn't start the dune-building process. It needs an "embryo dune" to establish itself on.

That embryo dune is often created by annual **pioneer plants**. The most important of these is **Sea Rocket (*Cakile maritima*)**. This tough, succulent plant is the "first responder." It can germinate and survive on the bare beach, trapping the first grains of sand and adding organic matter to the soil. It creates the stable patch that allows the key "ecosystem engineer" to move in.

Here is the problem: **We are missing the first chapter of our story.** Our models are simulating a dune system *without* its critical first responder. We have no "character sheet" for *Cakile maritima*. We don't know its "rules of life."

- What are its key functional traits (e.g., its shape, its root-to-shoot ratio)?
- What are the *exact* environmental cues that make its seeds germinate?
- How much sand burial can it survive?
- How does it respond to drought or heat?

Without this data, our models are scientifically incomplete. This Master's thesis will solve this problem. It is a biological detective story to find these missing rules.

### Objective of the Master's Thesis

The main goal of this thesis is to "write the user manual" for *Cakile maritima*. The student will be the first to conduct a targeted investigation to find the missing biological data needed to add this species to the Living Dunes model.

This is a project in functional ecology. The student's primary objective is to quantify the key functional traits and environmental response curves of *Cakile*. This means finding the *actual numbers* that define this species. The student will answer fundamental ecological questions like:

1. What are its morphological and allometric rules? (e.g., What is its max-height, its root/shoot ratio, and how does its height relate to its biomass?)
2. What are its germination rules? (e.g., What is the optimal temperature and moisture for seeds to sprout? Does burial depth help or hinder germination?)
3. What are its growth rules? (e.g., How does the plant's growth rate change in response to different levels of sand burial or drought?)
4. What are its survival rules? (e.g., What are the environmental limits—how much burial, drought, or heat—that cause mortality?)

The final deliverable of this thesis will be a brand new, data-driven species config file that can simulate embryonic dune development. This file, built from the student's own experimental data, will become the new European standard for simulating this critical pioneer species in our coastal models.

Download full PDF

**Locatie:**

campus Ledeganck, coastal zones

**Website:**

Meer informatie op: frederikvand.github.io/living_dunes/

Onderwerp voorbehouden voor Joran Van den Eynde

*Deze masterproef werd reeds 1-maal toegekend!*

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## 48343: Reducing nitrogen pollution through the identification of biological nitrification inhibitors

| | |
|---|---|
| Promotor(en): | Tom Beeckman, Hans Motte |
| Begeleider(s): | Fabian Beeckman, Alexia Antoniou |
| Contactpersoon: | Alexia Antoniou |
| 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 ($NH_3$) into nitrite ($NO_2^-$) and nitrate ($NO_3^-$). 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 ($N_2O$). 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 validated by assessing their reduction on nitrous oxide emissions in microcosm studies and 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. Further characterization and validation will depend on the progress of the project and the interest of the candidate. Possibly, the effect of the microbiome and the physicochemical soil characteristics on the inhibitor efficacy may be tested by applying different soils in the new soil assay; structure-activity relationships studies may be conducted to assess active substructures and optimize inhibition; or pot experiments with plants to assess the nitrification inhibition potential in a more realistic environment may be performed. 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
- Ammonium and nitrate measurements (spectrophotometry)
- DNA/RNA extraction from soil
- (RT-)-qPCR
- 16S-sequencing
- Pot experiments

**Locatie:**

VIB-UGent Center for Plant Systems Biology

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## 48279: Resilience After Fire: Ecological Recovery Processes in Burned Landscapes

|  |  |
|---|---|
| Promotor(en): | Jan Van Uytvanck |
| Begeleider(s): | Marijke Thoonen |
| Contactpersoon: | Marijke Thoonen |
| 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:**

Many ecosystems depend on fire, but climate change is causing fires to become more intense and frequent.

Management after fire therefore needs to shift from emergency response to a proactive, science-based approach.

### Doelstelling:

This research examines how planned restorative burns compare to uncontrolled wildfires, with the goal of developing resilient landscapes that protect people, nature, and the economy.

Core indicators (soil composition, vegetation structure) are measured in plots located in burned, unburned, and controlled-burn areas in de Mechelse Heide en de Kalmthoutse Heide.

Fire impact and recovery are analysed using statistical models and satellite imagery, linked to management actions and ecosystem traits.

Fieldwork runs from June to September.

### Locatie:

Gent, Mechelse Heide, Kalmthoutse Heide

### Samenwerking met bedrijf of non-profit organisatie

Bedrijf: Instituut voor Natuur- en Bosonderzoek (INBO)
Samenwerking: begeleider

### Onderwerp voorbehouden voor Aline Mesjasz

*Deze masterproef werd reeds 1-maal toegekend!*

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## 48472: Rewilded dunes: does large grazer introduction restores dynamic dunes

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:

Coastal dunes are dynamic ecosystems that provide critical habitats for specialized flora and fauna. Historically, many European dunes have been stabilized through afforestation or intensive management, reducing natural disturbance regimes and leading to succession toward dense grasslands or scrub. This stabilization often results in the loss of early-successional habitats, which are key components of Natura 2000 habitat types such as 2130 (fixed coastal dunes with herbaceous vegetation) and 2120 (shifting dunes along the shoreline with Ammophila arenaria). Rewilding -introducing large herbivores like cattle, horses, or even deer- has emerged as a strategy to restore natural processes. Grazers can create heterogeneity by trampling and grazing, reopening patches of bare sand and reducing dominance of stabilizing species like Ammophila arenaria. This theoretically benefits plant diversity and early-successional species.

### Doelstelling:

This thesis aims to investigate how rewilding with large grazers influences the ecological integrity of coastal dune systems along the Flemish West Coast, with a particular focus on wild bees and wasps. Historically, these dunes were characterized by extensive open habitats maintained by natural disturbances such as wind dynamics and occasional flooding. However, human interventions have significantly reduced these processes, leading to succession toward dense grasslands and scrub. These changes have profoundly affected the availability of nesting substrates and foraging resources for arthropods, especially wild bees (Apidae) and wasps (Vespidae, Sphecidae), which depend on bare sand for nesting and diverse floral assemblages for food. Rewilding initiatives that introduce large herbivores aim to reverse this trend by creating structural heterogeneity and reopening patches of bare sand. This study will quantify how such interventions alter vegetation composition and structure compared to original open dunes, and assess whether these changes align with Natura 2000 habitat types such as 2120 (shifting dunes) and 2130 (fixed dunes with herbaceous vegetation). Furthermore, it will evaluate the diversity and community composition of wild bees and wasps in rewilded versus stabilized dunes, testing whether rewilding effectively restores key microhabitats critical for these taxa. Finally, the research will explore how habitat heterogeneity relates to functional traits such as nesting strategy and diet breadth, and determine whether rewilding supports species of conservation concern or primarily favors generalist species.

**Locatie:**

**Onderwerp voorbehouden voor Liam Welsh**

*Deze masterproef werd reeds 1-maal toegekend!*

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## 48425: Scaling patterns in squamates: a comparative analysis with a focus on burrowing adaptations

| | |
|---|---|
| Promotor(en): | Dominique Adriaens, Anthony Herrel |
| Begeleider(s): | Morgane Taillades |
| Contactpersoon: | Morgane Taillades |
| 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 squamates, the skin is the first barrier with the external environment and plays essential roles including camouflage, locomotion, regulation of body temperature and water balance, and protection against physical damage. This skin is organized into scales, those arrangements, known as pholidosis, shows remarkable diversity in size, shape, and organization. Moreover, scaling patterns vary not only among species but also across body regions, suggesting functional specialization.

In burrowing species, the skin even experiences more specific and extensive mechanical constraints, such as friction and substrate resistance forces, so that it can be expected that skin properties and scale morphology and patterning may influence burrowing performance. Limbless squamates, where the entire body circumference interacts with the soil during underground locomotion, not only exhibit increased contact with the substrate compared to their limbed counterparts but also rely on the friction for forward underground movement. The skin must thus be resistant to environmental constraints while preserving other essential functions, such as freedom of movement.

**Doelstelling:**

Few studies have quantified scaling patterns across squamates or explored their link to burrowing strategies. This project aims to fill that gap by characterizing scaling patterns in a representative group of squamates and identifying adaptations associated with burrowing life strategies. The objectives are:

- To describe scale traits qualitatively and quantitatively (shape, orientation, surface topography, overlap, density…). Different methods (photogrammetry, 3D laserscanning, µCT scanning) will be used to quantify skin shape
- To test mechanical properties of the skin (elasticity, friction resistance) and relate these to ecological variables such as degree of fossoriality and substrate type.
- To identify morphological adaptations from phylogenetic heritage.

**Locatie:**

campus Ledeganck, onderzoeksgroep Evolutionary Morphology of Vertebrates

**Website:**

Meer informatie op: www.ugent.be/we/biology/evo-morph/en/research/projects/project_now/hfsp_amphisbaenia_25

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## 48513: Signals in the cloud forest: the evolution of floral scent and colour in a megadiverse orchid tribe

| | |
|---|---|
| Promotor(en): | Lars Chatrou, Kenneth Bauters |
| 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 many flowering plants, successful reproduction depends on the transfer of pollen by animal pollinators such as bees, beetles, flies, or butterflies. Achieving this reliably is no small feat, and floral colour and scent are among the key signals plants have evolved to attract these visitors.

The orchid family (Orchidaceae) is the most species-rich plant family on Earth, with an estimated 25,000-30,000 species distributed worldwide except Antarctica. Its greatest diversity occurs in tropical and subtropical regions, with the Neotropics - particularly cloud forests - representing a major hotspot. Orchid evolutionary success is intimately tied to interactions with pollinators, which range from extreme specialization on a single insect species to more generalised strategies that attract a broad suite of pollinators. While some orchids depend on elaborate forms of mimicry to deceive one highly specific pollinator, others thrive through generalist pollination—an approach that can be especially advantageous in marginal or unpredictable habitats.

The subtribe Pleurothallidinae is one of the largest radiations within Orchidaceae, comprising over 5,000 species primarily distributed throughout the Neotropics, with exceptional richness in the Andean cloud forests of Colombia and Ecuador. Despite this remarkable diversity, pollination data for Pleurothallidinae remain sparse. However, the available evidence suggests that many species are pollinated predominantly by flies (Diptera). Patterns emerging from the literature indicate that flower colour, trichomes, and floral scent together function as key attractants for a wide variety of fly lineages.

Hypothesis

In this MSc project, you will test the hypothesis that key floral traits - particularly flower colour and floral scent - have evolved multiple times independently within Pleurothallidinae. This would indicate that similar floral adaptations reflect convergent evolution in response to pollinator pressures, rather than being inherited from a common ancestor.

**Doelstelling:**

The project will involve assembling comparative floral trait data from both living collections in botanic gardens and from the scientific literature. These data will be analysed in the context of available phylogenies to assess how often similar floral signals have evolved across Pleurothallidinae and how these may be associated with different pollination systems.

The availability of numerous Pleurothallidinae species cultivated in greenhouse collections is a major asset for this project. The Botanic Garden of Ghent University offers access to many species from genera such as Dracula, Pleurothallis, Stelis, and Masdevallia. Additional sampling opportunities exist through nearby collections in Meise, Leiden, and Kew. Collaboration with specialists in Orchidaceae at the Royal Botanic Gardens, Kew, will ensure access to the phylogenetic datasets needed to test the project's main hypothesis.

What you will learn:

- Headspace sampling of floral scent (volatile organic compounds) from living orchid flowers
- Gas chromatography - mass spectrometry (GC-MS) in the Separation Science laboratory (Prof. Frederic Lynen, Faculty of Sciences, Ghent University)
- Data processing: transforming complex scent profiles into trait characters usable for evolutionary analysis
- Phylogenetic comparative methods for testing evolutionary hypotheses

**Locatie:**

Campus Ledeganck & Plantentuin; campus Sterre

**Onderwerp voorbehouden voor Jaro De Nauw**

*Deze masterproef werd reeds 1-maal toegekend!*

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## 48183: Stress in honeybee colonies (Apis mellifera) due to predation by the Asian hornet (Vespa velutina)

| | |
|---|---|
| Promotor(en): | Dirk de Graaf, Dries Bonte |
| Begeleider(s): | Heleen Van Ransbeeck |
| 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.

Since its establishment, V. velutina has spread rapidly and has become a significant threat to both biodiversity and apiculture. The species competes with native wasps for resources, preys upon native insects, and exerts strong predatory pressure on honeybees (Apis mellifera). Its intensive hunting strategy induces a stress response in honeybee colonies, known as “foraging paralysis,” whereby the honeybees no longer forage to protect themselves from being caught by a hornet. This behavioral disruption can lead to reduced foraging efficiency, weakened colonies, and ultimately, impaired pollination services.

Quantitative data on predation frequency and colony-level behavioral responses remain limited. Recent technological advances, such as the BEEP monitoring system, enable automated and non-invasive monitoring of hive performance. In addition, Hall et al. have developed an algorithm capable of distinguishing Yellow-legged hornet sounds from honeybee sounds, offering a novel opportunity to detect predation events acoustically and monitor hornet activity in real time. These tools open new avenues for studying hornet–honeybee interactions and their impact on colony dynamics.

**Doelstelling:**

The aim of this study is to assess the impact of the Yellow-legged hornet (Vespa velutina) on the development and stresslevel of honeybee (Apis mellifera) colonies. Using an innovative sound-based hornet detection system, BEEP monitoring devices, and a knocker–accelerometer system, this research will quantify predation frequency and evaluate its effects on colony performance. Specifically, the study will aim to confirm the occurrence of foraging paralysis in apiaries and identify how hornet activity correlates with changes in colony behavior and development.

**Locatie:**

campus Sterre

**Opmerkingen:**

De student dient in de zomer van 2026 grotendeels beschikbaar te zijn. Met piekseizoen van augustus tot en met oktober.

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## 48492: Synthetic reconstruction of diatom–bacteria interactions in mudflat biofilms

| | |
|---|---|
| Promotor(en): | Willem Stock, Koen Sabbe |
| Begeleider(s): | Willem Stock, Yeseren Kayacan |
| Contactpersoon: | Willem Stock |
| 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, eukaryotic microalgae, are the dominant primary producers in intertidal mudflats. A substantial fraction of the carbon fixed during photosynthesis is released as extracellular polymeric substances (EPS), a complex mixture of polysaccharides and various other organic compounds. Within these biofilms, different bacterial guilds participate in a sequential degradation process. Specialist degraders hydrolyze complex EPS polymers into smaller, more accessible monomers and oligomers. These intermediate products then fuel a second guild of generalist bacteria that rely on simpler substrates. This cross-feeding cascade supports the microbial loop in benthic systems. The diatoms seem to regulate its EPS production and composition to steer the functionality of the bacterial community in its proximity to be beneficial for itself. Deciphering these EPS driven interactions is challenging because it requires not only an understanding of the metabolic capacities of the bacterial partners, but also of the reciprocal feedbacks between diatom and bacteria within this microscale

**Doelstelling:**

This dissertation aims to experimentally dissect the interactions between a benthic marine diatom and its associated bacterial guilds through the development of a synthetic microbial community. In the first phase, we will characterize a set of bacterial isolates. Their phenotypic traits, including their capacity to grow on different carbon substrates and their interaction with the diatom, will be combined with genomic data to classify them into functional guilds (primary degraders, secondary consumers). In the second phase, we will experimentally test cross-feeding interactions between selected bacterial isolates to verify predicted metabolic dependencies. Using the diatom as a focal organism, we will then assess how variations in EPS quantity and composition influence bacterial community dynamics and feedback on algal growth and physiology. This project will provide insight into how microbial cooperation and competition shape carbon cycling in benthic systems and how diatoms potentially use biochemical signaling to engineer their microbial niche.

**Locatie:**

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## 48380: Testing the pace-of-life syndrome in beetles - Is personality consistent across life and linked to life history traits?

Promotor(en): Birgit Szabo
Begeleider(s):
Contactpersoon: Birgit Szabo
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:**

One hypothesis about why animals show differences in behaviour, i.e. personality, is because this variation is linked to life history traits and represent different strategies to maximise fitness. In this study, we tested yellow flour beetles across 4 tests to collect behavioural data on boldness, exploration, and sociability. Furthermore, we tracked the individuals development measuring their size as they grew, the days taken to pupate, days taken to emerge from the pupa, size of the pupa and beetle, sex and life span. We tested individuals once a week throughout their life. Experimental data on personality is rarely collected for this long, mostly by tracking wild individuals for a long time, but not in an invertebrate.

Data on boldness and exploration have already been collected only the analysis of the social test is left. So this project is about analysing existing videos: 25h of videos, repeated testing of 51 individuals over 25 weeks (from larvae to beetle). This topic will include the development of an ethogram of social behaviour (no published ethogram of social interaction is available in the literature so far), behavioural analysis using BORIS (behavioural recording software) and statistical analysis using state of the art methods such as mixed modelling and structural equation models.

There data enables us to ask a few interesting questions: (1) How stable is behaviour over time when measured for many repetitions (standard in the field is 2 repetitions, we did 25)? (2) Is behaviour consistent across metamorphosis (larvae versus beetle)? (3) Is behaviour associated with life-history measures forming a pace-of-life syndrome? We are looking for a motivated student that will collect high quality data from the videos. The student will be included as a coauthor on the resulting paper.

**Doelstelling:**

**Locatie:**

Dunant / Ledeganck

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## 48477: The contribution of spore traits to the dispersal of ectomycorrhizal fungi

| | |
|---|---|
| Promotor(en): | Annemieke Verbeken |
| Begeleider(s): | Ruben De Lange |
| 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 most ecosystems worldwide, ectomycorrhizal (ECM) fungi are central in ecosystem functioning and essential to maintain a healthy balance, regulating plant growth and fitness. They produce fruitbodies with the sole purpose of producing and dispersing sexual spores. Theoretically, the discharged spores are widely disseminated by air currents. Although this mode of dispersal is ubiquitous among fungi, there seem to exist some limitations to anemochory and consequently, other dispersal mechanisms must exist. Various theories have been put forward of which zoochory is potentially the most viable. More specifically, we want to explore the role of fungivorous invertebrates in ECM fungal dispersal. We believe that ECM fungi have certain morphological adaptations that might facilitate dispersal by invertabrates, either through passive transport (epizoochory) or by ingestion (endozoochory).

**Doelstelling:**

In this thesis we want to test if spore ornamentation has a positive effect on dispersal success by means of feeding essays and microscopical analysis. The student will have to perform fieldwork for collecting both soil invertebrates (slugs and woodlice) and fungal fruitbodies (based on a preselection of species), set up cafeteria experiments, perform microscopical and statistical analysis.

**Locatie:**

campus Ledeganck

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## 48232: The effect of dispersal rates on adaptation of populations with consumer-resource dynamics under environmental forcing

| | |
|---|---|
| Promotor(en): | Felipe Kauai Pereira, Dries Bonte |
| Begeleider(s): | |
| Contactpersoon: | Felipe Kauai Pereira |
| 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:**

Nature displays many periodic signals, such as daily temperature swings or tidal rhythms. Populations must adapt to these oscillators in order to thrive and avoid extinction. Recently, the classic consumer-resource model of Rosenweig-MacArthur has been studied under environmental forcing. That is, under periodic resource availability. Think, for instance, of a resource that increases and decreases in availability as a function of time. More explicitly, if y is the resource amount and x time, we might look at something of the sort y = sin(x). The relevant literature for additional information on these ideas can be found in the following manuscrips:

1. Bieg C, Gellner G, McCann KS. 2023 Stability of consumer–resource interactions in periodic environments. Proc. R. Soc. B 290: 20231636. https://doi.org/10.1098/rspb.2023.1636

2. Rosenzweig ML, MacArthur RH. 1963 Graphical representation and stability conditions of predator– prey interactions. Am. Nat. 97, 209–223.

An important result from the study of Bieg et al. (2023) is the fact that adding environmental forcing to stable populations can act as a destabilizing process, leading populations to chaos/extinction. These interactions depend, however, on the biological properties of populations, such as growth rates, as well as on the speed of environmental forcing itself (i.e., degree of oscillation). In this context, this master project will seek to answer the question of how dispersal rates impact the stability of consumer-resource dynamics under environmental forcing. The question arises naturally when one contemplates the role that dispersal plays, for example, in driving populations to new resourceful environments when conditions are not optimal. Think of bird migrations, for instance.

**Doelstelling:**

The goal is to develop a deep understanding of the manuscripts cited and expand their scope. Also, the student will learn to analyze many important theoretical arguments that drive scientific progress in the field of ecology and is expected to expand his/her skill set in mathematical analysis and computer programming.

**Locatie:**

Campus Ledeganck

**Opmerkingen:**

The student needs to be acquainted with basic mathematical skills, such as notions of ordinary differential equations, and have programming skills in a common programming language, such as python, java, c++ ...

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## 48233: The effect of genetic systems of sex determination on the spread of reproductive endosymbionts in spatially concentrated populations

Promotor(en): Felipe Kauai Pereira, Nicky Wybouw
Begeleider(s):
Contactpersoon: Felipe Kauai Pereira
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:**

Reproductive endosymbionts that are maternally transmitted, such as Wolbachia, spread through host populations by manipulating reproduction. Notably, cytoplasmic incompatibility (CI) is a well studied reproductive manipulation, where uninfected females that are fertilized by infected males lay eggs that are not entirely viable. As a result, females that carry infection, and have no problems being fertilized by either infected or uninfected males, have a reproductive advatange and eventually rise in frequency. However, CI is expressed differently relative to the genetic system of sex determination. For instance, in haplodiploids CI may disturb demographic aspects of the host population such as sex ratio distribution. One outstanding questions to be tackled is the quantitative differences in infection dynamics with respect to the underlying host genetic system. Moreover, although theoretical models of CI to understand rates of endosymbiont spread in host populations provide important insights for understanding these interactions, as well as to predict infection spread for applied purposes, these models often neglect the effect of space on host-symbiont associations. For example, how dispersal rates of individuals (which is a spatial property) influence the speed with which Wolbachia spreads through host populations? This one of the questions to be addressed within this project.

**Doelstelling:**

The goal of this master project will be to understand quantitative differences between Wolbachia spread in haplodiploids compared to diplo-diploid host populations in space. More specifically, the student will learn to develop agent-based models and analyze mathematical models to understand how these interactions unfold in time. Additional information on the related problems and scientific context can be found in the following manuscrips:

1. Kauai, F., and N. Wybouw. 2025. " Reciprocal Host–Wolbachia Interactions Shape Infection Persistence Upon Loss of Cytoplasmic Incompatibility in Haplodiploids." Evolutionary Applications 18, no. 7: e70138.

2. Michael Turelli, EVOLUTION OF INCOMPATIBILITY-INDUCING MICROBES AND THEIR HOSTS, Evolution, Volume 48, Issue 5, 1 October 1994, Pages 1500–1513

3. Wybouw, N., Van Reempts, E., Zarka, J. et al. Egg provisioning explains the penetrance of symbiont-mediated sex allocation distortion in haplodiploids. Heredity 131, 221–229 (2023)

**Locatie:**

**Opmerkingen:**

The student needs to be willing to understand some basic mathematical concepts. Also, programming skills with languages such as python, java or c++, is required.

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## 48247: The fish scale as an open book: reading the life history of common sole (Solea solea)

| | |
|---|---|
| Promotor(en): | Adelbert De Clercq |
| Begeleider(s): | Karen Bekaert, Bavo De Witte |
| 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 crystals or otoliths. These otoliths need to be extracted from the auditory capsule in the skull of the fish. Otoliths are embedded, and sections are polished and sometimes stained to help visualise the growth lines within the crystalline structures. It is these growth lines, similar to growth lines in a tree stump, that can be counted to determine the age of the animal. This technique is well established for age determination of fishes. A small part of the commercial fish catch is used to collect samples. Age reading via otoliths, although accurate, gives a single time point and thus life history of a single animal has to be investigated indirectly via calculations based and age-weight-length relationships. Additional information such as chemical composition of the otolith can be used. 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 ethically advantageous, because scales regenerate quickly and thus do not kill the animal when lost. Moreover, scales can be sampled from the same individual over time thus representing an opportunity to track the life history of an individual fish. This is however challenging for wild animals, as they need to be tagged and traced, and recaptured for scale collection. As scales are close to the surface of the animal, and mineralised structures are ideal sinks to capture and store small molecules, inorganic composition as well as isotope composition can possibly provide more information of the life history of an animal if chemical profiles of the scale can be linked to chemical profiles of water or sediment.

**Doelstelling:**

The aim of the project is to develop the scale as a minimal invasive age and life history reading tool. Although, initial exploration of the scales of many marine fish species has to happen first, preliminary data has been collected from common sole (Solea solea), the most economically important fish species for Belgium. You will train in age reading techniques used by the sclerochronology group at the Flemish Institute for Agriculture, Fisheries and Food (ILVO). In collaboration with the Evolutionary Developmental Biology group of Ghent University, you will sample scales of different sizes, and life history stages of the common sole, visualise the growth rings, describe the scale morphology and visualised pattern, and count growth rings to assess the age of the animals. To validate possible age and life history readings on scales, otoliths of the corresponding animals 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 exist. If possible, chemical analysis of scales will be explored in order to assess if chemical profiles can be determined and if these chemical profiles can be matched to known chemical profiles of the water column or sediments.

**Locatie:**

Campus Ledeganck (Gent), InnovOcean Campus (ILVO-MARIEN, Oostende)

**Samenwerking met bedrijf of non-profit organisatie**

Bedrijf: Instituut voor Landbouw-, Visserij- en Voedselonderzoek (ILVO)
Samenwerking: begeleider

**Onderwerp voorbehouden voor Kirsten Van der Straeten**

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## 48497: The functional response of soil communities to increased snow cover and moisture availability in High Arctic tundra

| | |
|---|---|
| Promotor(en): | Elie Verleyen, Bjorn Tytgat |
| 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 Arctic is experiencing rapid climate change as a result of the polar amplification of global warming. Besides increased temperatures, climate models also predict that during the 21st century, precipitation in the Arctic will increase with 50-70%. This might have important biological consequences because in polar regions, water is often a limiting resource. In addition, changes in winter precipitation can change the onset and duration of snow cover and snow depth. This might result in a shorter growing season for phototrophs, a higher moisture availability, and because snow is a good insulator, also a better protection against cold temperatures during winter. The latter might in turn lead to a prolonged period of above zero temperatures in the soils and hence increased heterotrophic activity, resulting in higher emissions of the greenhouse gasses CO2 and CH4. The effect of increased snow cover and water availability on tundra soil communities might, however, depend on local conditions including the amount of water already available and the topography.

In the summer of 2017, a long-term field experiment was initiated in Kongsfjord in Spitsbergen, Svalbard. Two snow fences were installed on the extremes of a dry-wet gradient in High-Arctic tundra. Snow fences create turbulence when wind passes through them, causing snow to drop and accumulate down-wind of these structures. In total, 6 plots (each with 3 subplots) were subjected to increased snow cover using snow fences, and 6 control plots (each with 3 subplots) were left untreated. Samples were collected at the onset of the experiment and in 2024 to track long-term changes in the soil microbial community structure and diversity resulting from these treatments. An amplicon sequencing study revealed striking shifts in community structure in both bacteria and (micro-)eukaryotes with the dry tundra showing the highest response. However, how these changes in snow cover affect the functioning of the soil communities remains largely unknown.

**Doelstelling:**

In this MSc project the student will analyse changes in the abundance of critical functional genes involved in carbon and nutrient cycling based on high-throughput metagenomics sequencing. The student will be involved in the library preparation for sequencing and the subsequent bioinformatics analysis using a standardized pipeline and packages available in R. The metagenomics data will be integrated with greenhouse gas measurements to assess the effect of increased snow cover on the functioning of these tundra soils.

**Locatie:**

Sterre (S8) and K.L. Ledeganckstraat

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## 48479: The lateral roots of 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: https://www.beeckmanlab.be/research/horsetails-elucidate-evolution-lateral-root-branching

**Opmerkingen:**

The project might also need to clone some constructs.

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## 48468: The neuroprotective function of glial GLB-1 during hypoxia and reoxygenation stress.

Promotor(en): Bart Braeckman
Begeleider(s): Giuliano Lecompte
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:**

Globins are a superfamily of proteins characterized by the globin fold and a broad biochemical repertoire. Although ubiquitous in nature, the physiological roles of many globins, including several human globins, remain poorly understood. A promising model to explore globin function lies within Caenorhabditis elegans, which encodes for an impressive number of 34 globins (compared to 6 to 8 globins in most vertebrates).

Among these, the myoglobin-like GLB-1 can reversibly bind oxygen with high affinity, and theoretical analyses suggest that it may thereby facilitate oxygen diffusion during low-oxygen conditions (hypoxia). Moreover, as the globin-fold often enables interactions with reactive oxygen species (ROS), GLB-1 may also scavenge ROS. These potential functions are critical to survive hypoxia-reoxygenation stress, and are further supported by the strong transcriptional regulation of HIF-1, the master regulator of the hypoxic survival response.

Neurons are particularly susceptible to oxygen fluctuations because of their high oxygen demands and ROS susceptibility. Notably, GLB-1 is constitutively and highly expressed in glial cells, which closely associate with neurons and support their function. Within this context, we hypothesize that glial GLB-1 facilitates oxygen diffusion into the neurons, safeguarding their function during acute or chronic hypoxia. Similarly, glial GLB-1 may scavenge ROS and protect neurons from oxidative stress that is primarily generated during reoxygenation.

A fundamental understanding of how glial GLB-1 provides neuronal protection during hypoxia-reoxygenation stress could provide novel insight explaining the hypoxic lifestyle of many small invertebrates: nematodes, flatworms and gastrotrichs. More broadly, it could information on how vertebrate neuroglobin provides neuronal support in the brains of hypoxia-tolerant mammals and the human retina.

**Doelstelling:**

In this master thesis, we will use C. elegans to verify whether glial GLB-1 maintains neuronal function during and after hypoxia-reoxygenation stress. First, we will perform quantitative PCR on neuron-specific hypoxia marker genes to identify the oxygen range wherein neurons of wild-type and globin-1 mutant worms start to experience hypoxia. For this, we will use existing RNA libraries of worms that were differentially exposed to various oxygen concentrations. Within that neuronal hypoxic zone, we will conduct behavioural assays that validate neuronal function (smell , taste, touch, ...), both during hypoxia and following reoxygenation. For this, you will learn how to create, maintain and work within enclosed hypoxic environments.

**Locatie:**

Campus Ledeganck

**Onderwerp voorbehouden voor Thibault Van Peteghem**

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## 48491: The role of diversity and biotic interactions in the productivity of benthic diatom communities

Promotor(en): Willem Stock, Koen Sabbe
Begeleider(s): Willem Stock
Contactpersoon: Willem Stock
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:**

Benthic diatom communities in tidal flats are known for their high productivity. These microalgae form a dense and dynamic biofilm on the sediment in early spring. They are responsible for a significant portion of primary production in intertidal areas and form the basis of the food web. The structure and composition of these communities are influenced by deterministic processes (environmental conditions, competition between species) and stochastic processes (random colonization and local extinctions). The interaction between these processes determines not only the species richness but also the functionality (for instance the efficiency of carbon fixation and amount of sediment stabilization) of the biofilm. However, we currently lack a clear understanding of the extent to which biodiversity and biotic interactions contribute to the primary productivity of these intertidal biofilms.

**Doelstelling:**

In this thesis, we will use an experimental approach to investigate the role of diatom diversity in the primary production of tidal flat communities. Using a dilution-to-extinction method, natural diatom communities will be gradually diluted into communities with varying levels of diversity. By monitoring the growth and composition of these experimental communities, we will investigate how biotic interactions (such as competition and mutualism) contribute to community structure. At the same time, we will measure total primary production to quantify the relationship between diversity and ecosystem function. The focus of this thesis will be on experimental laboratory work, supplemented by limited fieldwork for sampling. In the lab, techniques such as fluorometry and microscopy will be used. A key challenge of this experiment will be to contextualize the experimental observations within an ecological and theoretical context, specifically the relationship between biodiversity, ecosystem stability, and productivity.

**Locatie:**

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## 48469: The role of GLB-1 in providing systemic protection during a secondary hypoxia-reoxygenation event.

| | |
|---|---|
| Promotor(en): | Bart Braeckman |
| Begeleider(s): | Giuliano Lecompte |
| 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:**

Globins are a superfamily of proteins characterized by the globin fold and a broad biochemical repertoire. Although ubiquitous in nature, the physiological roles of many globins, including several human globins, remain poorly understood. A promising model to explore globin function lies within Caenorhabditis elegans, which encodes for an impressive number of 34 globins (compared to the typical 6-8 globins in vertebrates).

Among these, the myoglobin-like GLB-1 can reversibly bind oxygen with high affinity, and theoretical analyses suggest that it may thereby facilitate oxygen diffusion during low-oxygen conditions (hypoxia). Moreover, as the globin-fold often enables interactions with reactive oxygen species (ROS), GLB-1 may also scavenge ROS. These potential functions are critical to survive hypoxia-reoxygenation stress.

Under normal oxygen conditions (normoxia), GLB-1 is predominantly expressed in glial cells, which closely associate with neurons and support their function. However, after hypoxic exposure (reoxygenation), GLB-1 expression increases tremendously and shifts from glia-dominant expression to systemic expression, including neurons, intestine, and muscles. This upregulation likely occurs under control of Hypoxia-Inducible Factor (HIF), the master regulator of the hypoxic survival program. In this upregulated state, we hypothesize that GLB-1 may facilitate oxygen delivery throughout the entire worm and/or provides systemic ROS protection to survive any secondary hypoxia-reoxygenation event.

High-affinity myoglobin-like proteins, like GLB-1, are consistently found in small invertebrates that frequently experience fluctuating hypoxia, such as nematodes, flatworms and gastrotrichs. Understanding whether and how GLB-1 confers hypoxic protection could establish these proteins as a key factor for the survival of small invertebrates in chronic and fluctuating hypoxic habitats. Moreover, these animals lack a circulatory system and are therefore generally presumed to lack any hypoxia-induced mechanism that enhances oxygen delivery. Contrary to this assumption, this work has the potential to show that, instead, they rely on a molecular mechanism wherein the HIF-dependent upregulation of globin proteins increases cellular oxygen delivery.

**Doelstelling:**

In this master thesis, we will use C. elegans to validate whether systemically upregulated GLB-1 provides protection against secondary hypoxia-reoxygenation stress. The student will first learn how to create and maintain an enclosed hypoxic environment to pre-condition both wild-type and globin-1 mutant worms. These worms will be subjected to both physiological and phenotypic assays, the type of which will depend on the status of our research at that time. Physiological assays could involve measuring various aspects of energy metabolism such as metabolic rate (micro-calorimetry), oxygen-consumption (oxygen quenching fluorometry) and the production of anaerobic metabolites (colorimetry), or the accumulation of mitochondrial ROS (fluorometric probe). Phenotypic assays could involve measuring recovery-time, survival, locomotion and reproduction during or after a secondary hypoxia-reoxygenation event.

**Locatie:**

Campus Ledeganck

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## 48463: The role of microscopic banks in population dynamics of kelp vegetations

| | |
|---|---|
| Promotor(en): | Olivier De Clerck |
| Begeleider(s): | María Bonafont Castells |
| Contactpersoon: | María Bonafont Castells |
| 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 a group of brown seaweeds that form ecologically and economically important underwater forests and portray a characteristic life cycle. They alternate between a macroscopic sporophyte phase (diploid) and a microscopic gametophyte phase (haploid).The gametophyte stage has been hypothesized to persist in the field for prolonged periods of time, reproductively inactive depending on environmental conditions. In doing so, they may function as a seed bank analogue for land plants, referred to as the "bank of microscopic forms".

Although this concept has been proposed for decades, direct evidence of its presence and functioning directly in the field remains extremely limited. The existence of such bank would serve as a reservoir of genetic diversity, enabling rapid post-disturbance recovery, and buffer populations against seasonal or stochastic environmental stress. Understanding their presence, persistence and ecological relevance is therefore crucial.

**Doelstelling:**

This thesis aims to track the contribution of a gametophyte generation to the macroscopic sporophyte population of the kelp Undaria pinnatifida (natural population in Belgium) in time. The work will combine monthly field sampling, lab experiments and genetic (parentage) analysis to disentangle the characteristics that would describe the persistence of a bank of microscopic forms for this species.

**Locatie:**

**Website:**

Meer informatie op: https://phycology.ugent.be/

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## 48248: The scale of AI: using artificial intelligence to improve automated fish scale reading.

Promotor(en): Adelbert De Clercq
Begeleider(s): Hanne De Rijcke, Siebren Cosijn
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:**

Are you a biologist with deep interest in artificial intelligence (AI) and loves to program your way out of problems? If yes, keep reading.

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 crystals or otoliths. Otoliths are embedded, and sections are polished and sometimes stained to help visualise the growth lines within the crystalline structures. It is these growth lines, similar to growth lines in a tree stump, that can be counted to determine the age of the animal. An alternative to otoliths for age reading are the scales of fish. Scales also show growth lines, called circuli and annuli, and well-established life history reading protocols exist especially for salmonids. Using scales for life history reading is ethically advantageous, because scales regenerate quickly and thus do not kill the animal when lost. Age reading via otoliths and scales happens through human expert readers, and although proven to be accurate, takes large amounts of time. In addition, training new experts is a considerable investment, and multiple experts need to read the same otoliths in order to maintain data quality and reading consistency. A well-developed AI on the other hand, can work fast and with a consistent approach, given that the AI produces good accuracy and is trained properly. The latter implies that the quality of training data-set is of key importance, a well-known fact for builders and users of AI applications.

**Doelstelling:**

The aim of the project is to develop an accurate and consistent AI model that can produce results which will allow researchers to read the age on fish scales. Preliminary tests of an AI model were run on a training dataset of European seabass scales, of which we know the precise ages due to being processed by expert age readers of the sclerochronology lab of the Flemish Research Institute for Agriculture, Fisheries and Food (ILVO). However, further refinement and tests need to be run. In addition, a dataset of Atlantic salmon (Salmosalar) scales for which we know exact ages (in days) and other life history events is available from the Evolutionary Developmental Biology group at Ghent university, and is ready for being probed with AI models. Collaboration between the two lab groups will be important. As the quality of the training dataset is of key importance, you will also develop recommendations related to how training datasets for this specific application should be build, as well as recommendations on how to capture data to run through AI based age reading tools on fish scales.

**Locatie:**

campus Ledeganck (Gent), InnovOcean Campus (ILVO-MARIEN, Oostende)

**Samenwerking met bedrijf of non-profit organisatie**

Bedrijf: Instituut voor Landbouw-, Visserij- en Voedselonderzoek (ILVO)
Samenwerking: begeleider

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## 48470: Thermal physiology and metabolic adjustment in invasive passerine birds

Promotor(en): Cesare Pacioni
Begeleider(s): Diederik Strubbe
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:**

Understanding how small invasive passerine species adjust their physiology to temperature variation is essential for predicting their success and spread in new environments. These species often establish populations in climates that differ from their native range, and their physiological ability to cope with these conditions may determine whether they can persist and expand. Physiological adjustments, particularly changes in metabolic rate, are key for regulating energy expenditure, maintaining survival, and supporting fitness. These adjustments are especially relevant under climate change, where increasing temperature extremes may frequently push birds beyond their thermoneutral zone (TNZ).

**Doelstelling:**

This thesis will examine how small invasive passerines regulate their metabolism above and below the TNZ, providing insight into their ability to cope with changing environments and assessing their potential to thrive in novel climates.

What you will do:

• Learn to safely handle birds

• Learn to set up and run respirometry experiments

• Take key morphological measurements

• Analyse raw respiratory data to obtain metabolic rate values

**Locatie:**

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## 48442: Ulva growth and morphogenesis by ensuring stable colonization and functional activity of the associated microbiome

| | |
|---|---|
| Promotor(en): | Olivier De Clerck, Anne Willems |
| Begeleider(s): | Siyu Ma |
| Contactpersoon: | Olivier De Clerck |
| 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:**

Seaweeds are always associated with microbial organisms of which bacteria are the most important. Specifically for sea lettuce (Ulva) previous research demonstrated a close interaction between the seaweed and specific bacterial strains. Up to which extent the associated bacteria form a stable community is not well researched at present. Using a combination of field sampling and lab experiments the candidate student will isolate bacteria, characterise their function and try to make synthetic communities that are stable with respect to environmental perturbations.

**Doelstelling:**

Objective

- Isolate and characterize bacterial strains from Ulva-associated microbiomes, focusing on growth-promoting traits such as IAA production, phosphate solubilization, nitrogen fixation, and siderophore production.
- Select non-antagonistic strains and assemble 3–5 SynComs.
- Evaluate the effects of SynComs on Ulva growth and morphogenesis under controlled laboratory conditions.
- Assess the functional stability and colonization ability of SynComs.

**Locatie:**

Sterre S8, Ledeganck

**Website:**

Meer informatie op: https://phycology.ugent.be/

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## 48295: Unravelling coumarin's enigmatic mode of action

| | |
|---|---|
| Promotor(en): | Bartel Vanholme |
| Begeleider(s): | Robin De Wulf |
| Contactpersoon: | Robin De Wulf |
| 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:**

Coumarin is a well-known secondary metabolite found in a plethora of plant species. It is formed as a by-product of the phenylpropanoid pathway, presumably from the cinnamic-acid intermediary. Exogenous application of coumarin to plants yields a multitude of developmental effects, altering plant growth and development throughout all life stages. Recent research within our group focusses on unravelling the coumarin signalling network. In literature and from our own research, coumarin has been linked to interact with multiple plant hormones, but it remains hard to unravel the complete coumarin signalling network.

**Doelstelling:**

Your objectives and role within the coumarin research will be to unravel this complex coumarin signalling mechanism. Using two coumarin insensitive lines, you will study one coumarin-induced phenotype and dive deeper into the underlying regulatory mechanisms. The goal will be to determine regulatory elements that coumarin employs to induce this phenotype while utilizing the knowledge of coumarin's interaction with the known phytohormones.

**Locatie:**

Campus Zwijnaarde (PSB)

**Onderwerp voorbehouden voor Eliott Liberale**

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## 48462: Unravelling cryptic diversity within the diatoms species complex Cylindrotheca closterium

| | |
|---|---|
| Promotor(en): | Eveline Pinseel, Wim Vyverman |
| Begeleider(s): | Anne-Laura Monten |
| 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:**

Marine planktonic microorganisms are often assumed to form only a few cosmopolitan species, given their enormous population sizes, passive dispersal potential, and the apparent absence of geographic barriers in the ocean. However, growing evidence reveals that many of these microorganisms comprise cryptic species, leading to extensive, previously unrecognized genetic diversity within planktonic communities.

One such clade of potentially highly diverse marine microbes are diatoms. Diatoms are unicellular stramenopile microalgae, and represent one of the most diverse and ecologically important phytoplankton groups, contributing around 20% of global net primary productivity. Many diatom lineages include cryptic species complexes, such as the globally common Cylindrotheca closterium complex.

Unravelling species boundaries in such complexes requires both molecular and experimental approaches. C. closterium is especially suitable for this, as it has a small reference genome and established laboratory protocols for sexual crossing. This species exhibits two reproductive modes: heterothallism, where sexual reproduction occurs between compatible mating types, and homothallism, where it occurs within a single clone. Although heterothallism predominates in pennate diatoms, increasing evidence shows variation in mating systems even within morphologically similar species.

Despite their ecological importance, the drivers and mechanisms underlying these reproductive differences remain unclear. How reproductive barriers emerge—whether prezygotic or postzygotic, and under allopatric or sympatric conditions—is still poorly understood. Clarifying these dynamics is crucial for understanding how genetic diversity and speciation arise in marine diatoms and other planktonic microorganisms.

**Doelstelling:**

The objective of this master's thesis is to unravel the global species-level diversity and reproductive barriers within the cryptic marine diatom species complex Cylindrotheca closterium by combining experimental and molecular approaches.

The student will conduct laboratory crossing experiments using C. closterium strains collected from diverse geographic regions (polar, temperate, and tropical environments). These experiments will assess reproductive compatibility between strains and identify potential pre- or postzygotic barriers that may contribute to species diversification within the complex.

Additionally, the student will characterize molecular diversity among global C. closterium strains. Molecular analyses will be performed by the student to compare genetic relationships and explore how genetic, geographic, and reproductive patterns align, or differ between strains.

Finally, the student will integrate various species concepts to better define boundaries within the C. closterium complex. This integration, will provide insights into the ecological and evolutionary drivers behind diatom diversification.

Through this project, the student will acquire hands-on experience in microscopy, diatom culturing, molecular techniques and laboratory experiments. The combined expertise of the promotors and the practical guidance of the supervisor will ensure that the student receives the necessary support to successfully complete the thesis.

**Locatie:**

campus Sterre, S8

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## 48009: 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**

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## 48286: Unravelling species complexes and cryptic species in African rain forests, using genomic data

| | |
|---|---|
| Promotor(en): | Lars Chatrou |
| Begeleider(s): | |
| Contactpersoon: | |
| 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:**

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

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## 48219: Unravelling the regulation and functions of starchy endosperm cell death in maize kernels

| | |
|---|---|
| Promotor(en): | Moritz Nowack |
| Begeleider(s): | Fontanet Manzaneque Juan Bautista |
| Contactpersoon: | Moritz Nowack |
| 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:**

Cereal crops constitute the largest source of human food and animal feed, providing approximately 43% of global caloric intake. Among them, Zea mays (maize) ranks first in annual production, exceeding one billion metric tons. The maize kernel endosperm is composed of four major cell types: the basal endosperm transfer layer, the endosperm adjacent to the scutellum, the aleurone, and the starchy endosperm (SE). The SE serves as the primary storage tissue of the seed, accounting for about 80% of its dry weight. Within the SE, starch and protein synthesis are crucial processes that determine grain filling. After filling is completed, SE cells undergo death; however, the mechanisms and molecular regulation of this process remain poorly understood. Notably, SE cells that fill first are also the first to die, indicating that a tightly regulated programmed cell death (PCD) process marks the final stage of SE development. This project is based on the hypothesis that modulating PCD may enhance starch and protein accumulation in the maize SE, potentially improving yield and contributing to food security in the context of climate change.

**Doelstelling:**

Using single-nucleus RNA-sequencing data of maize endosperm, we identified candidate transcription factors central to SE molecular networks. The andidate genes were screened in rapid heterologous systems, including transfection of Nicotiana benthamiana leaves and maize mesophyll protoplasts, revealing six transcription factors capable of inducing cell death and activating the expression of PCD marker genes. In this project, you will target these genes to generate higher-order mutants using CRISPR-Cas9 and create endosperm-specific dominant-negative variants to modulate SE PCD. Next, you will analyze the mutant plants to detect aberrations in PCD progression, as well as kernel development and yield. With this approach we will 1) test the hypothesis that transcriptionally regulated cell death controls a PCD process in the starchy endosperm, and 2) be able to gain information about the functions of PCD in the starchy endosperm with respect to kernel filling and yield in maize as an important crop plant.

As a master student, you will become a full member of the PCD research team (https://www.nowacklab.be/) at the internationally reknowned VIB-UGent Center for Plant Systems Biology, one of the leading plant science institutes in Europe (https://www.psb.ugent.be/). If the topic has piqued your curiosity, don't hesitate to reach out to Prof Moritz Nowack (moritz.nowack@ugent.be; moritz.nowack@vib.be) to arrange a visit of the lab and a discussion about details of the project. We are looking forward to getting to know you!

**Locatie:**

Campus Ardoyen / Tech Lane Ghent Science Park

**Website:**

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

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## 48438: Unveiling the hidden diversity of Amanita in Togo's forests

| | |
|---|---|
| Promotor(en): | Annemieke Verbeken, Kudzo Atsu Guelly |
| Begeleider(s): | |
| Contactpersoon: | Annemieke Verbeken |
| 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:**

Amanita is a globally important ectomycorrhizal (ECM) genus and plays a key ecological role in African forest ecosystems, including the Sudanian woodlands of Togo (West Africa).

All known Amanita species are endemic to the continent and are associated with the indigenous ectomycorrhizal forming trees, except fro some species introduced with exotic trees such as Pinus.

Although several Amanita species from the region have been documented and described, many taxa remain uncharacterized, and the true diversity of the genus is likely underestimated.

Existing identification keys and taxonomic resources for African Amanita are often incomplete or outdated, making accurate species identification challenging. This knowledge gap hampers ecological studies and limits our understanding of the genus' contribution to local forest functioning.

**Doelstelling:**

This thesis aims to address these issues by documenting Amanita diversity in Togo and refining the taxonomic framework needed for reliable identification.

You will study dried specimens and annotate and document microscopical characters.

A selection of specimens will be sequenced and ITS barcodes will be obtained. Reference specimens are available in the fungaria of Gent and Meise.

**Locatie:**

campus Ledeganck

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## 48486: Validating DNA metabarcoding as a novel tool for the analysis of moss-associated diatoms in historic moss herbarium specimens

| | |
|---|---|
| Promotor(en): | Koen Sabbe, Eveline Pinseel |
| Begeleider(s): | Charlotte Goeyers |
| Contactpersoon: | Charlotte Goeyers |
| 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:**

Moss herbarium collections offer a unique archive of Arctic-alpine biodiversity spanning nearly two centuries, particularly for siliceous microalgae such as diatoms. While preserved diatom frustules from historical moss samples have been successfully used for light microscopy-based analyses in the past, much less is known about how well diatom DNA is preserved in these collections. This hampers the development of a taxonomy-free tool to assess moss diatom communities in Arctic-alpine terrestrial ecosystems and how they have been impacted by environmental change.

### Doelstelling:

In this MSc thesis, the student will compare two fundamentally different biodiversity assessment methods (light microscopy (LM) versus DNA metabarcoding). Historic moss specimens (1829–1970) from Iceland, Greenland, and Svalbard were retrieved from the Natural History Museums of Vienna and Copenhagen, and diatoms were already morphologically assessed by LM. This dataset will serve as the baseline for validation with DNA metabarcoding and might be expanded with data from alpine localities.

The student will validate DNA metabarcoding as a tool for reconstructing historic moss-associated diatom communities over time and compare the results with an existing morphological dataset from the identical samples. If the student is interested, and if time allows, there is a possibility to include LM-based analyses from yet to be analyzed alpine moss collections. Comparing LM versus DNA in the same historic samples will allow us to (1) test the reliability of historic DNA from herbarium material; (2) identify biases in either LM or DNA metabarcoding approaches; and (3) unravel cryptic diversity that was not detected using LM. Ultimately, this MSc thesis project will contribute to unlocking historical moss collections for the assessment of microbial communities – a key step in understanding how microbial communities responded to climate change in the last few centuries.

### Locatie:

campus Sterre S8

### Opmerkingen:

The project is suitable for a student with interest in DNA metabarcoding and biostatistics/-informatics. Training will be provided for DNA metabarcoding, R-based analyses, and bioinformatics, although basic R skills are essential. As outlined above, LM-based analyses can be included if the student is interested.

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## 48263: What drives species apart?

| | |
|---|---|
| Promotor(en): | Nicky Wybouw |
| 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:

All animal and plant species arise by speciation, the evolutionary process of splitting a single species into two reproductively incompatible lineages. A hundred years ago, Wallin hypothesized that animal and plant speciation may be driven by microbial symbionts, a radical idea that was largely forgotten for decades. Researchers followed the work of Dobzhansky and Muller and focused on nuclear gene incompatibilities to explain speciation. However, recent work has been gathering evidence that supports Wallin's idea and uncovered a certain group of symbionts that promotes reproductive isolation. In this thesis, we will explore the relative contribution of symbionts and nuclear genes in the reproductive isolation of animals.

### Doelstelling:

This project will use multiple Tetranychus spider mite species and their bacterial symbiont Wolbachia as a model system. The student will be able to rely on an established panel of lab strains and will work within an ongoing international research project. Different research lines can be offered to students, ranging from experimental evolution and host behaviour, to molecular biology and genetics.

**Locatie:**

Campus Ledeganck

**Website:**

Meer informatie op: www.nickywybouw.org/

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## 48281: Which ecological factors drive the selection of breeding bird territories the Zwin salt marsh?

| | |
|---|---|
| Promotor(en): | Jan Van Uytvanck |
| Begeleider(s): | Jan Van Uytvanck, Wouter Faveyts |
| 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 the Zwin saltwater marsh, vegetation and vegetation structure are largely determined by tidal dynamics. Nevertheless, salt marshes are often grazed by cattle and sheep as an additional management measure (e.g., to prevent overgrowth by Sea Couch).

The different grazing activities also create additional structural variation in the vegetation. This likely has an important influence on the fauna present.

**Doelstelling:**

In this study, we aim to investigate how the choice of breeding territories of species such as Skylark, Meadow Pipit, and Redshank is influenced by the interaction between grazing, tidal dynamics, and vegetation structure. From this, we hope to gain insights for effective management of saltwater marshes.
Existing data and map layers (vegetation maps, species surveys, hydrological maps, habitat preferences of grazers) will be used, supplemented with fieldwork (territory mapping) in April, May, and June 2026. Breeding bird data from previous years will also be incorporated into the analyses.

**Locatie:**

Zwin Knokke, UGent Ledeganck, thuis

**Samenwerking met bedrijf of non-profit organisatie**

Bedrijf: Provincie West-Vlaanderen, Agentschap Natuur & Bos, INBO
Samenwerking: begeleider

**Onderwerp voorbehouden voor Juliette Debruyne**