

# Overzicht niet gekozen masterproeven 2017-2018 per promotor

**Beeckman**

**Tom**

**1503** Development and optimization of transgenic rice cell culture

**abstract:** Nitrogen is one of the most important limiting factor directing crop yields. It is required for the composition of proteins, DNA molecules, and several chemical compounds of importance for the plants. Nitrate (NO<sub>3</sub><sup>-</sup>) and ammonium (NH<sub>4</sub><sup>+</sup>) are the two main forms available for the plant in the soil, where it is taken up by the roots to be processed into amino-acids. Many researches are ongoing to unravel the gene networks and pathways that control the assimilation of NH<sub>4</sub><sup>+</sup> and NO<sub>3</sub><sup>-</sup>. One goal is to improve the nitrogen use efficiency of the plants, i.e. increasing yields obtained for the same amount of fertilizers (nitrogen) applied on the field. In this context, we performed a RNA-sequencing in rice fed upon different nitrogen sources (NH<sub>4</sub><sup>+</sup>, NO<sub>3</sub><sup>-</sup>) and identified candidate genes that possibly affect nitrogen use efficiency. These genes will be used as monitoring tools of the nitrogen use efficiency of the plants in response to various chemical compounds. For this purpose, we need to develop a rice cell culture which will be transformed to integrate the selected genes, and which will be used for a compound screen analysis. The main goal of this Master project is to develop and optimize a system of rice cell culture and to optimize a transformation protocol to generate cells with a reporter of the gene to be screened for the compound screen. Depending on the interests of the student, various side projects can be discussed such as a more in depth analysis of the RNA-sequencing data-set (bioinformatics).

**onderzoeksgroep:** PSB Plant Systems Biology - Root Development

**Copromotor(en):**

Motte Hans

**Begeleider(s):**

Pélessier Pierre-Mathieu

**opmerking:**

**voorbehouden:**

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## **1504** Nitrification inhibitors in fertilizers: a positive effect on plant growth and environment?

**abstract:** Nitrogen is one of the most important nutrients for plant growth and therefore, it is intensively fertilized on agricultural soils. Nitrogen is mainly present in two forms: ammonium (NH<sub>4</sub><sup>+</sup>) and nitrate (NO<sub>3</sub><sup>-</sup>). During nitrification, ammonium is converted into nitrate by nitrifying soil microorganisms. Nitrate, however, leaches from the soil and contributes to groundwater contamination. Moreover, nitrate is converted to nitrous oxide, a greenhouse gas which contributes to global warming. In a current research project, possible inhibitors of nitrification will be tested, which as such might prevent abundant nitrate formation, leaching and greenhouse gas production. Therefore, different techniques will be performed: microbial (culturing bacteria and archaea, determining the effect of inhibitors on community structures and activities in soil), plant physiological (phenotyping, yield determination), molecular (qRT-PCR, GFP/GUS report lines) and environmental (determining chemical soil composition and nitrate leaching). Different aspects can be highlighted depending on the interests of the student.

**onderzoeksgroep:** PSB Plant Systems Biology - Root Development

### **Copromotor(en):**

Motte Hans

### **Begeleider(s):**

Beeckman Fabian

### **opmerking:**

### **voorbehouden:**

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## **1505** Small molecules to increase phosphate use efficiency

**abstract:** Crop productivity relies heavily on phosphate fertilization, while rock phosphates resources are becoming more scarce, which is a threat for farming. In addition, the efficiency of fertilizer phosphate uptake by cultivated plant roots is rather low due to conversion of fertilizer phosphate into phosphate forms which are not available for uptake by plants. Phosphates which have not been taken up by plant roots will return to apatite rock (aging) and are lost for plant nutrition. In this project, it is aimed to increase phosphate uptake and/or use efficiency via application of small molecules. These molecules were selected by their capacity to interact with SPX1 (a central phosphate signal) or SPX1 expression in *Arabidopsis thaliana*. In the proposed master dissertation, the goal is to evaluate the genetic and molecular effect of a number of selected small molecules in *Arabidopsis thaliana* to characterize their mode of action. In addition, the effect of the molecules on plant growth and development will be evaluated micro- and macroscopically. During this thesis, a large variety of lab techniques such as plant tissue culture, phenotyping, GUS-staining, RNA-extraction, Quantitative Reverse-Transcriptase PCR, RNA sequencing, microscopy (light, DIC, confocal), image analysis... will be used.

**onderzoeksgroep:** PSB Plant Systems Biology - Root Development

### **Copromotor(en):**

Motte Hans

### **Begeleider(s):**

Crombez Hanne

### **opmerking:**

### **voorbehouden:**

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**abstract:** Cell-to-cell signaling is essential for many processes in plant growth and development. Much work has concentrated on traditional plant hormones. However, recent findings highlight that peptide signals have emerged as an important class of regulators in intercellular signaling during plant development. Our work, along with that of other research groups, has led to the identification of a novel secreted peptide family in Arabidopsis named GOLVEN. During previous characterization of GOLVEN genes transcription we remarked that GOLVEN6 (GLV6) had a very specific expression pattern associated to lateral root formation. Additional experiments lead us to postulate that GLV6 peptide signaling is part of a mechanism controlling the very first asymmetric cell divisions required for primordium initiation and essential for the progression of lateral root development. Since the mechanisms controlling the first asymmetric divisions during primordium formation are largely unknown, we aim to unravel the GLV6 signaling pathway. In order to identify molecular players of the GLV6 signaling pathway, an EMS mutagenesis screen was launched which recently led to the identification of MITOGEN ACTIVATED PROTEIN KINASE 6 (MPK6). Currently we are validating the role of MPK6 as well as other MAPKs in the GLV6 signaling pathway during lateral root initiation. In a next step, we will perform a shotgun phosphoproteomics experiment to identify specific substrates of MPK6. This thesis proposal will allow you to take part in an in-depth functional analysis of MPK6 as well as candidate substrates in GLV6 signaling during lateral root formation and help us to gain insights in this exciting, unexplored research field. During your thesis, you will not only learn to use a large variety of essential lab techniques such as plant tissue culture, PCR, qRT-PCR, Western blotting, light and confocal microscopy, GUS staining as well as general phenotyping, but you will also learn to master techniques such as stable transformation of Arabidopsis, cloning and the cutting-edge genome editing technology, CRISPR-CAS9 for the more ambitious amongst you.

**onderzoeksgroep:** PSB Plant Systems Biology - Root Development

**Copromotor(en):**

Fernandez Ana

**Begeleider(s):**

Vangheluwe Nick

**opmerking:**

**voorbehouden:**

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**abstract:** According to our research on the behaviour and reproductive biology of Anostraca (large Branchiopoda Crustacea) from temporary pools, males of some species live much longer than females. We demonstrated that adults maintain a chemical communication with the offspring in the eggs (resting eggs or cysts) at the bottom of the pond. This communication prevents nauplii from early hatching (before the pond dries out). Beladjal et al., 2007 showed that such signal is species-specific, but interspecific communication between different species in the same pool also exists (related signaling molecules?). The properties of these chemicals are unknown. The purpose of this topic is to identify the different aspects of the substance. The research focuses on the chemical aspects of a pheromone (structure, chemical group, durability, specificity, ...) from lab cultures of *Streptocephalus torvicornis* (Anostraca). We only expect one pheromone, unique for the species. The majority of crustacean pheromones are identified as peptides. It is likely that the same applies to our unknown substance (although it can also be a mixture of different molecules). The aim of this research is to add more information about this pheromone from different perspectives (ecology, behaviour, biochemistry).

**onderzoeksgroep:** Terrestrial Ecology & Vakgroep Organische en Macromoleculaire Chemie (WE07)

**Copromotor(en):**

Gheysens Tom

**Begeleider(s):**

Beladjal Lynda

Gheysens Tom

**opmerking:****voorbehouden:**

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**1373** A phenomic approach to understand dispersal

**abstract:** Many ecological problems associated to global change are characterized by human disruption of spatial dynamics. Habitat fragmentation constrains colonization and gene-flow, climate change forces organisms to track their optimal niche by moving pole- or upward and invasive species spread into new locations and outcompete their native counterparts. Spatial dynamics are always mediated by dispersal, whether it is natural or enforced. Phenotypic variation in dispersal occurs from gene expression, to physiology, morphology and behaviour, yet it is unclear which kind of phenotypic variation is the most relevant or carries the most variability and to which degree this variation depends on the mode of dispersal. The aim of this project is to acquire high-dimensional phenotypic data, from genes to behaviour to gain a deep understanding of the phenomic make-up of individual dispersal phenotypes, and to understand the importance of intraspecific variation in dispersal phenotypes for ecological dynamics. This goal will be reached by making use of an experimental model system (the spider mite *Tetranychus urticae*), combined with detailed cutting edge approaches to compare philopatric and dispersive individuals at the level of gene expression, metabolites, life history, morphology and behaviour. Relevant reading: BAGUETTE ET AL. 2015. An Individual-Centered Framework For Unravelling Genotype-Phenotype Interactions. Trends in Ecology & Evolution BONTE, D. & DAHIREL, M. (2017). Dispersal as a central and independent trait in life history. Oikos

**onderzoeksgroep:** Terrestrial Ecology

**Begeleider(s):**

Goossens Steven

**opmerking:****voorbehouden:**

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**1374** Bringing the Serengeti to the lab: the evolution of migratory strategies according to spatiotemporal variation in resources

**abstract:** Seasonal changes in resource availability induce large-scale migrations of animals. Seasonal variation in food abundance for instances induces intercontinental migration of birds, or more local mass migrations of large mammal herbivores on the African plains. In contrast, nomadic strategies are typical for animals inhabiting environments with unpredictable changes in resources (think of Saiga antelopes in Eurasian steppes). These large scales migrations are driven by evolved movement rules, by which individuals can overcome huge fitness costs. To date, insights on the evolutionary and environmental drivers of migratory strategies are principally derived from field observations, but experimental evidence is lacking. This project aims to develop challenging experimental evolution using a small arthropod herbivore as a model (the spider mite) to test if and how fast movement rules can evolve in response to environmental predictability, to which degree changes in movement rules affect population dynamics, and to which degree connectivity barriers will disrupt these population dynamics. The project can be combined with modelling according to student's interests. Relevant reading: MUELLER, T. & FAGAN, W.F. (2008). Search and navigation in dynamics environments – from individual behaviors to population distributions. *Oikos* 117: 654-664 FRONHOFER, E., STELZ, J.M., LUTZ, E., POETHKE, H.-J. & BONTE, D. (2014). Correlated extinctions select for less emigration but larger dispersal distances in the spider mite *Tetranychus urticae*. *Evolution* 68: 1838-1844

**onderzoeksgroep:** Terrestrial Ecology

**Begeleider(s):**

Mortier	Frederik
Masier	Stefano
Bonte	Dries

**opmerking:**

**voorbehouden:**

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**1381** What is the effect of climate change on size distributions and population persistence in a simple food web?

**abstract:** Ecologists continuously seek for a (master) law that explain diversity of life on earth. The metabolic theory of Ecology (MTE) – a theory which essentially demonstrated that interactions and life histories are tightly linked to body size- provides such a framework in single populations. Movement and dispersal does, however, also depend on body size, thereby providing a link between the MTE and metacommunities. The distribution of body sizes in communities will thus depend on selection pressures generated by variation in spatial structure (fragmentation, patch availability). We created a theoretical model which predicts how optimal size distributions of a consumer change in accordance to the spatial distribution of its resource.

Climate change is threatening biodiversity and exerting new selective pressures on individual traits. Moreover, according to the Metabolic Theory of Ecology, variation in most individual traits (e.g. ingestion rate, walking speed, etc. (Peters 1983)) might be reduced to variation in one single trait: body size. Therefore, we created a theoretical model which predicts how the optimal size distribution of a consumer changes in accordance to the spatial distribution of its resource. Within this master thesis, this existing model will be extended by introducing climate change. This might for instance be done by defining a climate window which moves at a fixed speed over the landscape, simulating range shifts. As such, the effect of climate change on the optimal size distribution of a consumer will be examined.

**onderzoeksgroep:** Terrestrial Ecology

**Begeleider(s):**

Hillaert                      Jasmijn

**opmerking:**

**voorbehouden:**

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## 1512 Understanding invasions by learning from failed experimental invasions

**abstract:** Numerous native species shift their range in response to climate change, and global trade has led to the transportation of many invasive species from their native range into new locations. By outcompeting their native counterparts, biological invaders pose a major threat to biodiversity. In addition to competition, negative effects of invasion may arise by negative ecological interactions with introduced enemies, parasites, herbivores, etc. but also by evolutionary dynamics which may either moderate or exacerbate the impacts of invasion. On the other side of the coin, some species succeed to resist invasion and impede the establishment and spread of the non-natives. The many idiosyncratic patterns observed today render long-term predictions of the success and impact of invasions difficult to make. Such inference is especially hindered by the lack of any comparative approach since unsuccessful invasions are hardly recognized. Understanding why most invaders fail at the first hurdle, while a selected subset of individuals pass through each stage of the invasion process and become successful invaders is necessary to unravel the mechanistic basis of invasion. In this project we aim to test to which degree successful and unsuccessful invaders differ in their phenotype and to identify the relative impact of evolution and environment on invasion success. To accomplish these objectives, the student will use experimental methods (combined with novel molecular phenotypic tools – according to the student's interests) to gain an integrative understanding of the ecological and evolutionary characteristics of the invasion process.

**onderzoeksgroep:** Terrestrial Ecology

**Begeleider(s):**

Masier	Stefano
Mortier	Frederik

**opmerking:**

**voorbehouden:**

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**abstract:** Dispersal is considered a key life history trait for most organisms. Broadly defined dispersal is a permanent movement away from an origin and settlement at a new location. Because dispersal in nature is difficult to quantify, it is often treated as purely stochastic. However, recent research showed that there are tradeoffs between competition, dispersal and other traits, where species with an inferior ability to use resources, can compensate by moving more frequently and over longer distances. These species gain an edge through the discovery and early colonization of fresh resource patches. However, these dispersers have to invest energy in movement and deal with the risks involved in crossing an inhospitable matrix and settling in a novel environment (costs of dispersal). In this thesis, we want to take it one step further and look at these possible tradeoffs within a species by using a polyphagous herbivore spider mite (*Tetranychus urticae*) as a model system. Similar to spider ballooning, spider mites can use wind currents to passively disperse through the air. In the two-spotted spider mite, there is significant variation in the propensity for individuals to exhibit the aerial dispersal behavior. As this aerial movement of mites is undirected, it comes at a high risk because the mites cannot know if they will end up in a suited environment. Our main hypothesis is that mites that disperse early, will be inferior competitors but more able to deal with the stress of a novel environment (plant defenses). To test this hypothesis we plan to separate early dispersers from more resident individuals and test their ability to compete with another species and settle in novel environments. This work could provide valuable information for invasion and conservation biology. Because animals that naturally are expanding their range due to global changes, will cope differently with competition and new environments than individuals of that same species that are philopatric and possibly moved to new habitats by humans. Depending on the interests of the student the thesis can focus mainly on metapopulation ecology, range expansion and invasions, or target the differences between dispersers and non-dispersers using molecular tools, life history and morphological measurements.

**onderzoeksgroep:** Terrestrial Ecology

**Begeleider(s):**

Goossens                      Steven

**opmerking:**

**voorbehouden:**

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**1517** The effects of anthropogenic impacts on the bioirrigation behaviour of sediment inhabiting fauna.

**abstract:** Bioirrigation is the process in which organisms pump oxygen- and food-rich water into their burrows for respiration and feeding purposes. This also oxidises surrounding anoxic sediments, thus creating an oxygenised microzone around the burrows. As the degradation of organic matter is most efficient in the presence of oxygen, these oxidised zones strongly promote the remineralisation of organic matter, which sinks onto the seafloor from the water column. This then frees up nutrients which can be released into the water column again. Especially in shallow coastal seas the bioirrigation process can strongly affect benthic-pelagic coupling. For certain bioirrigating species e.g. the Sand mason (*Lanice conchilega*) it is known that their pumping behaviour changes depending on the population density, but for other prominent bioirrigators in the North Sea such research has not yet taken place. Human activities activities (bottom trawl fishing, aggregate extraction, installation of offshore wind farms) at sea can alter sediment conditions, to which many species are highly sensitive. Species respond to these changes by either disappearing, or altering their occurrence (e.g. changes in densities). The student will be involved in fieldwork to collect organisms and sediment for experimental research. The objective is to quantify bioirrigation rates of several species found in the North Sea, and test whether these are density and context (sediment type) dependent. With this information we can then investigate hypothetical scenarios in which local species communities change (species composition or density). This thesis contributes to an ongoing project aiming to understand the consequences of local anthropogenic activities on ecosystem functioning.

**onderzoeksgroep:** Marine Biology

**Copromotor(en):**

Vanaverbeke Jan

**Begeleider(s):**

De Borger Emil

**opmerking:**

**voorbehouden:**

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**1392** Dictyota's Dilemma's: early development and plasticity in brown algae

**abstract:** During embryogenesis of plant systems the basic body plan of the organism is laid down. In a first step, the sides of the zygote that will develop into the basal attachment structure and the apical photosynthetic organs are determined in a process called cell polarisation. Because of practical advantages over land plant zygotes, the brown alga *Fucus* serves already for more than 150 years as a research model for cell polarization and early development in plant systems. Egg cells are liberated as radial symmetrical 'soccer ball-shaped' cells. After fertilization the cell is polarized according to the direction of the incoming light in a single step. Recent developments show a totally different image for embryogenesis in the common genus *Dictyota*. The spherical 'soccer ball-shaped' egg cells are also liberated in the surrounding medium, but elongate immediately after fertilization into a 'rugby ball-shaped' cell. In contrast to *Fucus* and most animal systems the embryo is polarized in two steps and the determination of the attachment pole can be postponed long after the first cell division. This suggests an unseen degree of developmental plasticity in the establishment of the apical-basal axis and asymmetric cell division. It is hypothesized that on basis of the accumulation of one or more pheromones and kairomones in the surrounding medium the zygote can determine whether it should postpone the development of its attachment structure, possibly promoting colonization of new habitats and inhibiting competition. In this research, it is envisaged to acquire more insights in the mechanisms that can influence the timing of polarization with the help of molecular tools, lab experiments and field work. The subject is diverse and can be reoriented in different directions depending on the personal interest of the student.

**onderzoeksgroep:** Phycology & PSB Plant Systems Biology-Root Development

**Copromotor(en):**

Bogaert                      Kenny

Beeckman                    Tom

**Begeleider(s):**

Bogaert                      Kenny

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**abstract:** Coral reefs are among the most biologically diverse and economically important ecosystems on the planet, providing ecosystem services that are vital to human societies and industries through fisheries, coastal protection, building materials, new biochemical compounds, and tourism. Yet in the last decade, coral reefs have continued to deteriorate as a result of human influences. A common phenomenon is the transitions from coral dominated systems to algal reefs. Many of these shifts involve the brown alga Lobophora. The latter seaweed, distributed worldwide in tropical and temperate regions, represents a major benthic component in tropical reefs. Its capacity to dominate large reefs areas following coral mortality and herbivory declines, attracted ecologists interest since the 80s. Surprisingly, its species richness has only recently been revealed, with an estimated >100 species distributed worldwide. To understand the causes behind Lobophora genetic diversity and ecological success, we will apply a population genetic approach. No population genetics study has yet been done on this genus. This thesis aims to examine if sexual versus asexual reproduction influences the capacity of the seaweed to outcompete corals. Thereto we study the mating system: defining the sexual phenotype (hermaphroditic or dioecious, selfing or outcrossing), detecting asexual/sexual reproduction, determine the haploid:diploid ratios; investigate the fine-scale population genetic diversity and structure within and among Caribbean (Curacao, Bonaire, Sababank) and Macaronesian (Canary Islands, Madeira, Azores, Cap Verde) populations of 3 species using 8-10 microsatellite; and evaluate the genetic drift of Lobophora populations (at fine to large scales). Practical work involves: (1) DNA extraction and microsatellite amplification, (2) Scoring of polymorphisms, (3) analysis of genotypic diversity, and (4) analysis of genetic structure. The project may also include fieldwork.

**onderzoeksgroep:** Phycology

**Copromotor(en):**

Vieira Christophe

**Begeleider(s):**

Vieira Christophe

**opmerking:**

**voorbehouden:**

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**abstract:** Knowledge of global patterns of species richness is fundamental for contemporary studies in ecology, evolution and conservation. Surprisingly, recent studies on global patterns of species diversity were primarily conducted across heterotroph taxa (e.g. foraminifera, fishes, mammals, corals; Tittensor et al. 2010), but did not consider the major oceanic and coastal primary producers, namely phytoplankton (e.g. cyanobacteria, diatoms, dinoflagellates, green algae, coccolithophore) and seaweeds (brown, green and red macroalgae). The biodiversity in some of these autotroph groups far surpasses most of the macro-heterotroph taxa, and adding these data could possibly alter the current picture of global patterns of marine species richness. Nevertheless, we are lacking such data for marine primary producers including seaweeds. Kerswell (2006) and Keith et al. (2014) provided a genus-level richness global distribution for the seaweeds. Genus richness, however, does not necessarily reflect species richness as recently shown in a prominent group of brown seaweed (Dictyotales; Steen et al. in prep.). The master thesis will specifically aim at examining global patterns of species richness across the three seaweed clades (Chlorophyta, Rhodophyta, Phaeophyceae). The student will assemble a dataset of geographical distribution of the marine seaweeds based on online databases (e.g. AlgaeBase) and available seaweed checklists for specific regions. Global spatial distribution maps of species richness will be derived from this dataset for all seaweeds, and for separated clades (e.g. phylum, family, order) to define specific richness distribution patterns. If the student progresses quickly on this part of the project, he/she will then assess the extent to which environmental conditions can predict species richness in seaweeds, following Keith et al. (2014) methodology.

**onderzoeksgroep:** Phycology

**Copromotor(en):**

Vieira Christophe

**Begeleider(s):**

Vieira Christophe

**opmerking:**

**voorbehouden:**

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**1519** Supertree: toward a comprehensive phylogeny for brown seaweeds (Phaeophyceae, Ochrophyta)

**abstract:** Large and comprehensive phylogenetic trees are desirable for studying macroevolutionary processes. The highly Phaeophyceae ('brown seaweeds'), comprises of over 2000 species (Guiry and Guiry, 2017). The Dictyotales, Ectocarpales, Fucales, and Laminariales are the phaeophycean orders that include the most species. Several species have significant commercial value, such as the genera Laminaria, Undaria, Macrocystis, Sargassum, and Fucus. Over the past few years, molecular-assisted taxonomic studies have significantly contributed to our knowledge of the biodiversity within several phaeophycean groups. Silberfeld et al. 2011 conducted a phylogenetic study with a subsample of species from each order to refine the understanding of ordinal-level phylogenetic relationships. Nevertheless, a comprehensive phylogeny of the Phaeophyceae, encompassing all presently known species, is now lacking. The master thesis will consist in producing a comprehensive phylogeny for the brown seaweeds. Thereto, we will apply a supertree approach. The student will assemble smaller subtrees for all Phaeophycean clade from previously published data. And if necessary, the student will construct trees de novo for some clades, by compiling sequences from the NCBI nucleotide database for a selection of mitochondrial, nuclear and chloroplast markers to construct clade-specific phylogenies; perform multiple sequence alignment; define the best-fit models of nucleotide substitution for each marker; and reconstruct phylogenetic relationships using Bayesian and maximum likelihood techniques on the multilocus dataset lower taxonomic level. A Phaeophycean super-tree will be summarized as the summary tree derived from the set of source compiled from the literature or de novo constructed, employing the super-tree state-of-the-art methods. If the student progresses well, a time calibration of the Phaeophycean phylogeny will be performed, as well as primary macroevolutionary studies on specific trait. Knowledge of Python or Perl scripting and of phylogenetic analyses are strongly recommended.

**onderzoeksgroep:** Phycology

**Copromotor(en):**

Vieira                      Christophe

**Begeleider(s):**

Vieira                      Christophe

**opmerking:**

**voorbehouden:**

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**1520** The battle of the ploidies, detecting differences in rate and mode of phenotypic evolution between haploid and diploid cells

**abstract:** Whole genome duplication (WGD) or polyploidisation provides an organism with an extra copy of the genome, which is entirely redundant and consequently has the potential to evolve new functionality. Despite this advantage of WGD, the stability of polyploid cells is limited mainly due to problems during cell division. Previous work demonstrated that many polyploid plants became established in stressful environments. We therefore hypothesize that stress can enhance polyploid establishment because their plastic phenotypes and genotypes can enable rapid adaptive changes that allow survival. To test this hypothesis, we are running an "long" term evolutionary experiment based on haploid and artificially induced diploid strains of the unicellular green algae *Chlamydomonas* growing in both benign and stressful environments. Using fitness assays, flow cytometry and RNA sequencing data you will follow up phenotypic evolution of the different lines over time and try to detect differences in phenotypic evolution between cells of different ploidy.

**onderzoeksgroep:** Phycology & PSB-Bio-informatics group

**Copromotor(en):**

Van de Peer Yves

**Begeleider(s):**

Aydogdu Eylem

Bafort Quinten

**opmerking:**

**voorbehouden:**

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## 1521 The battle of the ploidies, differences in genome evolution between haploid and diploid cells

**abstract:** Whole genome duplication (WGD) or polyploidisation provides an organism with an extra copy of the genome, which is entirely redundant and consequently has the potential to evolve new functionality. Despite this advantage of WGD, the stability of polyploid cells is limited mainly due to problems during cell division. Previous work demonstrated that many polyploid plants became established in stressful environments. We therefore hypothesize that stress can enhance polyploid establishment because their plastic phenotypes and genotypes can enable rapid adaptive changes that allow survival. To test this hypothesis, we are running an "long" term evolutionary experiment based on haploid and artificially induced diploid strains of the unicellular green algae *Chlamydomonas* growing in both benign and stressful environments. It is expected that the artificial diploid strains may not tolerate two copies of a single genome in a single nucleus very well, and therefore go through some dynamic genomic rearrangements especially in the early stages of their polyploid" existence. Using population wide pooled whole genome sequencing you will follow up genomic changes over time, look for signatures of selection, and detect whether polyploidisation does provide the expected genomic flexibility that increases evolvability."

**onderzoeksgroep:** Phycology & PSB-Bio-informatics group

### **Copromotor(en):**

Van de Peer Yves

### **Begeleider(s):**

Aydogdu Eylem

Bafort Quinten

### **opmerking:**

### **voorbehouden:**

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## 1522 Developing a CRISPR/Cas genome engineering toolkit for seaweeds

**abstract:** Despite the ever-increasing number of organisms with a published genome, only a few genomes of multicellular seaweeds have been reported. Consequently, molecular biological research is limited in a large group of red, brown and green algae with ecological and economic value. This research project wants to tackle this problem through development and implementation of reverse genetic research in these important marine primary producers. Recently, the phycology group of UGent (<http://www.phycology.ugent.be>) has been involved in sequencing and annotating the genome of *Ulva mutabilis* (sea lettuce), an emerging model organism for green macroalgae. *Ulva* is an important species in coastal benthic ecosystems around the world and is not only cultivated as food and feed, but also for bioremediation, in integrated aquaculture systems and as a putative biofuel source. Furthermore, *Ulva* is a laboratory model organism since it is easy to grow and maintain in culture as a clonal haploid gametophyte, has a short generation time, a small genome and can be stably transformed with vector plasmids. Molecular cloning and perturbation is a prerequisite for functional biology studies. In this research project, we want to develop a genome engineering toolkit and generate mutant lines to study carbon concentrating mechanisms. We have identified several putative regulators of CO<sub>2</sub> capture and carbon transport from the environment to the chloroplast in *Ulva*. To study these genes in detail, we will generate different vectors based on the CRISPR/Cas technology that will allow us to knock-out, knockdown or activate genes-of-interest. Furthermore, we will develop base-editing technology and tools to isolate and/or visualise genomic regions based on CRISPR/Cas. The generated vectors will be used to transform *Ulva*, after which the functionality and efficiency will be evaluated. This research project will assist in the establishment of *Ulva* as a model organism for seaweed molecular biology.

**onderzoeksgroep:** Phycology

**Copromotor(en):**

Jacobs Thomas

**Begeleider(s):**

Blomme Jonas

**opmerking:**

**voorbehouden:**

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**abstract:** Global climate change represents a major threat to marine ecosystems and species worldwide. Continuously increasing greenhouse gas emissions cause changes in oceanographic conditions such as temperature and pH, which in turn affect biological systems at levels ranging from individuals to entire communities. Understanding the response of marine organisms to a changing environment as a consequence of global change is therefore crucial. One of the mechanisms through which organisms can respond to fast environmental changes is transgenerational plasticity (TGP). TGP occurs when environmental conditions experienced by the parents influence the phenotype of the offspring. If the parental environment is a good predictor of the offspring environment, TGP can be adaptive and may buffer populations against rapid environmental change, providing time for genetic adaptation to catch up. In this master thesis, we will study the transgenerational impact of both ocean warming and ocean acidification on several ecophysiological traits in the brown macroalga *Dictyota dichotoma*, a key component of European coasts. Specifically, we will test how the length, timing, and magnitude of environmental stressors experienced by the parents can affect the transgenerational response observed in offspring. Thereto, we will collect algae from a European population of *D. dichotoma*. These algal individuals will then be used to conduct parents-to-offspring experiments, in which part of the parental generation will be conditioned to ocean warming and acidification while another part will be exposed to ambient conditions. Differences in fitness of the offspring when subjected to the same stressor conditions will yield information on the importance of TGP. The fitness-related traits we will measure include photosynthetic efficiency, respiration, survival, and fecundity. Practical work: fieldwork, laboratory experiments, PAM fluorescence, and algal respiration measurements.

**onderzoeksgroep:** Phycology

**Begeleider(s):**

Delva	Soria
Bogaert	Kenny

**opmerking:**

**voorbehouden:**

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**1525** Assessment of biodiversity and ecosystem services in crater forests in Western Uganda

**abstract:** Western Uganda comprises one of the most diverse tropical areas in the world. From a pure biodiversity point of view, forested areas surrounding crater lakes are of particular importance given the extreme fragility and at the same time peculiarity of these woodland ecosystems. However these woodland areas are seriously disturbed due to human agricultural practices and illegal felling for timber. Crater forests are important breeding areas and corridors for wildlife and therefore, it is necessary to find a balance between forest conservation and community-use for supporting local livelihoods. Since October 2017, the Belgian Directorate-General for Development Cooperation and Humanitarian Aid supports a 5-year programme in Western Uganda that includes the conservation and participatory forest management of several community forest fragments. The objective of this programme is to develop local livelihoods, but at the same time protect environmental conditions and avoid further degradation of woodlands. In order to facilitate the forest management of these crater forests in the near future, it is essential to make a thorough study of the diversity present in these forests and characterize the ecosystem services that they provide to the community.

The student should apply for a VLIR-UOS grant to cover for travel costs. In case this grant does not get awarded, the student should be able to cover travel costs him/herself. Per diem costs are covered by the supervisor.

**onderzoeksgroep:** Terrestrial Ecology

**Copromotor(en):**

Lens Luc

**Begeleider(s):**

de la Peña Eduardo

Evenepoel Hilke

**opmerking:** The student should apply for a VLIR-UOS grant to cover for travel costs. In case this grant does not get awarded, the student should be able to cover travel costs him/herself. Per diem costs are covered by the supervisor.

**voorbehouden:**

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**abstract:** Tanzania is home to one of the largest tree covers in the world, but woodland areas are also at risk. Woodlands near populated areas are dramatically felled for firewood or turned into charcoal. Reduction in woodland areas is estimated in a 3% year. Forests are important breeding areas and corridors for wildlife and therefore, it is necessary to find a balance between forest conservation and community-use for supporting local livelihoods. Since October 2017, the Belgian Directorate-General for Development Cooperation and Humanitarian Aid supports a 5-year programme in Northern Tanzania that includes the conservation and participatory forest management of several community forest fragments. The objective of this programme is to develop local livelihoods, but at the same time protect environmental conditions and avoid further degradation of woodlands. Two areas that are currently protected are the Selela and the Burger community forests. In order to facilitate the forest management of these community forests in the near future, it is essential to make a thorough study of the diversity present in these forests and characterize the ecosystem services that they provide to the community.

The student should apply for a VLIR-UOS grant to cover for travel costs. In case this grant does not get awarded, the student should be able to cover travel costs him/herself. Per diem costs are covered by the supervisor.

**onderzoeksgroep:** Terrestrial Ecology

**Copromotor(en):**

Lens Luc

**Begeleider(s):**

de la Peña Eduardo

Evenepoel Hilke

**opmerking:** The student should apply for a VLIR-UOS grant to cover for travel costs. In case this grant does not get awarded, the student should be able to cover travel costs him/herself. Per diem costs are covered by the supervisor.

**voorbehouden:**

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**1531** Fatty acid metabolism of copepods (Crustacea: Copepoda) under a global change scenario: a molecular approach

**abstract:** There is a growing concern about the ability to produce enough nutritious food to feed the global human population by the end of this century. Nevertheless, hope goes to marine resources like aquaculture as sources of proteins and fatty acids. In addition, global change is expected to impact the overall functioning of marine ecosystems, as well as the productivity of these marine resources and the efficiency of energy transfer from primary producers to top consumers. Copepods are small crustaceans and a major food source for marine fish larvae, both in the wild and in commercial production. They are known to contain high levels of so-called essential fatty acids (EFAs), being fatty acids (FA) that fish and humans cannot produce themselves and need to be obtained through their diet. However, how they assimilate and modify these FA remains largely unknown. In this light, this master thesis will contribute to the understanding of the biosynthesis and bioconversion of FA by copepods, and to which extent climate change will affect these processes. In recent decades, aspects of molecular biology and bioinformatics have found their way into the field of marine ecology. Through the use of transcriptomics, we can uncover the molecular pathways of FA biosynthesis and metabolism in copepods. Depending on the interests of the student, differences in gene expression under different abiotic regimes, different food regimes or different life stages will be analyzed. The practical work will consist of field work, short-term feeding experiments, molecular lab work and bioinformatics. Prior experience in molecular lab work would be an asset, as well as eagerness to learn bioinformatics.

**onderzoeksgroep:** Marine Biology

**Begeleider(s):**

Boyen                      Jens

**opmerking:**

**voorbehouden:**

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**1532** From sustainable aquaculture to ecosystem services: biodiversity assessment of epiphytic communities associated to seaweed farm in the Belgian North Sea

**abstract:** At-Sea Technologies is a Belgian joint venture company developing farming systems for large-scale seaweed aquaculture. In contrary to Asian countries producing seaweeds from industrial aquaculture system, European seaweed production is limited and comes mostly from wild harvests. Nevertheless, an increasing number of companies have shown their interest for seaweed products and import Asian seaweeds due to the low European production. Belgian authorities have developed a marine spatial plan for the Belgian Part of the North Sea and put aside sea area for sustainable aquaculture. Because of the eutrophication, integrated and extractive aquaculture systems including seaweed production are foreseen. In this context, At-Sea Technologies is farming brown seaweed (*S. latissima*) in Nieuwpoort on innovative cultivation supports. Besides biomass production and nutrients extraction, seaweed farming changes ecosystem properties by providing biogenic supports for the development epiphytic communities. Therefore, UGent and At-Sea Technologies started to monitor the communities associated to a Norwegian seaweed farm in order to model fish stocks response to the extra food supplied by the aquaculture system. The present work proposes to assess biodiversity of epiphytic invertebrates associated to seaweed farming in the Belgian Part of the North Sea from an ecosystem services perspective. The study consists in field sampling campaigns in Nieuwpoort on the offshore cultivation site and laboratory measurements to weight and identify the organisms. The obtained data will give insight in the complexity of the seaweed farm and associated invertebrates.

**onderzoeksgroep:** Marine Biology & ENVOC (Environmental technology and clean technology), LA11

**Copromotor(en):**

Dewulf Jo

**Begeleider(s):**

Groenendaal Bert

Pycke Benny

De Troch Marleen

Préat Nils

**opmerking:**

**voorbehouden:**

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## 1533 Responses of copepods to stressors in temperate and tropical estuaries

**abstract:** Estuaries are coastal ecosystems that are under increasing pressure from anthropogenic impacts such as industry and agriculture. Worldwide, large populations live in close proximity to estuaries and local communities (especially in developmental countries) depend on its resources. With environmental conditions varying greatly on seasonal and daily basis, aquatic organisms in estuaries are naturally well-adapted to physiological stress in a changing environment. This makes estuarine systems useful models to study ecological and evolutionary responses of organisms to stressors such as pollution and climate change. These stressors will have an impact on the ecosystem's primary producers and can cause a cascade of unfavorable responses throughout the food web. The basic process in food web dynamics is the transfer of energy from one trophic level to another. This can be seen as the assimilation of solar energy into primary production, and energy flow from plants to herbivores to predators. Copepods are small crustaceans found at the base of the food web in all aquatic ecosystems and play a pivotal role both as consumers of primary production and as a food source for higher trophic levels. These copepods contain high levels of fatty acids which have a crucial role in the maintenance of physiological functions of many organisms. Fatty acids are also important trophic markers that can be used to track the transfer of energy in food webs. Balanced fatty acid profiles in copepods are important for a healthy and stable ecosystem and the impact of stressors will be translated in changes in fatty acid profiles, a reduced energy transfer efficiency to higher trophic levels and less fish biomass in the ecosystem. The student will help process copepods sampled in the Westerschelde estuary (the Netherlands) and the Guayas estuary (Ecuador), help with fatty acid extractions in the lab, fatty acid profiling using gas chromatography and the analysis of chromatograms. The student should be keen to work with a microscope and in a lab environment. There might be a chance for field work in Ecuador, but the student will be responsible for financing his/her own travel costs or can apply for a travel grant.

**onderzoeksgroep:** Marine Biology

**Copromotor(en):**

Dominguez Granda Luis Elvin

**Begeleider(s):**

Wellens Siel

**opmerking:**

**voorbehouden:**

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**1535** Authenticity and quantification of mixed seafood samples using real-time PCR

**abstract:** Seafood is a high quality and healthy food item, but the European seafood production is insufficient to feed the human population. As a result, the vast majority of seafood in Europe is imported. Many seafood products contain mixtures of different species, meaning that all species should be clearly mentioned on the product labels. However, this may be subject to fraud. Many seafood products are processed which makes morphological identification impossible. DNA-based approaches may offer an efficient and reliable method to investigate whether the product label accurately reflects the content of the seafood sample. In this thesis, a quantification tool will be validated to assess the percentage of particular fish species present in processed products. These results will be compared with the product label to identify potential fraud. For this purpose qPCR and the more sophisticated method digital droplet PCR (ddPCR) will be applied to establish copy numbers of target DNA which, in turn, will be used to count the initial share of fish ingredients used in seafood processing.

**onderzoeksgroep:** ILVO (Oostende)

**Copromotor(en):**

Robbens                      Johan

**Begeleider(s):**

Maes                              Sara

**opmerking:**

**voorbehouden:**

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## **1536** Determining the microfouling bacterial communities linked to corrosion in ballast water tanks of marine vessels

**abstract:** Biofouling formation on vessels and other submerged structures is a dynamic process, with primary colonization by bacteria and diatoms happening within hours. These microbial organisms, together with extracellular polymeric substances, facilitate the adhesion of more particles and larger organisms. Biofouling causes severe economic and ecological costs. For example, the adhesion of macro-organisms increases the resistance of ship hulls, which leads to a much higher fuel consumption. Already much research has been conducted on the relation between macro-fouling and coatings in order to develop environmental friendly antifouling agents. However, insight in the coupling between the physico-chemistry of the coating and the developmental processes of most marine micro-fouling organisms is largely lacking. Corrosion is an oxidative process, which can be substantially reduced by adding low oxygen gas to the medium. Sulphur-oxidizing bacteria have been linked to this corrosion process, but it remains unclear whether this type of bacteria are really present in ballast water tanks in marine vessels or if other micro-organisms can be linked to corrosion as well. In this thesis, we aim to identify the different bacterial communities in the ballast water tanks of marine vessels. Comparison of sites with different degrees of corrosion, including control sites with no corrosion, in different ships' ballast water tanks, will highlight which specific bacterial groups can be linked to the corrosion process. Both taxonomic analyses, using DNA sequencing methodologies, and the determination of some biochemical and morphological characteristics will be performed.

**onderzoeksgroep:** ILVO (Oostende)

### **Copromotor(en):**

Hostens                      Kris

### **Begeleider(s):**

Maes                         Sara

### **opmerking:**

### **voorbehouden:**

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## 1537 Metabarcoding macrobenthos communities in the North Sea: do DNA and morphology tell the same story?

**abstract:** Human activities such as marine aggregate dredging, construction of wind turbines and dredge disposal alter the species composition and structure of the seafloor. Such changes in habitat, especially impact the organisms living in the sediment, because benthic organisms have low dispersal once they reach adulthood. As such, they cannot easily escape the stressful habitat. At ILVO, we conduct long term monitoring studies to investigate how macrobenthic communities change in relation to these human activities. Species are identified using morphological characteristics, and their abundance/biomass are determined, so biodiversity indices can be calculated. This approach requires taxonomic expertise, and is often time consuming. DNA approaches may complement, and speed up the characterisation of these communities, but so far comparative studies between morphology-based and DNA-based methods for the North Sea are lacking. In this thesis, we aim to identify samples from the four typical macrobenthic communities found in the Belgian part of the North Sea (*Macoma balthica*, *Abra alba*, *Nephtys cirrosa* and *Ophelia borealis*) using both approaches, being morphological identification and amplicon sequencing. Diversity estimates calculated from DNA that is directly obtained from the ethanol preservative as well as from mixed tissue samples will be compared for their accuracy to morphologically identified macrobenthic samples.

**onderzoeksgroep:** ILVO (Oostende)

**Copromotor(en):**

De Backer                      Annelies

**Begeleider(s):**

Maes                              Sara

**opmerking:**

**voorbehouden:**

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**abstract:** Short description of the project: Root growth and development are controlled by an intricate gene regulatory network. One of the still enigmatic fundamental processes of root development is programmed cell death (PCD). PCD is the ultimate differentiation step of several tissues in the root, for instance the xylem and the root cap, and is crucial for regular root growth. However, which molecular mechanisms prepare a cell for initiation and execution of PCD is still largely unknown. The focus of your project will lie in the investigation of the signaling network that is activated in the minutes prior to cell death to trigger the active suicide of the cell. You will be part of the international Programmed Cell Death team investigating the molecular fundamentals of developmental cell death process in the model plant *Arabidopsis thaliana*. Our projects deploy the latest genetics, proteomics, and cell biological approaches, and will provide you with an excellent hands-on experience in one of the leading plant science institutes in Europe. For more info, or if you would like to visit our lab at PSB, please mail to [moritz.nowack@vib.be](mailto:moritz.nowack@vib.be) ! Aim: At the end of your master's project you will have undergone a thorough training in methods of molecular biology, genetics and developmental cell biology in a young team of scientists (<http://www.psb.ugent.be/programmed-cell-death>). Scientifically, you will have gained insight into PCD regulation during root development in the model species *Arabidopsis thaliana*, and contributed to the understanding of this complex biological process by detailed functional analysis of key signaling events that regulate cellular differentiation and PCD. Eventually, your research might contribute to find the new solutions we urgently need to sustainably provide food and plant-based material for an ever increasing human world population. Techniques: CRISPR-based genome editing PCR (molecular cloning, genotyping, qPCR) Phenotypic analysis of mutant or mis-expression lines in *Arabidopsis* Gene expression analysis by promoter::reporter fusions Protein localization by protein::reporter fusions Analyses of protein-protein interactions (Y2H, TAPtag) Electron Microscopy, Confocal Microscopy, Spinning Disc Microscopy

**onderzoeksgroep:** PSB Plant Systems Biology - PCD Programmed Cell Death

**Copromotor(en):**

Nowack Moritz

**Begeleider(s):**

Buono Rafael

**opmerking:**

**voorbehouden:**

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**1540** Into darkness: shifts in bat and night-active insect communities in response to tree composition and landscape context.

**abstract:** The current global change is affecting communities worldwide leading to shifts in community composition but also in biomass. Human societies manage the landscape to their needs often leading to intense fragmentation and isolation of habitat patches. The TREEWEB research platform is designed to explore how both tree composition shifts and fragmentation affect communities across the food chain and ecosystem functioning. In this project we want to look at the response of night-active insects and their predators, bats, to changes in tree species composition but also to different isolation. Field work will include setting up bat loggers, setting up light traps, and collecting the insects. The field work will take place between July and September 2018. Lab work will include identification of the insects and processing of the bat logger data. This project will benefit from the many dataset already available within the TREEWEB to complement the data analysis. This project require to be able to go independently to different forest fragments (maybe also in the night) which require that the student be in possession of a car.

**onderzoeksgroep:** Terrestrial Ecology

**Begeleider(s):**

Dekeukeleire Daan

**opmerking:**

**voorbehouden:**

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**1541** Silent spring: changes in trophic interactions between birds and insects along a fragmentation gradient.

**abstract:** Trophic interactions are essential for ecosystem functioning transferring energy, matter and nutrients up and down the food chains. Yet current management of the landscape leads to high fragmentation with many detrimental impacts on these interactions. The TREEWEB research platform is designed to explore how both tree composition shifts and fragmentation affect communities across the food chain and ecosystem functioning. In this project we want to look at the links between insects and bird communities in forest fragments of different size and isolation but also with different tree composition. Field work will include collecting the bird communities data through bird calls, collecting the insect communities using flight traps. Most of the field work will take place in the spring (March – May) 2018, a field technician will be available to help the student collect the data. Further field work in summer may be carried over depending on the student interests. Lab work will consist of identification of the insect samples. In this project many additional dataset will be made available for the student, for instance on bark-dwelling arthropod communities which might provide nice addition to the analysis. This project require to be able to go independently to different forest fragments which require that the student be in possession of a car.

**onderzoeksgroep:** Terrestrial Ecology

**Begeleider(s):**

Dekeukeleire Daan

**opmerking:**

**voorbehouden:**

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**1544** Site conditions of Atlantic old acidophilous beech and oak forests on poor sandy plains

**abstract:** In this project we'll focus on European protected Atlantic old acidophilous beech forests (habitat 9120) and oak forests (habitat 9190) on poor sandy plains in the Kempen, a region in Northern-Flanders. Well-developed old forests on sandy soils are rare in Flanders, and even rare in the whole Northwest of Europe. We often assume that oak forests on acid, nutrient poor, sandy plains are a climax stage, but there are strong indications that another climax type (habitat 9120) develops if the soil profile changes. Therefore we wish to answer the following research questions: • What are the environmental differences between 9190 and 9120 on sandy soils? • When, how and how fast is this secondary succession occurring? To answer these questions we study a chronosequence of forests on sandy soils in the phytogeographic district of 'the Kempen', a priori selected executing a GIS-analysis. We collect data in the field (vegetation measurements, soil samples) and gather information about the management and historical landuse of the sites. Based on this information we will be able to investigate the site conditions of both habitat types in more detail. This thesis can be situated in the framework of the INBO-project HabNorm (2015-2019). In this project biotic and abiotic site characteristics of international and regional important vegetation types are quantified and thresholds to ensure a sustainable conservation status are defined. The student will be part of an enthusiastic team (forest ecophysiology and soil-experts). First, the student will do measurements in the field. Second, the student will use data from our FlaVen-dataset. He/she will gain experience with specific software to collect and manage vegetation data and improve his/her R-, Access- and GIS-skills. Also a literature study is needed about the environmental conditions of the habitat type on (historic) reference sites. The student will be stimulated to organize discussions with different experts. At the end we aim an A1-publication as a final product. References De Keersmaecker L, Rogiers N, Vandekerckhove K, De Vos B, Roelandt B, Cornelis J, De Schrijver A, Onkelinx , Thomaes A, Hermy M, Verheyen K (2013). Integrating the concept of ancient forest plant species into a Potential Natural Vegetation map - a case study from Flanders, northern Belgium. *Folia Geobotanica* 48, 137-162. Leuschner C. & Rode M.W. (1999). The role of plant resources in forest succession: changes in radiation, water and nutrient fluxes, and plant productivity over a 300-yr-long chronosequence in NW-Germany. *Perspectives in Plant Ecology, Evolution and Systematics* 2: 103-147. Leuschner C (1997) Das Konzept der potentiellen natürlichen Vegetation (PNV): Schwachstellen und Entwicklungsperspektiven [The concept of Potential Natural Vegetation: weaknesses and perspectives for modification] (in German). *Flora* 192, 379-391.

**onderzoeksgroep:** Terrestrial Ecology&INBO Brussel Team Milieu&Klimaat

**Copromotor(en):**

De Keersmaecker Luc

**Begeleider(s):**

De Keersmaecker Luc

Raman Maud

**opmerking:****voorbehouden:**

**1545** The effect of species-area relation on local conservation status indicators: case study on indicator forest herbs

**abstract:** The European habitats directive mandates the monitoring of the habitat types and species it protects. In a six yearly report, each member state has to give figures on the percentage of each habitat type that is in a favourable conservation status. This favourable status is based on the evaluation of a set of indicators which determine the local conservation status. For Flanders (and most other regions and countries), these indicators are defined as stand wide or patch wide indicators. For example, to have a favourable status of the habitat type Asperulo-Fagetum (9130) more than 5 key herb species should be present at the stand scale. In order to monitor the quality of the Flemish network of habitat types, a set of permanent plots is followed up. This is done for the simple reason that permanent plots can be revisited and re-evaluated more easily than a stand or patch of habitat. However, some indicators (e.g. the number of key forest herbs) are difficult to evaluate at plot scale as they are originally defined at stand scale. In order to have better insight in this problem, we want to study the effect of the species-area relation on the number of key forest herbs. Based on this relation, we can indicate how many plots are needed from a certain stand or forest before we can evaluate the key herb species indicator. To study the species-area curves, we will first explore the available data. Both the Flemish forest inventory, as well as the monitoring of the Flemish forest reserves and the inventories for forest management plans all use the same 16x16m vegetation plots. From these, we can extract plots that are grouped within a similar forest stand of a certain forest habitat type. Preferably, a species poor habitat (likely Fago-Quercetum, 9120) and a more species rich one (e.g. Stellario-Carpinetum, 9160) will be selected. Based on the available data, we will select a study area (e.g. Meerdaal forest) to gather additional data. In this study area we will map the presence of key herb and tree species in stands of the selected habitat types (for example 9120, 9160). This field work needs to take place in March and April. Based on the number of species at stand level, we will evaluate whether the stand is in a favourable condition for this indicator. Secondly, we will evaluate the area needed to significantly discriminate the group of favourable and unfavourable stands and the threshold (number of herb or tree species for this number of plots) that needs to be used to distinguish both groups. Useful references: Storch 2016. The theory of the nested species-area relationship: geometric foundations of biodiversity scaling. *JVS*, 27: 880-891 <http://onlinelibrary.wiley.com/doi/10.1111/jvs.12428/abstract> Van Calster & Damgaard 2017. Integral occurrence probability: combining cover and relative shoot frequencies based on bounded point-to-plant distances. *JVS*, 28: 824-837 <http://onlinelibrary.wiley.com/doi/10.1111/jvs.12527/full>

**onderzoeksgroep:** Terrestrial Ecology&INBO Brussel Teams Boscologie&-beheer en Biometrie,methodologie en kwaliteitszorg

**Copromotor(en):**

Van Calster Hans

Thomaes Arno

**Begeleider(s):**

Thomaes Arno

Van Calster Hans

**opmerking:**

**voorbehouden:**

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**abstract:** Global warming and population growth severely impact agricultural production and agricultural adaptation should occur sustainably without affecting ecosystems. One way to address this is by understanding processes that determine plant productivity. In our research team we study how leaves grow and how we can expand the area with which they harness solar energy and convert CO<sub>2</sub> to chemical energy that can be used by the plant to grow. Maize is one of the most economically important crops that can be grown in distinct geographical regions around the world. In addition, maize has both cereal and fodder value, making it an extremely versatile crop. Over the past years, we gained information on the molecular and cellular mechanisms of how the maize leaf grows in the length direction. However, we noticed that an increased growth in the length direction is not linearly correlated to an increase in lamina width and area. In this project, the student will study the relationship between proximo-distal and mediolateral regulation of maize leaf growth, starting from leaf size mutants.

**onderzoeksgroep:** Vakgroep Plantenbiotechnologie en Bio-informatica - onderzoeksgroep Systems Biology of Yield

**Copromotor(en):**

Nelissen                      Hilde

**Begeleider(s):**

nog te bepalen

**opmerking:**

**voorbehouden:**

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**1546** The role of the peptidase DA1 and the E3-ligase BIG BROTHER in regulating cell proliferation and senescence in plants

**abstract:** How plants grow from a small seed to their final stature appeals to the imagination of many people. Uncovering the molecular mechanisms that determine plant organ growth and size is therefore a challenging and fascinating research topic. The E3-ligase BIG BROTHER (BB) and the peptidase DA1 work in concert to restrict cell proliferation and leaf longevity in Arabidopsis. Mutants of these genes produce larger organs that contain more cells whereas overexpression reduces growth. Recent findings have demonstrated the importance of this pathway for yield in crop plants, such as maize and Canola. Molecularly, BB activates the latent peptidase DA1 by ubiquitination in a novel activation-repression mechanism. Subsequently, the activated DA1 destabilizes positive regulators of growth, such as UBP15 and the transcription factors TCP14 and TCP15. In addition, DA1 cleaves and destabilizes BB in a negative feedback loop, resulting in a unidirectional transition from cell proliferation to cell expansion. Recently, we have found that two additional ubiquitin-specific proteases, UBP12 and UBP13, interact with DA1 in vivo. These de-ubiquitinating enzymes might play an important role in plant growth and development by de-activating DA1 and thus promoting cell division. During this master thesis, we will apply various challenging molecular techniques, such as recombinant protein production, in vitro ubiquitination and de-ubiquitination and phenotypic assays (leaf size measurements, microscopy, mutant complementation) to further explore this growth regulating pathway.

**onderzoeksgroep:** Vakgroep Plantenbiotechnologie en Bio-informatica - onderzoeksgroep Systems Biology of Yield

**Copromotor(en):**

Vanhaeren Hannes

**Begeleider(s):**

Vanhaeren Hannes

**opmerking:**

**voorbehouden:**

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**1547** Resolving the Neotropical Magnoliaceae phylogeny: what does the chloroplast genome predict?

**abstract:** The relationships between the major sections and species of the Neotropical Magnoliaceae remains unresolved due to lack in informative DNA sequences, and an underrepresentation of the diversity in the phylogenetic analyses up to date. In this thesis, both problems will be overcome by using a new technique: Hyb-Seq, which is a combination of target enrichment (=> low-copy nuclear genes) and genome skimming (=> high-copy genomic data, cf. chloroplast, ITS, ...). The technique works with DNA probes that amplify short DNA sequence reads, which is a great advantage as (fragmented) DNA extracted from herbarium specimens can be used as input. Many Neotropical Magnoliaceae species are documented in herbaria and therefore these Magnolia species can be included when applying this technique. In this thesis, the student will 1) execute DNA extractions, 2) measure the DNA content and quality, 3) run the bio-informatics on the raw genomic data: assemble and align datasets of chloroplast genes, 4) reconstruct phylogenetic hypotheses: ML-trees, Bayesian-trees,... and interpret the found relationships in terms of the species distributions and morphology.

**onderzoeksgroep:** Spermatophytes

**Copromotor(en):**

Samain Marie-Stéphanie

Goetghebeur Paul

**Begeleider(s):**

Veltjen Emily

**opmerking:****voorbehouden:**

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Interference or exploitation competition? Experimental studies on the interspecific interactions of cryptic species and the importance of priority effects.

**abstract:** Interference - one species interferes with the ability of another species to obtain resources - and exploitation competition - the superior species depletes the resource faster or better, not leaving enough resources available for inferior species - are the two main types of competitive interactions between closely related species. These types of competition mostly increase with relatedness between species, according to classical competition theory (Darwin, 1859). As a consequence, competition is predicted to be high in cryptic species - closely related species that are morphologically indistinguishable, but show consistent genetic differences. Cryptic diversity is prominently present in coastal nematodes and the best studied model 'species' in this context is *Litoditis marina*, which is mostly found associated with decomposing macroalgae. Both competition and facilitation between these cryptic species have been reported in closed, homogeneous microcosms. Changing the composition of the cryptic species changes the interactions between them and abiotic factors - temperature and salinity- also have an influence on the interactions between the species. The nature of this competition, however, is not clear yet. Moreover, species that start a new population early in a certain patch may have a greater chance of being dominant than later arriving species (priority effects) and this may help to explain why the species are able to co-occur in different species compositions in the field . In this master thesis, we will test whether interference competition and priority effects exist within the cryptic species complex of *Litoditis marina*. Marine nematodes produce mucus trails, which may interfere with the growth of other species. In lab experiments we can test if the presence of such mucus trails, without the presence of the nematodes, influences the population growth of other species. In other lab experiments, we can test if competitively inferior species may be able to remain dominant in a certain patch if they have a bigger starting population and/or an earlier arrival compared with a competitively superior species. This thesis will consist mainly of laboratory work (setting-up experiments, molecular techniques, ...).

**onderzoeksgroep:** Marine Biology

**Copromotor(en):**

Derycke Sofie

De Meester Nele

**Begeleider(s):**

De Meester Nele

**opmerking:**

**voorbehouden:**

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**1551** Interspecific and intraspecific competition in a changing world: next-generation-sequencing and lab experiments in a cryptic species complex

**abstract:** According to classical competition theory, interspecific competition increases with relatedness between species (Darwin, 1859), rendering coexistence of cryptic species - closely related species that are morphologically indistinguishable, but show consistent genetic differences - unlikely. Cryptic diversity is prominently present in coastal nematodes and the best studied model 'species' in this context is *Litoditis marina*, which is mostly found associated with decomposing macroalgae. Both competition and facilitation between these cryptic species have been reported in closed, homogeneous microcosms. Changing the composition of the cryptic species changes the interactions between them and abiotic factors - temperature and salinity- also have an influence on the interactions between the species. Moreover, evidence for intraspecific competition within cryptic species was found. Nevertheless, several studies have shown that cryptic species can co-occur at small geographical scales. Four of the cryptic species of *Litoditis marina* frequently co-occur in the littoral zone of the south-western coast and estuaries of the Netherlands. The underlying mechanisms of this co-occurrence remain unknown. Species may be able to co-occur if they show differential niches in feeding behaviour. Next-generation-sequencing can be used to determine the bacterial diets of the cryptic species to test if such a niche differentiation exist. In this master thesis, different combinations of the species (interspecific competition) and different starting densities (intraspecific competition) will be tested to elucidate the effects and the relative importance of intra- and interspecific competition in this cryptic species complex. Response variables tested can be population growth rate and diet composition. Moreover, climate change models predict changes in salinity and temperature, so different abiotic conditions will be studied, in order to investigate possible effects of global change on the interactions and thus on the co-occurrence of the species. This thesis will consist mainly of laboratory work (setting-up experiments, molecular techniques, ...).

**onderzoeksgroep:** Marine Biology

**Copromotor(en):**

De Meester Nele

Derycke Sofie

**Begeleider(s):**

De Meester Nele

**opmerking:**

**voorbehouden:**

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## 1552 Investigating the effects of global warming on the microbiome of fouling fauna: impacts on the N-cycle

**abstract:** Marine environments are being threatened by global change. Increased atmospheric CO<sub>2</sub> concentrations lead to global warming on the one hand, and on the other hand to a decrease in ocean pH. Moreover, marine coastal areas are increasingly used for the production of marine renewable energy, mainly by installing offshore wind farms. As such, artificial hard substrates are being introduced in areas that are otherwise characterized by sandy sediments. These artificial hard substrates are being colonized by a fouling fauna: for instance the bivalve *Mytilus edulis*, the amphipod *Jassa herdmani* and tunicate *Diplosoma listerianum*. They can serve as a predictable and resource-rich surface for microbial communities and are to be considered as biogeochemical hotspots in the aquatic environment producing considerable amounts of N<sub>2</sub>O, and in this way affecting the N-cycle. N<sub>2</sub>O is considered a highly potent greenhouse gas, and thus also contributing significantly to global warming. In this thesis, we will investigate the microbial communities involved in these processes, and how they are affected by climate change. We will incubate the organisms, described above, under the current situation and a predicted global warming scenario to perform detailed investigations on their microbiome. We will (1) investigate the composition of the entire microbial biofilm by 16S rDNA sequencing, and (2) perform a detailed analysis of functional genes involved in the N-cycle by targeted Next Generation Sequencing on the functional genes *nirK/nirS* and *nosZ*. In this way, (1) prokaryotic families with a documented role in N-cycling can be detected, such as N-fixing and anammox bacteria and nitrifying Archaea and bacteria and (2) the expression of functional genes related to N<sub>2</sub>O will be investigated. These results can give us insights about the impact of fouling fauna on the N-cycle and the possible effects of global warming on these processes.

**onderzoeksgroep:** Marine Biology

**Copromotor(en):**

De Meester Nele

**Begeleider(s):**

De Meester Nele

**opmerking:**

**voorbehouden:**

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**1553** Pollutants and cryptic species: can toxicants alter the microbiome of cryptic species and influence their abiotic tolerances?

**abstract:** Anthropogenic activities have been altering natural environments for decades, where contamination by man-made pollutants poses a great risk for ecosystem health and biological diversity. Environmental risk-assessment methods have been developed and applied in order to prevent and/or mitigate human impacts, like single-species toxicity tests. Single-species are widely used as bio-indicators of pollution and environmental degradation, and data resulting from such assays are often used by regulatory agencies in the establishment of environmental regulations. However, the existence of cryptic species requires attention and care when interpreting data from single-species assessments. Cryptic species are morphologically indistinguishable, but show consistent genetic differences and may show species-specific tolerances towards pollutants. This was already proven for cryptic species of the marine nematode *Litoditis marina*. Pollutants may also influence the microbiome (bacteria associated with the gut) of a species. A species' microbiome may also be important for specific abiotic tolerances (e.g. salinity fluctuation) and was also proven to be different among the cryptic *L. marina* species. As a consequence, pollutants may not only influence the microbiome but also the abiotic tolerances of the species. In this thesis we will test if the microbiomes of the species will change depending on pollutants and if their tolerance for specific abiotic conditions will be influenced. An experiment will be conducted with different cryptic species, pollutants and abiotic conditions. Next Generation Sequencing will be used to determine the microbiome of the species and to elucidate the effect of pollutants on it.

**onderzoeksgroep:** Marine Biology

**Copromotor(en):**

De Meester Nele

**Begeleider(s):**

De Meester Nele

**opmerking:**

**voorbehouden:**

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**1554** Pollutants and cryptic species: investigating transgenerational effects on the performance and the microbiome of cryptic species.

**abstract:** Anthropogenic activities have been altering natural environments for decades, where contamination by man-made pollutants poses a great risk for ecosystem health and biological diversity. Environmental risk-assessment methods have been developed and applied in order to prevent and/or mitigate human impacts, like single-species toxicity tests. Single-species are widely used as bio-indicators of pollution and environmental degradation, and data resulting from such assays are often used by regulatory agencies in the establishment of environmental regulations. However, the existence of cryptic species requires attention and care when interpreting data from single-species assessments. Cryptic species are morphologically indistinguishable, but show consistent genetic differences and may exhibit species-specific tolerances towards pollutants. This was already proven for cryptic species of the marine nematode *Litoditis marina*. Besides species-specific differences in resistance to pollution, resistance may also be transgenerational: some individuals may be more resistant toward pollutant than others and can pass this on to next generations. Pollutants may also influence the microbiome (bacteria associated with the gut) of different individuals/species. The microbiome (bacteria associated with the gut) of a species possibly plays an important role on organisms' tolerance to different toxicants. In this thesis we will subject species to pollutants and check their performance (population growth, behaviour, ...). Moreover effects on the microbiome will be checked with Next Generation Sequencing to test if an effect on their microbiome can be found. Subsequently, we will collect the next generations of these species and raise them in treatments without pollution, to investigate if the species' microbiome remains affected. Moreover, we will also subject them to pollutants, to see if they react differently than organisms from which previous generations have never been in contact with toxicants.

**onderzoeksgroep:** Marine Biology

**Copromotor(en):**

De Meester Nele

**Begeleider(s):**

De Meester Nele

**opmerking:**

**voorbehouden:**

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**1556** Remote sensing of coastal algal blooms using hyperspectral imaging

**abstract:** In the Belgian coastal zone and adjacent lagoons (such as the Spuikom in Oostende), dense algal blooms occur from early spring to autumn. These fuel coastal food webs but can also become a nuisance (e.g. massive foam accumulation by the colonial haptophyte *Phaeocystis*). Monitoring such blooms is crucial for understanding and predicting their occurrence. Because the blooms are spatially complex and highly dynamic, optical remote sensing, with its high spatial and temporal resolution, is ideally suited for monitoring purposes. While current satellites carry sensors with low spectral resolution (allowing only a very general description of algal biomass), future sensors will be hyperspectral. Detailed spectral information will open up new perspectives for discriminating algal taxonomic and functional groups on the basis of differences in light absorption (~pigment composition), fluorescence, but also size and shape. In the thesis, which forms part of the Belgian project HYPERMAQ, we will analyze absorption and reflectance spectra of micro- and macroalgae from both cultures and field samples, in order to explore the development of new algorithms for discriminating algal groups in turbid coastal waters using hyperspectral remote sensing. The thesis will involve bio-optical analysis (spectrophotometry, spectrofluorometry), pigment analysis and hyperspectral imaging of both algal cultures and field samples from the Spuikom and the North Sea.

**onderzoeksgroep:** Protistology & Aquatic Ecology

**Copromotor(en):**

Vyverman Wim

**Begeleider(s):**

Castagna Mourao e Alexandre

**opmerking:****voorbehouden:**

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**abstract:** *Magnolia lacandonica* is an Endangered tree species which belongs to the family Magnoliaceae. The species is endemic to the Lacandon tropical rainforest of Chiapas, Mexico. Several populations occur in protected areas, but the number of trees which occur outside protected areas has been drastically reduced due to conversion of rainforest to agriculture and pasturelands. By using conservation and landscape genetic analyses, we want to 1/ test for population structure: are the sampled populations true genetic demes, or are there multiple populations together making up a genetic deme? 2/ estimate the health of the species overall: are there specific populations that show a high amount of genetic variation?, and 3/ understand the impact of habitat fragmentation in a spatial context. With the insights on the genetics of the species, it is aimed to propose a realistic in situ conservation management plan, to execute in cooperation with the local Lacandon community of Nahá (municipality Ocosingo) and a conservation NGO in the municipality of Yajalón.

**onderzoeksgroep:** Spermatophytes

**Copromotor(en):**

Goetghebeur Paul

**Begeleider(s):**

Veltjen Emily

**opmerking:**

**voorbehouden:**

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**1558** Bio-inspired calcium carbonate nanoparticles as antimicrobial agents.

**abstract:** Bio-inspired calcium carbonate nanoparticles as antimicrobial agents. The Evolution and Optics of Nanostructures (EON) group seeks a student to work at the interface of chemistry/materials science and biology in developing a new antimicrobial material. The avian eggshell is a complex structure consisting of several layers of calcium carbonate and minerals within an organic matrix. In many species, a non-calcified layer called the cuticle covers the outer surface. We have shown that bird species breeding in wetter environments have cuticles composed of mineralized vaterite ( $\text{CaCO}_3$ ) or hydroxyapatite ( $(\text{Ca}_{10}(\text{PO}_4)_6(\text{OH})_2)$ ), nanometer-scale spheres (D'Alba et al. 2016). These nanospheres provide an effective barrier to bacterial attachment (D'Alba et al. 2017) and the rough topography that they confer to eggshell surfaces may explain their antimicrobial effect. Size of nanospheres may also impact the effectiveness of these properties. However, these hypotheses have not been experimentally tested. This project has two aims: 1) to fabricate  $\text{CaCO}_3$  nanospheres of varying dimensions and 2) to test the antimicrobial effects of these bio-inspired nanospheres. References L. D'Alba, R. Torres, G.I.N. Waterhouse, C.M. Eliason, M.E. Hauber and M.D. Shawkey In press. What does the eggshell cuticle do? A functional comparison of avian eggshell cuticles. *Physiological and Biochemical Zoology*. L. D'Alba, R. Maia, M.E. Hauber and M.D. Shawkey. 2016. Evolution of eggshell cuticle in relation to nesting ecology. *Proceedings of the Royal Society of London B* 283:1836.

**onderzoeksgroep:** Evolution and optics of nanostructures (EON)

**Begeleider(s):**

nog te bepalen

**opmerking:**

**voorbehouden:**

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## 1559 Color and morphological change after alcohol preservation in reptiles

**abstract:** Colors are known to fade if a specimen is preserved in alcohol (e.g. Bagnara et al. 1968, Bagnara et al. 2007). However, in reptiles, only the upper dermal layer appears to be affected. How long alcohol takes to degrade pigments or how deep in the dermal layer it penetrates is still unknown. Elucidating these questions is critical for studies on reptiles coloration involving museum specimens. To answer them, we have selected two lizard families: agamids (Agamidae) and cordylids (Cordylidae). The student will compare museum specimens preserved in alcohol to fresh tissue samples collected in the field and preserved in both alcohol and Trump's fixative. We predict that (1) over time degradation will occur from the upper towards the lower layer and that (2) melanophores (melanin-containing cells), due to their strong architecture and deeper dermal position, will be less affected. The study will combine multiple methods such as light microscopy, scanning electron microscopy (SEM) and transmission electron microscopy (TEM). Further, based on locality information, the student may be able to link the project with an examination of color change across a latitudinal gradient in South Africa. The focus of the study is open to discussion as long as the broad scope of the original project is maintained. Students with an interest in evolution, ecology, physiology, biomimicry, conservation or any combination thereof, are strongly encouraged to apply. References: Bagnara et al. 2007. On the blue coloration of vertebrates. *Pigment Cell Research*, 20: 14-26 / Bagnara et al. 1968. The dermal chromatophore unit. *The Journal of Cell Biology*, 38(1): 67-79.

**onderzoeksgroep:** Evolution and optics of nanostructures (EON)

**Copromotor(en):**

D'Alba Liliana

**Begeleider(s):**

Goldenberg Jonathan

**opmerking:**

**voorbehouden:**

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**abstract:** Habitat quality is a main determinant of reproductive success and survival, and differences in the habitat quality of occupied territories often lead to fitness differences between individuals. However, individuals can employ a range of alternative life-history strategies to cope with their environment, and predicting which strategy is optimal for a given environment therefore is not straightforward. In this thesis, we will test how habitat quality and life-history strategies interact to determine the breeding success of the Placid greenbul (*Phyllastrephus placidus*), a cooperatively breeding Afrotropical forest bird. How habitat quality affects optimal life-history strategies is particularly important for avian cooperative breeders, where offspring may delay dispersal and may help their parents during the following breeding seasons. For instance, it has been shown that Seychelles warblers (*Acrocephalus sechellensis*) originating from lower-quality territories are likely to attain higher fitness when breeding independently, while individuals raised on a high-quality territory are better of aiding their parents. This thesis will focus on Placid greenbul populations from the Taita Hills in southeastern Kenya, an area where the remaining forest patches are small and heavily fragmented. In this area, Placid greenbuls breed from November until March, either as a pair or as social groups with 1 – 5 subordinates, of which 0 – 3 contribute to nestling provisioning (i.e. are actively helping individuals). To quantify habitat quality of these fragmented forest patches, we will study patterns of feather growth bars (termed 'ptilochronology'). Such bars represent circadian feather growth rates, and thus reflect the nutrient uptake by an individual bird within 24h. This thesis will build on placid greenbul feathers samples and data on social structure and reproductive success gathered for three consecutive breeding seasons. The student will first carry out detailed measurements of growth bar patterns on the feathers collected from the Taita Hills populations, and will then use statistical techniques to test hypotheses regarding the interplay between habitat quality, Placid greenbul social structure and reproductive success.

**onderzoeksgroep:** Terrestrial Ecology

**Copromotor(en):**

Lens Luc

**Begeleider(s):**

Strubbe Diederik

**opmerking:**

**voorbehouden:**

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**1431** Climate change in marine soft-sediments: understanding cascading effects on community biodiversity and ecosystem functioning

**abstract:** Communities are composed of species connected to each other through a network of direct and indirect interactions that may either dampen or augment stressor effects on populations. Prediction of ecosystem change and resilience to stressor regimes therefore requires understanding of the interactions of species populations within the ecosystem. Benthic macrofaunal invertebrates play a pivotal role in the functioning of shallow soft-sediment ecosystems such as estuaries, coastal lagoons and continental shelf seas, e.g. through direct trophic interactions and/or indirect ecosystem engineering interactions. Responses of these populations to environmental change will thus cascade through communities, affecting biodiversity and ecosystem functioning. In this thesis you will investigate how climate change induced extinctions and changes in density of populations of clams and polychaetes influence community performance. Soft-sediment communities will therefore be incubated under high pCO<sub>2</sub> conditions using the long-term water and sediment incubation facilities available in the research group of Marine Biology (UGent). Analysis of food web dynamics, biogeochemical cycling and community diversity under variable environmental settings and in the presence of variable densities of the selected macrofaunal key species populations will contribute to a better understanding of the ecosystem-wide interactions that underpin resilience of shallow soft-sediment coastal habitats to climate change.

**onderzoeksgroep:** Marine Biology

**Copromotor(en):**

Moens Tom

De Troch Marleen

**Begeleider(s):**

Ee Zin Ong

**opmerking:**

**voorbehouden:**

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## 1562 Quantifying benthos evolutionary adaptation capacity to ocean warming and acidification

**abstract:** The enhanced emission of greenhouse gasses (e.g. CO<sub>2</sub>) have raised global sea surface temperatures (SST) at approximately 0.13 °C per decade since the current period of climate warming started in the mid 1980s. Climate models suggest that patterns of mean and extreme SST will alter across the globe. In addition, ocean CO<sub>2</sub> absorption alters sea water carbonate chemistry and pH, with temperate shallow marine ecosystems currently experiencing a one order of magnitude faster decrease in pH (i.e. ocean acidification) as compared to global estimates. This unprecedented fast rate of acidification likely has consequences for marine biodiversity as resident species of different taxonomic and functional groups have already been shown vulnerable to scenarios of ocean acidification as projected by climate change models to occur in the next century. Consequently, the investigation of the combined effects of concurrent ocean warming and acidification on the physiology, condition and survival of marine benthos has been put forth to improve our understanding of the mechanisms that underpin resilience of coastal soft-sediment ecosystems to climate change. In addition to the examination of such stressor effects on the performance of organisms, the likelihood to adapt to these stressors should be assessed. For example, phenotypic plasticity may facilitate the persistence of populations at the short term, i.e. the rate at which environmental changes currently take place, while evolutionary genetic adaptation will likely be required to persist at the long-term. During this thesis you will experimentally investigate the response and potential for evolutionary adaptation of different species of benthic invertebrates (clams and polychaetes) by quantifying phenotypic variability and response to combined effects of ocean acidification and warming (i.e. high pCO<sub>2</sub> conditions). Therefore adults will be incubated under high and ambient pCO<sub>2</sub> conditions and genetic variation in tolerance of their offspring will be quantified in a full-factorial breeding design including multiple seawater temperature and pH levels.

**onderzoeksgroep:** Marine Biology

**Copromotor(en):**

Moens	Tom
De Clerck	Olivier

**Begeleider(s):**

Van Colen	Carl
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**opmerking:**

**voorbehouden:**

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## Van Der Straeten Dominique

**1565** Elucidating the genetic basis of the Green Revolution in wheat

**abstract:** To attain food security in 2050, the global agricultural production should increase by 60 to 110 %, while using less water, nutrients and fossil fuel. Wheat is one of the most widely grown crops and provides approximately 20% of the total calories to the world's population, hence, safeguarding yield in wheat is one important way to achieve this goal. In wheat, the so-called 'Green Revolution' led to more than a doubling in wheat production in the 1960s. The genetic basis underlying the Green Revolution was a mutation in the DELLA gene. Research in Arabidopsis revealed how DELLA proteins translate internal signals and environmental cues into responses regulated by the plant hormone gibberellic acid (GA). In wheat, very little is known on the molecular basis of DELLA function. The DELLA mutation, which was introduced during the Green Revolution and is present in over 70% of wheat cultivated worldwide, is associated with some negative aspects, especially when the mutants are grown in dry environments. To design strategies to overcome the associated yield penalties, we want to identify the proteins that are produced by the mutant DELLA gene and understand how these proteins regulate specific growth- and developmental responses in wheat. This master thesis will study a unique set of transgenic lines expressing GFP-tagged DELLA variants, using microscopy and protein biochemistry approaches. This research will be performed in close collaboration with the Innovation Center of Bayer CropScience in Ghent. Consequently, this thesis provides a unique opportunity to learn how fundamental research is translated to applications that promote sustainable agriculture.

**onderzoeksgroep:** FPB(Functional Plant Biology) & Bayer Cropscience Gent

**Copromotor(en):**

Van De Velde Karel

Rohde Antje

**Begeleider(s):**

Van De Velde Karel

**opmerking:**

**voorbehouden:**

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## Vandegehuchte Martijn

**1567** Connectivity in the dark underground

**abstract:** The soil is one of the most important environments for terrestrial life. It does not only provide the needed resources for plants, it additionally harbours an exceptional high diversity of organisms. Because the soil is heterogeneous, organisms also need to move in order to maximise their fitness. In contrast to aboveground terrestrial environments, we lack insights on the causes, consequences and modes of belowground dispersal. It is for instance known that many organisms facilitate each other, by the development of organismal 'highways' and 'pipelines'. The aim of this Msc project is to gain experimental insights on how the spatial organisation of plant roots, and the level of relatedness among plants impact spread of belowground herbivores. One major objective of the project is to test to which degree belowground movements are mirrored in the aboveground productivity.

**onderzoeksgroep:** Terrestrial Ecology

**Copromotor(en):**

Bonte Dries

**Begeleider(s):**

Zhang Peihua

**opmerking:**

**voorbehouden:**

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**1568** Loss of enemies and evolution of defense

**abstract:** Biodiversity is currently decreasing at unprecedented rates across the world, while at the same time species are shifting their ranges under the influence of climate change, leading to novel species communities. Species at higher trophic levels are often the first to locally go extinct, while plants typically expand their ranges faster than their natural enemies. Both scenarios lead to a simplified enemy community. The enemy release hypothesis predicts that under a lower enemy pressure, plants should invest less in energetically costly defense and more in growth and reproduction. However, field observations often reveal an opposite pattern, with plants investing more in defense when the enemy community consists of fewer species. This could be a consequence of different enemy species exerting opposing selection pressures on defense traits, thus stabilizing defense levels. If some enemies are lost, this may enable the plant to fully invest in defense against the remaining enemies. The aim of this project is to test these contrasting hypotheses using synthetic communities of different spider mite species on a shared host plant species. Enemy communities will be varied from simple to complex, and selection on plant defense traits will be tested using a common-garden approach.

**onderzoeksgroep:** Terrestrial Ecology

**Copromotor(en):**

Bonte Dries

**Begeleider(s):**

Vandegehuchte Martijn

**opmerking:**

**voorbehouden:**

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## 1569 Plant-enemy interactions in the city

**abstract:** Urbanization is a major driver of environmental change. Two important consequences of urbanization are an increase in temperature –the so-called urban heat island effect– and fragmentation of habitat. Both these aspects of urbanization are known to have far-reaching effects on the ecology of species and communities. However, the implications for the evolution of species interactions and community structure are less well understood. This project focuses on three plant species (*Arabidopsis thaliana*, *Jacobaea vulgaris*, and the invasive *Senecio inaequidens*) and their associated community of invertebrate enemies. Several hypotheses will be considered. For example, we expect the invasive *S. inaequidens* to cope better with an urban environment than its native counterpart. Plants in urban environments may be attacked by fewer invertebrates, because only generalist invertebrate species with a good dispersal ability may reach fragmented urban habitat patches. However, the invertebrates may perform better under higher temperatures. The final aim is to determine how plant and enemy performance as well as food web structure change along an urban-rural gradient, and whether differences in plant traits are a result of phenotypic plasticity or evolution.

**onderzoeksgroep:** Terrestrial Ecology

**Copromotor(en):**

Bonte Dries

**Begeleider(s):**

Qu Jiao

**opmerking:**

**voorbehouden:**

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**Vanholme**

**Bartel**

## 1571 Molecular mechanism of bioactive aromatic compounds in plants: cis-cinnamic acid as case study

**abstract:** Plant growth and development is tightly regulated by the phytohormone auxin. We recently found that the naturally occurring molecule cis-cinnamic acid (c-CA) can perturb auxin homeostasis by interfering with auxin transport in the plant. Treating plants with c-CA results in the inhibition of primary root growth and proliferation of lateral roots. The altered root architecture can give plants an advantage under water or nutrient depleting conditions making c-CA an excellent candidate for application in agricultural practice. To resolve the molecular mode of c-CA action and obtain a mechanistic insight into its perception further research is necessary. During your master thesis you will be involved in functional characterization of some of the early c-CA response genes. You will work with the model plant *Arabidopsis thaliana* and analyze primary and lateral root growth. The relative role of specific biochemical pathways will be studied by means of mutants blocked in particular steps of the pathway, as well as by the use of specific drugs to inhibit particular enzymes. Finally, structural analogs of c-CA will be tested to provide us with information on the structural characteristics of c-CA conferring bioactivity.

**onderzoeksgroep:** Dept. Of Plant Systems Biology (PSB), VIB

**Begeleider(s):**

El Houari Ilias

**opmerking:**

**voorbehouden:**

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# Vanthournout Bram

**1573** Arachnid colour in the city.

**abstract:** Human activity can induce profound changes in natural habitats, creating anthropogenic environments that differ in (a)biotic characteristics compared to natural systems and exerting strong selection pressures on affected species. There is increasing awareness that these changes target both ecological and evolutionary dynamics on similar time and spatial scales. However, these eco-evolutionary feedback loops can seriously hamper the predictive ability of species response models to habitat change. It is therefore of paramount significance to gain deeper knowledge on such interactions using suitable study systems and expanding the types and range of traits under investigation. One such example is colour in ectothermic species that causes darker coloured individuals to heat up faster through solar radiation but, at the same time, are at risk of overheating. Especially in urban environments, with a higher temperature, strong selection is expected for lighter individuals that potentially thermoregulate more efficiently. In this thesis we take full advantage of the extensive sampling along an urbanisation gradient that has been performed within the SPEEDY project (SPatial and environmental determinants of Eco-Evolutionary DYnamics: anthropogenic environments as a model). In this thesis we investigate whether the level of urbanisation influences the colouring of arachnids (spiders and/or mites) by determining the thermal profile using a thermal camera. A microspectrophotometer will be used to determine the spectrum of reflected wavelengths which allows to quantify the colour of an individual. Depending on the interests of the student, additional sampling and behavioural experiments on live specimens are possible.

**onderzoeksgroep:** Evolution and optics of nanostructures (EON)

**Copromotor(en):**

Shawkey Matthew

Bonte Dries

**Begeleider(s):**

Vanthournout Bram

**opmerking:**

**voorbehouden:**

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**abstract:** Springtails (Collembola) are soil-dwelling arthropods that are characterized by a tail-like appendage (furcula) that allows them to jump when threatened. Besides this remarkable anti-predator adaptation some collembola species exhibit a striking, iridescent colouration. These colours are not formed by pigment but through highly ordered nanostructures causing scattering of light and changing colours when viewed from different angles. These nanostructures are found on scales covering the entire body, in a similar way to scales on butterfly wings. The function of this colouration is currently unknown, living in low light conditions and having limited eyesight only distinguishing light and dark, make it unlikely that it plays a significant role in sexual selection. This thesis will be part of ongoing research in the EON-group on iridescent colour and can focus on two research topics, depending on the interest of the student. One is testing the hypothesis that the iridescent colour is important for thermoregulation as the nanostructures could reduce radiation absorption through light scattering and thus be a way to control heating. This is especially important in small ectothermic arthropods such as springtails. Behavioural experiments and the use of microspectrophotometry that allows to quantify colour through determining the reflectance in different wavelengths of the spectrum, including infrared, will be used. A second research topic will investigate the speed of evolution of iridescent colouration. Springtails are an excellent model system to test this as they can easily be bred in the lab and have short generations times. We will set up selection lines of springtails species with golden and violet colouration to test whether the reflectance spectra can be shifted through artificial selection. Moreover, inbreeding lines will be established as it is thought that inbreeding will directly affect the highly ordered nanostructuring in a negative way, changing the iridescent properties. For this research line, Scanning Electron Microscopy and Transmission Electron Microscopy will be used, next to microspectrophotometry.

**onderzoeksgroep:** Evolution and optics of nanostructures (EON)

**Copromotor(en):**

Shawkey                      Matthew

**Begeleider(s):**

Vanthournout              Bram

**opmerking:**

**voorbehouden:**

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**1580** Diversity and community structure of Arctic soil microbiomes along gradients in environmental and microclimatic conditions

**abstract:** Nowhere is climate change more visible than in the Arctic, making it the most critical reference region for the detection and understanding of global change and its effects on biodiversity and ecosystem functioning. In terrestrial Arctic biomes, particularly soils appear to respond very sensitively to changes in temperature and moisture availability as a result of their close proximity to freezing. It follows that relatively small climatic changes may have profound impacts on these soil ecosystems and their biota. This rapid response is also due to the fact that biogeochemical cycling and ecosystem functioning in Arctic environments are to a large extent controlled by microorganisms. While environmental changes imposed by global warming affect the composition of Arctic terrestrial microbiomes, there is increasing evidence that warming of the Arctic and altered precipitation regimes will also have repercussions on the global climate system because of the crucial role these soils play in greenhouse gas storage and emission. More in particular, over millennia, the cold Arctic climate has minimized the breakdown of organic matter leading to large quantities of carbon and nitrogen stored in the permafrost. However, climate change can accelerate the microbial breakdown of this organic matter, which results in the release of greenhouse gasses such as carbon dioxide (CO<sub>2</sub>), methane (CH<sub>4</sub>) and nitrous oxide (NO) to the atmosphere. While bacterial communities including methanogens and prokaryotes involved in N-cycling are being increasingly studied, relatively little is known about the diversity of microbial eukaryotes and small invertebrates in these soils and their cryptogamic vegetation covers. This student project is part of the EU BiodivERSA project CLIMARCTIC and aimed at studying the biodiversity and community structure of eukaryotic (micro-)organisms in response to microclimatic conditions in dry and wet tundra systems in Svalbard. To achieve this, Illumina high-throughput amplicon sequencing of the 18S rRNA, CO1 and ITS2 genes from environmental samples will be combined with measurements of local environmental and microclimatic conditions. The practical work is computer-intensive and will mainly involve bioinformatics analysis of the sequencing data. After quality filtering, the amplicons will be clustered into operational taxonomic units (OTUs) using a customized pipeline largely based on UPARSE. All OTUs will be assigned to curated taxonomic databases. The data will be analysed using ordination and clustering techniques in R.

**onderzoeksgroep:** Protistology & Aquatic Ecology

**Copromotor(en):**

Tytgat Bjorn

**Begeleider(s):**

De Maeyer Lotte

**opmerking:**

**voorbehouden:**

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**abstract:** Benthic microbial mat communities in lakes from high latitude polar desert biomes are localized hotspots for biodiversity and primary production compared to their surrounding soil ecosystems. High-throughput amplicon sequencing of the 16S and 18S rRNA genes from microbial mat communities in over 230 lakes from the Arctic and Antarctica revealed marked bipolar differences in the taxonomic structure and biodiversity. In the Arctic, the phylogenetic diversity in most Eukaryotic and several bacterial groups was higher compared to Antarctica, with several key clades being absent in the latter region. These findings can be explained by the contrasting configuration of ice-free land and the different tectonic and climatic histories of both Polar Regions. More in particular, diverse lacustrine microbial food webs probably tracked Pleistocene latitudinal range-shifts in the Northern hemisphere, while in Antarctica, glacial-interglacial cycles and the long-term isolation of the continent likely resulted in the regional extinction of major clades and the survival of well-adapted taxa in ice-free regions. Despite these strong differences in food web structure, little is known about potential contrasts in the functional diversity between Arctic and Antarctic microbial mat communities. This student project is aimed at studying the functional genes present in a selection of 15 lakes from Antarctica and the Arctic by using a shotgun metagenome sequencing approach on an Illumina HiSeq 2500 platform. The practical work will mainly involve bioinformatics analysis to annotate the gene fragments into contigs and for gene annotation. Two pathways will be run in parallel; one using a direct annotation approach of quality trimmed reads, the other one following a co-assembly into contigs and binning into functional and taxonomic groups. Assembly algorithms will be used for de-novo assembly, while functional annotation will be done using automated online pipelines.

**onderzoeksgroep:** Protistology & Aquatic Ecology

**Copromotor(en):**

Vyverman Wim

**Begeleider(s):**

Tytgat Bjorn

**opmerking:**

**voorbehouden:**

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**1582** Reconstructing 260,000 years of aquatic-ecosystem dynamics in equatorial East Africa, using sub-fossil remains of benthic invertebrates and fish

**abstract:** The ICDP (International Continental Scientific Drilling Programme) project DeepCHALLA aims to reconstruct climate and landscape history in equatorial East Africa over the past ~260,000 years, through multi-disciplinary analysis of the sediment record of Lake Challa, a 90-meter deep crater lake near Mt. Kilimanjaro. The targeted period encompasses the entire known history of our own species, *Homo sapiens*, and thus has the potential to both reveal how climate change influenced human cultural and technological progress, and how and when our ancestors started to impact their living environment. An important indicator of past climate change is the succession of lake highstands and lowstands through time, since this reflects episodes of higher and lower rainfall than today. These lake-level fluctuations can be traced, for example, in the succession of so-called draped (spread-out) and ponded (focused) sediment packages revealed in seismic-reflection profiles. However it can also be traced by analyzing changes in the abundance and diversity of benthic invertebrates, since this reflects whether seasonal water-column mixing maintained an adequate level of oxygen near the lake bottom. The composition of these fossil assemblages is thus an indicator of the depth of the water column at the time of their burial. In Lake Challa, water level must have dropped at least 50 m to expand benthic habitat from its steep-sided rocky margins to the soft mud bottom in the center of the lake. Therefore, benthic invertebrates may be particularly effective indicators to determine the exact timing and magnitude of lake-level fluctuations during the so-called African Megadrought period between ~115,000 and 100,000 years ago, i.e. around the time when our ancestors first migrated out of Africa towards the Middle East, to eventually reach Europe. The sediment samples available for this study permit paleo-environmental reconstruction with a temporal resolution of ~400 years. Originally extracted for paleomagnetic analyses, the relatively large size of these samples increases the probability of containing fossil remains of benthic groups such as snails, ostracods and non-biting midges, particularly during lowstand episodes. If the lake was shallow enough to allow growth of submerged macrophytes, then also bryozoan statoblasts can be expected. The most important 'by-catch' during these analyses will be fish remains: scales, vertebrae and teeth. Consequently this study will also reveal precisely when fish first colonized this isolated crater lake (presumably a mouth-brooding female cichlid fish brought in by a fish eagle), and whether these early immigrant fish maintained a local population continuously until the present. In that case they are the ancestor to the endemic tilapia *Oreochromis hunteri* living in Lake Challa today. This thesis project involves the processing and sieving of the sediment samples, after which the residue is scanned under a binocular microscope (20-80x magnification) to identify and count the recovered fish and invertebrate remains. Time spent on each sample will be relatively low, since not much taxonomic difficulties will be encountered during identification. Nevertheless it is advisable to start with a set of ~150 samples (~1600-year resolution), and aim for greater temporal resolution in the most dynamic parts of the record, if time permits. Interpretation of the results will involve comparison with data sets on other indicators of the lake's environmental history, produced by project partners at UGent and abroad.

**onderzoeksgroep:** Limnology

**Copromotor(en):**

Van der Meeren Thijs

**Begeleider(s):**

Ryken Els

**opmerking:**

**voorbehouden:**

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**1583** Ecology of the model benthic diatom species *Seminavis robusta*

**abstract:** Species that are used as models for biological and molecular research are usually selected for pragmatic reasons, such as ease of cultivation and experimental manipulation, genome size, etc. Research results obtained for these species is then often considered to be representative of the group they represent. However, in many cases it is not known whether this is justified, as very little is known about the ecology of these species in natural environments. During the last decade, the marine benthic diatom *Seminavis robusta* has been developed as a model species in the lab of the promoters. Extensive information is now available on its species structure, physiology and molecular and chemical biology (including whole genome sequence and transcriptomic data). Ongoing PhD research has shown that this 'species' actually represents a cluster of closely related species, which occur together in coastal lagoons and can hybridize but have distinct physiological and molecular-genomic features. This makes this model diatom an ideal candidate to study speciation mechanisms in diatoms. However, to date we have virtually no information about the ecology of this species cluster in nature. Such information may reveal important information on adaptation and hence the underlying mechanisms driving speciation. In this thesis, an ecological study of this species complex in coastal habitats in Belgium and the SW Netherlands will be performed. RT-qPCR protocols will be developed to monitor seasonal and spatial dynamics of different populations of these cryptic species. Environmental information (temperature, light, nutrients, presence of grazers or parasites, etc.) will be monitored simultaneously. Microscopy will be used to study the life cycle dynamics of the populations (size reduction cycle and sexual events).

**onderzoeksgroep:** Protistology & Aquatic Ecology

**Copromotor(en):**

Sabbe Koen

**Begeleider(s):**

nog te bepalen

**opmerking:****voorbehouden:**

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**1584** Elucidating the role of cGMP during sexual reproduction of *Seminavis robusta*, a pennate diatom

**abstract:** Diatoms are a key group of micro-algae that live in a glass-like shell and have a fascinating life cycle. In this so-called cell size reduction-restitution cycle, every cell division results in a small decrease in size of one of the two daughter cells, resulting in a gradually declining average cell size of diatom population. Below a species-specific cells size, however, sexual reproduction becomes possible, resulting in recombination of parental genomes and the establishment of the original larger cell size. The diatom *Seminavis robusta* is the current model system for studies of the life cycle and sexual reproduction in pennate diatoms. This species has two mating types ('sexes'), which are morphologically identical, but behave differently during sexual reproduction. During the mating process, these two mating types were shown to communicate through the action of multiple pheromones. Several RNA-seq experiments looking at the transcriptomic response to these pheromones were carried out in our lab. These experiments suggest a possible role for cyclic GMP (cGMP) signaling in the mating process. During this master thesis, we will attempt to find out whether cGMP signaling is indeed involved in the mating response. To this end, we will (1) test the effect of a range of cGMP inhibitors and analogues on different stages of the mating process (response and production of pheromones, pair formation, meiosis etc.), (2) use a cGMP ELISA kit to determine whether there is a spike in cGMP concentration in the cells as a response to the pheromones and during the mating process, and (3) carry out qPCR experiments to verify the findings of the available RNA-seq data.

**onderzoeksgroep:** Protistology & Aquatic Ecology

**Copromotor(en):**

De Veylder Lieven

Sabbe Koen

**Begeleider(s):**

Bilcke Gust

**opmerking:**

**voorbehouden:**

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## 1585 Physiological diversity in the *Cylindrotheca closterium* species flock

**abstract:** As in many diatoms, evidence from phylogenetic studies and crossing experiments revealed that the pennate diatom species *Cylindrotheca closterium* is genetically very diverse and is in fact not a single species but a species complex existing of several, yet morphologically indistinguishable species. In addition, genetic diversity within these cryptic species is extensive, raising important questions as to which mechanisms maintain this extraordinary diversity. In this student project, the variation in physiological traits within and between cryptic species will be studied in a phylogenetic framework. Using high throughput imaging, fitness-related traits (growth rate, cell size, reproductive success) of a reference set of genotypes will be measured under a representative range of environmental conditions (focusing on salinity, temperature, light intensity and photoperiod, nutrient resource ratios). Subsequently, trait variation will be analysed in a phylogenetic context and will allow to determine the degree of fundamental niche overlap between more or less related lineages. Time permitting, predictions based on these analyses will be tested in competition experiments using multiple genotypes under constant or variable conditions.

**onderzoeksgroep:** Protistology & Aquatic Ecology

### **Copromotor(en):**

Chaerle Peter

Sabbe Koen

### **Begeleider(s):**

Chaerle Peter

### **opmerking:**

### **voorbehouden:**

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**1586** Soil microbial biodiversity patterns in Antarctic nunataks

**abstract:** Because of the virtual lack of macroscopic organisms, microbial foodwebs dominate ecosystem functions and biogeochemical cycling in Antarctic terrestrial ecosystems. Considering the long history of geographical isolation, a key question is to which extent these microbiomes are taxonomically and functionally different from those found in similar environments elsewhere, such as in the Arctic region or other cold deserts. This student project focuses on soil crust communities in nunataks of the Sør Rondane Mountains (East Antarctica) with the primary aim to investigate bacterial, archaeal and eukaryote biodiversity patterns and relate these to local environmental conditions (e.g. substrate type, local temperature regime, snow cover, etc). These data will form the basis for habitat suitability modeling using remote sensing observations of habitat features. Importantly, these biodiversity inventories will also be part of a continent-wide baseline study of microbial biodiversity, given the increasing risk of the introduction of alien species via human activities on the continent. Techniques used will include metabarcoding using Illumina high throughput sequencing and the application of in-house bioinformatics pipelines to generate diversity data, which will be analysed using multivariate statistical tools. Time permitted/depending on the student's interest, part of the project can also be devoted to the analysis of remote sensing data in order to obtain a first habitat classification of the region.

**onderzoeksgroep:** Protistology & Aquatic Ecology

**Copromotor(en):**

Verleyen Elie

Tytgat Bjorn

**Begeleider(s):**

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**opmerking:****voorbehouden:**

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