

Overzicht onderwerpen masterproeven 2019-2020 per promotor

Adriaens

Dominique

1651 Does a flexible tail also makes it prehensile? Musculoskeletal anatomy of mammalian tails

abstract Prehensility in the tail is an adaptation that arose in several vertebrate and invertebrate lineages. Prehensility is the ability to grab around a substrate, which can assist in an arboreal lifestyle to act as a 5th arm, combining both high flexibility and strength. Prehensile animals differentiate themselves from animals with flexible tails with the ability to suspend their entire body weight using their tail. This research focuses on the prehensile tails of mammals. In trying to understand the morphological basis that underlies the prehensile capacities in mammals, we compare the skeletal morphologies and its associated muscular organisation between prehensile and non-prehensile taxa. For this study we will be using (soft tissue stained) CT scanning, dissections on fresh material, and histology. We will be making CT scans of tail in which we can visualize and compare the vertebral morphologies, as well as CT scans of soft tissue-stained material to visualize the musculature. Also dissections will be performed on fresh material to determine the muscular arrangement within the tail. The exact specimens that will be used are yet to be determined based on availability.

onderzoeksgroep: Evolutionary Morphology of Vertebrates

Begeleider(s):

Luger Allison

opmerking

voorbehouden:

1652 Ontwikkelen van didactische werkvormen ter bevordering van het onderwijs over evolutie en evolutietheorie

abstract Het aanbrengen van hoe evolutie werkt, en waar de evolutietheorie voor staat, maakt onderdeel uit van het leerplan in het secundair onderwijs. Om dit in een klascontext aan te brengen, is dit nog steeds een uitdaging in bepaalde centrumscholen. Bij sommige leerlingen ligt de evolutietheorie namelijk gevoelig, ondermeer omwille van religieuze redenen. Los van de verplichte eindtermen, lijkt het evident dat alle jongeren zelf de kritische reflectie moeten kunnen maken, en met kennis van zake de evolutietheorie naast creationisme moeten kunnen leggen om zelf af te kunnen leiden wat aanvaardbaar en onderbouwd is, en wat niet. Gebruik van de juiste didactische werkvormen, die verder gaan dan het beschrijven van feiten, maar eerder principes verduidelijken en procesmatig denken stimuleren, staan hier dan ook centraal. Binnen deze masterproef zal er gewerkt worden naar geschikte formats om kritisch denken en begrip van de evolutietheorie bij deze doelgroep te bevorderen. Dit impliceert dat eerst in kaart moet worden gebracht wat de voorkennis en visie is over evolutie bij leerlingen, om uiteindelijk het leereffect van de werkvormen te kunnen uittesten. Het onderzoek richt zich tot het identificeren van de kernpunten die maken dat iets als evolutie en evolutietheorie moeilijk wordt geaccepteerd, ongeacht de manier waarop de gekende feiten worden aangebracht. Het onderzoek binnen deze masterproef zal zich dus richten tot (1) bevraging bij enkele doelscholen naar de kennis en houding tov evolutie en evolutietheorie, (2) in kaart brengen van de toegepaste werkvormen, (3) het identificeren van mogelijke beperkingen in deze werkvormen, zoals wordt ervaren door leerlingen, (4) het uitwerken van nieuwe werkvormen, (5) het uittesten van de werkvormen via leerkrachten in enkele doelscholen, en (6) het evalueren van het leereffect.

onderzoeksgroep: Evolutionary Morphology of Vertebrates & Vakgr. Wijsbegeerte en moraalwetenschap & Vakgr. Onderwijskunde

Copromotor(en):

Braeckman Johan

Van Braak Johan

Begeleider(s):

Vershelde Dominick

opmerking Gezien het onderwerp aangebracht werd door de student, evenals het gaat om een biologisch-didactisch onderwerp, werd het voorstel uitgeschreven in het Nederlands.

voorbehouden: Joeri Deldycke

1653 Study of the postcranial musculoskeletal system in burrowing amphisbaenians

abstract Mostly due to their hidden life style, limbless burrowing vertebrates have received only little scientific attention since the beginning of the 20th century. However, although they have no legs, they show many specializations and occupy a wide range of different habitats. Amphisbaenians are a group of highly specialized burrowing squamates. Most of them are limbless and possess a strongly ossified and compacted skull with different cranial shapes to dig permanent galleries into the ground. Despite good descriptions of the skull anatomy in the literature, only a few studies have dealt with the postcranial system. However, some preliminary data show that they can produce really high burrowing forces using the postcranial system. To better understand the exact anatomical structures and biomechanics of efficient burrowing in amphisbaenians, more qualitative and quantitative data on that system are thus needed. During this master thesis, CT-scans will be reconstructed in 3D using Amira software and then landmarked to compare the 3D shape of the bones. Dissections of representatives of limbless burrowing amphisbaenians will then be realized to characterize the muscular morphology. The analysis of force plate data will finally give us information about the maximum pushing force that amphisbaenians can perform. Statistical analyses will then be conducted within a well resolved phylogenetic framework and should allow us to understand the relation between the burrowing performance and the modification of the postcranial musculoskeletal system. These results will give new insights into the organization and adaptive evolution of the postcranial musculoskeletal system in fossorial taxa.

onderzoeksgroep: Evolutionary Morphology of Vertebrates

Begeleider(s):

Lowie Aurélien

opmerking

voorbehouden:

Beeckman Tom

1654 Root development in the early land plant *Selaginella moellendorffii*

abstract *Selaginella moellendorffii* is a lycophyte, which is the oldest lineage having with extant members having true roots. This makes *S. moellendorffii* an interesting model to study how roots evolved. In contrast to euphyllophytes (including ferns and seed plants) that have monopodial root systems with lateral root formation from a main root, lycophytes are only able to branch their roots via dichotomous bifurcation of the root tip. In the Root Development group of Tom Beeckman, the *S. moellendorffii* roots are studied both morphologically as genetically, including the generation of a gene expression dataset during the branching. Depending on the interest of the student, the master thesis can focus on (1) morphological aspects, with a primarily use of different microscopy techniques (technovit sectioning and light microscopy, fluorescence microscopy and different stainings, confocal microscopy, in situ hybridization using genetic probes from our dataset), (2) genetic aspects, to identify and validate conserved factors in root development and mainly use biotechnological approaches (phylogenetic analyses, gene expression analysis (RNA-extraction, qRT-PCR), gateway cloning, complementation of *S. moellendorffii* genes in *Arabidopsis* (transformation and phenotyping)), (3) developmental and phytohormonal aspects, including the evaluation of root growth on different conditions (hormone treatments,...) to possibly induce root branching or develop a transformation protocol for *S. moellendorffii* (in vitro plant tissue culture, stereomicroscopy, Agrobacterium mediated transformation), or a combination of the abovementioned techniques.

onderzoeksgroep: PSB Plant Systems Biology - Root Development

Copromotor(en):

Motte Hans

Begeleider(s):

Motte Hans

opmerking

voorbehouden: Ward Poelmans

abstract The architecture of the root systems of plants has a strong impact on plant productivity and consequently also on agricultural productivity and the productivity of whole ecosystems. Therefore, the formation of lateral roots, which allows root systems to branch and expand, is a very important developmental process for both agriculture and nature. A lateral root originates from a small group of pericycle cells that go through a series of strongly regulated cell divisions, thereby giving rise to a lateral root primordium. In the lab of Prof. Beeckman, the underlying molecular mechanisms that drive the initiation and development of lateral roots are being studied. Thanks to these efforts, the GOLVEN6 gene was found to play an important role in the regulation of the initial cell divisions in the pericycle. Overexpression of GLV6 disrupts the asymmetry of the first cell division, which is essential for subsequent primordium development. As a result, overexpression of this gene results in a striking phenotype; a complete lack of lateral roots. The GLV6 gene encodes a small signaling peptide (also called peptide hormone). The importance of peptide signaling in plants is a relatively recent discovery. Consequently, the research field that focusses on plant peptides is still young and growing. The last few years, lots of peptide hormones have been discovered and they were found to play a role in numerous developmental and physiological processes. However, for the large majority of these peptides, the underlying molecular mechanisms via which they exert their function have yet to be discovered. The elucidation of the GLV6 signaling pathway will therefore not only yield important information about its role in lateral root primordium initiation, but will also contribute to our general understanding of plant peptide signaling. At the moment, an RNA-sequencing experiment is being performed that will clarify which genes are up- and downregulated by GLV6 during lateral root initiation. Once this list of GLV6 target genes is available, their involvement in the GLV6 signaling pathway, and their role in lateral root development will be carefully analyzed. This master's thesis will contribute to that work. The student will be involved in the validation of the transcriptional regulation of the newly discovered genes by GLV6 (primer design, RNA-extraction, qPCR). The expression patterns of these target genes will be analyzed (DNA-extraction, design of reporter constructs, cloning, plant transformation, confocal laser scanning microscopy). Gain-and loss-of-function mutants will be generated and their lateral phenotypes will analyzed on a macro- and microscopic level (light microscopy, DIC-microscopy, peptide and hormone treatments,...). The goal of this project will thus be to gain a better understanding of the role of some of the GLV6 target genes during lateral root development.

onderzoeksgroep: PSB Plant Systems Biology - Root Development

Begeleider(s):

Jourquin

Joris

opmerking

voorbehouden: Tom Cooremans

1507 Pheromones inhibit the hatching of diapausing Anostraca (Crustacea: Branchiopoda)

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:

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:

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):**

Bonte	Dries
Masier	Stefano
Mortier	Frederik

opmerking**voorbehouden:****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
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opmerking**voorbehouden:** Kaat Mertens

1650 The spatial configuration of resources and its effect on food web structure

abstract The organisation of biodiversity and species networks is largely determined by the availability and spatial configuration of resources. Evidence is emerging from theory that this organisation at lower trophic levels affects body size distributions and thus the structure of the entire food web. Empirical evidence is, however lacking. We here aim to test how the spatial organisation of marram grass in the coastal dunes impacts functional aspects of invertebrate (arthropod) communities and their organisation into plant-associated food webs. Once this relationship can be unravelled, marram grass coverage can be used as an important early warning tool to assess dune biological value.

onderzoeksgroep: Terrestrial Ecology

Copromotor(en):

Vandegehuchte Martijn

Begeleider(s):

Bonte Dries

Vandegehuchte Martijn

opmerking onderwerp 1511 werd vorig jaar ook ingevuld, maar kent vervolg

voorbehouden: Noemie Van den Bon

1656 How do soil legacy effects alter the composition of grassland vegetations?

abstract This master thesis is part of a long-term study where the compositions of grassland vegetation communities are compared between soils with different histories. The field experiment started in 2015 when 104 plots of 2.5 x 2.5 m² were set up in an existing grassland. The aim of the experiment is to examine how plant traits (grasses/forbs, and fast growing/slow growing species) influence the soil and to what extent in real plant communities this leads to plant soil feedbacks. In the experiment, each plot consists of three subplots. For one of the subplots in each plot the vegetation was removed and a specific plant community was sown. This plant community consisted of three grasses, three forbs, or a mixture of three grasses and three forbs. Communities were sown with either fast growing or slow growing plant species. Sown plots were regularly weeded to maintain the sown community identity. In 2016, for a second subplot in each plot the vegetation was removed and this subplot was sown with the same plant community. In 2017 the vegetation of all three subplots (original, sown 2 years ago and sown 1 year earlier) was removed and a standard plant community of 35 species was sown in each subplot. Last year the composition of the vegetation in each subplot was determined. For the master thesis, the student will carry out vegetation recordings in all subplots and the effects of the characteristics of conditioning plant communities on the established vegetation will be analyzed.

onderzoeksgroep: Terrestrial Ecology

Copromotor(en):

Bezemer Martijn

Begeleider(s):

Bezemer Martijn

opmerking met thesiscontract

voorbehouden: Nuria Simoens

1657

The effect of brood parasites on the fitness and spatial distribution of a solitary, aggregating wasp

abstract Brood parasitism is a specific type of parasitism in which the parasite's offspring feed on the host's nest provisions. The cuckoo might be the best known example, but brood parasites of arthropods are very interesting, less-known study systems. For the solitary, aggregating digger wasp *Bembix rostrata*, the brood parasitic fly *Senotainia albifrons* lays its larvae on the prey provisioned by the female digger wasp at her nest. The impact of such a brood parasite on the individual and population level is not well understood. This master thesis topic will investigate the effect of brood parasitism on host individual fitness, possible response of spatial bet hedging (spatially spreading nests to mitigate risk) by the digger wasp and the effect on spatial distribution of nests and population size. In the dunes at the Belgian Westcoast (from De Panne until Nieuwpoort), several populations of *Bembix rostrata* will be monitored using capture-mark-recapture (CMRC). In each population, several censuses will be made, including marking and measuring individuals of *B. rostrata*, indicating their nests, assessing the parasite load, etc. Using CMRC-analysis, spatial point and social network analysis, the impact of the brood parasite on the individual and population level of *B. rostrata* will be investigated.

onderzoeksgroep: Terrestrial Ecology**Begeleider(s):**

Batsleer Femke

opmerking The student must be willing to do at least 6-8 weeks (end of June-mid August) of fieldwork in the (sometimes hot and sunny) dunes. The study sites can easily be reached by train and bike.

voorbehouden:**1659**

The underlying mechanism of polyphagy in parthenogenetic herbivores

abstract Description: Sexual reproduction is the main reproductive strategy in animals. Evolutionary theory states that a sexual mode of reproduction is favored because it generates high levels of genetic variation and hereby facilitates the adaptation of populations to environmental changes. Parthenogenetic, or asexual, lineages can evolve from sexual populations, but theory predicts that these should be evolutionary dead-ends with a very limited adaptive potential. Surprisingly, within the Arthropod phylum, a number of parthenogenetic plant-feeding species have evolved that are evolutionary robust and are found feeding on several plant hosts in the wild. These parthenogenetic herbivores may have developed high levels of adaptive phenotypic plasticity to feed on different plant hosts or they may be a collection of specialists that only eat from one specific plant host. This thesis tests these two hypothesized mechanisms of polyphagy in parthenogenetic herbivores using *Bryobia* spider mites as a model system. The student will perform several transplant experiments and will quantify different fitness components. Depending on the student's interests, a molecular or more ecological series of experiments can be included. Molecular techniques can include next-generation sequencing, qPCR, cloning, and phylogenetic analysis. Key Words; herbivore, phenotypic plasticity, parthenogenesis

onderzoeksgroep: Terrestrial Ecology**Copromotor(en):**

Wybouw Nicky

Begeleider(s):

Wybouw Nicky

opmerking**voorbehouden:**

1660 Do healthspan-promoting genes and chemical compounds delay sarcopenia in *C. elegans*?

abstract Healthspan is the period in life when one is generally healthy and free from serious disease. In the light of a European project and in a collaborative effort with other laboratories, we aim to find pathways and mechanisms involved in the extension of healthspan in the nematode *C. elegans*. Candidate mechanisms for healthspan extension will be preselected from (1) *C. elegans* genes selected from RNAi screens and (2) pure compounds or botanical preparations reported to ameliorate healthspan. In our lab, selected genes, compounds and extracts will be studied in more detail. At the phenotypic level, several distinct healthspan-promoting effects can be observed, including elevated stress resistance, improved muscle and/or neuronal functioning and efficient metabolism. In this project, we will study the phenotypical consequences on muscle integrity of genes, polymorphisms and chemical compounds selected as healthspan promoting candidates. Sarcopenia, the age-related degeneration of muscle mass in humans, has also been observed in old *C. elegans* worms. In old worms, sarcomeres tend to show disorganization with less dense packing and irregular orientation, clearly deviating from the tightly parallel symmetric rows of sarcomeres seen in young adults. We will score muscle integrity at advanced age by using a myo 3::GFP translational reporter to study body wall muscle, given that MYO-3 is a myosin heavy chain protein, essential for thick filament formation in muscle sarcomeres. Via confocal images and an automated image analysis tool, we will objectively score this reporter strain and aim to assess delayed sarcomere disorganization upon RNAi-treatment of selected candidate genes or the administration of chemical compounds.

onderzoeksgroep: Aging physiology and molecular evolution

Begeleider(s):

Dhondt

Ineke

opmerking This subject is only available for students with excellent technical skills in microscopy and have the competence to work with utmost care and a high level of responsibility.

voorbehouden:

1661 Functional analysis of *Caenorhabditis elegans* globin-3 in the somatic gonad.

abstract Globins are globular heme-binding proteins that are widely distributed throughout life. Globin diversity is exceptional in nematodes and in the *C. elegans* genome 34 globin genes were discovered. Globin-3 attracted our attention as it is one of the few globins that gives a clear phenotype upon knockout: sterility. This globin is expressed in 20 to 30 neurons and in a specific region in the somatic gonad. It is expressed as two isoforms, predicted to be membrane-bound: one in the plasma membrane and one in the mitochondria. In this project, we will functionally characterize these two GLB-3 isoforms. After exact localization inside the worm, we will study how gonadal GLB-3 influences fertility. Gonad morphology in the glb-3 mutant will be studied and the ovulation process will be quantified because glb-3 is known to be expressed in the proximal somatic cells of the ovary. We will also focus on the putative interaction partners, the superoxide dismutases, as GLB-3 is expected to act as a superoxide generator.

onderzoeksgroep: Aging physiology and molecular evolution

Begeleider(s):

Loier

Tim

opmerking

voorbehouden:

1662The effect of healthspan-promoting genes and compounds on stress-response pathways in *C. elegans*.

abstract Healthspan is the period in life when one is generally healthy and free from serious disease. In the light of a European project and in a collaborative effort with other laboratories, we aim to find pathways and mechanisms involved in the extension of healthspan in the nematode *C. elegans*. Candidate mechanisms for healthspan extension will be preselected from (1) *C. elegans* genes selected from RNAi screens and (2) pure compounds or botanical preparations reported to ameliorate healthspan. Armed with a selection of genes, compounds and extracts that cause healthspan extension, we will look for the molecular mechanism that supports this improved health. Healthspan of transgenic worms, expressing GFP-reporters of well-known cytoprotective signaling pathways, will be extended by RNAi of selected genes or by addition of selected chemical compounds or botanical extracts. More specifically, in this project, we will focus on DAF-16/FOXO, a well-known key regulator increasing longevity – and likely healthspan. Thereto, we will study the activation of its target SOD-3 in a *sod-3::GFP* reporter strain undergoing the healthspan extension treatment. GFP expression will be quantified via fluorimetry using a multi-well plate reader. By using similar approaches, we will also verify the activation of HSP-4 (an Hsp70-related protein), a stress-induced regulator of aging related signaling in the endoplasmic reticulum. Taken together, this project will provide insights into distinct signaling mechanisms in *C. elegans*, involved in the control of healthspan.

onderzoeksgroep: Aging physiology and molecular evolution**Begeleider(s):**

Dhondt

Ineke

opmerking**voorbehouden:****1663**

The role of glial cells in BLI-4 mediated lifespan extension observed in axenically cultured worms

abstract The nematode model organism *Caenorhabditis elegans* has a mean lifespan of about three weeks when cultured under standard laboratory conditions, i.e. grown at 20°C on agar plates seeded with *Escherichia coli*. However, when worms are cultured in a sterile nutrient-rich medium devoid of bacteria (axenic medium), their lifespan is doubled. The exact mechanisms underlying the lifespan extension observed under axenic dietary restriction (ADR) are still enigmatic. Our recent work has shown that knocking down the proprotein convertase *bli-4* by means of RNAi, completely abolishes the lifespan extending effect of ADR. Furthermore, lifespan experiments in worm strains that allow for tissue-specific RNAi have shown that BLI-4 activity is required in the neurons to establish ADR longevity. However, an earlier cell-specific transcriptomics study in *C. elegans* indicated that *bli-4* expression is very low in neurons but much higher in the neighbouring glia cells, which may have also been covered in our 'neuron-specific' RNAi strain. This leads us to the new hypothesis that ADR-mediated lifespan extension may require BLI-4 activity in glial cells, rather than in neurons. In order to confirm this, we aim to create a *C. elegans* strain that is sensitive to RNAi treatment exclusively in glial cells. Lifespan experiments using this strain will indicate if knockdown of *bli-4* in the glial cells results in abolishment of the long lifespan commonly observed in axenic cultures. BLI-4 is predicted to be expressed as 10 alternative splicing forms and likely these isoforms are specific to certain tissues. Mutant and RNAi analysis have thought us before that six of these isoforms are not involved in ADR longevity and some are likely expressed in the hypodermis where they are involved in the moulting process. In a second part of the thesis, we will try to localize expression of the relevant BLI-4 isoforms using GFP reporter constructs. We hypothesize that at least one of them is expressed in the glial cells. During this master dissertation, a wide array of techniques may be applied: nematode and bacterial culturing methods, RNA interference, lifespan assays, PCR and QRT-PCR, molecular cloning, CRISPR/Cas, transgenesis, fluorescence microscopy.

onderzoeksgroep: Aging physiology and molecular evolution**Begeleider(s):**

Vandemeulebroucke

Lieselot

opmerking**voorbehouden:**

abstract Heart disease is the most important cause of mortality in westernized nations, with heart failure, which is when the heart cannot pump sufficient blood, being the most prominent cause of hospitalizations in Europe. More than half of the heart failure patients have heart failure with preserved ejection fraction (HFpEF). HFpEF occurs in patients that present with additional disorders such as diabetes and hypertension. There is currently no successful treatment for HFpEF. There is increasing evidence that the blood vessels that feed the heart tissue are dysfunctional during HFpEF and preliminary results show that a reduction in blood vessel density is present in HFpEF. Gene analysis data also shows that genes from the Wnt signalling pathway are downregulated. This is important because in other models, downregulation of these genes drives vessels to regress leading to hypoxia. Coupled with this vessel loss and hypoxia, preliminary data also exhibits a reduction in Wnt mediated anti inflammatory proteins, such as TSG6. This suggests that the loss of Wnt signalling could create an inflammatory cardiac environment both by vessel loss and the downregulation of anti-inflammatory pathways. This research represents a new perspective on HFpEF, focusing on blood vessel dysfunction and inflammation rather than heart muscle cell dysfunction.

onderzoeksgroep: Aging physiology and molecular evolution & Department of Cardiovascular Sciences
KU Leuven

Copromotor(en):

Jones Elizabeth A.V.

Begeleider(s):

Simmonds Steven

opmerking

voorbehouden: Jana Raman

1665

Impact of offshore wind farms on the soft-sediment macrobenthos and benthic ecosystem functioning

abstract By 2020 Belgium should acquire 13% of its energy from renewable resources. One option to reach this deadline has been the construction of offshore wind farms in the Belgian part of the North Sea. Three offshore wind farms are already operational in the Belgian part of the North Sea and four more concession areas are granted for construction. By 2030, all Belgian offshore windfarms together should produce as much renewable energy as windfarms on land. A monitoring programme was set up to identify the ecological effects of this anthropogenic disruption on the soft-sediment macrobenthos (organisms living in the sediment and larger than 1mm). Ongoing monitoring shows that the effects of wind turbines on benthic communities are, if present at all, very local. These effects are manifested through organic enrichment of the sediment via the fall-out of organic deposits from the hard substrate fauna colonizing the turbine submarine foundations. This increased food availability favours macrobenthic communities, which is shown in both higher densities and biodiversity in close (<50 m) vicinity to certain types of wind turbine foundations. In September 2019, a multidisciplinary integrated monitoring campaign will be conducted to investigate the small-scale effects of wind turbine presence on local hydrodynamics, hard substrate fauna colonizing the turbines, geological imprints of locally altered hydrodynamics on the sediment and benthic communities along with characterization of their habitat. The student involved will be able to take part in this one week campaign in the offshore windfarms. Back in the home lab, she/he will identify the macrobenthic organisms in the sediment samples until species level and possible changes in the environment will be evaluated using biotic (biomass, abundance, diversity on and around the turbines) and abiotic variables (sediment grain size, organic material, hydrodynamics). Also benthic ecosystem functioning can be assessed by measuring carbon mineralization rates in sediments in a transect along the wind turbines.

onderzoeksgroep: Marine Biology

Copromotor(en):

Moens

Tom

Begeleider(s):

nog te bepalen

opmerking

voorbehouden:

abstract The application of phylogenetic trees has revolutionized the field of botany in the past 30 years or so. For a long time, chloroplast markers have been the most widely used type of data to infer phylogenies. With phylogenies, based on chloroplast DNA sequence data, all kinds of fascinating questions have been addressed, for example related to ecology, biogeography, molecular evolution, or the evolution of life history features. The application of next generation sequencing techniques is particularly exciting for plant phylogenetics. Using a relatively cheap sequencing approach called genome skimming, it is possible to routinely generate genomic data from all three plant genomes, so not just from the chloroplasts only. An ongoing project on a genus of South and Central American tropical trees has demonstrated the value of a genome skimming approach, even when sequencing from herbarium material. So far, this project has revealed something remarkable: the phylogeny based on chloroplast data is in strong conflict with the phylogenies based on nuclear and mitochondrial data. The most probable explanation so far is an old hybridization event that facilitated chloroplast capture. This is how far we have got, and you can take this project further. What tree species are we talking about? The name of the genus is *Oxandra*, which belongs to the soursop family, with the scientific name Annonaceae. The Annonaceae consist of roughly 2500 species of trees and lianas, almost exclusively confined to wet tropical rain forests on all continents. You may know the delicious fruit of *Annona muricata*, 'zuurzak' in Dutch, or the enticing smell of *Cananga odorata*, better known as ylang-ylang, both of which are species of this family. The genus *Oxandra* comprises 27 species of small to large (50 m!) trees. They occur from Mexico down to the Atlantic rain forests of Brazil, with many species having their home in the Amazon. Now, here is the reason why we wanted to know more about the evolution of this genus: based on leaf, flower and fruit characters, and reproductive systems it is difficult to paint a coherent picture of the genus. This could be an indication that these species did not evolve from a single common ancestor. This hunch turned out to be true... but only if you look at phylogenetic trees based on chloroplast data. Nuclear and mitochondrial data, on the other hand, indicate that most species of *Oxandra* are monophyletic, that is, did evolve from a single common ancestor. The analyses up to now are based on 18 species of *Oxandra*. In order to advance our understanding of the processes that produced the conflicting phylogenetic patterns, you will expand the sampling of species of *Oxandra* and some closely related genera. Questions that you will focus on in your project are: - is the phylogenetic conflict of chloroplast phylogenies vs. nuclear and mitochondrial phylogenies maintained after increasing species sampling? - does the monophyly of *Oxandra* in nuclear and mitochondrial phylogenies involve all species, or are there aberrant species falling outside this clade? - can the phylogenetic patterns be related to morphological or life history features of the tree species? - is it possible to describe the scenario that led to the ancient hybridization (species involved, geographical area)? Techniques that you will use are: - laboratory techniques: high-throughput sequencing, involving DNA isolation, DNA library preparation, and sequencing - bioinformatics: data assembly and annotation - phylogenetics: aligning, likelihood and Bayesian phylogenetics, character optimization. Do come knocking on my door when you are a motivated student with a broad interest in different biological disciplines like evolutionary biology, botany, genomics, biogeography.

onderzoeksgroep: Spermatophytes

Begeleider(s):

Chatrou

Lars

opmerking

voorbehouden:

abstract With over 20% of plant species threatened worldwide, intensified efforts to conserve plant diversity are urgently needed. The first step for protecting a threatened species is to evaluate its conservation status in the framework of the IUCN (International Union for the Conservation of Nature) Red List of Threatened Species. Evaluating threat based on the Red List Categories and Criteria is an authoritative, comprehensive and widely used approach in conservation biology. Indeed, many decisions made by governments, natural resource managers, and conservation planners rely often solely on the "Red List" published by IUCN. The conservation status of many plant species is yet to be assessed. In 2016, the Red List included assessments of almost 22,000 plant species, just over 6% of the estimated global total of ca. 352,000 flowering plant species. The situation is especially critical for countries where the political situation has made fieldwork, to collect specimens and data, impossible for botanists. Angola is a case in point. In the last few years, however, this situation has much improved opening opportunities to collect new data. During this project, the student will build an accurate checklist of all Cyperaceae species occurring in Angola; discern whether these species are endemic, native or introduced; search for collection locality data in online databases, identify and study herbarium specimens, and geo-reference locality records. Using this data, he/she will then calculate the Area of Occupancy (AOO) and the Extent of Occurrence (EOO) of species, and build species files for IUCN Species Information Service (SIS) Toolkit. Also, the student will build a species richness map based on the collected data, and aim to establish correlations with areas of high species richness in other taxa, and/or specific habitat types. The objectives of this project are: - to learn how to apply state-of-the-art conservation research tools, - to effectively include threatened species into the IUCN Red List of Threatened Species - to gain an understanding of (patterns of) Cyperaceae species richness in Angola. The techniques used in this project are: - literature study, study and use of (digital) herbarium specimens and records. - identifying species using species identification keys and species descriptions. - using GIS tools like GeoCAT, R packages such as ConR, and database tools like the IUCN SIS toolkit - species richness assessments

onderzoeksgroep: Spermatophytes

Copromotor(en):

Larridon

Isabel

Begeleider(s):

nog te bepalen

opmerking

voorbehouden:

abstract More than 250 specimens of *Carex* species from Sub-Saharan Africa are present in the collections of the Ghent University Herbarium (GENT), and together they represent about 50 species. Further collections are available in the herbarium of the Botanic Garden Meise (BR). Many of these identifications of these specimens are questionable, tentative, uncertain, or not carried out up to species level. Understandable, because until recently no workable identification key for these plants was present. Previously, there were regional keys and (very) old keys, and often these keys were based on very incomplete overviews of the floristic wealth in Sub-Saharan Africa. Remarkable progress was made due to a recent treatment of the genus by German botanist Berit Gehrke, who published a key, accompanied by good descriptions, with which all *Carex* species south of the Sahara can be identified. In the context of the ongoing efforts to write a Cyperaceae treatment for the Flore d'Afrique Centrale in collaboration with Botanic Garden Meise, this project aims to revise the *Carex* species from the Democratic Republic of Congo, Rwanda and Burundi. In general, this project will contribute to a better understanding of the African *Carex* species and increase the quality of the collections of the GENT and BR herbaria by ensuring the specimens bear the correct identification. The techniques / materials used in this project are: - Literature study: available information about *Carex* species from Sub-Saharan Africa. - Study morphological characters and identify species based on identifications key using binocular microscope, loupe, etc. - Molecular study: Sanger sequence the species not yet included in the Global *Carex* Group mega-phylogeny to place them in a phylogenetic framework. - Species distribution: preparation of distribution maps by means of (online) software based on herbarium data.

onderzoeksgroep: Spermatophytes

Copromotor(en):

Goetghebeur Paul

Larridon Isabel

Begeleider(s):

Chatrou Lars

Goetghebeur Paul

Larridon Isabel

opmerking

voorbehouden:

abstract Tropical rain forests are the most species-rich terrestrial ecosystems, containing astonishing numbers of species in almost any group of organisms. This master thesis dives into the evolutionary build-up of this diversity. There is a long-standing debate on the pattern of species accumulation in tropical rain forests over evolutionary time, known as the museum vs. cradle debate. The museum hypothesis goes back to Alfred Russell Wallace, who proposed that tropical forests accumulated species over long periods of time due to their age and climatic stability. Ledyard Stebbins coined Wallace's idea the 'museum hypothesis', and suggested that the climatic stability is connected to low extinction rates and the survival over evolutionary time of archaic forms. Contrasting with the museum model, is the model of rapid speciation in clades, so-called radiations. This model, coined the 'cradle hypothesis' would necessarily involve extinction rates that are elevated compared to those associated with the museum model. An excellent plant group for testing these hypotheses is the family Annonaceae, containing ca 2500 species of trees and lianas that almost exclusively are found in tropical rain forests on all continents. In recent years we have learned a lot about the phylogenetic relationships within this plant family. Also, we know that the common ancestor of the family was around some 100 million years ago. However, we only have a limited understanding of patterns of diversification (speciation minus extinction) that gave rise to the present-day diversity. The reasons for this are twofold: first, our efforts to estimate the age of Annonaceae are seriously hampered by lineage-specific heterogeneity of molecular substitution rates. Indeed, processes at the level of DNA have a huge impact on our understanding of large-scale processes covering millions of years. The second cause is the incompleteness of species sampling in most family-wide analyses so far. Tree shape of the two main clades of the Annonaceae, the subfamilies Annonoideae (1400 species) and Malmeoideae (900 species), is very different. Our preliminary results suggest that the species in the Malmeoideae have accumulated at an even pace, which would be consistent with the museum model. Phylogenetic patterns in the Annonoideae, on the other hand, appear more radiation-like with periods without traceable speciation being followed by abrupt and fast bursts of speciation. Your task will be to further explore evolutionary ages and diversification patterns in the light of these observations. You will bring together data from several data sets and from online data repositories, and gathered a data set containing all species of Annonaceae, for which sequence data of multiple plastid markers are available. Using mainly Bayesian statistical approaches you will infer phylogenies and clade ages, and infer diversification patterns. Questions that you will focus on in your project are: - do pattern and rates of species evolution in Annonaceae conform to the museum model or the cradle model? - does the accumulation of species over evolutionary time follow a pattern that is universal for the entire family, or do clades within the family have different diversification patterns? - do diversification patterns differ among the major continents containing tropical rain forests (South America, Africa, Asia)? - are differences in patterns and rates of species evolution, if present, attributable to species characteristics, for example of flowers or fruit? - how large are the uncertainties of the results, and what is the effect of using different assumptions in the analyses? Techniques that you will use are: - bioinformatics and phylogenetics: data gathering, aligning, likelihood and Bayesian phylogenetics, including inference of ages and diversification patterns. The ability to use R would be helpful, but isn't required and can be learned during the project. Also, no preliminary knowledge of Bayesian statistics is required. By far the most important is enthusiasm for and an interest in biological disciplines like evolutionary biology, botany, biogeography, and a feel for data analyses.

onderzoeksgroep: Spermatophytes

Begeleider(s):

Chatrou

Lars

opmerking

voorbehouden:

1670 Auxin immunolocalisation and chemical screening in macroalgae

abstract Macroalgae attach the substrate by means of (i) adhesive secretion; (ii) rhizoids differentiation which differentiate into (iii) hapters upon contact with the substrate Zygotes of Dictyota are being used to study cell polarisation and asymmetric cell division in plant systems because of some practical advantages of broadcast spawning algae (Bogaert et al. 2017). Soccer ball-shaped egg cells elongate quickly after fertilisation into rugby ball-shaped cells with two poles. The cell normally polarizes and one pole differentiates into the basal cell fate (developing the rhizoid or attachment structure) and the other into the apical cell fate (becoming the thallus). The rhizoids will attach the embryos to the substrate and mature in branched discoid hapters that may develop a large physical attachment surface. In chemical biology, molecules are applied as conditional tools to reveal the underlying mechanisms of growth and development. Exogenous application of natural or synthetic analogs of signaling molecules or pharmacological agents may interfere with the polarisation process and be of value for the study of the developmental processes such as rhizoid development. For example exogenous application of auxin analogs interferes with the process of apical-basal patterning by inducing embryos with two cell poles with a basal cell fate: embryos with two rhizoids instead of one (Bogaert et al. 2018). The hypothesis is that exogenous application of auxins interferes with the establishment of an intercellular gradient of auxin. While preliminary evidence suggests such a gradient, the existence of intercellular auxin gradients is controversial. The first projects objective, is to test this hypothesis by means of auxin immunolocalisation of developing cells of algae. Secondly, the master student will deliver pioneering work in establishing a protocol for an automated chemical screening protocol that will be used to discover new molecules affecting asymmetric cell division, rhizoid emergence and rhizoid maturation into hapters. Although pre-plated compound collections are commercially available, the challenge is in developing a proper and robust screening assay: (i) screening protocols for Arabidopsis protoplasts and tobacco BY-2 cells need to be modified for Dictyota zygotes or spores. (ii) Using imaging software we will make first steps to automate the read-out using cell shape and hyalinity of the rhizoid cells. Using chemical screening we envisage to develop compounds that (i) provide a powerful tool to study early algal development and (ii) may result in an applications as anti-biofouling agents or attachment promoting components in seeding lines and canvasses. References: Bogaert KA, Beeckman T, De Clerck O (2017) Two-step cell polarization in algal zygotes. Nature Plants 2017 3: 16221 Bogaert KA, Blommaert L, Ljung K, Beeckman T, De Clerck O. (2018) Auxin function in the brown alga Dictyota dichotoma. Plant Physiology <https://doi.org/10.1104/pp.18.01041>

onderzoeksgroep: Phycology & PSB Plant Systems Biology-Root Development

Copromotor(en):

Beeckman Tom

Begeleider(s):

Bogaert Kenny

opmerking**voorbehouden:**

1671 How is Sea lettuce taking up CO₂? A closer look at transcription factors.

abstract Sea lettuce, or *Ulva mutabilis*, is a model organism for green multicellular algae. Most algae have developed carbon concentrating mechanisms (CCMs) to actively take up CO₂ from their aquatic environments. CCMs have mainly been studied in the single-celled green algae *Chlamydomonas*. At the molecular level, CCMs involve several proteins that transport CO₂ across various membranes and other enzymes that facilitate carbon assimilation. CCMs are inducible systems; at least two transcription factors control their expression in *Chlamydomonas*. Physiological research has clearly indicated the presence of a CCM pathway in *Ulva* and the molecular tools to dissect their function has only become possible in recent years. Homologs for all essential CCM proteins have been identified in the *Ulva* genome, including transcription factors putatively regulating them. In this master thesis project, we want to explore the function of transcription factors which are putative regulators of CCMs in *Ulva* using a molecular toolkit that we have developed. We will generate transcriptional and translational reporters, generate gain- and loss-of-function lines, perform gene expression (qRT-PCR, Western Blot) analysis and identify targets of these transcription factors (ChIP).

onderzoeksgroep: Phycology & PSB Plant Systems Biology-Plant Genome Editing

Copromotor(en):

Jacobs Thomas

Begeleider(s):

Blomme Jonas

opmerking Most practical work will be performed in VIB (Plant Systems Biology)

voorbehouden:

1672 On sex, stress and whole genome duplications

abstract Whole genome duplication: or autopolyploidisation provides an organism with an extra copy of the genome. As this copy is entirely redundant it has the potential to evolve new functionality. Consequently polyploidy is considered to be a major factor contributing to (plant) evolution. Nevertheless polyploidisation is a rather stressful event as the extra copy of the genome hampers cell division and causes considerable transcriptional and epigenetic upheaval. Stress: Several lines of evidence suggest that polyploid success is somehow linked to environments that are considered to be stressful to their lower ploidy ancestors. Three non mutually exclusive hypotheses have been proposed to explain this link: 1) stressful conditions promote polyploid formation, 2) polyploidisation causes an immediate fitness advantage allowing polyploids to grow where their ancestors cannot survive 3) polyploids have an increased evolvability and consequently adapt faster to a changing environment. Sex: At the climax of the sexual cycle of the unicellular green algae *Chlamydomonas reinhardtii* a common (5%) deficiency in the fusion products of + and - gametes prevents the formation of zygospores, giving rise to natural polyploids that reproduce asexually. In this thesis we will integrate these three elements by creating an exciting experiment in which wild type *Chlamy* is grown facultatively sexual in a number of stressful environments that are considered advantages for polyploids (finding such an environment will be the first module of this thesis). Subsequently we will test whether the polyploids increase in number and are able to establish themselves and outcompete their ancestors. By using the proper controls (facultative sexuals in a benign environment, asexual haploids and asexual diploids) we will be able to distinguish between the immediate fitness effect of polyploids (hypothesis 2) and the increased polyploid production (hypothesis 1). Lab work involves: Algal culturing, growth assays, coulter counter and flow cytometry, there is a possibility to do molecular work and/or transcriptome analysis as well.

onderzoeksgroep: Phycology & PSB-Bio-informatics group

Copromotor(en):

Van de Peer Yves

Begeleider(s):

Bafort Quinten

opmerking

voorbehouden:

1673

Some like it hot (but not too long) – brown algal response to climate change.

abstract Seaweed ecosystems worldwide are under increasing pressure from changing environmental conditions as a result of global climate change. To date, a large amount of studies have indicated the sensitivity of several seaweed species to warming and acidification. However, there is increasing evidence that seaweed responses to climate change interact with local variables such as seasonal daylength cycles. The effect of these variables should therefore be studied simultaneously in order to make realistic predictions regarding the persistence of seaweeds under specific scenarios of climate change. To address this issue, we will study the single and interactive effects of temperature and daylength on reproduction and growth in the brown macroalga *Dictyota dichotoma*, a key component of European coastal ecosystems. Specifically, we will subject algae originating from several European populations to different combinations of these stressors in order to better understand how latitudinal or seasonal differences in daylengths affect the sensitivity of *Dictyota* populations to global warming. In addition, we will use these data to construct models, aimed at predicting the future distribution of the European *Dictyota* populations under distinct scenarios of global climate change as described by the Intergovernmental Panel on Climate Change (IPCC).

onderzoeksgroep: Phycology**Begeleider(s):**

Delva Soria

opmerking**voorbehouden:****1674**

The more the merrier?

abstract Whole genome duplication (WGD) or polyploidisation provides an organism with an extra copy of the genome. As this copy is entirely redundant it has the potential to evolve new functionality. Consequently polyploidy is considered to be a major factor contributing to (plant) evolution. Nevertheless polyploidisation is a rather stressful event as the extra copy of the genome hampers cell division and causes considerable transcriptional and epigenetic upheaval. Several lines of evidence suggest that polyploid success is somehow linked to environments that are considered to be stressful to their lower ploidy ancestors. Three non mutually exclusive hypotheses have been proposed to explain this link: 1) stressful conditions promote polyploid formation, 2) polyploidisation causes an immediate fitness advantage allowing polyploids to grow where their ancestors cannot survive 3) polyploids have an increased evolvability and consequently adapt faster to a changing environment. In this thesis we will focus on the second hypothesis. Immediate changes of polyploidisation such as a change in cell size and geometry and gene expression changes are supposed to create a niche shift which can either be an advantage when the environment changes or can allow the polyploids to disperse and spread in regions that are inaccessible to their the lower ploidy ancestors. This initial ecological differentiation is hypothesised to reduce interploidy competition and can consequently be a first step in the establishment of a polyploid species. We will try to quantify this niche shift by measuring growth parameters of wild type and neopolyploid plants along gradients of different environmental variables. Growing lines of different ploidies in competition will subsequently enable us to study how interploidy competition affects the amount of niche differentiation. Because land plants growth is notoriously slow and requires a lot of space all experiment will be conducted on the most wonderful plant model species you can imagine: the unicellular green algae *Chlamydomonas reinhardtii*. Lab work involves: Algal culturing, growth assays, coulter counter and flow cytometry, there is a possibility to do molecular work and/or transcriptome analysis as well.

onderzoeksgroep: Phycology & PSB-Bio-informatics group**Copromotor(en):**

Van de Peer Yves

Begeleider(s):

Bafort Quinten

opmerking**voorbehouden:**

1675 Characterization of physical and biological properties of newly discovered honey bee viruses.

abstract Honey bees are important pollinators of plants including economically important agricultural crops. However, honey bee populations are declining worldwide due to multiple factors, including pathogens, agrochemicals and loss of habitat. Honey bee viruses are an important factor contributing to colony losses and can be aggravated by the presence of the parasitic mite *Varroa destructor*. Most honey bee viruses are positive sense single-stranded RNA viruses belonging to the order of Picornvirales and Tymovirales. Double-stranded DNA viruses belonging to the Baculoviridae and Iridoviridae have also been reported. Bee viruses can be transmitted vertically within species or horizontally within species and different bee genera. Other parasites, such as the mites *Varroa destructor* and *Tropilaelaps* spp. can serve as vectors for these viruses and facilitate their transmission. For example, deformed wing virus (DMV) replicates inside *Varroa destructor*, leading to greater titers of the virus inside the bee. Recently, we conducted a metatranscriptome study of eight social and wild bee species, in which we combined polyadenylated RNA enrichment with high-throughput RNA sequencing. We identified over 20 known bee viruses, as well as several plant viruses and other pathogens. However, we also discovered two novel RNA viruses (bee iflavirus 1 and bee macula-like virus 2) and two novel DNA viruses (OcNV and a densovirus) which are related to pathogenic insect viruses. Understanding the transmission and pathology of these newly discovered viruses are important steps in understanding their role in bee health and may lead to new methods to improve honey bee health. This project aims to elucidate the physical and biological properties of these novel. The virus particles will need to be isolated and purified for electron microscopy and infection studies in bee hosts will need to be conducted.

onderzoeksgroep: Lab. of Molecular Entomology and Bee Pathology (WE10)

Begeleider(s):

Demaeght

Peter

opmerking

voorbehouden:

abstract Farmers are obligated by EU-regulations to cover their land as much as possible throughout the year. This benefits the soil during wet periods because erosion is less likely and nutrients are fixed. During dry periods this cover helps the soil by prevention of evaporation and the addition of humus which helps to keep moist. To avoid a continuous environment for pests and diseases to reproduce, farmers are keen to use green manure crops from other plant families than their actual productive crops. Phacelia (*Phacelia tanacetifolia*) and Mustard (*Brassica* sp.) are very popular. If the weather in the fall is good, these green manure fields can provide an important influx of pollen and nectar for honeybees. Some beekeepers are happy with these crops because they believe every additional food supply before winter is welcome. Other beekeepers blame these crops for higher winter mortality rates. They argue the 'winter bees', having a higher amount of vitellogenin to survive the long winter period, become exhausted if they have to become a 'summer bee' again to forage the green manure. In this masterthesis we will find out what the impact is of fall flowering crops on honeybees. Both on the individual bee level and the colony level. A field-experiment will be designed and executed by the student. Honeybee colonies will be placed in an area with high amounts of flowering green manure crops and in areas with no flowering crops in autumn. Bee samples will be taken throughout fall, winter and spring and vitellogenin-level will be analysed. The potential influx of nectar and pollen will be calculated by observations of the surrounding fields that are flowering. The actual influx will be measured by Arnia's remote-sensing-systems. These systems have a very accurate scale and log the weight of a hive. Daily weight gain will be measured and compared between the apiaries with and without flowering green manure crops in the neighbourhood. Together with the vitellogenin-analyses and the follow-up of the colonies during winter and spring, this masterthesis will result in an answer to the question if the flowering green manure crops are beneficial or harmful for honeybees.

onderzoeksgroep: Lab. of Molecular Entomology and Bee Pathology (WE10)

Begeleider(s):

Laget Dries

opmerking

voorbehouden:

de la Peña

Eduardo

abstract Western Uganda comprises one of the most diverse tropical areas in the world. Forested areas surrounding volcanic crater lakes are of particular importance given the extreme fragility and at the same time peculiarity of these ecosystems. Crater forests are important breeding areas and corridors for wildlife (several species of Colobus monkeys and chimpanzees occur naturally in the area). However, crater lakes are seriously disturbed due to human agricultural practices, uncontrolled cattle grazing and illegal felling for timber and firewood. Since October 2017, BOS+ financed by the Belgian Directorate-General for Development Cooperation and Human Rights supports a 5-year programme in Western Uganda that focuses on the conservation, restoration and sustainable management and use of forest areas. The main purpose of this MSc topic is to assess the distribution and recruitment of key fruit-tree species pivotal for macrofauna in these ecosystems (volcanic crater forests in West Uganda).

onderzoeksgroep: Terrestrial Ecology

Copromotor(en):

Lens Luc

Begeleider(s):

Cooper Matt

de la Peña Eduardo

opmerking

voorbehouden: Lynn Schepens

1678 Cranial musculoskeletal variation in Anolis lizards

abstract Anolis lizards represent a prime example of convergent evolution. Species occurring on different islands developed a similar morphology depending on the habitat they occupy. Six different ecomorphs can be distinguished: trunk, trunk-ground, trunk-crown, crown-giants, twig and grass-bush anoles. Recent research showed that each of these ecomorphs has a typical head shape. Surprisingly, while it was previously hypothesized that head width was the most important in determining bite force, this study showed that head height, rather than width, influences bite force. This implies that there are important differences in the cranial musculoskeletal morphology causing these differences in bite force (such as muscle orientation, relative muscle volume of jaw closing muscles, etc.). In order to identify traits that are affecting bite force, CT-scans and 3D-reconstructions will be made of the cranial musculoskeletal system of lizards belonging to the different ecomorphs. These 3D-reconstructions can then first be used to identify musculoskeletal traits that strongly differ between ecomorphs or that are similar within ecomorphs. Subsequently, by linking the observed variation in the cranial musculoskeletal system to measured bite forces, traits can be identified that are causing differences in bite forces. Next to improving our insight in cranial musculoskeletal variation and its link to performance, this study will also allow to test whether convergent evolution in external morphology is reflected in internal morphology.

onderzoeksgroep: Evolutionary Morphology of Vertebrates

Begeleider(s):

De Meyer

Jens

opmerking**voorbehouden:****1679** Musculoskeletal variation in the dewlap of Anolis lizards

abstract Most Anolis lizards are characterized by a dewlap, a skin flap just beneath the chin, which is used to communicate with other individuals. The dewlap strongly differs in morphology and performance (extension rate and duration), both within and between species. The dewlap mechanism itself is related to the hyoid apparatus. While previous studies already found that certain aspects of the hyoid musculoskeletal system can influence the extension rate, there are still a lot of aspects un(der)studied, such as muscle volume, fiber orientation and mineral density of the bones involved. To analyze this, CT-scans will be made of several Anolis lizard species, belonging to different ecomorphs (lizards belonging to the same ecomorph live in a similar habitat and have a similar morphology). These scans will then be used to make 3D-reconstructions of the dewlap musculoskeletal system. As such, it can be tested 1) how the musculoskeletal system differs between species and sexes and 2) whether species belonging to the same ecomorph have a similar musculoskeletal system. This will enhance our insight in the dewlap mechanism of Anolis lizards.

onderzoeksgroep: Evolutionary Morphology of Vertebrates

Begeleider(s):

De Meyer

Jens

opmerking

voorbehouden: Emile Cardinael

1680 Chemical genetics dissection of cell division orientation in Arabidopsis

abstract Due to the presence of a cell wall, plant cells are fixed within their tissue context and cannot move relative to each other during development. Plants thus need to rely on directed cell elongation and cell division to generate a full three-dimensional (3D) structure. In order to create a 3D structure, plants use formative or periclinal divisions (PD) that generate additional cell files (parallel to the tissue axis). This results in radial growth and the formation of new organs. It is clear that a very precise control of cell division orientation is crucial to allow normal 3D growth to occur. Thus, a central question in plant biology is what mechanisms govern division plane orientation. Given its importance, strikingly little is known about the mechanisms that orient division plane in a developmental context. In this project, we will use a chemical genetics strategy to screen for small chemical molecules that specifically promote PD in a cell-based system and study the transcriptional and proteomic changes that occur upon treatment with these small molecules. In our lab, we have already developed a cell culture-based system that enables us for high throughput chemical perturbation studies of the PD event. We will then perform a chemical genetics screen (using the in-house Compound Screening Facility) by adding a library of 10.000 chemical molecules to the cells in 96-well plates and analyzing the effect after two-four days of growth. Identified interested chemicals will be tested for their effect on PD in wild-type Arabidopsis roots. We will also systematically dissect different properties of selected chemical molecules using a set of subcellular markers (e.g. cytoskeleton, cell polarity and hormone signaling). For one or two selected small molecules, we will study the transcriptional and proteome changes upon treatment by RNA sequencing and MS/MS respectively. Genes or proteins significantly changed in abundance upon treatment will further studied using localization studies, determining loss and gain-of-function phenotypes and establishing protein interactors using IP-MS/MS and TAP technologies.

onderzoeksgroep: FPB(Functional Plant Biology) & PSB Vascular Development

Begeleider(s):

Yang BaoJun

opmerking**voorbehouden:****1681** Single cell transcriptomics of the root meristem in Arabidopsis

abstract Plant cells are organized in files along the body axis and growth is maintained through divisions within these files of cells. To create a new three-dimensional organ, plants trigger cells in a specific zone to undergo a different type of division (periclinal), forming additional cell files. Vascular cells have ability to undergo many of these periclinal division, generating the tissues that make up wood in trees and that are responsible for transport of nutrients and water throughout the plant. Recently, two transcription factors have been identified that together are necessary and sufficient to trigger periclinal divisions in these tissues. However, at this point it is not known what cell biological components are responsible for this switch of division plane. In this MSc project, we aim to understand what properties of the cell are altered that ultimately lead to a change in division orientation. In our lab, we have developed a system that enables us to induce periclinal divisions in any cell type of interest. As soon as 4 hours after induction, we can observe the first periclinal divisions, which gives us the perfect tool to find out what factors are important for this type of division. Using a set of subcellular markers (e.g. for cell geometry, cytoskeleton, cell polarity and hormone signaling) we will systematically dissect different properties of cells undergoing periclinal division and compare this, over time, to "normally" dividing cells. This also includes the use of antibodies specific for different types of cell wall modification. In addition, we will perform 3D electron microscopy to look at dividing cells at ultra-high resolution. This will enable us to physically see what is happening to substructures and molecules inside the cell during (periclinal) division. The combined approaches in this project will greatly enhance our knowledge of the cell biology concerning this important type of division.

onderzoeksgroep: FPB(Functional Plant Biology) & PSB Vascular Development

Begeleider(s):

Wendrich Jos

opmerking**voorbehouden:** Celien Van de Velde

1682 Fish distribution maps and marine protected areas to reduce fishing mortality of bycatch species

abstract Can we identify areas where bycatch species can be protected from excessive fishing mortality? This is the objective of this thesis. Bottom trawl fisheries catch a variety of fish species, but only few fish species are highly valuable at the fish market, such as Dover sole (*Solea solea*). A suite of other fish species, including vulnerable fish species such as sharks and rays, are considered as bycatch. The return of bycatch species to the sea, defined as discarding, induces unnecessary mortality of these bycatch species. This thesis will examine whether this unnecessary bycatch mortality can be avoided by closing areas to fishing. To this end, the student will assess whether bycatch species are occurring in hotspots, i.e. in locations with a disproportionately high abundance of the species and whether (some of) these hot spots have a proportionally low abundance of the target species? In other words, the hypothesis of this thesis is that bycatch species can be protected by closing areas where fishers do not lose much of the catches of their target species. The hypothesis will be addressed using commercial (landings) data from beam trawlers and from scientific surveys in the North Sea and the English Channel. Scientific surveys are conducted once or twice a year using standard trawls in pre-determined locations. The student will be encouraged to join a scientific survey to better grasp the experimental design and experience the sampling process. Fish distribution maps will be generated using these scientific survey data. The generated fish distribution maps will be independent from commercial fishing practices, i.e. fish catches are reflecting natural abundances. As such, hot spots of target and bycatch species will be identified. Commercial fish data (landings data from commercial beam trawlers) will also be plotted and compared to survey data to evaluate whether commercial catches are purely reflecting fish abundances (as predicted from scientific surveys) or also include targeted fishing behaviour (based on the experience of fishers). The assessment of spatial distribution of fish and fisheries will have to account for the potential influence of spatial resolution, seasonal variability, annual displacement of fishing effort and aggregation behaviour of fish species. These distribution maps will provide scientific support to evaluate whether catches of bycatch species are located in different areas than catches of the main commercial fish species? This evaluation will provide the baseline to discuss the potential for closed areas to protect bycatch species. Students with a good background in R software and an interest in geostatistics are privileged. Keywords: fish distribution maps; Belgian fisheries; bycatch and discards, spatial management

onderzoeksgroep: Marine Biology & ILVO Oostende

Copromotor(en):

Depestele Jochen

Vansteenbrugge Lies

Begeleider(s):

Depestele Jochen

opmerking

voorbehouden:

abstract In order to achieve an increase in the plant's intrinsic yield and biomass, expansion of knowledge on the mechanisms of plant growth and its regulatory circuits is necessary. Since next to cell division, cell elongation determines the development and growth of plants, the mechanisms behind this process will form the primary focus of the research. Even if plant cell walls consist of less than 10% of cell wall proteins, the role of the latter in cell elongation is crucial. This complex group of enzymes will mediate and regulate the different processes necessary for the cell to elongate. Since the structure and function of cell wall enzymes is influenced by post-translational modifications, we assume that cell elongation also depends on these post-translational modifications. A couple of interesting cell wall proteins were selected for further investigation. This pool of proteins was narrowed down by gene expression data of the genes coding for them to a couple of promising candidates whose activity might be regulated by post-translational modifications. The protocol for cell wall protein extraction in rice coleoptiles, plant organs that solely grow via cell elongation after a defined period of time, has been optimized in our lab, so protein activity during cell elongation in these organs can now be studied, as well as the difference in glycan profiles of the cell wall proteins in normal versus fast elongating cells. Furthermore, pharmacological data obtained after the use of N- glycosylation blockers during coleoptile growth show an effect on the elongation. These data will have to be supported by mutant analyses. Mutants in the N-glycosylation pathway have been created, and need to be analyzed. Cell wall proteins are not only heavily N-glycosylated, but also contain a lot of O-glycans. It would be interesting to explore this type of post-translational modification as well. The effect of (partial) blocking the O-glycosylation pathway on cell elongation will need to be investigated, and mutants with respect to enzymes in this pathway need to be created via the exciting CRISPR-Cas9 genome editing tool. Aim Our goal is to unravel the role of post-translational modifications, and more specifically of N- and O- glycosylations during cell elongation in normal versus fast elongating cells, by combining functional analyses and pharmacological approaches. Techniques Plant handling – Coleoptile elongation assay – Molecular analyses (DNA/RNA extraction, qRT-PCR, CRISPR-Cas9 genome editing, rice transformation, etc.) – Functional analyses

onderzoeksgroep: Lab of Plant Growth Analysis (vakgroep KR01, Environm. Technology, Food Technoloav&Molecular Biotechnoloav)

Copromotor(en):

De Jaeger Geert

Begeleider(s):

Botterman Debbie

opmerking gelieve bij interesse stephen.depuydt@ghent.ac.kr te contacteren ivm huisvesting en praktische zaken! Dank!

voorbehouden:

abstract Given the challenges of feeding an ever-growing world population combined with the negative effects climate change will have on crop yields, it will be of critical importance to develop high yielding resilient crops. While the progress that has been made for rice in the last decades is nothing short of spectacular, higher yields of this staple crop will also be needed. In this research line, we mainly focus on examining the effects of genetic perturbation of components of the PLA1 pathway. It has previously been shown that overexpression of this protein in Arabidopsis and maize leads to an enhanced biomass and seed yield, while knockouts have the opposite effect. In the laboratory, we have generated transgenic rice lines overexpressing PLA1, as well as CRISPR knockout lines targeting negative regulators of PLA1. These lines are in different stages of the transformation cycle (ranging from T1 to T2), and will be subjected to a number of analyses. These analyses will involve kinematic analyses to get a detailed insight in how the growth of the plants is affected, in addition to coleoptile elongation assays to determine if this parameter is also affected. Additionally, we will also investigate gene expression in these plants for a number of genes using qPCR. Next to the PLA1 pathway, we also have a number of mutant plants ready that have been modified using CRISPR for a number of QTLs in mesocotyl elongation. These knockouts should lead to a longer mesocotyl which will make it easier for the rice seedling to push through the soil after germination. Depending on the interest of the student and the need of the laboratory, we are also able to generate a number of additional CRISPR mutants in the same or alternative pathways. These experiments will involve the design of gRNAs, molecular cloning and tissue culture of rice. Aim Our goal is to determine the effect of genetic perturbation of the PLA1 pathway on the yield of rice. Additionally, we will validate a number of QTLs reported to be involved in the elongation of the mesocotyl. Techniques Plant handling – Kinematic analysis - Coleoptile elongation assay – Molecular analyses (DNA/RNA extraction, qRT-PCR) - CRISPR - Molecular cloning – Tissue culture

onderzoeksgroep: Lab of Plant Growth Analysis (vakgroep KR01, Environm. Technology, Food Technoloav&Molecular Biotechnoloav)

Copromotor(en):

Nelissen Hilde

Begeleider(s):

De Saeger Jonas

opmerking gelieve bij interesse Stephen.depuydt@ghent.ac.kr te contacteren ivm housing en praktische regelingen! Dank.

voorbehouden:

Goormachtig

Sofie

The use of Plant Growth Promoting Rhizobacteria (PGPR) to alleviate drought stress in wheat (*Triticum aestivum*)

abstract Wheat is one of the most important agricultural crops globally. Today, it is grown on more land area than any other commercial crop and continues to be the most important food grain source for humans. Wheat yield increases have stagnated over the last decade and technological innovations such as GMO and hybrid line production has proven to be cumbersome. One other opportunities is to use Plant Growth Promoting Rhizobacteria (PGPR) which promote plant growth and help the plant to overcome different biotic and abiotic stresses. Deep sequencing analysis revealed several bacteria that correlate with growth of wheat plants in drought conditions and that might help the plant to alleviate drought stress. We apply those bacteria and analyze whether the inoculated plants are more protected against drought than the uninoculated ones by phenotypic analysis. In addition, we perform a molecular characterization of the plant-microbe interaction in order to understand the mechanisms behind the growth promotion. As a result, we will identify bacterial strains that can be used to promote wheat development with a decrease of water availability.

onderzoeksgroep: PSB Plant Systems Biology Rhizosphere Group

Begeleider(s):

Froussart Emilie

opmerking

voorbehouden:

1689 The use of root endophytic bacteria to boost lettuce growth at low temperature conditions

abstract The Compositae family, the most successful group of flowering plants in the world, encompasses over 200 domesticated species of which lettuce (*Lactuca sativa* L.) is the most important one from an economic point of view. In Belgium, from late spring to early autumn, lettuce can be grown up to consumable size in less than two months, while this period is almost tripled during the colder months of the year both at nurseries and the horticultural facilities. Hence, speeding up lettuce root and shoot development to enhance crop formation at low temperature conditions would benefit both seedling and crop producing companies. One way to tackle this problem is through the use of plant growth promoting rhizobacteria (PGPR). A significant subset of PGPR have been shown to promote plant growth in multiple stress conditions, including low temperature stress. However, much still needs to be discovered about the response of in planta plant signaling pathways upon interaction with PGPR, especially while coping with cold temperatures. Hence, this project aims at defining a root endophytic bacterial consortium to boost lettuce growth at suboptimal temperatures and to unravel the underlying molecular pathways.

onderzoeksgroep: PSB Plant Systems Biology Rhizosphere Group

Begeleider(s):

Persyn Antoine

opmerking

voorbehouden:

Hendrickx Frederik

1690 The genomics underlying fast, in situ evolution in a wing-polymorphic beetle

abstract Understanding the capacity of organisms to adapt to environmental change is a central topic in evolutionary, ecological and conservation research. Some recent studies have demonstrated that such adaptation may often occur surprisingly fast and suggests that natural populations may harbor a much larger pool of standing (adaptive) genetic variation than generally assumed. While standing genetic variation is generally assumed to be introduced by gene-flow, it remains poorly understood if single founding populations may contain sufficient variation for rapid, in situ, evolution. However, testing this idea is difficult as it requires the identification of alleles involved in adaptation at the molecular level and to follow changes in their frequency in real-time. A prominent case of rapid evolution is found in populations of the wing-polymorphic beetle *Pogonus chalceus*, where short-winged 'tidal' and long-winged 'seasonal' ecotypes have diverged in response to contrasting hydrological regimes. Colonization of 'tidal' habitats occurs by long-winged individuals, but these populations quickly (~20 years) evolve towards the short-winged ecotype. This process is very well illustrated in a recently created salt-marsh in Belgium, for which samples of the first colonizing long-winged individuals are available for genomic analyses. Given that the alleles underlying this ecotypic differentiation have been characterized during previous research, this system represents a unique opportunity to better understand how populations adapt genetically after the colonization of a new environment and how adaptive genetic variation is maintained within populations. More specifically, the aims of this project are (i) to quantify to what extent phenotypic changes are associated with genomic changes; (ii) to quantify the presence and frequency of adaptive alleles in the founding population; (iii) to follow frequency changes in these alleles through time and (vi) to decipher the origin of the short-wing associated alleles in the founding population. Practical work includes the preparation of Restriction-site Associated DNA libraries (RADseq) and bioinformatic analysis of the data.

onderzoeksgroep: Terrestrial Ecology & KBIN, Departement Entomologie

Copromotor(en):

Vangestel Carl

Begeleider(s):

Hendrickx Frederik

Vangestel Carl

opmerking

voorbehouden:

abstract Forest edges are characterized by surprisingly richer communities forming hotspots of diversity in otherwise fragmented landscapes. Conceptually the strength of these edge effects could be attributed to structural differences between the vegetation on both sides of the forest edges and to the spatially heterogeneous distribution of resources. In fragmented landscapes with discrete habitat patches such as forest remnants within an agricultural matrix, edge permeability will affect the connectivity between these discrete habitat and ultimately metapopulation dynamics and persistence. Understanding the edge features that control this permeability to animal movement and dispersal is therefore key to efficient species conservation in fragmented landscapes. The aim of this thesis will be to select a set of target (animal) species, to track their crossing behaviors of forest edges using various methods such as mark-recapture, directional traps or stable isotope. The edge permeability observed in the fields would then be used to develop a metric that would enable us to predict edge permeability and landscape connectivity from edge features.

onderzoeksgroep: Terrestrial Ecology

Copromotor(en):

Bonte Dries

Begeleider(s):

Hertzog Lionel

opmerking

voorbehouden: Lars Dekeyser

abstract Recently, a German study (Hallmann et al. 2017) suggests that insect communities in nature reserves in western Germany declined with over 75% in the past three decades. And a similar phenomenon has been observed in certain insect taxa in the Netherlands as well (Kleijn et al. 2018). The authors do not exclude that the intensification of agricultural practices might be an important factor, but there is no hard evidence for this assumption. And thus far, no attempts have been made to assess the current insect diversity nor its recent trends in Flanders. As a result, we have no idea about the insect biodiversity in agricultural land (versus semi-natural habitats) nor whether crucial ecosystem services (pollination, crop protection, food supply, ...) are still provided. Trying to get a grip on this system is what this project is all about. Apart from various but often detailed datasets on a number of insect families from the past, most samples and data will be gathered during the project itself. A representative number of sites in agricultural land (arable crops, pastures, meadows) and in adjacent semi-natural habitats will be investigated with an array of collecting methods that should provide us with a first indication on both the species richness and abundances. Though identification until species level is not excluded per se, in a first step we will rather focus on functional groups and other higher level taxonomic traits. In a second step the natural history of these functional groups will be screened (via literature research) in order to establish their role in the respective ecosystems and potential ecosystem services for mankind. In a final step an attempt will be made to construct an ecosystem model, focusing on the insect component. Profile: we seek a biologist with a pronounced interest in entomology, who likes fieldwork, is both accurate with data and material, creative, thinks out-of-the-box and is not afraid of modelling, i.e., a can-it-all. (S)he knows the different insect orders, and might be willing to extend her/his taxonomic knowledge.

onderzoeksgroep: Terrestrial Ecology & INBO Brussel

Copromotor(en):

De Bruyn Luc

Pollet Marc

Begeleider(s):

De Bruyn Luc

Pollet Marc

opmerking

voorbehouden:

abstract In the absence of genetic diversity, plants rely on the capacity of phenotypic plasticity to cope with shifts in environmental conditions. Understanding the mechanisms behind phenotypic plasticity and how local phenotypic adjustments are transferred to clonal offspring, will provide insight into its ecological and evolutionary significance. Epigenetic changes has recently been proposed to play a crucial role in rapid environmental adaptation. This project investigates the epigenetic and phenotypic variation (in terms of bud flush and bud set) of the Lombardy poplar, a single clone of *P. nigra* L. that is distributed worldwide since the beginning of the 18th century. Its clonal origin in combination with its widespread distribution in space and time, makes the Lombardy poplar an excellent study system to investigate how long-lived plant species with a prevailing vegetative reproduction can cope with widely contrasting environmental conditions, without variation at the genetic level. Cuttings were collected across Europe in winter 2016-2017 from 60 adult Lombardy poplars grown across Europe in different environments. The plants are grown in the greenhouse. This study includes bud flush and bud set observations in the greenhouse and the study of epigenetic variation (data-analysis) on vegetative offspring grown in a common greenhouse environment. Using statistical models, we investigate correlations among epigenetics, bud phenology and the climate at the home site of the Lombardy poplar trees. This project combines bud flush and bud set observations in the greenhouse (ILVO - Melle), with statistical data-analysis analysis of the greenhouse observations and epigenetic profiles (methylation sensitive AFLPs). Useful references: Vanden Broeck A., Cox K., Brys R., Castiglione S., Ciatelli A., Guarino F., Heinze B., Steenackers M., Vander Mijnsbrugge K. (2018). Variability in DNA Methylation and Generational Plasticity in the Lombardy Poplar, a Single Genotype Worldwide Distributed Since the Eighteenth Century. *Frontiers in Plant Science* 9(1635). <https://doi.org/10.3389/fpls.2018.01635>

onderzoeksgroep: Terrestrial Ecology & INBO Brussel

Copromotor(en):

Vanden Broeck An

Begeleider(s):

Vanden Broeck An

opmerking

voorbehouden:

abstract Assessing insect species richness and diversity, even in one single site, remains quite a challenging undertaking. For flying species, the most widely employed collecting methods are Malaise traps, pan traps and sweep nets, each with their specific benefits and restrictions. Contrary to Malaise traps, pan traps are far less frequently used despite their high effectivity and their standardized application. They come in all kind of shapes, sizes and colours, which has an effect on both the numbers and species obtained. At present, no unequivocal data are present on which trap types are best used in local or large scale surveys. Finding an answer to that question and turning this into a clear advice for future research is the goal of this project. And we do not start from scratch, on the contrary: extensive datasets from surveys in both the Palaearctic realm and the Neotropics (e.g., Chile, Ecuador, Martinique) are available, as well as sample sets from two field experiments conducted in two different marshland habitats in 2017 and 2018. Additional field work is most desirable and might a.o. entail assessing the proportion of species and specimens effectively being trapped. Indeed, the collected samples are merely the final product of possibly intricate processes that are not yet known or understood. The available datasets alone guarantee a number of peer-reviewed papers, and additional sample processing and field experiments only add more potential research outputs. Profile: we seek an allround biologist with a pronounced interest in entomology, who is both accurate with data and material, creative and thinks out-of-the-box. (S)he knows the different insect orders, and it is considered an asset to be into flying insects or to excited to gain knowledge on these taxa during the project. (S)he is expected to take charge of one or a few smaller fly families.

onderzoeksgroep: Terrestrial Ecology & INBO Brussel

Copromotor(en):

De Bruyn Luc

Pollet Marc

Begeleider(s):

De Bruyn Luc

Pollet Marc

opmerking

voorbehouden:

abstract Recent Red Lists (<https://www.inbo.be/nl/rode-lijsten-vlaanderen>) reveal that a large number of species is currently threatened in Flanders, not in the least insects. But as a German study (Hallmann et al. 2017) suggests, entire insect populations are at stake. Indeed, these authors showed that communities in nature reserves in western Germany declined with over 75% in the past three decades. And there are indications that the same processes are taking place in the Netherlands (Kleijn et al. 2018). So far, no attempts have been made to assess the current insect diversity let alone its recent trends in Flanders. The first aspect is the main goal of this project. To estimate the number of insect species at one single site alone is already a formidable challenge. Not only the individual species show seasonal activity patterns which requires (semi-) permanent monitoring efforts, but multiple collecting devices are necessary to gather flying, soil surface dwelling and subterranean species. Moreover, there is the issue of the taxonomic impediment: while there might be about 25,000 insect species in Belgium (not all of these occurring at the marshland site under investigation, of course), it is unlikely that a taxonomic expert for each of the collected insect groups can be found. And this knowledge cannot be expected from you individually either. A full year survey has been conducted in a nature reserve in Flanders in 2018 (Wellemeersen, Denderleeuw) including a Malaise trap and pan traps that might provide (part of) the necessary samples for processing. However, other approaches are also possible including additional fieldwork with e.g., the employment of a camera counter (<https://vroegevogels.bnnvara.nl/nieuws/automatisch-insecten-tellen-en-herkennen>). Depending on the approach (after discussion with you), a network of Belgian and foreign taxonomic experts can be involved which would also be part of the project. Profile: we are looking for an allround biologist with a pronounced interest in entomology, who is both accurate with data and material, communicative, creative and thinks out-of-the-box. (S)he knows the different insect orders and preferably more, or is willing/capable to extend her/his knowledge.

onderzoeksgroep: Terrestrial Ecology & INBO Brussel

Copromotor(en):

De Bruyn Luc

Pollet Marc

Begeleider(s):

De Bruyn Luc

Pollet Marc

opmerking

voorbehouden:

abstract This study investigates the effect of habitat loss and fragmentation on the genetic structure between populations of a species with an assumed low dispersal ability and narrow feeding niche. The dual resource specialization of *M. alcon* (single food plant (*Gentiana pneumonanthe* L.) and dependency of specific ant species (*Myrmica* sp.) makes it particularly sensitive to landscape modification and habitat alteration. Natural history collections provide immense opportunities to study past genetic diversity and evolutionary processes. They are also very useful to address conservation questions and investigate the impact of human pressure on populations over time. In this study we analyze the genetic diversity of present and past populations of the Alcon bleu (museum samples from KBIN) in order to provide insights in the effect of life history traits and human pressures on genetic diversity. This project combines a little bit of lab work under assistance of an INBO lab technician (at INBO, Geraardsbergen) with the analysis of genetic profiles (microsatellite analysis) and statistical data-analysis. Useful references: Vanden Broeck A., Maes D., Kelager A., Wynhoff I., Wallis de Vries M.F., Nash D.R., Oostermeijer G., Van Dyck H., Mergeay J. Gene flow and effective population sizes of the Alcon blue butterfly *Maculinea alcon* in a highly fragmented, anthropogenic landscape; (2017).

onderzoeksgroep: Terrestrial Ecology & INBO Brussel

Copromotor(en):

Maes Dirk

Vanden Broeck An

Begeleider(s):

Maes Dirk

Vanden Broeck An

opmerking

voorbehouden:

abstract European black poplar (*Populus nigra* L.) is a key species of the floodplain forest, which is the natural vegetation type on riverbanks in Western Europe (Habitat Code. H91E0). In common with many other European countries, floodplain areas in Belgium were subjected to urbanization. Native poplar stands were replaced by agriculture or by cultivated poplar plantations consisting of a narrow range of euramerican (*P.x canadensis*) and interamerican (*P. interamericana* ; *P. deltoides* x *P. trichocarpa*) hybrids. Exotic gene flow may have profound effects on the evolution of the native black poplar and a potential consequence is the increased extinction risk of the native species. In 2001, a species reintroduction project was set up and black poplar trees were planted along the riverside of the Meuse (Dilsen-Stokkem). These trees have now reached the reproduction stage, producing pollen and seeds that might contribute to the colonization of the gravel banks of the Meuse. This project aims to evaluate this re-introduction process. More specifically, this study aims to answer the following questions; Are the black poplar trees reproductive? Do they produce viable, seeds of pure *Populus nigra*? What is the genetic origin of the poplar seedlings that can be found on the gravel banks? Our methods combine field work with greenhouse experiments (seed experiments) and molecular genetic methods in the lab (paternity analysis on the species level). The final aim is to evaluate the re-introduction project and to produce guidelines for the restoration of floodplain forests with black poplar populations along the river Meuse at the Dutch-Belgian border. This project combines field-work (a few days in June and a few days in September – October), DNA-analysis in the lab under assistance of an INBO lab technician (at ILVO-Melle), greenhouse experiments (at ILVO – Melle) and statistical data-analysis. Useful references: Vanden Broeck A., Storme V., Cottrell J.E., Boerjan W., Van Bockstaele E., Quataert P., Van Slycken J. (2004). Gene flow between cultivated poplars and native black poplar (*Populus nigra* L.): A case study along the river Meuse on the Dutch-Belgian border. *Forest Ecology and Management* 197(1-6):307-310.

onderzoeksgroep: Terrestrial Ecology & INBO Brussel

Copromotor(en):

Vanden Broeck An

Begeleider(s):

Vanden Broeck An

opmerking

voorbehouden:

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 plots is followed up. This for the simple reason that 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 will mainly 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

Copromotor(en):

Thomaes	Arno
Van Calster	Hans

Begeleider(s):

Thomaes	Arno
Van Calster	Hans

opmerking

voorbehouden:

1700 The evaluation of agri-environment schemes to increase insect biodiversity

abstract A recent study received a lot of media attention, showing a 75% decline of flying insect biomass over the last 27 years. Insects play countless roles in ecosystem functioning. Hence, loss of insect biodiversity and biomass will provoke cascading effects in ecosystems (e.g. food webs, nutrient recycling, ...) and can impact ecosystem services (e.g. pollination, pest control, ...). Increased agricultural intensification plays an important role in explaining this decline. The European Partridge project (<https://northsearegion.eu/partridge/>) aims to improve the agricultural landscape which should increase biodiversity by 30% over 4 years. Through agri-environmental schemes, farmers sow flower strips and create beetle banks that should provide more food for Partridge chicks and increase insect biodiversity in general. The aim of the present study is to assess the effectiveness of these measures. Tasks: - Fieldwork o April – September in Ramskapelle and/or Isabellepolder o Survey of insects with traps (pit falls, sticky traps, pan traps, ...) and/or transect walks - Lab o Identification of trapped insects o Statistical analyses

onderzoeksgroep: Terrestrial Ecology & INBO Brussel

Copromotor(en):

De Bruyn	Luc
Pollet	Marc

Begeleider(s):

De Bruyn	Luc
Pollet	Marc

opmerking

voorbehouden:

Inzé Dirk

1701 Enhancing yield in maize by expanding the knowledge on the growth promoting PLASTOCHRON1 gene

abstract The economic value of maize greatly depends on grain and biomass yield. We recently showed that ectopic expression of the maize cytochrome P450 PLASTOCHRON1 (PLA1) enhances by more than 10% both biomass accumulation and grain yield in field trials performed both in Belgium and Iowa (USA). PLA1 produces a, yet unknown, yield promoting small molecule. The student will be involved in unraveling the chemical nature of this growth enhancing molecule as well as the gene regulatory network that is activated by PLA1. This project has a large potential to significantly contribute to further boosting crop yield. The project aims to identify additional genes in the regulatory network around PLA1 and to assess their putative role in yield enhancement; to identify the substrate/product of PLA1 and to evaluate the growth enhancing potential of the chemicals; and to obtain genome edited approaches to phenocopy the yield enhancing effect of the ectopic expression of PLA1. To achieve this aim the following techniques will be used: Growth assays and phenotyping (including automated imaging systems), genome editing in maize by CRISPR/CAS9, analysis of transcriptome and metabolome data, microscopy, cloning, maize genetics

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

Copromotor(en):

Nelissen	Hilde
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Begeleider(s):

Nelissen	Hilde
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opmerking

voorbehouden: Timothy Villers

abstract With the increasing world population, food resources become scarce and arable land area is decreasing. In addition, the effects of global warming can be perceived more and more each year, putting an even stronger pressure on the fragile food security equilibrium. During the summer of 2018, Belgium and Europe in general experienced the direct consequences of climate change, with an extremely dry summer and higher temperatures. Corn, potatoes, and vegetable fields were directly impacted. When plants start to perceive drought stress, they reduce their growth in order to limit the evaporative surface and save energy. This growth reduction is a very intriguing scientific question and unraveling the mechanisms behind it forms a first step towards breeding the climate-resilient crops of the future. With this thesis project, the student will participate in research on leaf growth inhibition under drought stress in the model species *Arabidopsis thaliana*. Leaf growth is a complex developmental process that is tightly regulated in order to react dynamically to changing environmental conditions such as drought. In very young *Arabidopsis* leaves, the growth reduction under drought is achieved through the inhibition of cell division and expansion. In the last years, research conducted on *Arabidopsis* and crop species highlighted an emerging role for the small phytohormone ethylene in the regulation of leaf growth and yield under drought. Despite the importance of understanding the drought-induced growth inhibition, the molecular mechanisms underlying this process remain largely elusive. With the proposed project, the student will help to unravel the role of ethylene in leaf growth inhibition under drought stress. By using last-generation technologies and genetic tools we will tackle this question at the molecular, cellular, and phenotypic level. We will measure and try to understand the ethylene accumulation under drought stress, with the use of reporter lines and mutants. Next, we will elucidate at the molecular level how ethylene triggers downstream pathways for leaf growth inhibition. This will involve molecular analyses such as (amongst others) expression analysis and in vitro assays, as f.e. luciferase assays, to confirm regulatory links between upstream ethylene factors and downstream growth-inhibitory genes. During the whole project, automated plant phenotyping platforms will be used to apply controlled drought stress to plants, accompanied by automatic daily imaging of the plants. Finally, image analysis of growing leaves at macroscopic and microscopic level will enable to track (cellular) growth dynamics under drought. The precise directions of this project are still to be defined according to the progress of the research and the interests of the student. Interested and motivated students are encouraged to contact the promoter or supervisor for further details.

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

Copromotor(en):

Dubois Marieke

Begeleider(s):

Dubois Marieke

opmerking

voorbehouden:

abstract Since November 2011, thanks to the financial support of the Belgian company Telenet, a large-scale reforestation programme has been implemented by BOS+ and the Mindo Cloudforest Foundation in Northwest Ecuador. This ca. 500 ha reforestation project has mainly focused on recovering degraded grazing lands near tropical cloudforest and subtropical forest areas. This programme ensures not only carbon storage, but the conservation of local biodiversity. The Chocó region harbours an astonishing 60% of global biodiversity on only 1,4% of the earth's surface but faces a lot of forest loss and degradation. So far, more than 450.000 trees have been planted and gradually restoration plots are yielding fully grown forests with a focus on connecting existing forest (reserves). The CaVeLab of Ghent University (Faculty of Bioscience Engineering) is monitoring tree growth and biomass production since 2012, but so far, an assessment of how fauna is responding to the restoration efforts has not yet been conducted. The restoration project has been organized following a hierarchical balanced design with plots in different regions, altitudes and climatic areas; and allowing comparisons between used and abandoned grazing lands, spontaneous revegetation and assisted reforestation. This set-up offers a unique opportunity to study along a restoration gradient how bird populations (and other groups of fauna) respond to reforestation efforts. This MSc topic is presented with the idea of filling this gap focusing on bird biodiversity. The work considered for this MSc-topic consists on the compilation of inventories of species (like the annual Christmas and global big day counts) and other available data on bird diversity, the analysis of such data-sets and finally field-work and observational studies focused on a specific group of birds to assess in different restoration and control plots to what extent functional and taxonomical diversity are restored.

onderzoeksgroep: Terrestrial Ecology

Copromotor(en):

de la Peña Eduardo

Begeleider(s):

de la Peña Eduardo

Eraly Debbie

opmerking

voorbehouden: Nele Devriendt

abstract White-eyes (Genus *Zosterops*) show the highest speciation rate in birds, yet little is known about how environmental niches evolve in these great speciators. This thesis will focus on the environmental niche variation in four closely related highland lineages inhabiting isolated sky-island systems in Kenya. Recent breakthroughs in environmental niche modeling (ENMs) have substantially improved our understanding of species-environment relationships. ENMs include a set of correlative approaches that link environmental conditions to occurrence information of single species to estimate environmental niches. During the thesis, you will apply two state-of-the-art approaches: MaxEnt and BIOMOD2 to assess species- vs. lineage-environment relationships. In particular, this approach will allow us to identify niche conditions that overlap among the different highland lineages by those who differ and hence will contribute to the understanding of the relative roles of ecological adaptation vs. isolation in the speciation of White-eyes across East Africa.

onderzoeksgroep: Terrestrial Ecology

Copromotor(en):

Engler Jan

Begeleider(s):

Engler Jan

opmerking

voorbehouden:

abstract Seabirds are positioned high up in the food chain, and their diet is assumed to reflect the relative abundance, availability and shifts in forage species. Seabirds are therefore considered useful indicators for the health of the marine environment. When recruit fish make up a considerable part of the diet, seabirds can be used as samplers of the younger stages of fish, be it commercial or non-commercial species, and to assess stock recruitment. Because of their small foraging ranges and specialized diets, terns are particularly sensitive to changes in local prey availability. Most diet studies of terns, however, have been restricted to chicks, whereas adult diets are still poorly documented. In 2001, the Research Institute for Nature and Forest initiated a monitoring program on the breeding and feeding ecology of Sandwich Terns in Belgium. From 2009 till 2018, this program was complemented by an extensive study in the Dutch Delta-area. In both countries, breeding success, condition of the chicks and the diet composition of both adult and juvenile birds was monitored during the breeding season. In 2016, a large-scale study on the adult diet of Sandwich Terns has been launched, comprising nearly 30 colonies across Europe. In this master thesis, the student will get access to all data collected over the last 15 years. These will be analysed in relation to fisheries data in order to see if the Sandwich Tern diet can be used as an indicator for the availability of small pelagic fish. Besides data analysis, the thesis also involves lab-work. In order to identify the diet of adult terns, faecal samples collected in 2018 and 2019 will be processed. This work comprises selecting, photographing, identifying and measuring fish remains (mainly otoliths). There will also be an option to take part in sample collection, behavioural observations, and chick measuring, although this is not mandatory.

onderzoeksgroep: Terrestrial Ecology

Copromotor(en):

Courtens Wouter

Stienen Eric

Begeleider(s):

Courtens Wouter

opmerking

voorbehouden:

1550

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):

De Meester	Nele
Derycke	Sofie

Begeleider(s):

De Meester	Nele
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opmerking**voorbehouden:**

abstract Marine environments are being threatened by global change. Increased atmospheric CO₂ 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 N₂O, and in this way affecting the N-cycle. N₂O 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 N₂O 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:

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:

abstract Marine environments are being threatened by global change. Increased atmospheric CO₂ concentrations lead to global warming on the one hand, and on the other hand to a decrease in ocean pH. Such shifts in ocean characteristics act as stressors upon biological communities, e.g. through interference with life-history traits and physiology; or through induction of changes in community composition, functioning, and biodiversity. Understanding the response of marine organisms to a changing environment as a consequence of global change is therefore crucial. In this thesis, the responses and reaction norms of nematode species on changing environmental variables will be quantified, and the underlying mechanisms will be investigated. The maintenance of a functional phenotype in a changing environment may involve plastic (acclimation) and/or adaptive responses, as well as heritable epigenetic effects. The latter compromise changes in gene expression that cannot be explained by changes in DNA sequences, but which can prime offspring for improved performance under climate change. Because epigenetic processes can be directly altered by the environment, they may not only provide a second system for natural selection to act upon, but empirical evidence also demonstrates that non-genetic carry-over effects may act as a significantly faster pathway for adaptation. DNA methylation is one of these important epigenetic inheritance systems. We will further fine tune a protocol on DNA methyltransferase inhibitors, to be able to elucidate the effect of epigenetic variation. Afterwards, we will perform experiments with and without these inhibitors on the performance of nematodes while inducing global change stressors. A comparison of phenotypic variation of hypomethylated individuals with controls under a range of environmental conditions and accounting for genetic variation will enable to assess the relative importance of epigenetic and genetic factors and test for their interplay.

onderzoeksgroep: Marine Biology

Copromotor(en):

De Meester Nele

Begeleider(s):

De Meester Nele

opmerking

voorbehouden:

abstract Marine environments are being threatened by global change. Increased atmospheric CO₂ concentrations lead to global warming on the one hand, and on the other hand to a decrease in ocean pH. Such shifts in ocean characteristics act as stressors upon biological communities, e.g. through interference with life-history traits and physiology; or through induction of changes in community composition, functioning, and biodiversity. Understanding the response of marine organisms to a changing environment as a consequence of global change is therefore crucial. Cryptic species are morphologically indistinguishable, but show consistent genetic and ecological differences and may exhibit species-specific functions in the ecosystem, which makes it an interesting model to study the effect of global change on life-history traits. Besides species-specific differences in reaction on global change, tolerances towards environmental change may also be transgenerational: some individuals may be more resistant toward environmental changes than others and can pass this on to next generations. This may be caused by differences in the microbiome (bacteria associated with the gut) of different individuals/species. In this thesis we will subject species to changing environmental conditions 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 changed conditions, to investigate if the species' microbiome remains affected. Moreover, we will also subject them to changed conditions, to see if they react differently than organisms from which previous generations have never been in contact with environmental change.

onderzoeksgroep: Marine Biology

Copromotor(en):

De Meester Nele

Begeleider(s):

De Meester Nele

opmerking

voorbehouden:

abstract In mixed-fisheries, where multiple species are caught simultaneously by the fishing gear bycatches of vulnerable species (with low reproduction potential) such as sharks, skates and rays remain a major challenge regarding the sustainable exploitation of marine ecosystems. Instruments that are currently used in European fisheries management, e.g. Total Allowable Catches (TACs), technical measures, that manage stocks over large geographical areas have not proven to be very effective in reducing fishing mortality on these species. Therefore, it is generally agreed that new management tools are required to protect these species. Spatiotemporal management tools, that attempt to regulate fishing effort allocation in space and time, are considered to be very effective at reducing fishing mortality to sustainable levels for many endangered species. After all, the spatiotemporal distribution of most fish species is not static, but varies due to migratory behaviour e.g. between feeding and spawning grounds. If migration patterns differ between species, obviously, the spatiotemporal overlap in local abundance is likely to differ as well. In this case, fishing vessels have the opportunity to exploit fishing grounds with relative high abundance of target species and low abundance of bycatch species. As a consequence, the fishery may remain economically viable while fishing pressure on bycatch species can be reduced. A prerequisite for the successful implementation of spatiotemporal fisheries management tools is that species have different migration patterns. This precondition will be addressed in this thesis using both observer and survey data. A modelling approach will be used to gain insights into the spatiotemporal distribution of target and vulnerable bycatch species appearing in the catches of Belgian fishing vessels in the southern part of the North Sea using. Nevertheless, few data on sensitive species is available to make accurate predictions on their spatiotemporal distribution. To circumvent this barrier, a recently developed joint species model (VAST, developed in R), in which information on environmental variables and other species can be included, will be used in this thesis. This will enable to identify correlations between species and provide insights into the extend Belgian fishing vessels can avoid bycatch species. Students that apply for this topic are required to have a good knowledge of R. Students with a good background in R software and an interest in geostatistics are privileged.

onderzoeksgroep: Marine Biology & UGent, Vakgroep Toegepaste Ecologie en Milieubiologie (BW09)

Copromotor(en):

Goethals Peter

Begeleider(s):

Sys Klaas

Vandecasteele Loes

opmerking

voorbehouden:

1712 Diversity and succession of nematode fauna in ant nests

abstract Ants are well-known ecosystem engineers that significantly affect soil processes and the distribution of other organisms. The large, conspicuous, dome-shaped nests of red wood ants are thermoregulated and are constantly supplied with food resources. These unique conditions make red wood ant nests biodiversity hubs for a diverse fauna of commensalistic and parasitic arthropods, including beetles, mites and spiders. A hitherto unexplored group in ant nests are nematodes. Given the unique microconditions in red wood ant nests, we expect that they house a rich and distinctive nematode fauna as well. The aim of this thesis is to characterize the nematode diversity in different niches (underground earth nest and organic mound) of red wood ant nests. As nematodes are ideal organisms to test succession patterns, we will compare the fauna between recently founded red wood ant nests and nests established for more than 10 years. This thesis starts with sampling in the field during the summer of 2019 followed by characterization of the nematode fauna in the lab. Subsequently, next-generation sequencing will be applied to assess nematode diversity in high-resolution.

onderzoeksgroep: Terrestrial Ecology

Copromotor(en):

Bert	Wim
Steel	Hanne

Begeleider(s):

Bert	Wim
Parmentier	Thomas
Steel	Hanne

opmerking**voorbehouden:****1713** Spatial dynamics and dispersal of arthropods associated with ants

abstract An enormous diversity of arthropods, so-called myrmecophiles, live inside ant nests and benefit from the resources and optimal nest conditions. We are gradually gaining insight into the advanced chemical and behavioral tactics employed by myrmecophiles, which enable them to penetrate into the heart of these well-defended fortresses. Unfortunately, dispersal in myrmecophiles has hitherto been overlooked. When, how and how often these organisms move to other spatially distinct nests is completely unknown. The aim of this thesis is to unravel dispersal mechanisms in myrmecophiles associated with red wood ants. These ants harbour a unique and diverse community of arthropods, including beetles, mites and spiders. These symbionts are characterized by different degrees of specialization, which is likely reflected in their dispersal strategies. Dispersal in the field will be assessed using pitfalls and detailed observations. Subsequent lab tests will be conducted to test whether different myrmecophile species can track host pheromones and other host-specific chemical cues. Preferentially, the candidate is able to start the field work in the beginning of July and has got a driver's license.

onderzoeksgroep: Terrestrial Ecology

Copromotor(en):

Bonte	Dries
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Begeleider(s):

Parmentier	Thomas
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opmerking**voorbehouden:**

1714 The feeding ecology of the harbour porpoise in a changing environment

abstract The harbour porpoise has returned in numbers to the southern North Sea, after a virtual absence between 1960 and 1995. This is probably due to a shift of the population towards the south, possibly caused by decreasing feeding opportunities in the northern and central North Sea. Whereas porpoises were common predominantly during late winter and spring months, and virtually absent during summer, nowadays also in summer and autumn a relatively high number of strandings occurs. As an endothermic animal living in a cold environment, regular feeding and finding the energetically most interesting food is very important for harbour porpoises. Therefore, investigations into its food preferences and feeding habits in our waters can reveal underlying reasons for the shifts in distribution observed, and the seasonality of its occurrence in the southern North Sea. Also, it may indicate if porpoises have access to the richest food sources, and if trends exist in their feeding ecology seasonally, and yearly between around 2000 and now. Stomachs of stranded harbour porpoises are available, with more to be collected during 2017 and 2018. Also, a number of treated stomach contents (dry) are available for analysis. The analysis consists of establishing the species of prey, and their size, mainly using fish otoliths and cephalopod beaks. Data on the stranded animals, such as date of stranding, sex, age and cause of death, are available.

onderzoeksgroep: KBIN, OD Natuur, Mariene ecologie & Management (Mareco)

Begeleider(s):

Haelters Jan

opmerking de thesis gaat door in Oostende; verplaatsingskosten openbaar vervoer worden vergoed

voorbehouden:

1715 Do diatoms display Gondwanan distributions? A biogeographic analysis of the unique, endemic freshwater diatom flora of Tasmania and New Zealand

abstract Preliminary evidence from contemporary and fossil data from the Southern Hemisphere (obtained in the labs of the promoters) suggests that a historic, Gondwana-like connection exists between the diatom floras of South America, Australasia and Antarctica. This would be a very surprising find, as to date no microbial organisms with Gondwana-like distributions are known. In order to address this question, a closer investigation of the endemic freshwater diatom flora of Tasmania and New Zealand is indispensable. The benthic diatom flora of the largely unspoiled, oligotrophic freshwater mountain lakes and tarns from these islands is characterized by a large number of endemics. While during the past 15 years several new species and even genera have been described from these regions, the diversity and geographic distribution of most genera remains largely undescribed and contains numerous new taxa. This seriously hinders a better understanding of the evolution of diatom biogeography and diversity in the southern hemisphere. This master project will contribute to filling the knowledge gap that exists on freshwater diatoms from the southern part of Australasia, and involves a taxonomic and biogeographic analysis of these diatom floras, and almost certainly also the description of species new to science. Diatom identification will be done using state-of-the-art microscopic techniques (light and scanning electron microscopy) at UGent and the Meise Botanical Garden.

onderzoeksgroep: Protistology & Aquatic Ecology & Nationale Plantentuin Meise

Copromotor(en):

Van De Vijver Bart

Vyverman Wim

Begeleider(s):

Sabbe Koen

Van De Vijver Bart

opmerking

voorbehouden:

abstract Like plants on land, phytoplankton fuels all food webs in the sea. Because of this essential role in marine ecosystems, and because it often shows a rapid response to environmental change such as pollution and climate warming, phytoplankton is closely monitored in Belgian coastal waters by the Flanders Marine Institute (VLIZ) in collaboration with the Protistology & Aquatic Ecology (PAE-UGent) lab. While in the past, monitoring was often based on microscopic identification and counts, various more standardized and/or high-throughput systems are now used, such as flow cytometry, FlowCam, metabarcoding (using molecular markers), underway fluorometry and pigment analyses. In contrast with the traditional microscopic methods, these techniques are also less time-consuming. However, these methods also have their disadvantages: some techniques appear to miss certain plankton groups, or have a lower taxonomic resolution than microscopy. This can have serious consequences as e.g. introduced or harmful algal species may be overlooked. The new methods in turn can help detecting small-sized species which can be easily overlooked in the microscope. It is therefore very important that the novel data types are compared with biodiversity assessments based on microscopy and vice versa to mutually assess their performance and accuracy. In this thesis, data from biweekly-monthly monitoring cruises with the VLIZ research vessel 'Simon Stevin' (to which the student will participate when possible), phytoplankton samples will be collected for microscopic and pigment analysis. High-Performance Liquid Chromatography (HPLC) will be used for the separation and quantification of phytoplankton pigments, allowing a partitioning of phytoplankton biomass in taxonomic groups. Microscopic analyses will be performed to get a detailed view of the taxonomic and functional diversity of the phytoplankton communities. Together with environmental data (temperature, turbidity, nutrients, zooplankton etc.), the data thus obtained will be compared with DNA sequencing-based and flow cytometric and FlowCam based diversity inventories. This will allow establishing a solid inventory of phytoplankton biodiversity and occurrence in Belgian coastal waters, which will form a standard for future biodiversity assessments in this area.

onderzoeksgroep: Protistology & Aquatic Ecology

Copromotor(en):

Debusschere	Elisabeth
Vyverman	Wim

Begeleider(s):

Sabbe	Koen
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opmerking

voorbehouden:

abstract In the Belgian coastal zone, dense algal blooms occur from early spring to autumn. These can be composed of phytoplanktonic microalgae, but in shallow waters (such as the Spuikom lagoon in Ostend) benthic seaweeds and microalgae are also important. Algal blooms of some species can cause a lot of problems, from the undesirable accumulation of foams (the haptophyte *Phaeocystis*) or seaweeds (*Ulva* green tides) on beaches, to blooms that are toxic (dinoflagellates and diatoms) for animals and humans. Monitoring such blooms is thus 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 obtained during field work in the Spuikom and the North Sea.

onderzoeksgroep: Protistology & Aquatic Ecology

Copromotor(en):

De Clerck Olivier

Vyverman Wim

Begeleider(s):

Castagna Mourao e Lima Alexandre

opmerking

voorbehouden:

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:****1718** Does heat absorption by iridescent feathers vary with lighting angle?

abstract Birds produce a variety of colors based on pigments and nanostructures. While pigments selectively absorb visible light, and produce either brown to black (melanins) or yellow to red colors (carotenoids), nanostructured tissues produce iridescent or non-iridescent structural colors through coherent light scattering. Structural iridescent feathers change color with the viewing angle. Most studies focus on colors as sexual or social signals or as agents of camouflage. However, colors also have significant thermal properties, as in light vs dark coloration. This is because colored tissues differentially reflect or absorb solar radiation that can directly affect feather surface temperature. Yet, only a few studies have addressed how iridescence may affect heat absorption. In this project the student will use spectrophotometric and thermal imaging methods to investigate how a change in lighting angle may affect heat absorption in iridescent feathers. We will use spectrophotometry to measure feather reflectance within the solar spectrum for different angles and model heat absorption rates within the near infrared. We will further use thermography to experimentally assess temperature gradients on feathers exposed to solar radiation altering the positioning of the light source. This study will provide the first test of whether iridescence can enable dynamic heating and cooling in birds.

onderzoeksgroep: Evolution and optics of nanostructures (EON)

Copromotor(en):

D'Alba Liliana

Begeleider(s):

Rogalla Svana

opmerking**voorbehouden:** Gerben Debruyne

1719 Evolution of coloration in the sunbirds (Nectariniidae)

abstract Coloration in animals can be produced by deposition of pigments and/or the arrangement of materials at the nanometer scale (structural color). While a shift in pigment-based coloration (e.g. from red to orange) requires complex chemical rearrangements, a comparable shift in structural coloration requires only changing the spacing of an existing nanostructure by 30-40 nm. Thus, we hypothesize that, due to its likely greater lability, structural coloration should evolve more rapidly than pigment-based coloration. The sunbirds are one of the most colorful groups of organisms on the planet, with colors ranging from deep violet to firey red. Moreover, these colors are produced by both pigmentary and structural mechanisms, making them ideal for testing this hypothesis. The student will both use existing color data and collect new data using spectrophotometry on museum specimens at the Africa Museum and RBINS. They will then compare rates of evolution (how quickly colors evolve through time) of structural vs pigmentary coloration using phylogenetic techniques.

onderzoeksgroep: Evolution and optics of nanostructures (EON)

Copromotor(en):

D'Alba Liliana

Begeleider(s):

Shawkey Matthew

opmerking

voorbehouden: Vandewiele Vicky

Strubbe

Diederik

1720 A mechanistic view of biological invasions: the common waxbill as a case study.

abstract The number of species introduced by humans beyond their natural distribution ranges continues to increase, and these introductions present ecologists with a unique opportunity to test how species respond to novel environments. Correlative models, built based on native-range presence records and spatial information on climate, often fail to accurately predict the invasive distribution of introduced species. Such mismatches between predicted and actual invader occurrence are often interpreted as evidence for 'niche shifts', however, correlative models are inherently unable to discriminate between species occupying different parts of their fundamental niche in different geographical areas versus a 'true' niche shift due to rapid evolutionary changes. Therefore this thesis will attempt to quantify the fundamental (thermal) niche of a successful invader, the common waxbill (*Estrilda astrild*), a sub-Saharan estrildid finch that has successfully spread across parts of Iberia. To do so, the thesis will rely on the NicheMapper modeling framework, an animal energetics model that allows key organismal heat and mass balances to be calculated from biophysical first principles under a single mechanistic framework. The thesis will first empirically derive a number of key parameter needed for calibrating the animal energetics models, and then apply these estimates in conjunction with climate, topography and land-use GIS variables to obtain spatially explicit estimates of common waxbill energetic requirements across Iberia, and across its native African range. Key physiological parameters will be measured in laboratory (aviary) settings using commercially available (pet) birds, and include morphological measures (mass, size and shape), feather characteristics (length, depth, density, solar reflectivity), temperature-dependent metabolic rates, core body temperature and (possibly) estimates of food (seeds and grains) consumption. The actual NicheMapper modeling will be done using the R software.

onderzoeksgroep: Terrestrial Ecology

Begeleider(s):

nog te bepalen

opmerking student zal cursus proefdierkunde volgen, promotor gaat aanstonds opleiding voor behalen FELASA C volgen.

voorbehouden: Michael Goedertier

abstract The introduction of invasive alien species ranks among top threats to biodiversity globally, and the number of non-native species introduced continues to rise. As only a fraction of those species introduced are able to establish, spread and cause damage, there is an urgent need for predictive tools that allow identification of those species likely to become high-impact invaders. Over the last two decades or so, species distribution models (SDM), which are statistical tools that correlate species occurrences with spatial environmental predictors, have become the tool of choice to generate spatially explicit prediction of invasion risk. Mismatches between predicted and actual invasive species occurrences are however frequently reported, casting doubt on the robustness and reliability of SDM-derived invasion risk forecasts. One of the main reasons hypothesized to underlie such model failure is the fact that standard SDMs ignore intraspecific niche variations, which likely is especially important for species with large native ranges – where local adaptation is common. Using the invasion of parts of Europe by common waxbills (*Estrilda astrild*), a sub-Saharan estrildid finch, this thesis will test whether incorporating within-species niche variation allows for more accurate predictions of its invasion potential across Europe. First, SDMs will be built based on published range maps describing the distribution of the 16 recognized subspecies of common waxbills across their native African range. Second, as there is considerable uncertainty about the extent to which these subspecies (which are typically based on 'expert opinion') represent biologically meaningful entities, a large number of museum specimens (kept at the Royal Belgian Institute of Natural Sciences) will be (a) georeferenced and (b) measured for a set of key functional traits (body sizes and shape, characteristics of plumage). Morphometric analyses will be used to test for, and if present delineate, functional morphogroups which will serve as the basis for SDMs. Finally, the thesis will evaluate the predictive accuracy of standard 'species-level' SDMs versus forecasts obtained by either range map or morphometrically derived 'intraspecific' SDMs.

onderzoeksgroep: Terrestrial Ecology

Copromotor(en):

Davis Amy

Begeleider(s):

nog te bepalen

opmerking

voorbehouden: Marie Stessens

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 pCO₂ 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):

De Troch Marleen

Moens Tom

Begeleider(s):

Vlaminck Ellen

opmerking

voorbehouden:

abstract Regime shifts are rapid reorganizations of ecosystems from one relatively stable state to another. Because the system state after the regime shift can be functionally different from that before the shift the occurrence of such shifts has considerable implications for the management of the marine environment and the provision of ecosystem services, particularly fisheries. Regime shifts can have a number of causes. Probably the best well studied are those caused by climatic oscillations which often occur on (very) large scales. Additionally, ecosystem state shifts can also occur on much smaller scales e.g. as the result of eutrophication, change in resource availability, overfishing or the introduction of alien species. Regime shifts driven by climate change and anthropogenic disturbances have been reported from many geographical areas for diverse groups of marine organisms such as fish, phyto- and zooplankton. However, our knowledge of whether such regime shifts also occur in marine benthic soft-sediment ecosystem is far less detailed. Through analysis of historic time series from different locations, this thesis will reveal insights in the stability of benthic communities in the Belgian Part of the North Sea (BPNS) and identify the role of climatic oscillations and/or historic and ongoing anthropogenic activities (e.g. fisheries, sand extraction and dumping of dredge materials) for community change. Such knowledge is currently lacking and these insights will assist in the management of coastal ecosystems in the current Anthropocene era. Potential topics include (1) a large-scale study of the distribution patterns of communities in the BPNS between 1970-1976 (i.e. the oldest sample series present for the area); (2) the analysis of long-term (1970-2015) benthic community change at selected stations of known anthropogenic pressure; and (3) the analysis of community biotic properties as early warning indicators of community change.

onderzoeksgroep: Marine Biology

Copromotor(en):

Moens Tom

Van Colen Carl

Begeleider(s):

Braeckman Ulrike

Moens Tom

opmerking

voorbehouden:

abstract The biodiversity found in coastal habitats is on the frontline of current environmental change resulting from anthropogenic activities related to the expanding exploitation of coastal areas. For example, changes in sedimentation regimes and water-borne suspended sediment concentrations resulting from changes in land-use and engineering activities in the coastal zone (e.g. dredging, aggregate extraction, beach nourishment) affect biodiversity and ecological value in coastal soft-sediment habitats. One such habitat are coastal lagoons where suspended sediments may deposit depending on interactions between geomorphological, hydrological and biological factors. Such infilling is enhanced in sheltered habitats further facilitated by pioneering vegetation that trap fine sediment particles resulting in increasing elevation, and a reduction in inundation time and the surface of low intertidal areas, illustrative for the succession towards a marsh habitat. In the Zwin tidal lagoon (Belgium and the Netherlands), sand deposits have led to the gradual filling up of the lagoon, causing loss of safe breeding opportunities and sleeping sites for the birds, as the former islands are becoming connected to the mainland and accessible to ground predators. The deposited sand probably originates from the increased marine erosion of the sandy beach and fore-dunes, so that the loss of biodiversity can be considered an example of coastal squeeze as a consequence of climate change. This situation has also led to the loss of mud and sandflats that provide a high biomass of intertidal prey organisms for wading birds, nektonic fish such as crustaceans, polychaetes and molluscs. The Flemish regional nature and forest agency is aiming to restore the rich biodiversity of this internationally important Natura 2000 site by carrying out large-scale restoration of the ecological dynamics in the Zwin area, and by turning former agriculture land into tidal nature. This thesis aims at studying the macrobenthos and nekton communities in the lagoon to evaluate the restoration success in the current and newly created tidal nature in the area.

onderzoeksgroep: Marine Biology

Copromotor(en):

Moens Tom

Begeleider(s):

Van Colen Carl

opmerking

voorbehouden:

abstract The detrimental consequences of inadequate folate levels in the diet together with the inefficacy of folate supplementation through pills or folic acid fortification in developing countries highlight the urgency of folate biofortification in crops. Past genetic research has achieved high levels of folates in few crops, however, as the folate species themselves are quite unstable, maintenance of their stability is one of the major present concerns; since it is of paramount importance that the attained levels remain available till the crop product reaches the consumer. Reports suggest that folates bound with other proteins/enzymes are quite stable (Gorelova et al., 2017). In the light of this, attempt to co-express mammalian folate binding proteins (FBP) in folate-overproducing rice led to overall folate stability (Blancquaert et al., 2015). This triggered the quest for identification of a plant FBP, which can optimally be employed in a folate biofortification program. Recently, a novel FBP has been identified in Arabidopsis, which upon expression in yeast resulted in higher folate uptake (Puthusseri et al., 2018). This project entails optimizing the expression of this FBP in bacteria and purification of the recombinant protein. The idea is to obtain high quantities of FBP that can further be assessed for its folate binding capacities through state of the art in vitro assays. This will eventually feed the folate biofortification program by providing a necessary tool for genetic approaches. We propose to transform the appropriate bacterial host with the plasmid containing the FBP cDNA with N-terminus 6x-his tag downstream to an inducible promoter. A single positive clone will be selected for protein expression/purification. Appropriate growth conditions and induction parameters will be optimized to express as much soluble protein as possible; this involves selecting the most suitable expression temperature and inducer concentration among a series of different temperatures/concentrations tested. Once the desired level of soluble FBP protein is attained in the bacterial cells, the recombinant protein will be purified using Ni-NTA beads affinity-based chromatography. Soluble protein will be dialyzed and dissolved in an appropriate buffer to ensure stability under long-term storage and activity. The proposed project offers a set of key molecular biology skills, like (1) bacterial media preparation, (2) bacterial transformation and selection of transformants on antibiotics, (3) Colony-PCR, (4) maintenance of bacterial cultures (dos and don'ts), (5) light spectrophotometry, (6) sonication based cell lysis, (7) protein buffer and sample preparation, (8) Sodium Dodecyl sulphate- polyacrylamide gel electrophoresis (SDS-PAGE), (9) gel-imaging, (10) affinity chromatography etc. References: Blancquaert, D., Van Daele, J., Strobbe, S., Kiekens, F., Storozhenko, S., De Steur, H., Gellynck, X., Lambert, W., Stove, C., and Van Der Straeten, D. (2015). Improving folate (vitamin B9) stability in biofortified rice through metabolic engineering. *Nat Biotechnol* 33, 1076-1078. Gorelova, V., Ambach, L., Rebeille, F., Stove, C., and Van Der Straeten, D. (2017). Foliates in Plants: Research Advances and Progress in Crop Biofortification. *Front Chem* 5, 21. Puthusseri, B., Divya, P., Lokesh, V., Kumar, G., Savanur, M.A., and Neelwarne, B. (2018). Novel Folate Binding Protein in Arabidopsis Expressed during Salicylic Acid-Induced Folate Accumulation. *J Agric Food Chem* 66, 505-511.

onderzoeksgroep: Functional Plant Biology (FPB)

Copromotor(en):

Ratnesh Mishra

Begeleider(s):

Ratnesh Mishra

opmerking

voorbehouden:

abstract Ethylene is a gaseous plant hormone that is a central regulator of a wide range of physiological processes in the plant life cycle from germination to senescence. It plays an important role in growth control during vegetative development with the “triple response” phenotype of dark-grown seedlings being one of its best characterized effects. In addition, ethylene is a major stress hormone, involved in the reaction to both abiotic and biotic stress factors. As the direct precursor of ethylene, the three-membered ring amino acid 1-aminocyclopropane-1-carboxylic acid (ACC) is a pivotal molecule in the regulation of its biosynthesis. Previous studies have shown that, while ethylene is gaseous and thus mostly diffuses over short distances, ACC, being water soluble, is the form under which the ethylene signal travels throughout the plant over long distances. During waterlogging or submergence, for example, transport of ACC from root to shoot results in an increased ethylene production and ethylene signaling at the level of the shoot. It has also been shown that ACC can be exported to the rhizosphere promoting the interaction with plant growth promoting Rhizobacteria (PGPR). These PGPRs are capable of using ACC as a carbon and nitrogen source, in turn reducing the available ACC/ethylene pool of the plant. Finally, in addition to ethylene-dependent signaling, ethylene-independent ACC signaling has also been suggested to be important in growth, for instance during root elongation in response to pathogen associated molecular patterns (PAMPs). These are only a few examples of the central role of ACC transport in plants. A detailed knowledge of ACC transport, including the function and location of different ACC transporters within plant tissues would not only reshape our view on the ethylene pathway regulation, but also creates interesting possibilities for future applications in agriculture. A few years ago, a first *Arabidopsis thaliana* ACC transporter LHT1 was identified. Based on information gained from this first ACC transporter and an *in silico* approach, we were capable of fine-tuning our search and characterization novel ACC transporters. The main focus in this master project is the characterization of novel ACC transporter(s) in the model plant *Arabidopsis thaliana*. In a first part of this project, ACC transport will be analyzed indirectly using the model organism *Saccharomyces cerevisiae*. This will include yeast transformation and culturing, and analysis of ethylene production from transformed yeasts (using laser photo-acoustics). In a second part, ACC transport will be analyzed directly in *A. thaliana* using loss and gain of function mutants. The techniques that will be used include plant tissue culturing, genotyping, phenotyping (by bioimaging), analysis of ethylene production, and qPCR. Furthermore, using the mutants, we will assess developmental specificity of the ACC transporter(s) as well as involvement in abiotic stress conditions (flooding and/or drought). Other everyday-techniques include PCR, gel electrophoresis, *E. coli* culturing, *E. coli* transformation, plasmid isolation. Reference Vanderstraeten, L., Van Der Straeten, D. (2017). Accumulation and Transport of 1-Aminocyclopropane-1-Carboxylic Acid (ACC) in Plants: Current Status, Considerations for Future Research and Agronomic Applications. *Frontiers in Plant Science*, 8(38):1-18

onderzoeksgroep: Functional Plant Biology (FPB)

Begeleider(s):

Vanderstraeten Lisa

opmerking

voorbehouden:

1727

Investigating the combined effect of global change and the installation of offshore windfarms: partim fouling fauna

abstract In order to meet the requirements for renewable energy demand, many European countries have installed offshore windfarms in their coastal environment. Along with the installation, monitoring programmes were put in place, mainly targeting towards assessing structural changes in the marine ecosystem. These monitoring programmes showed that wind turbines are rapidly colonised by large densities of fouling species, including non-indigenous species. It is to be expected that this fouling fauna affects the local environment in many ways. Fouling species filter organic material from the water column to feed and excrete faeces and pseudofaeces to their environment. Fouling species affect the nutrient budget as well, as they provide the environment with large quantities of ammonium. In addition, recent paper show that the presence of shell-bearing fouling species (i.e. the blue mussel) also results in the production of N₂O, a highly potent greenhouse gas. While the introduction of offshore windfarms, and their colonisation by fouling species is in essence a local change, it will interact with global change: temperature increase and ocean acidification. Both global change aspects are known to affect the behaviour of many organisms on the one hand, and the cycling of nutrients on the other hand. As such, it is important to understand how the interaction of both global and local change will affect the marine environment. Within this research topic, students will perform experimental research on the behaviour of selected fouling species, and how this affect the nutrient cycling, mimicking both current environmental and in future climatological settings. The students will be involved in field work, setting up and maintaining experiments, and analysing ecological datasets. The students will mainly work at the Marine Biology Research Group of Ghent University, making use of state-of-the-art experimental equipment.

onderzoeksgroep: Marine Biology en KBIN, OD Natuur, Mariene ecologie & Management (Mareco)

Copromotor(en):

Van Colen Carl

Begeleider(s):

Voet Helena

opmerking

voorbehouden:

abstract In the past decades, the Belgian part of the North Sea (BPNS) has been affected by a mixture of local and global pressures. Locally, an increasing trend to install offshore wind farms results in the introduction of artificial hard substrates and an increase in potentially non-indigenous fouling fauna. Plans to use these concession areas for aquacultural activities will further affect the food web structure and aggravate the emission of nitrous oxide (N₂O), a potent greenhouse gas. On a global scale, the International Panel for Climate Change (IPCC) 'business-as-usual' climate change scenario predicts a rise of ocean temperature by 3°C and a drop in oceanic pH of 0.3 by the end of this century. Monitoring programmes have showed that wind turbines are rapidly colonised by large densities of fouling species. It is to be expected that this fouling fauna and the presence of the artificial hard substrates themselves, affect the local environment in many ways. Fouling species filter organic material from the water column and excrete (pseudo)faeces into their environment, as well as affect the nutrient budget of the surrounding environment. As the large wind farm structures literally connect the water column with the surrounding sediment, all local fouling fauna and benthic organisms are potentially tightly linked in a new local food web. While the introduction of offshore wind farms and their colonisation by fouling species is in essence a local change, it will interact with global change: temperature increase and ocean acidification. Both global change aspects are known to affect the behaviour of many organisms on the one hand, and the cycling of nutrients on the other hand. As such, it is important to understand how the interaction of both global and local change will affect the marine environment. Within this research topic, students will perform experimental research on the food web of selected fouling and benthic species, mimicking both current environmental and in future climatological conditions in a large mesocosm set up. The students will be involved in field work, setting up and maintaining experiments, and analysing ecological datasets. The students will mainly work at MSO Ostend (carpooling to Ostend from Ghent is usually possible) and will make use of state of the art experimental equipment and mesocosm manipulation facilities.

onderzoeksgroep: Marine Biology en KBIN, OD Natuur, Mariene ecologie & Management (Mareco)

Copromotor(en):

Van Colen Carl

Begeleider(s):

Vlaminck Ellen

Voet Helena

opmerking

voorbehouden:

1729 Is the introduction of offshore windfarms affecting the marine environment: partim benthos

abstract In order to meet the requirements for renewable energy demand, many European countries have installed offshore windfarms in their coastal environment. Along with the installation, monitoring programmes were put in place, mainly targeting towards assessing structural changes in the marine ecosystem. The wind turbines are being colonized by large densities of fouling species, fish and large crustaceans are attracted to the installations, and close by the turbines, both benthic communities and sediment properties change. While these are important observations, we lack a deep understanding of the causes and consequences of these changes. This research line deals with an experimental assessment of the consequences of the fining of the sediments around wind turbines. Before the installation of the offshore wind farms, sediments in the area acted as very efficient areas of mineralization of organic matter. This process transforms organic matter into inorganic nutrients. These inorganic nutrients are returned to the water column where they can be consumed by primary production. As the sediment properties change, and as the inhabiting communities change as well, it can be expected that the efficiency of benthic processes is altered as well. Within this topic, students will be engaged in a combination of field sampling and experimental work, aiming at investigating the consequences of the observed changes in the biological and physical environment. Students will work mainly at the Marine Biology Research Group, making use of state-of-the-art experimental equipment. Students will gain expertise in field work, setting up and maintaining manipulative experiments, and analysing ecological data.

onderzoeksgroep: Marine Biology en KBIN, OD Natuur, Mariene ecologie & Management (Mareco)

Copromotor(en):

Braeckman Ulrike

Begeleider(s):

Toussaint Elise

opmerking

voorbehouden:

Vandegehuchte Martijn

1730 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 invertebrate herbivore species on a shared host plant species. Enemy communities will be varied from simple to complex, and real-time evolution of plant defense traits will be tested using a common-garden approach.

onderzoeksgroep: Terrestrial Ecology

Copromotor(en):

Bonte Dries

Begeleider(s):

Vandegehuchte Martijn

opmerking

voorbehouden:

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:

1731 Are the benthic communities of the NE Greenland shelf affected by climate change? A historical comparison.

abstract Benthic communities regulate numerous ecosystem processes and rely almost exclusively on the sinking of organic matter from the pelagic. The Arctic is one of the three regions on Earth that is warming more rapidly than anywhere else. In the last 20 years, drastic changes in sea ice cover and accelerated glacial melt were observed on the Northeast Greenland (NEG) shelf which might have altered benthic community structure and their function in this region. In September/October 2017, NEG soft-bottom communities were sampled along with environmental variables. We found that food availability for benthos was 7 times lower than in the early 1990s, while macrofauna abundances were 5 times lower. This suggests that the strong benthic-pelagic coupling, so characteristic for the Arctic, might have weakened since the 1990s. In this thesis, we would like to investigate the meiobenthic response to these changes in food availability, both in terms of abundances and community structure. These results will contribute to a better understanding of rapid climate change effects on this pristine and vulnerable ecosystem.

onderzoeksgroep: Marine Biology

Copromotor(en):

Braeckman Ulrike

Begeleider(s):

nog te bepalen

opmerking

voorbehouden:

1732 Meibenthos in the North Sea: a historical comparison.

abstract Meibenthos (sediment-dwelling organisms between 38 µm and 1 mm in size) is a group of infaunal organisms involved in the degradation of organic matter, and as such also strongly linked to the microbial loop. Meibenthos from the North Sea is well described along the coastlines of the Southern Bight of the North Sea and the West coast of the UK. Their spatial distribution and community composition in the central North Sea has been studied for the first time in the 1980s. Within the framework of a new integrated biodiversity assessment, samples from different benthic size classes were collected during a campaign crossing the entire North Sea from the Netherlands to Norway in May 2018. In this thesis, the biodiversity of the meiofauna component along this transect will be assessed and compared to the historical samples from the 1980s. We will relate spatial variability in meiofauna communities to food availability, abiotic habitat characteristics and distribution of other benthic size classes (macrofauna) and we will explore whether meibenthic communities from the North Sea have experienced changes in community composition (both taxonomic and functional) since the 1980s.

onderzoeksgroep: Marine Biology & NIOZ

Copromotor(en):

Braeckman	Ulrike
Soetaert	Karline

Begeleider(s):

nog te bepalen

opmerking

voorbehouden:

Vanthournout Bram

1733 Function and evolution of colour in springtails.

abstract Springtails (Collembola) are soil-dwelling arthropods that are characterized by a tail-like appendage that allows them to jump when threatened. Besides this remarkable anti-predator adaptation, some collembola species exhibit a striking iridescence that gives them a metallic colouration. These colours are formed by scales (much like a butterfly wing) that cover their entire body. We have recently discovered the mechanistic basis and found that nanostructures on the surface of the scale, together with scale thickness and pigment deposition control the production of golden to violet colours. The function of colouration is currently unknown, it is unlikely that it plays a significant role in sexual selection as collembola live in low light conditions and have limited eyesight. This thesis will be part of an ongoing research line in the EON-group and will focus on getting insight in scale function. Depending on the interest of the student, several research subjects are possible. These include the potential role of scales in thermoregulation and investigating the extent of scale evolution by setting up artificially selected (in)breeding lines in the lab and determining scale structure.

onderzoeksgroep: Evolution and optics of nanostructures (EON)

Copromotor(en):

D'Alba	Liliana
Shawkey	Matthew

Begeleider(s):

Vanthournout	Bram
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opmerking

voorbehouden:

1734 Spider 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. First results for the garden cross spider (*Araneus diadematus*) indeed indicate such a pattern of lighter individuals in urban areas. In this thesis, we will expand on these results and investigate the effect of urbanisation on spider colour and how this relates to thermoregulation. Spiders will be collected in urban and rural locations, their colour determined using spectrophotometry and a thermal heating and cooling profile will be established using a thermal camera. Depending on the interest of the student, behavioural experiments or a more mechanistic focus on the colour production (through pigment identification and SEM/TEM microscopy) can be added.

onderzoeksgroep: Evolution and optics of nanostructures (EON)

Copromotor(en):

Bonte Dries

Shawkey Matthew

Begeleider(s):

Vanthournout Bram

opmerking

voorbehouden:

Verbeken Annemieke

1735 African fungal communities, diversity of three vegetation types compared

abstract Sub-Saharan Africa is characterized by three vegetation types dominated by ectomycorrhizal (ECM) associations: Central African Guineo-Congolian rainforests, West African Sudanian woodlands and East African Zambezi Miombo woodlands. Little is known concerning composition and distribution of fungal communities in these vegetation types. We sampled root tips in the rainforests of Cameroon, in the Sudanian woodlands of Togo and the Miombo woodlands of Zambia. Root tips were sampled in multiple plots per vegetation type and IonTorrent was used to sequence the ITS2 region from the root tips. The composition of the ECM fungal community was studied and revealed strong correlation with edaphic factors, with many ECM fungi occurring in either woodland (high pH, together with low C, N and organic material) or rainforest (low pH, together with high C, N and organic material). The ECM community composition thus differed amongst the three vegetation types, with the main regions of overlap occurring in the riparian forests in between the vegetation types. However, the samples contain much more information, for example on endophytes or endomycorrhizal fungi. The aim of this project is to study the community composition of non-ECM fungal communities in these African samples. Occurrence of species across vegetation types will be analysed using ordination methods and spatial distribution of the fungal communities will be mapped across the sampled plots using GIS methods. Different functional groups will be studied and compared. Do they follow the same trends as ECM fungi, or will new patterns be revealed?

onderzoeksgroep: Mycology

Copromotor(en):

De Crop Eske

Begeleider(s):

nog te bepalen

opmerking

voorbehouden:

abstract Bats are parasitized by different organisms, including bugs, fleas and flies. The flies (Diptera) feed on the blood of the bat host. There are many recent studies on bat flies that discuss specificity, sexual infection patterns and population structure. However, we know almost nothing about the parasites of those ectoparasitic flies. They can be infected by Laboulbeniales (fungi). These Ascomycota were described in the last century and occur on many groups of insects. They are outstanding in the giant kingdom of fungi because they are not at all forming mycelium but are composed of a few cells that form a thallus on the outside of the host. Laboulbeniales on bat flies have not been found for several decades, but recently, during fieldwork in Central and Western Europe, a number of bat flies were collected, infected with Laboulbeniales from the genus *Arthrorhynchus*. Cryptic diversity is common in fungi and might also be present in the two species that we found on European bat flies. The question is whether it is actually two species or whether it concerns two species complexes where a morphological "species" hides several species that can only be distinguished molecularly. The aim of this master thesis is to investigate diversity in the genus *Arthrorhynchus* by detailed microscopic study in combination with molecular work. Based on DNA sequences that will be generated during this study, relationships can be mapped. The student also gets acquainted with the unique morphology, nomenclature and taxonomy of the under-studied but fascinating Laboulbeniales fungi.

onderzoeksgroep: Mycology

Copromotor(en):

Haelewaters Danny

Begeleider(s):

nog te bepalen

opmerking

voorbehouden:

abstract Up to ten years ago, natural regeneration of beech was problematic in the forest of Sonian (south of Brussels). This problem was already described as early as the beginning of the 20th century (Colleaux, 1923). Several studies were performed to analyze and explain this problem (cfr. Grulois et al. 2002; 2003), but none could clearly point out one particular reason. Since a few years however, natural regeneration is plentiful, although the circumstances and explanatory factors (predation by wood pigeons, compaction of the soil) have not changed. Foresters and scientists are facing a mystery. A new possible explanation for the former lack of regeneration may give a clue to solve this puzzle. Ectomycorrhizal fungi have been proven to be essential in the establishment of natural regeneration of beech, as they provide the connection to transport nutrients from the parent trees to the seedlings. Due to atmospheric pollution (first sulfur, later nitrogen) some of the essential ectomycorrhizal species may have disappeared from the forest. Seedlings did germinate but did not manage to develop further to saplings, as the connection to parent trees was missing. Since the last decade, deposition levels have dropped and a beginning of recovery of the soil is registered (Verstraeten et al. 2017) This new hypothesis has not been tested yet. We want to test this hypothesis by organizing targeted soil samplings in the forest, at sites with and without saplings but with similar forest structural conditions. Using next generation sequencing, the soil samples will be analyzed on the presence of OTUs of ectomycorrhizal fungi, combined with chemical analysis, to test whether there are significant differences between the sites with and without regeneration. Colleaux H. 1924. Excursions forestières en 1923, dans Bulletin de la Soc. Centr. forestière de Belgique, pages 140-150 and 214-226. Verstraeten, A. et al. 2017. Response of temperate forest N status to long-term recovery from acidification and decreasing atmospheric N deposition. IUFRO World Congress paper. [https://pureportal.inbo.be/portal/nl/publications/natuurlijke-verjonging-van-het-zonienwoud--regeneration-naturelle-de-la-foret-de-soignes\(43321520-9ec0-471c-b275-356a6d581a00\).html](https://pureportal.inbo.be/portal/nl/publications/natuurlijke-verjonging-van-het-zonienwoud--regeneration-naturelle-de-la-foret-de-soignes(43321520-9ec0-471c-b275-356a6d581a00).html) [https://pureportal.inbo.be/portal/nl/publications/natuurlijke-verjonging-van-het-zonienwoud--regeneration-naturelle-de-la-foret-de-soignes\(01b73e83-6c4e-407f-abc9-d2cbccd4647b\).html](https://pureportal.inbo.be/portal/nl/publications/natuurlijke-verjonging-van-het-zonienwoud--regeneration-naturelle-de-la-foret-de-soignes(01b73e83-6c4e-407f-abc9-d2cbccd4647b).html)

onderzoeksgroep: Mycology

Copromotor(en):

De Keersmaecker	Luc
Vandekerkhove	Kris

Begeleider(s):

nog te bepalen

opmerking

voorbehouden:

abstract Most macro-organisms on the planet follow the so-called 'latitudinal diversity gradient'. This pattern refers to the higher biodiversity in the tropics compared to the poles, which has been shown for all major groups of plants and animals. On the other hand, there are the microbes. Microbes have traditionally been considered to follow the 'everything is everywhere' model. This model predicts that everything is everywhere, but the environment selects. At the interface of both are the fungi. They have traditionally been considered to follow the microbial model, but more recently strong geographical patterns were discovered. Biogeographic patterns of fungi have always been poorly understood, but this is now rapidly changing. Recent publications show that many groups of fungi tend to follow the latitudinal diversity gradient and are most diverse in the tropics, but there is one important exception. These are the ectomycorrhizal fungi. Ectomycorrhizal fungi are symbionts with plant roots of many trees and shrubs. The fungus provides water and nutrients to the plant in exchange for carbohydrates. Ectomycorrhizal fungi exhibit a biogeographic pattern counter to the latitudinal diversity gradient. Their diversity increases away from the tropics and towards the temperate/boreal regions. The evolutionary basis for this pattern has rarely been explicitly tested. Many ectomycorrhizal fungi display disjunct distribution patterns that might be explained by vicariance or long-distance dispersal events. The hyper-diverse ectomycorrhizal milkcap genus *Lactarius* (Russulaceae, Basidiomycota) has a worldwide distribution and displays such disjunct distributions. Most species live in the temperate and boreal climatic zones but recent analyses reveal that early diverging clades in *Lactarius* contain only sub-Saharan African species. This study wants to reconstruct the evolutionary history of the genus and test where it originated. The African clades represent 3 subgenera that are new to science. An important goal of this study is also to reveal their unique morphological features and describe the new species they contain.

onderzoeksgroep: Mycology

Copromotor(en):

Nuytinck Jorinde

Begeleider(s):

nog te bepalen

opmerking

voorbehouden:

abstract In the genus *Russula*, within subgenus *Compactae* section *Lactarioides*, two common, well-known, big, white-spored species are very closely related: *Russula delica* (Witte russula) and *Russula chloroides* (*Smalplaatrussula*). Molecular phylogenetic analyses however revealed that there might be more than these 2 species in the section. The topic of this project is to find microscopic features that confirm this new species delimitation. We expect that spore size and ornamentation (which is amyloid in *Russula*) might be good candidates for distinguishing the species. We have plenty *Russula delica* and *R. chloroides* collections from all over Europe that can be used and the student is expected to take part in collecting trips to see and describe fresh collections. The student will participate in all stages important for mycological research: field work, lab work (extraction, pcr), phylogenetic analyses and microscopy. This master dissertation will result in the description of at least one new species.

onderzoeksgroep: Mycology

Begeleider(s):

De Lange Ruben

opmerking

voorbehouden:

1740Trees matter: Comparison of the ectomycorrhizal community of *Fagus* and *Quercus* lanes on sandy soils.

abstract We know that ectomycorrhizal associations are vital for many tree species, especially in stress conditions (periods of drought, nutrient poor situations, presence of parasites), those trees that are associated with EM fungi will be more resistant and their photosynthesis will be more efficient. Since EM is especially an answer to lack of nitrogen, we see that in Flanders, due to the nitrification, many rare and nitrogen-sensitive EM fungi are lacking in the middle of the forest, but are still present in lane or park situations. The hypothesis that will be tested here is that in lanes on sandy soils *Quercus* trees are richer in EM associations than *Fagus* trees, since these sandy regions were originally covered with *Quercus*-*Betula* forests and the *Fagus* trees naturally occur on more loamy soils. Therefore, comparable plots (*Quercus* lanes and *Fagus* lanes with trees of the same age, same traffic situation etc.) will be monitored for EM fungi. A second hypothesis is that, due to decreasing nitrogen contents in this region during the last decade, EM associations are restored. We have data of these plots in 2000, and will compare the current situation with the situation 20 years ago. The student will do fieldwork in the period august-november and identify all collected fruitbodies in the different plots. The data will be analysed and compared with the historical data.

onderzoeksgroep: Mycology**Begeleider(s):**

De Lange Ruben

opmerking**voorbehouden:** Florence Beel**1741**Under the spell of a ring - species delimitation in two morphologically similar lineages from different continents within the genus *Lactifluus*.

abstract The milkcap genus *Lactifluus* is a species-rich genus, known for its cryptic diversity and species complexes. Contrary to its sister genus *Lactarius*, it is mainly distributed in the tropics. *Russula* and *Lactarius* s.l. are commonly known as typical agaricoid fungi without any trace of a velum generale or partiale, but in some tropical regions we find russulas and milkcaps with a ring (annulus) and/or distinctly developed veil on the cap. Within *Lactifluus*, species with a ring are only known from two lineages: an African and a Neotropical lineage. Within these lineages, annulate and non-annulate species are mixed and interspecific relationships are poorly known. During recent field expeditions to Africa and the Neotropics, species from both lineages were collected, of which several new species. The goal of this project is to delimit species within these two lineages, using a combination of a genealogical approach based on multiple genes, Bayesian species delimitation and a meticulous microscopical study of each species.

onderzoeksgroep: Mycology**Copromotor(en):**

De Crop Eske

Begeleider(s):

nog te bepalen

opmerking**voorbehouden:**

abstract Biological Soil Crusts (BSCs) dominate primary production and are the main food source for vertebrate herbivores in high Arctic polar desert biomes. BSCs are also the first colonizers of exposed soils after glacial retreat in which they act as ecosystem engineers through soil stabilization, regulation of soil temperature and altering the carbon, water and nutrient content of the underlying substrates. As such, BSCs are essential in fixing atmospheric nitrogen and nurturing environments poor in organic matter. The colonization of bare soils by BSCs is therefore considered to be the initial process of a succession ultimately leading to the 'Greening of the Arctic' and the succession to shrub tundra. BSCs are to a varying degree composed of cyanobacteria, eukaryotic microalgae, lichens, mosses, fungi, and heterotrophic bacteria. The relative dominance and taxonomic composition of these groups appears to depend on microclimatic conditions (i.a. moisture availability), soil stability (e.g. wind-water erosion, cryodisturbance), and the pH and salinity of the underlying soils. Recent studies also indicate that the geochemical characteristics of the underlying substrate exert a strong selective force on the composition of BSCs in polar deserts. Rock types differ in their weathering potential and elemental composition, including inorganic N and P concentrations. BSCs in turn contribute to pedogenesis through i.a. acidification and podzolification associated with the accumulation of organic matter and microbial activities, and trapping of dust particles. Nevertheless, our understanding of the structuring role of bedrock type on the diversity, composition and functioning of BSCs in polar regions is incomplete, which evidently prevents region-wide upscaling to assess the role of BSCs in the 'Greening of the Arctic'. This is largely due to the lack of large-scale studies covering broad geographic ranges and adopting a polyphasic approach. The objective of this MSc project is to investigate the effects of bedrock type on the composition, development and functioning of microbial communities and BSCs in west Svalbard and Nordaustlandet along transects of developmental stages in glacier forefields. Svalbard has a high geological diversity at a relatively small spatial scale, making the region an ideal study site for this type of research. You will use high-throughput amplicon sequencing of marker genes in combination with pigment analysis. These data will be integrated with vegetation surveys and geochemical and mineralogical characteristics of the substratum soils using multivariate statistics. Ultimately, these data will help predicting the rate and direction of early responses of polar deserts to climate change and their altered ecological and biogeochemical functions.

onderzoeksgroep: Protistology & Aquatic Ecology

Copromotor(en):

Tytgat	Bjorn
Vyverman	Wim

Begeleider(s):

De Maeyer	Lotte
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opmerking

voorbehouden:

abstract Anthropogenic warming is amplified in the Arctic as evidenced by a temperature rise exceeding 2 to 3 times the global mean. These changes already impacted on terrestrial ecosystems in the form of melting of glaciers and permafrost and the Northward migration of vegetation belts or the so-called 'Greening of the Arctic'. Paleolimnological studies have also revealed significant shifts in diatom and invertebrate communities across the entire Arctic in response to climate warming through lengthening of the growing season since the 1850's. At the same time, these studies revealed human-impact related changes in the catchments of the lakes in previously presumed relatively pristine systems. The development of protocols to study ancient DNA and the advent of high-throughput sequencing techniques are allowing us to reconstruct ecosystem-wide changes in lakes and their catchments with an unprecedented level of detail. In this MSc thesis high throughput sequencing (HTS) of 18S rRNA and COI genes in ancient DNA will be combined with fossil pigments and microscopy based inventories of fossil diatom communities to study the effect of past changes in climate and land-use in a high Arctic lake in Ny Alesund (Svalbard) during the past c. 2000 years. Lakes in Svalbard are ideally suited for this purpose, because previous paleolimnological studies using more traditional approaches revealed clear changes in the vegetation and lacustrine communities in response to the last two major climate excursions during the past 1500 years, namely the Medieval Climate Anomaly and the Little Ice Age. Moreover, the region is experiencing accelerated glacier retreat during the past 100 years, as well as important human impacts, such as mining and the reintroduction of reindeer in 1987 after an absence of 100 years. The HTS data will be processed using an established bioinformatics pipeline. The proxy data will be analysed in R and combined with existing reconstructions of past climate changes and historical records of human activity in the region.

onderzoeksgroep: Protistology & Aquatic Ecology

Copromotor(en):

Tytgat Bjorn

Vyverman Wim

Begeleider(s):

De Maeyer Lotte

opmerking

voorbehouden:

abstract High Arctic tundra acts as an important global carbon sink due the positive balance between photosynthesis by plants and biological soil crusts (BSCs), and the slow degradation of organic matter in response to low soil temperatures. The Arctic organic carbon reservoir includes newly produced biomass as well as old organic matter that has accumulated in the soils over millennia. It is estimated that up to 50 % of the global soil organic carbon is buried in Arctic permafrost. However, with climate change being amplified in the Arctic, coupled climate-vegetation models predict at least three potential future trajectories for tundra systems in the Northern Hemisphere. First, increased temperature results in thawing of the permafrost leading to increased microbial degradation of the ancient organic matter and the release of greenhouse gasses CO₂ and CH₄ into the atmosphere. Second, the predicted temperature rise in the Arctic can result in an accelerated 'Greening of the Arctic', following the extension of moss and shrub dominated vegetation belts towards the North leading to increased primary production and CO₂ fixation at high latitudes. A third prediction is that most Arctic regions will be affected by a more extended snow cover during autumn, winter and spring. This might have important implications for Arctic tundra systems, given that snow cover acts as a thermal insulator for the soils, in turn enabling the microbial breakdown of organic matter at near 0 °C temperatures. Based on automatic measurements it has been shown that microbially mediated CH₄ production during the cold period is at least as high as during summer, with slowly dropping CH₄ emissions during winter and a short peak at spring onset. Importantly, increased snow cover can result in a shortening of the summer growing season for photoautotrophs, and thus tipping the balance of tundra from being a carbon sink to a source. However, microbial activity under snow cover remains largely unexplored and it is unclear which (groups of) microorganisms are active and which functions and at what rate (particularly methanogenesis) they perform in different types of tundra. This MSc thesis will make use of a unique dataset collected along a gradient from dry to wet tundra in Svalbard during three seasons (spring, summer and winter). Samples from the three seasons will be studied using metagenomics and metatranscriptomics sequencing approaches, to study the up- and downregulation of genes involved in carbon and nutrient cycling. These data will be linked with field-based measurements of CH₄ and CO₂ dynamics during the three seasons in order to better predict carbon fluxes under future climate warming scenarios.

onderzoeksgroep: Protistology & Aquatic Ecology

Copromotor(en):

Tytgat Bjorn

Vyverman Wim

Begeleider(s):

De Maeyer Lotte

opmerking

voorbehouden:

1745

260,000 years of aquatic-ecosystem dynamics in a crater lake near Mt. Kilimanjaro (East Africa) using fossil remains of aquatic insects, ostracods, mollusks and fish

abstract The ICDP project DeepCHALLA aims to reconstruct climate and landscape history in equatorial East Africa over the past 260,000 years through multi-disciplinary investigation of the uniquely long and continuous sediment record of Lake Chala, a 90-meter deep crater lake near Mt. Kilimanjaro. As this period encompasses (almost) the entire known history of our own species, *Homo sapiens*, this project has the potential to both reveal how climate change has 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 high-stands and low-stands through time, since this reflects episodes of higher or lower rainfall than today. These lake-level fluctuations can be traced by analyzing changes in the zoobenthos community, because its composition reflects the proximity of near-shore habitat and whether the offshore lake bottom is adequately oxygenated. When water level in Lake Chala dropped 50 m or more, benthic habitat expanded from its steep-sided rocky margins to the soft mud bottom in the center of the lake. Therefore, zoobenthos fossils may be particularly effective indicators to determine the currently uncertain timing and magnitude of climate change in East Africa during the so-called African Megadrought period (~115,000-100,000 years ago), when severe climatic aridity is believed to have stimulated the 'Out-of-Africa II' migration of ancient modern humans out of Africa towards the Middle East, and eventually to Europe. The research material available for this study are sediment samples from turbidites, layers of mud sandwiched between the regular sediment matrix and containing a greater diversity and abundance of zoobenthos fossils. The most important 'by-catch' will be fossil fish remains: scales, vertebrae and teeth of the tilapia *Oreochromis hunteri* living in Lake Chala today. Consequently this study will also reveal precisely when the ancestor of this endemic fish species first colonized the isolated crater lake (presumably a mouth-brooding female cichlid fish was brought in by a fish eagle), and whether the surviving progeny of this first fish have maintained a local population continuously until the present. This thesis project involves the sieving of sediment samples, after which the residue is scanned under a binocular microscope (20-80x magnification) to identify and count the fish and zoobenthos fossils. Not much taxonomic difficulty will be encountered, therefore time spent on each sample will be relatively low, and the number of samples can be high enough to cover the lake's entire history with high temporal resolution. Interpretation of the results will involve statistical comparison with data sets from other indicators of the lake's environmental history, produced by UGent and international project partners.

onderzoeksgroep: Limnology

Copromotor(en):

Van der Meeren Thijs

Begeleider(s):

nog te bepalen

opmerking Gelijkaardig aan maar toch verschillend van topic 1582 van vorig jaar, dat dus mag worden geschrapt of vervangen.

voorbehouden:

abstract Despite being located in a densely populated region with major shipping and harbour activities, the Schelde estuary is a very important and unique ecosystem which in contrast to most European estuaries still has extensive freshwater and brackish tidal marshes. During the last decades, water quality in the Schelde has significantly improved (mainly due to better sewage treatment). At the same time, constant dredging activities (to keep the harbour of Antwerp accessible for large ships) impact the geomorphology and hydrodynamics of the estuary. During the last years, there is a worrying trend towards more suspended matter and higher turbidity in the estuary. This can have major impacts on the whole ecosystem, as it affects sediment dynamics (land-sea material transfer, erosion-deposition dynamics, etc.) but also the biogeochemical functioning of the estuary (e.g. it can lead to lower primary production due to light limitation, or less efficient zooplankton grazing). In the MSc project, the role of phytoplankton in the dynamics of suspended flocs (e.g. floc aggregation, size and sedimentation) will be investigated. During photosynthesis or as a result of stress, micro-algae exude carbon-rich exopolymeric substances (EPS) which can further aggregate to larger transparent exopolymeric substances (TEP). These sticky substances promote the formation of flocs by incorporating dead and living cells, suspended matter etc., and can as such impact sedimentation and carbon fluxes in the estuary. Moreover, these flocs are hotspots of microbial activity and are probably grazed by various zooplankton, which in turn affects their dynamics. To date however, very little is known about the factors that influence the dynamics of EPS and TEP formation by phytoplankton, and how this affects floc size and dynamics. In this thesis, the student will combine the analysis of field data and laboratory experiments to study phytoplankton controls on floc dynamics. In the framework of the OMES project (<http://www.omes-monitoring.be/en>), long-term data sets on environment and biology (including phytoplankton and recently also EPS/TEP) in the Schelde estuary are available. Analysis of these data will be combined with dedicated experiments with phytoplankton isolates using state-of-the art observational (e.g. imaging flow cytometry) and -omics technologies to understand the role of key species and processes in the formation of EPS and TEP, and how this influences floc size, stability and sedimentation.

onderzoeksgroep: Protistology & Aquatic Ecology

Copromotor(en):

Sabbe

Koen

Begeleider(s):

nog te bepalen

opmerking

voorbehouden:

abstract In Antarctica, extremely low temperatures, seasonal differences in sunlight and biologically available liquid water and nutrients pose serious restrictions to life. Microorganisms are therefore the dominant lifeforms in the scarce ice-free regions. To date, microbial diversity studies in terrestrial habitats in Antarctica mainly focused on soils in coastal ice-free regions or so-called oases, while less accessible inland regions such as nunataks largely remain unstudied. These inland locations are however characterized by even more extreme conditions, as they ultra-oligotrophic and drier, and nutrients are only available through weathering of the mineral substrates. A recent study in a few inland polar deserts revealed that the conditions are so extreme to the extent that organisms acquire their energy from atmospheric trace gases such as CO and H₂. A recent barcoding approach of samples from inland locations in the Sør Rondane Mountains (East Antarctica) developed by the laboratory of Protistology and Aquatic Ecology also revealed the presence of micro-eukaryotes which are difficult to place in known higher taxonomic groups. It is therefore very likely these organisms represent novel diversity and taxa new to science. In this MSc project high-throughput shotgun sequencing metagenomics will be used to assess the taxonomic and functional potential of microbial communities (i.e. (micro)eukaryotes, prokaryotes and DNA viruses) from several nunataks in the Sør Rondane Mountains (East Antarctica). The samples were taken along gradients in moisture and organic carbon availability, as well as mineral substrate type. The student will gain experience in bioinformatics and state-of-the-art metagenomics analysis using an in-house data processing pipeline. The results will serve as a basis to identify nunataks that need to be protected by the Committee for Environmental Protection as part of the Antarctic Treaty system.

onderzoeksgroep: Protistology & Aquatic Ecology

Copromotor(en):

Verleyen Elie

Willems Anne

Begeleider(s):

Tytgat Bjorn

opmerking

voorbehouden:

abstract Information on water quality parameters (e.g., suspended particulate matter, phytoplankton biomass) is usually obtained by measuring such parameters in the field or lab. If information from many lakes needs to be obtained on a regular basis (e.g. for lakes used for recreation or drinking water provision), the cost of field work and lab analyses can become very high. Information on water quality can however also be retrieved from spectroscopic measurements, as optically active particles in the water (e.g. phytoplankton cells) impact the spectrum of the water-leaving radiance. Remote sensing information obtained from satellites can as such be used to collect information on water quality for large spatial areas at high temporal frequency, reducing the costs of water quality monitoring. As a result, remote sensing observations of water quality are now routine for large water bodies and the necessary tools for applications to small water bodies are also becoming available. However, because lakes in Belgium are usually small, we need data from sensors with high spatial resolution, and these typically have a lower temporal resolution (~5 days frequency). In this thesis, we will explore the incorporation of time series of operational remote sensing water quality retrievals with meteorological information (modelling and remote sensing) for the prediction of water quality in Belgium inland waters at high temporal resolution.

onderzoeksgroep: Protistology & Aquatic Ecology

Copromotor(en):

Sabbe Koen

Begeleider(s):

Castagna Mourao e Lima Alexandre

opmerking

voorbehouden:

abstract Antarctic lakes are hotspots of biodiversity and primary production compared to the polar deserts in their surrounding catchments. This is because liquid water is readily available, and the water column and lake-ice cover provide a buffer against the sub-zero air temperatures, and the high PAR and UV radiation during spring and summer. Benthic microbial mats are the most conspicuous life forms in these lakes. These mats consist of structured assemblages of cyanobacteria and in some case mosses, which provide a substrate for other photo-autotrophs such as diatoms and green algae, as well as heterotrophic bacteria, protozoans and micro-invertebrates. A few millimeters to centimeters below this photosynthetic active layer, bacteria remineralize organic matter in anoxic conditions. The resulting nutrients are efficiently recycled by the photo-autotrophs in the microbial mats, resulting in a higher primary production compared with that in the (ultra)oligotrophic surrounding lake water. Recent studies in the PAE research group using high-throughput sequencing of specific marker genes uncovered an unknown diversity and a high amount of endemism in various phyla and supergroups in both bacteria and eukaryotes. These studies, as well those based on more classical genetic fingerprinting approaches, also revealed depth-related changes in microbial community structure in response to differences in the light climate and disturbance by lake ice. The functional potential of these organisms and how biochemical pathways vary in response to lake depth and related variables is however still unknown. We hypothesize that benthic mats at shallow depths are more subjected to lake ice disturbance and UV radiation and therefore functionally different compared with those in deeper parts of the lakes. This is likely reflected in depth-related differences in nutrient and carbon pathways, as well as the production of photoprotective compounds. In this MSc project samples collected along a depth gradient in a lake from Skarvsnes (Lützow-Holm Bay, Enderby Land) in East Antarctica will be studied using shotgun sequencing on an Illumina HiSeq platform. This will result in billions of sequences containing genomic information of (micro)eukaryotes, bacteria and DNA viruses. The student will process the metagenomics data using an in-house bioinformatics pipeline and combine the output with field measurements of the carbon and nitrogen cycles. The project will result in a better understanding of the functioning of microbial mats and a biochemical model for carbon and nutrient dynamics along a depth gradient in Continental Antarctic lakes.

onderzoeksgroep: Protistology & Aquatic Ecology

Copromotor(en):

Verleyen Elie

Begeleider(s):

Pargana Aikaterini

Tytgat Bjorn

opmerking

voorbehouden:

abstract Diatoms are one of the most successful groups of microalgae in aquatic ecosystems. In the last decades they have received increasing interest of scientists trying to understand how they impact the functioning of aquatic ecosystems, but also in an industrial context as they have great potential to produce interesting biomolecules. Like many algae, diatoms alternate vegetative and sexual phases in their life cycle. Importantly, their average cell size in population slowly declines during the vegetative growth. This is related to the peculiar structure of diatom's rigid (siliceous) cell wall. The cell wall has a box and lid structure, with one part (the lid or epitheca) being slightly larger than the other part (the box or hypotheca). During the mitotic cell division the two parental thecae become the new epithecae of the daughter cells, whereas the smaller hypothecae are synthesized de novo, which results in a decreased cell size. If this size reduction would go on indefinitely, the cells would become too small and die. To avoid this, diatoms have developed a capability to sense their own size. Once the cells reach species specific size threshold, they transform into mature cells which are capable to keep dividing mitotically or reproduce sexually to restore their initial size. How diatoms control their life cycle and monitor the cell size remains to date unknown. In the PAE lab, we investigate this size sensing mechanism and how it translates into changes in their behavior. To accelerate this development, we established a new model system, *Cylindrotheca closterium*, in which we can routinely and controllably reduce cell size and symmetry by cutting of the long ends of the cells. Given the universal occurrence of cell size sensing in diatoms, we expect that the fundamental control mechanism is strongly conserved. We will search for the potential candidate genes using reference genomes of two diatom models developed in the lab, namely *C. closterium* and *Seminavis robusta*, and by performing comparative analyses of their transcriptomes above and below the SST. We expect to find highly conserved genes coding novel hypothetical proteins related to mitotic spindle formation, cytoskeleton dynamics during mitosis and cell cycling that may be involved in size sensing. For in-vivo tests of the selected candidates, we will use advanced Gibson assembly cloning to prepare plasmids with genes of our interest fused to GFP (green fluorescent protein), express them in *Cylindrotheca closterium* and finally localize the expressed proteins within the cell. We are mostly interested in altered expression and localization of the proteins during different stages of the cell cycle and in cells with modified size. In this MSc project we will use basic and advanced molecular biology techniques such as GO enrichment analysis, PCR, cloning, cell transformation, fluorescent microscopy and flow cytometry.

onderzoeksgroep: Protistology & Aquatic Ecology

Copromotor(en):

Sabbe Koen

Begeleider(s):

Belisova Darja

opmerking

voorbehouden:

abstract Diatoms are a successful group of microalgae, responsible for up to 20% of the global oxygen production and c. 40 % of the oceans' primary productivity, through the fixation of carbon dioxide via photosynthesis (photoautotrophy). In recent years, however, it has become clear that many diatoms, especially benthic species, can combine photosynthesis with the uptake of organic substrates to proliferate, a process called mixotrophy. This realization has led to a paradigm shift in our thinking of carbon and nutrient flows through marine foodwebs. In addition, mixotrophy also offers interesting perspectives for algal biotechnology. At the high cell densities required for cost-effective algae production, cultures very often suffer from self-shading, which limits their potential yield. The use of mixotrophic species could offer a solution for this bottleneck and increase the microalgal productivity by means of adding cheap (waste) organic substrates in the presence of light. The aim of this master thesis project is studying how the availability of light, its spectral composition and organic carbon supply rate influence the physiology and growth of the model mixotrophic diatom *Cylindrotheca closterium*. Experiments will be carried out in continuous culture in 2L bioreactors, allowing to control the supply rates of carbon dioxide, inorganic nutrients, and organic carbon as well as light intensity and quality. Growth conditions will be varied from photoautotrophy (only light, no organic C supply) over mixotrophic to heterotrophy (no light, only organic carbon supply). Throughout the experiments, cell growth and morphology as well as chlorophyll and lipid content will be monitored using an Amnis Imagestream X flow cytometer and photosynthetic activity will be followed using PAM measurements. At representative conditions and time points, RNA will be harvested to study the changes in gene expression patterns and identify the metabolic pathways activated during mixotrophic growth.

onderzoeksgroep: Protistology & Aquatic Ecology

Copromotor(en):

Chaerle Peter

Begeleider(s):

Audoor Sien

opmerking

voorbehouden:

abstract The scarce ice-free areas in Antarctica are among the most extreme terrestrial environments on Earth. As a consequence, foodwebs are strongly truncated, with few metazoans consuming organic matter and microbial biomass. This topic fits in a project aimed at elucidating the factors that shape the biodiversity of these microbiomes and control their contribution to biogeochemical processes. This information can be used to develop conservation strategies, guide long-term monitoring efforts and to predict responses to future environmental changes. The region of the Belgian Antarctic base Princess Elisabeth, the Sør Rondane Mountains in East Antarctica is far less well-studied than more coastal locations and in the McMurdo Dry Valleys, yet is very interesting given its long-term exposure and potential role as ice-free refugia during Neogene and Pleistocene glacial maxima. We are studying freshly collected environmental samples from a radius of 200 km around the Princess Elisabeth Station to generate a comprehensive inventory of the taxonomic and functional diversity of microbial communities in these habitats using high throughput sequencing approaches. The project also includes monitoring of field setups such as snow fences and open top chambers to mimic rising temperatures. An additional aim is to cultivate and characterize key bacterial taxa from these environments which harbour many groups new to science. Depending on the progress of the project the following techniques will be used: protocols for DNA extraction from environmental samples, PCR amplification, library preparation, amplicon sequencing, characterization of the bacterial community by sequence analysis of Illumina data sets (bioinformatics), sequence analysis of shotgun metagenomics data sets, comparative analyses of different samples and use of visualisation tools and statistical analyses. In addition, newly isolated bacterial strains from the region can be characterized using phenotypic test and/or complete genome analyses.

onderzoeksgroep: Protistology & Aquatic Ecology & Labo Microbiology (WE10)

Copromotor(en):

Vyverman Wim

Begeleider(s):

Lambrechts Sam

opmerking

voorbehouden:

abstract The rhizosphere is defined as the soil compartment that is directly affected by root exudates. Due to the nutrients released by the plant, microorganisms are able to proliferate in this ecological niche. Several bacteria that inhabit the rhizosphere colonize the rhizoplane (surface of the roots) and some of them are able to go further and colonize the plant's inner tissues, specifically, the inter-cellular spaces. These bacteria are called endophytes and the environment where they live is the endosphere. In these compartments several plant-microorganism interactions occur. The free living bacteria that have beneficial effects on the plant's health are known as Plant Growth Promoting Rhizobacteria (PGPR). Mainly, these organisms are capable of helping plants cope with biotic (phytopathogens) or abiotic (drought, salinity, flooding, low temperatures) stress through different mechanisms such as biofertilization (phosphate solubilization, nitrogen fixation, siderophore production), phytohormones modulation (Indole-3-acetic acid biosynthesis, ACC deaminase biosynthesis) and biocontrol activity (production of DAPG, HCN, phenazines). Specifically, this project will be focused in one particular abiotic stress which affects crop yield due to its effect on plant growth rate: low temperatures. It has been demonstrated that some PGPR can protect plants against cold, e.g. through plant cell wall strengthening, or the modulation of plant carbohydrates metabolism. Thus, the main aim of this project will be to characterize the plant growth promotion performance of different endophytes under low temperatures, to determine their potential as bioinoculants. In order to do so, some of the strains already isolated from three different plants (*Arabidopsis thaliana*, *Valerianella locusta* and *Poa annua*) will be studied. The selection process of the strains will be based on the presence of two PGP traits: the production of Indole-3-acetic acid and the ACC deaminase activity. The genome of the selected strains will be sequenced and analyzed, to verify the presence of other genes involved in plant growth promotion. Special attention will be given to those traits related to plant growth promotion such as hormone modulation, biofertilization and biosynthesis of antifungal compounds. The presence of genes involved in endophyte lifestyle will be also studied, such as motility and chemotaxis, the presence of plant polymer degrading enzymes, ROS detoxification and iron acquisition. Finally, the strains capacity to promote plant growth will be tested in *Arabidopsis thaliana* grown under cold temperatures.

onderzoeksgroep: Lab. Microbiology, Dept. Biochemistry and Microbiology(WE10) & PSB Rhizosphere group

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voorbehouden:

abstract This topic fits in the framework of a European research project that explores plant-associated microorganisms with the aim to improve the production of bioactive secondary plant metabolites that are of high value for pharmaceutical applications. The focus is on members of the Boraginaceae plant family that produce the naphthoquinones shikonin and alkannin derivatives (A/S) that have a broad spectrum of biological properties, such as tissue regeneration, wound healing, and antimicrobial, anti-inflammatory, and anticancer activities. Up to now bacterial endophytes have been isolated from Boraginaceae plants and partially identified. The selection of bacterial strains will be based on a broad taxonomic range of microorganism previously isolated from the roots of different *Alkanna tinctoria* plants. It is known from other studies that certain parameters such as plant hormones and mineral nutrients can increase the production of A/S. Therefore the goal of the project is to select bacterial strains that may contribute to these parameters and test these strains and combinations of these strains for their effect on plants in terms of plant growth promotion and production of secondary metabolites. Bacterial strains will be phenotypically characterized in laboratory cultures and tested for their effect on plants using hairy root cultures and/or in vitro plants. The ones exhibiting desired traits for inducing plant growth promotion and secondary metabolites production will be grown together in order to establish its compatibility. Selected strains or combination will be inoculated on plants under greenhouse conditions in collaboration with the project partners. Different parameters for plant development like length, number of leaves, root area and content of A/S will be recorded and analyzed. Strains or combinations that show a positive effect will be further characterized by studying their complete genome sequence in comparison with other non-effective bacterial endophytes.

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