

Overzicht onderwerpen masterproeven 2017-2018 per promotor

Adriaens

Dominique

1369

Ecomorphology of climbing versus terrestrial chameleons: studying the functional morphology of the tail system

abstract Prehensile or grasping tails have proven to be functionally very interesting for many vertebrate lineages, having evolved independently within for example fishes, reptiles and mammals. Various squamates have evolved such prehensile tails independently and use it to accommodate their arboreal lifestyle, allowing them to grasp onto branches to keep their balance. Our research focuses on the chameleons who are known for their variety in lifestyles. One genus in particular, *Bradypodion*, shows a lot of variation from terrestrial animals to entirely arboreal, the latter which possess prehensile tails. What is especially interesting is that this variation occurs both at an inter- and intraspecific level. The aim of this thesis project is to look into this chameleon tail morphology (musculoskeletal system), and perform a comparative functional morphological study across the *Bradypodion*, comparing the prehensile tails of the arboreal animals with the tails of the terrestrial species. This allows us to see to what degree there is convergent evolution in grasping tails, also when comparing them with outgroup species to determine what morphological characters can be attributed to adaptation and/or phylogeny. Morphological analyses will rely on μ CT scanning, including soft tissue visualisation and 3D reconstruction using contrast staining techniques. Functional analyses will rely on quantifying material properties of the different components of the tail (bending stiffness), as well as do performance testing on living animals (depending on availability of live specimens). Further understanding of how the skeletal system interacts (bony elements articulating with each other and with vertebrae), and how this translates to strength and flexibility, will be tested using 3D printed models. This thesis research is part of an on-going collaboration with Musée National d'Histoire Naturel (Paris – Prof. Anthony Herrel) and Clemson University (USA – Prof. Michael Porter), a project that focuses on evolutionary morphology and biomimetic applications of prehensile systems.

onderzoeksgroep: Evolutionary Morphology of Vertebrates

Begeleider(s):

Luger Allison

opmerking

voorbehouden:

Beeckman

Tom

1218

Evaluation of the role of Calcium as an integrator of nutrient sensing and root system architecture adaptation

abstract The root system of plants is a tremendously flexible structure that allows plants to explore the soil in search of water and nutrients. Depending on the availability of nutrients, the root system can become longer or shorter and more or less branched. In addition, the number of root hairs can be adjusted to increase the uptake surface. How nutrient availability is translated in root branching is poorly understood. Here, we will investigate the role of Calcium as a second messenger through which the nutrient status is translated in a cellular response that underlies root adaptive growth responses. Here the student will explore the existing literature for the state of the art, define a critical point that needs to be investigated, and lay down a strategic plan to address the raised issue(s). During the master thesis, the student will pursue to solve this problem.

onderzoeksgroep: PSB Plant Systems Biology - Root Development

Copromotor(en):

Vanneste Steffen

Begeleider(s):

Vanneste Steffen

opmerking

voorbehouden:

1370

The evaluation of nitrification inhibitors to suppress the growth of nitrifying micro-organisms and the effect on plant development.

abstract Nitrogen is one of the most important nutrients for plant growth and therefore, it is intensively fertilized on agricultural soils. Nitrogen is mainly present in two forms: ammonium (NH₄⁺) and nitrate (NO₃⁻). Ammonium is converted in nitrate by nitrifying soil micro-organisms. Nitrate however leaches from the soil and contributes to groundwater contamination. Moreover, nitrate is converted to nitrous oxide, a greenhouse gas which contributes to global warming. In a current research project, possible inhibitors of ammonium nitrification will be tested, which as such might prevent abundant nitrate formation, leaching and greenhouse gas production. This includes optimizing growth conditions of different nitrifying bacteria and archaea, their cultivation (including molecular identification) and evaluation of their growth (spectrophotometric methods). Finally, in vivo assays will be developed with Arabidopsis reporter lines to evaluate the effect of the inhibitors on plant growth. This project offers science with possibilities for industrial applications and the unique opportunity to work with elusive archaea and bacteria.

onderzoeksgroep: PSB Plant Systems Biology - Root Development

Copromotor(en):

Motte Hans

Begeleider(s):

Beeckman Fabian

opmerking

voorbehouden:

1371

Unraveling the role of GOLVEN6 signaling in lateral root initiation in *A. thaliana*

abstract Cell-to-cell signaling is essential for many processes in plant growth and development. Much work has concentrated on traditional plant hormones. However, recent findings highlight that peptide signals have emerged as an important class of regulators in intercellular signaling during plant development. Our work, along with that of other research groups, has led to the identification of a novel secreted peptide family in Arabidopsis named GOLVEN. During previous characterization of GOLVEN genes transcription we remarked that GOLVEN6 (GLV6) had a very specific expression pattern associated to lateral root formation. Additional experiments lead us to postulate that GLV6 peptide signaling is part of a mechanism controlling the very first asymmetric cell divisions required for primordium initiation and essential for the progression of lateral root development. Since the mechanisms controlling the first asymmetric divisions during primordium formation are largely unknown, unravelling the GLV6 signaling pathway will certainly contribute to our understanding concerning cell-to-cell communication in the control of this process. In order to identify molecular players of the GLV6 signaling pathway, an EMS mutagenesis screen was launched which recently led to the identification of seven suppressors of the GLV6 phenotype. This thesis proposal will allow you to take part in an in-depth functional analysis of the newly identified genes involved in GLV6 signaling during lateral root formation and help us to gain insights in this exciting, unexplored research field. During your thesis, you will not only learn to use a large variety of essential lab techniques such as plant tissue culture, PCR, qRT-PCR, light and confocal microscopy, GUS staining as well as general phenotyping, but you will also learn to master techniques such as transient and stable transformation of Arabidopsis, cloning and the cutting edge genome editing technology, CRISPR-Cas9 for the more ambitious amongst you.

onderzoeksgroep: PSB Plant Systems Biology - Root Development

Copromotor(en):

Fernandez Ana

Begeleider(s):

Vangheluwe Nick

opmerking

voorbehouden:

Bert

Wim

1372

Diversity and ecology of nematodes associated with mushrooms

abstract Nematodes can be found everywhere, but almost nothing is known about nematodes in mushrooms. Preliminary results demonstrated that many species are potentially transmitted by insects that are associated to mushrooms. Either fungi, insects and nematodes are among the most diverse groups of living organisms. Most of the research on nematodes is driven by economic motives, especially for parasitic nematodes of plants and animals and several habitats are still virgin territory and several nematodes appear to be new to science. This study will provide the first comprehensive overview of nematode diversity inside fungi. . This master thesis includes sampling of fungi in the field, sampling of insects collected with a special insect-emergence trap, extraction of nematodes from fungi and identification of both fungi and nematodes, and identification of the insects that are associated with the nematodes. Because this group of nematodes is not yet well investigated and several species are morphologically not well characterized, morphological data will be supplemented with molecular data. This includes DNA-extraction of nematodes, PCR and sequencing of species specific DNA regions that are also useful for phylogenetic analyses. The objectives of this thesis are: 1) to give a checklist of nematodes associated with fungi; 2) to investigate the ecology of nematodes associated with fungi; 3) acquire insight into transport mechanisms of nematodes; and 4) reveal the specificity of nematode-fungi relations.

onderzoeksgroep: Nematology

Begeleider(s):

Slos Dieter

opmerking

voorbehouden:

Bonte

Dries

1226

Experimental and theoretical study on optimal body size distributions within different landscape configurations

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 and now aim to validate our prediction with real data within this Msc project. This will be accomplished by collecting different arthropod species within the coastal dunes. In dunes, tussocks of marram grass (Ammophila Arenaria) are imbedded in a single matrix of sand and thus provide an ideal model system for this question. By sampling arthropods in patches with varying spatial configuration of the resources, the student will confront the collected data on species numbers and size with several alternative outcomes from a developed simulation model.

onderzoeksgroep: Terrestrial Ecology

Begeleider(s):

Hillaert Jasmijn

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):

Masier Stefano

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:

abstract Flanders has nearly 2000 ha of greenhouses, representing a revenue of nearly 370 million euro's. Economically, tomato is the most significant crop. A greenhouse represents a relatively closed environment, in which several climate variables (i.e. temperature, humidity) are monitored daily. A recent implementation of a European law encourages growers to produce residue poor tomato crop. Hence biocontrol options become more and more important. Pest species, like mites, affecting the crop often occur naturally. The beneficials or the predatory mites, are introduced as biocontrol. Little is known about the spatial distribution of the mite pest species in the greenhouses. For this thesis we will use an existing IBM (individually based model) describing the movement patterns of the mites on a single plant to inform us about more general movement patterns in the greenhouse. An experiment in which we monitor plants on a daily basis and release a small population of mites in the middle of the greenhouse will be carried out. The dispersal pattern observed will be verified against the predicted one from the IBM, allowing to describe the flow of mites along a tomato plant line and between lines. This will result in crucial information which is used in a population dynamical model able to simulate different biocontrol

onderzoeksgroep: Terrestrial Ecology

Copromotor(en):

Moerkens Rob

Sluydts Vincent

Begeleider(s):

Bonte Dries

Moerkens Rob

Sluydts Vincent

opmerking

voorbehouden:

abstract Adaptive evolution towards novel environmental conditions, also referred to as ecological specialization depends to a large extent on the interplay between gene flow among populations and the experienced local environmental conditions that determine the strength of selection. In spatially heterogeneous environments, the level of gene flow among differentially adapted populations and the attained population sizes will depend on the spatial grain of the landscape as well as on the degree of habitat matching, i.e. to which degree immigrants selectively settle in environments in which they are adapted to thus attain their highest fitness. The scale of spatial adaptation will thus be impacted by the species' dispersal behaviour and the spatial configuration of the environmental heterogeneity. Ecological specialization is expected to evolve in coarse grained landscapes. In contrast, fine-grained landscapes will promote the evolution of generalist strategies, unless individuals disperse among the fine-grained landscape in a non-random way, and settle in alike habitat to which they were born and adapted. In turn, ecological specialisation through local adaptation is expected to select against dispersal in heterogeneous landscapes and to enforce evolutionary dynamics, thereby affecting ecological dynamics by reducing rescue effects if local populations go extinct by either stochastic or deterministic processes. Depending on the severity of these disturbances at spatiotemporal scales, dispersal is expected to evolve, thus interchanging maladapted for adapted genes and to reduce local adaptation and ecological specialisation. Using the spider mite as a model system in experimental evolution, the project aims to test how spatial environmental heterogeneity and disturbance affects the rate of adaptive evolution of ecological specialization, and to which degree feedbacks imposed by the joint evolution of dispersal and local adaptation affect metapopulation dynamics. Relevant reading: DE ROISSART, A., WANG, S. & BONTE, D. (2015). Spatial and spatiotemporal variation in metapopulation structure affects population dynamics in a passively dispersing arthropod. *Journal of Animal Ecology* 84: 1565-1574 DE ROISSART, A., WYBOUW, N., RENAULT, D., VAN LEEUWEN, T. & BONTE, D. (2016). Life history evolution in response to changes in metapopulation structure in an arthropod herbivore. *Functional Ecology* 30: 1408-1417

onderzoeksgroep: Terrestrial Ecology

Begeleider(s):

Mortier

Frederik

opmerking

voorbehouden:

abstract Tree species diversity, identity and the level of forest fragmentation are expected to impact arthropod diversity, but also their impact on ecosystem functioning. Orb web spiders provide a unique model species that allow simultaneous inference of both inter- and interspecific variation in behaviour on prey capture. By measuring web characteristics, relevant foraging decisions can be quantified into detail, and linked to changes in environmental conditions. By making use of the TREEWEB design (<http://www.ecology.ugent.be/treeweb/>), the student will test to which degree foodweb functioning in a selection of forests is affected by spatial and diversity drivers. Intensive field work is foreseen in August-September, and can be extended with surveys in spring. Relevant reading: <http://biorxiv.org/content/early/2016/09/21/076497>

onderzoeksgroep: Terrestrial Ecology

Begeleider(s):

Lantman

Irene

opmerking

voorbehouden:

1378

The interaction between microbiome and evolutionary dynamics.

abstract New synthesis moves away from viewing only genes as the keystones for adaptation to novel environments. Microbiomes – the community of microorganisms inhabiting multicellular organisms - are increasingly recognised as an important force impacting life history, behaviour and thus fitness. Species communities are structured by drift, selection, gene-flow and migration, and microbiomes are hypothesised to follow these rules as well. They eventually maximise performance of their host. The main research questions will be: (1) Do we find a connection between the microbiome community of the spider mites and their fitness on a certain plant species and how does this evolve in time? (2) Is there a link with the transcriptome of the mite? In this research, the two-spotted spider mite (*Tetranychus urticae*) is introduced to new host plants and individuals will be sampled for their microbiome at certain time points during the adaptation to the new host. Besides, you will do fitness tests and a transcriptome study to investigate whether the microbiome affects host performance. The research will be carried out in Ghent or in Groningen, whichever is most pragmatic for everyone involved.

onderzoeksgroep: Terrestrial Ecology & GELIFES (Univ. Groningen)

Copromotor(en):

Etienne Rampal (R.S.)

Begeleider(s):

Bisschop Karen

opmerking This MSc thesis is in collaboration with professor Etienne from the University of Groningen, which may indicate some appointments in Groningen. The experiments can be performed in Ghent or in Groningen according to the preference of the student.

voorbehouden:

1379

The spatial and community context of ecological specialisation: a modelling approach

abstract Adaptive evolution towards novel environmental conditions, also referred to as ecological specialization depends to a large extent on the interplay between gene flow among populations and the experienced local environmental conditions that determine the strength of selection. In spatially heterogeneous environments, the level of gene flow among differentially adapted populations and the attained population sizes will depend on the spatial grain of the landscape as well as on the degree of habitat matching, i.e. to which degree immigrants selectively settle in environments in which they are adapted to thus attain their highest fitness. The scale of spatial adaptation will thus be impacted by the species' dispersal behaviour and the spatial configuration of the environmental heterogeneity. The community context is additionally expected to be an equally strong driver of such adaptive processes through direct and indirect effects but we lack insights on its importance relative to the abiotic context. Contrary to processes of direct selection under natural as well as experimental conditions, this spatial and community context of adaptive evolution received considerably less attention. Insights into the eco-evolutionary dynamics in metapopulations and metacommunities are thus of uttermost relevance if we aim to move towards a more predictive ecology of population and community dynamics in fragmented landscapes. By applying a modelling approach, potentially combined with insights from experimental work (see other thesis proposal), the project aims to develop theoretical insights on the dynamic interplay between habitat fragmentation, species-interactions and the evolution of life histories and dispersal. The student will use Python as a modeling platform. relevant reading: BOEYE, J., KUBISCH, A. & BONTE, D. (2014). Habitat structure mediates spatial segregation and therefore coexistence. *Landscape Ecology* 29: 593-604 DELGADO, M., BARTON, K.A., BONTE, D. & TRAVIS, J. (2014). Prospecting and dispersal: their eco-evolutionary dynamics and implications for population patterns. *Proceedings of the Royal Society B* 281: 20132851

onderzoeksgroep: Terrestrial Ecology

Begeleider(s):

Mortier Frederik

opmerking

voorbehouden:

1380 The spatial and social network of a highly endangered digger wasp.

abstract The digger wasp *Bembix rostrate* is a highly endangered insect species in the Flemish inland and coastal dunes. In order to prepare proper conservation measures, we need to understand how the population is structured in fragmented grey dunes, and to which degree individual females make use of different patches for nestling. Such insights can be gathered from a detailed capture-mark-recapture study and will allow inference of both the species' social and spatial network structure. The species is active from the end of June till September and intensive field work in the coastal dunes will be required. Data will be analysed using cutting edge spatial and network statistics.

onderzoeksgroep: Terrestrial Ecology

Begeleider(s):

Bonte Dries

opmerking

voorbehouden: Gertjan Bisschop

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

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

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

onderzoeksgroep: Terrestrial Ecology

Begeleider(s):

Hillaert Jasmijn

opmerking

voorbehouden:

1384The effect of healthspan-promoting genes and compounds on the heat shock response 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, (2) polymorphisms favoring healthy aging discovered in cohorts of healthy aged persons and (3) pure compounds or botanical preparations reported to ameliorate healthspan. Armed with a selection of genes, polymorphisms, 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. In this project, we will focus on HSP-16.1, a heat shock-related stress response protein. This gene is a direct mediator of heat shock transcription factor (HSF-1) signaling, known to play an important role in lifespan signaling. Via the reporter strain hsp-16.2::GFP, appearance of GFP fluorescence upon activation, due to RNAi-treatment of selected genes or administration of specific chemical compounds, can be quantified using a multi-well plate reader. In addition, we will study another heat shock protein which is a robust marker for mitochondrial stress, HSP-6. Its potential interactions with healthspan-promoting signaling cascades makes this protein an extremely interesting candidate to reveal healthspan promoting mechanisms of the selected genes or extracts. Taken together, this project will provide insights into distinct sets of healthspan-promoting signaling mechanisms in *C. elegans*, involved in the control of healthspan.

onderzoeksgroep: Aging physiology and molecular evolution

Copromotor(en):

Dhondt Ineke

Begeleider(s):

Dhondt Ineke

opmerking

voorbehouden:

1385The requirement of trehalose in proteome stabilization of long-lived *Caenorhabditis elegans* daf-2 mutants: systemic or tissue-specific?

abstract For a very long time, researchers have been intrigued by ageing, its underlying molecular mechanisms and regulation. However, despite being almost universal among animals, this process has yet to be fully elucidated. The long-lived daf-2 (Insulin/IGF-pathway) mutant of the nematode *Caenorhabditis elegans* has been widely used for studying mechanisms of life span extension and the underlying changes in gene expression and metabolism. daf-2 mutants show a decrease in protein synthesis and degradation, and the sugar trehalose is thought to have a major role in maintaining protein stability and homeostasis. Trehalose is an alpha-linked non-reducing disaccharide of glucose, involved in protection against environmental stress, such as desiccation, anoxia and heat. In *C. elegans* there are two trehalose-6-phosphate synthase genes: tps-1 and tps-2, and their expression is partially required for lifespan extension in daf-2 worms. The aim of this project will be to examine whether a protective role of trehalose in supporting the daf-2 longevity phenotype is required in the whole organism (systemically) or in specific tissues only. To do so, we will first determine the tissues in which tps-1 and tps-2 are expressed, by using green fluorescent protein (GFP) tags. Afterwards, we will select a few tissues in which we will specifically knockdown the two trehalose synthase genes in the daf-2 genetic background by RNA interference (RNAi) and score the animal's lifespan, to evaluate the role of trehalose synthesis in diverse tissues on daf-2 longevity.

onderzoeksgroep: Aging physiology and molecular evolution

Begeleider(s):

Zečić Aleksandra

opmerking

voorbehouden:

1386 Unravelling the mechanisms of lifespan extension under axenic dietary restriction (ADR).

abstract The free-living nematode *Caenorhabditis elegans* has a mean lifespan of about three weeks when cultured under standard laboratory conditions, i.e. grown on agar plates seeded with *Escherichia coli* bacteria and incubated at 20°C. However, when these worms are cultured in a semi-defined, nutrient-rich medium devoid of bacteria (axenic medium), their lifespan is doubled. The mechanisms underlying this lifespan extension under axenic dietary restriction (ADR) are still enigmatic, but our recent work has shown that knockdown of the *bli-4* gene completely abolishes the lifespan extending effect of ADR. *BLI-4* is a proprotein convertase that is involved in neuropeptide processing. As a first part of this dissertation, we aim to discover in which tissues *BLI-4* is required to establish the lifespan extending effect of ADR by knocking down this gene tissue-specifically using RNA interference. If *BLI-4* would appear to be important in the neurons, we aim to unravel in which subclasses of worm neurons *BLI-4*'s presence is essential for lifespan extension. Several subclasses of worm neurons have been identified based on their neurotransmitters (dopamine, serotonin, acetylcholine, octopamine, glutamate, GABA, tyramine). During this master dissertation, a wide array of techniques might be applied: nematode and bacterial culturing methods, lifespan assays, RNA interference, PCR and RT-PCR.

onderzoeksgroep: Aging physiology and molecular evolution

Begeleider(s):

Vandemeulebroucke Lieselot

opmerking

voorbehouden:

Braeckman Ulrike

1387 Bio-irrigation by two important polychaete species in the Belgian Part of the North Sea

abstract The sea floor is an important component of the coastal marine ecosystem, as it is the environment where large amounts of organic material are deposited after the annual phytoplankton bloom. Mineralisation of this organic matter results in fluxes of nutrients to the water column, where they fuel the next phytoplankton bloom. Mineralisation is most efficient in the presence of oxygen. Oxygen concentrations in coastal sediments are largely affected by the activities of sediment inhabiting fauna. Previous research showed that the Sand mason (*Lanice conchilega*), a tube-building polychaete, ventilates the sediment with overlying water, thereby increasing the oxygen content of the sediment and stimulating the mineralization of organic matter. A similarly looking polychaete species (*Owenia fusiformis*) lives in more rigid tubes, and is more tolerant to sludge disposal. While it is highly abundant in certain areas of the Belgian Part of the North Sea, there is no information on its effects on the sedimentary environment. Here, we will investigate whether *Owenia fusiformis* should be considered as important for benthic ecosystem functioning as *Lanice conchilega*. By experimental research, we will compare the bio-irrigation rates of both species, and test whether these are density - and context - (sediment type) dependent. This is highly relevant, as human activities (aggregate extraction, installation of offshore wind farms) at sea result in a fining of the sediments. Consequently, *Lanice conchilega* is now occurring in high densities where it has been absent before, and the suitable habitat for *Owenia fusiformis* can be increasing as well. This thesis therefore contributes to an ongoing project aiming at the understanding of the functional consequences at the ecosystem scale, from local anthropogenic activities.

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

Copromotor(en):

Vanaverbeke Jan

Begeleider(s):

Toussaint Elise

opmerking

voorbehouden:

abstract Human activities in the coastal zone have strong effects on the physical environment: beam trawling, dredging and dumping activities, aggregate extraction and the installation of offshore windmill farms can affect the sediment drastically. The effect of these changes is generally investigated through an assessment of how fauna is impacted but this does not provide answers on how the functioning of the ecosystem is affected. The majority of coastal sediments consist of clean, coarse sands. These sands act as a filter for the water column, where efficient biogeochemical processes result in fast mineralization of organic matter. On several areas on the Belgian part of the North Sea, we observed that these sediments are either covered by finer sediments, or that finer particles are incorporated in the sand matrix. The efficiency of the mineralization processes (process whereby organic material is changed to its anorganic elements) depends on the availability of oxygen in the sediment. Clean sands are characterized by the presence of oxygen in high concentrations, but the "fining" of such sediments can result in decreased oxygen concentrations, and hence in a decreased mineralization efficiency. Within this thesis, a series of experiments will be performed, along an artificially created gradient of fined sediments. The sediments, and fauna, will be incubated in lab-experiments, and organic matter (diatoms) will be added. During the experiments, the student will investigate how the mineralization rates are affected by the "fining" of the sediment. The student will be involved in sampling, setting up and maintenance of highly specialized experiments, and will get in touch with biogeochemical modeling. The thesis contributes to an ongoing project investigating the effect of fining of sediments at the scale of the Southern Bight of the North Sea.

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

Copromotor(en):

Vanaverbeke Jan

Begeleider(s):

Toussaint Elise

opmerking

voorbehouden:

abstract The Zanzibar yam, or *Dioscorea sansibarensis* (syn. *D. macroura*) is a species of true yam native to Madagascar and tropical Africa. The species is found in a wide belt from Madagascar to Guinea in West Africa and South to Mozambique. It is also invasive in Taiwan and Singapore, as well as in Florida. *D. sansibarensis* is a fast growing vine that reproduces almost exclusively by vegetative reproduction through aerial bulbils the size of a plum and through underground tubers. Tubers and bulbils are inedible and extremely toxic. In fact, the Baya people from what is now the Central African Republic are known to grow *D. sansibarensis* specifically for use in the manufacture of poison arrows. Tubers are also sometimes left in the fields of edible yam to kill wild pigs responsible for crop losses. The compound(s) responsible for the toxicity of *D. sansibarensis* has not been isolated to date. Leaf tips of *D. sansibarensis* are unusual in that they also harbor symbiotic bacteria. We isolated bacteria from *D. sansibarensis* specimens across Europe (including from the UGent botanical garden), and we found that these bacteria belong to a new species found exclusively in association with the Zanzibar yam: *Orrella dioscoreae*. Remarkably, the symbiotic bacteria are transmitted hereditarily through pre-colonized bulbils and tubers. How symbiont transmission occurs and how it relates to symbiont function is still unknown. The aim of this master thesis project is to investigate the life cycle of the symbiosis and draft hypotheses about its function through the use of advanced microscopy-based techniques. The findings will serve as a scaffold for functional analysis of the symbiosis. Research environment and techniques: This project will allow the student to draw from the scientific expertise of two laboratories housed in the Faculty of Sciences. The Laboratory of Microbiology will provide guidance on genome analysis of the bacterial symbionts, phenotypic assays (e. g. in vitro biofilm formation, bacterial signaling and quorum sensing, plant hormone production) and system-wide analysis of functions involved in colonization and symbiotic function. The Research Group Spermatophytes will provide guidance and support in plant histology and microscopy techniques (fixing and embedding, (ultra)microtome sectioning, epifluorescence and laser scanning confocal microscopy, fluorescence staining and in situ hybridisation).

onderzoeksgroep: Lab. Microbiology, Dept. Biochemistry and Microbiology - WE10

Copromotor(en):

Leroux Olivier

Begeleider(s):

Carlier Aurelien

Leroux Olivier

opmerking

voorbehouden:

1239 From alga to holobiont: characterisation of endosymbiotic bacteria in the invasive green algal species *Caulerpa cylindracea*

abstract Siphonous green seaweeds are among the morphologically most complex algae and also among the most notorious invasive species in many parts of the world. Their ecological success has repeatedly been linked to their association with endo- as well as epiphytic bacteria. Recent studies based on 16S rDNA sequencing have identified associated bacteria. However, little has been explored concerning the functional diversity and community structure assembly. It has been proposed that microbe interactions aid in the success of the seaweed and can in some cases provide a competitive advantage to invasive species. To investigate the relationship between bacteria and green seaweeds, metagenomic data of the associated bacteria of native and invasive species of *Caulerpa* will be analysed. A combination of in situ experiments will be performed by manipulating abiotic conditions to assess changes in bacterial community composition. Natural population collection as well as in situ experiments will take place in the Mediterranean Sea. Fieldwork is essential for the project, diving experience desirable. Furthermore, laboratory experiments will be conducted to identify *Caulerpa* growth in the presence of certain prominent bacterial species as well as the effects of abiotic stresses on bacterial recruitment by the seaweed.

onderzoeksgroep: Phycology & Lab. Microbiology, Dept. Biochemistry and Microbiology - WE10

Copromotor(en):

Willems Anne

Begeleider(s):

Morrissey Kathryn

opmerking

voorbehouden:

abstract The marine realm represents some of the most ecologically and socioeconomically significant ecosystems on the planet. Unfortunately, coastal marine ecosystems, along with the goods and services they provide, are threatened by global climate change. Continuously increasing greenhouse gas emissions cause changes in oceanographic conditions such as temperature and pH, which in turn affect biological and social systems. Shifts in ocean characteristics likely act as stressors by inducing changes in life-history traits and physiological performance of organisms. The outcome of a changing climate is dependent on a combination of factors, including the rate and magnitude of climate change, the adaptive potential of the species (standing genetic variation, population structure, etc.), plastic and possibly also epigenetic responses. As a result of climate change (rising temperatures, unpredictability of the weather, etc.) populations may either shift (climate tracking), adapt (evolve) or go extinct. The adaptive potential of populations is mainly determined by population size and available genetic diversity. However, the adaptability of spatially structured populations may also be affected by dispersal: positively by spreading beneficial mutations across subpopulations, but negatively by moving locally adapted alleles between locally adapted populations. Hence, there is a clear need to characterize spatial patterns of neutral as well as adaptive genetic variation in natural populations in order to understand the effects of local adaptation and dispersal on species persistence. This thesis focuses on the brown alga Dictyota. Natural populations of the selected organisms will be sampled in Europe. We will take advantage of a genotyping by sequencing (GBS) approach to develop genome-wide marker data from a sample of natural populations to infer demographic processes and find signatures of local adaptation. A technique that has been successfully applied in recent population genomic studies is restriction-site-associated DNA sequencing (RADseq) in conjunction with Illumina technology. Population genomic analysis will be carried out to examine geographic patterns of neutral and adaptive genetic diversity within and among populations, geographic population genetic structuring and gene flow, historical population dynamics, and loci under selection. Measures of neutral and adaptive genetic diversity will be estimated using population genomic techniques in combination with FST outlier analysis. This research will be realized through a cooperation of the Phycology Research and Marine Biology Research Groups (UGent) and the Department of Applied Mathematics, Biometrics and Process Control (UGent). The project combines fieldwork, lab experiments, molecular tools and modeling approaches.

onderzoeksgroep: Phycology & KBIN & BW10

Copromotor(en):

De Baets Bernard

Derycke Sofie

Begeleider(s):

nog te bepalen

opmerking

voorbehouden:

abstract The marine realm represents some of the most ecologically and socioeconomically significant ecosystems on the planet. Unfortunately, coastal marine ecosystems, along with the goods and services they provide, are threatened by global climate change. Continuously increasing greenhouse gas emissions cause changes in oceanographic conditions such as temperature and pH, which in turn affect biological and social systems. Shifts in ocean characteristics likely act as stressors by inducing changes in life-history traits and physiological performance of organisms. The outcome of a changing climate is dependent on a combination of factors, including the rate and magnitude of climate change, the adaptive potential of the species (standing genetic variation, population structure, etc.), plastic and possibly also epigenetic responses. This thesis will examine the extend of local adaptation on temperature response of the brown algal seaweed, *Dictyota dichotoma*. This species represents a major component of the total algal biomass along Northeast Atlantic and Mediterranean coasts. The student will sample populations along a North-South gradient [fieldwork] and characterize their physiological response (survival, growth, fecundity) under different temperature and pH conditions [lab experiments]. In addition, the role of transgenerational plasticity and epigenetics, will be deduced from a series of experiments centered on parent-offspring comparisons, measurements of heritability. This research will be realized through a cooperation of the Phycology Research and Marine Biology Research Groups (UGent) and the Department of Applied Mathematics, Biometrics and Process Control (UGent). The project combines fieldwork, lab experiments, molecular tools and modeling approaches.

onderzoeksgroep: Phycology & BW10

Copromotor(en):

Bogaert	Kenny
De Baets	Bernard

Begeleider(s):

Bogaert	Kenny
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opmerking

voorbehouden:

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

onderzoeksgroep: Phycology & PSB Plant Systems Biology-Root Development

Copromotor(en):

Beeckman	Tom
Bogaert	Kenny

Begeleider(s):

Bogaert	Kenny
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opmerking

voorbehouden:

abstract Although Darwin's theory of evolution is a gradualist theory based on the accumulation of small changes in the phenotype over time. Ever since Huxley, it has been argued that the theory would be equally correct if the changes were large and evolution was saltational. The most notorious proponent of saltational evolution was undoubtedly Richard Goldschmidt, who indicated that dramatic mutations as chromosomal rearrangements could result in "hopeful monsters" (i.e. organisms with a drastically changed phenotype, that might survive under some circumstances). Whole genome duplications (WGDs) are an example of such a macro-mutation and it has been argued that the resulting polyploids are such hopeful monsters. Plant evolution is characterized by a number of WGDs, and quite a large amount of them occurred around the K-Pg extinction event suggesting higher polyploid survival and/or an increased number of WGDs in the stressful conditions at that time. Furthermore, polyploids might have a higher adaptive potential in stressful or new environments as suggested by the relatively high abundance of recent polyploids in stressful environments, and higher invasiveness of polyploid plants. Does polyploidy become beneficial in stressful environments? In this thesis, you will seek for an answer to this question by sampling natural populations of the green alga *Chlamydomonas* along a stress gradient (latitudinal, pollution or altitude) and by quantifying the diploid/haploid ratio of these populations (using flow cytometry, fluorescent microscopy and by analyzing cell morphology). The results will allow you to draw a conclusion whether there is a correlation between the occurrence of these rare diploids and the environmental variances. "

onderzoeksgroep: Phycology & PSB-Bio-informatics group

Copromotor(en):

Van de Peer Yves

Begeleider(s):

Aydogdu Eylem

Bafort Quinten

opmerking

voorbehouden:

abstract How much do we know about the biodiversity of marine macroalgae along European coastlines? Many seaweed floras have been published over the past decades, resulting in a comprehensive overview of macroalgal diversity along our shores. However, the bulk of these marine flora's have been published in the 20th century, and hence understanding of seaweed diversity is largely based on morphological data only. Since the 1990ies, molecular systematics has drastically changed our understanding of species boundaries in algae. One of the main outcomes of DNA-taxonomy is the discovery of cryptic species: species that are genetically distinct, but morphologically indistinguishable. This has an important impact on our view of marine biodiversity. In addition, species diversity in the sea (and on land) is constantly changing as a result of global environmental change and the introduction of non-native species. The aim of this study is to assess macroalgal biodiversity along our shores, using a combined morphological and molecular approach, focusing on two marine regions: the semi-natural rocky shores of northern France, and the artificial and human-impacted shores of Zeeland. Both areas will be extensively sampled for marine algae, including macroscopic as well as microscopic seaweeds. Specimens will be characterized morphologically as well as molecularly by DNA sequencing, and species diversity will be assessed by DNA sequence analysis. These data will provide important insights in 1) actual species diversity of marine macroalgae along our shores, and concordance or discordance with morphology-based assessments of biodiversity, 2) possible shifts in species diversity over the past decades (e.g. species declines or introduced species), 3) the factors shaping and changing seaweed diversity. This research will be realized through a collaboration of the Botanic Garden Meise and the Phycology Research Group (UGent). Practical work will involve: Sampling along the rocky shores of northern France and artificial substrates in the Netherlands, morphological work and microscopy, study of herbarium collections, molecular lab work including DNA-sequencing, and DNA sequence analysis.

onderzoeksgroep: Phycology & Nationale Plantentuin van België

Copromotor(en):

Leliaert

Frederik

Begeleider(s):

nog te bepalen

opmerking

voorbehouden:

abstract Bryopsis is a genus of siphonous marine macroalgae. Species are widely distributed in coral reefs throughout the tropics and along rocky coastlines in temperate regions. Bryopsis itself is easily recognizable by its typical elegant feather-shaped morphology, but the genus has a notorious long history of confusing species circumscriptions. Previous studies have attempted to delimit species based on morphological criteria, and over 100 species have been described. This traditional taxonomy, however, is problematic because the morphology of Bryopsis can easily change with the environment. DNA-sequence data are therefore particularly valuable for testing traditional species boundaries. In addition, DNA sequencing of archival type material can solve taxonomic and nomenclatural problems. Bryopsis is also interesting from an ecological and biogeographical perspective. A number of species seem to be restricted in their geographical range, while other species have attained global distributions, or are known as invasive species. A molecular phylogenetic approach in combination with evolutionary analysis of traits (e.g. temperature tolerance) will be important to understand the evolutionary and biogeographical history of the genus. In short, the aims of this thesis are thus to 1) clarify the species-level taxonomy of Bryopsis using DNA-based approaches, and 2) elucidate the evolutionary history of the genus using a molecular phylogenetic approach. This research will be realized through a cooperation of the Botanic Garden Meise and the Phycology Research Group (UGent) and. Practical work will involve: Sampling in natural habitats (e.g. rocky shores of northern France and artificial substrates in the Netherlands), study of herbarium collections, molecular lab work, including DNA-sequencing of type material, DNA sequence analysis.

onderzoeksgroep: Phycology & Nationale Plantentuin van België

Copromotor(en):

Leliaert Frederik

Begeleider(s):

Leliaert Frederik

opmerking

voorbehouden:

abstract Polyploids, organisms that underwent a whole genome duplication (WGD), possess one or more extra copy of their genome, which is free to evolve new functionality. Many WGDs are accordingly found in very successful eukaryotic lineages characterized by particular biological innovations and/or diversifications. However, the possession of two complete genomes is generally not well tolerated by cells leading to harmful effects on the overall fitness and fertility? of the organism. This results in a paradox between the observed immediate negative effects of WGD, and their attributed long-term positive effects. Previous work demonstrated that many plant polyploids became established during the last mass extinction event. Present-day polyploids are also more abundant in stressful environments such as the Arctic. We therefore hypothesize that stress can enhance polyploid establishment because their plastic phenotypes and genotypes can enable rapid adaptive changes that allow survival. To test this hypothesis, we propose an evolutionary experiment based on unicellular green algae (the model system Chlamydomonas), of which we make polyploid strains and subject them to a wide variety of stressors to quantify their survival. Second, we will perform competition assays to compare the fitness of polyploids with the non-polyploid ancestors. Practical work will involve: Setting up an evolutionary experiment; Asexually batch culturing of established diploid and haploid lines for over 300 generations in various environmental stress regimes (to allow the cells to evolve). Evaluation of the end populations for adaptation rate, fitness and therefore, evolutionary success of haploid and diploid lines. Determination of the occurrence of new diploid lines arising spontaneously under stress. Isolation of genomic DNA in every 50 generations for later sequencing and genotyping experiments (NGS-Illumina) which will allow us to investigate genome evolution following polyploidization, leading the success of a species.

onderzoeksgroep: Phycology & PSB-Bio-informatics group

Copromotor(en):

Van de Peer Yves

Begeleider(s):

Aydogdu Eylem

Bafort Quinten

opmerking

voorbehouden:

abstract Plant growth is the result of a balanced regulation between cell proliferation and expansion, and relies on nutrient availability and beneficial environmental conditions. The Target of Rapamycin (TOR) kinase has been identified as the central actor in directing growth in eukaryotes. Extensive studies in yeast show the involvement of TOR in several cellular and metabolic processes including cell cycle progression, cell division, lipid synthesis, protein synthesis, autophagy and ribosome biogenesis. In mammalian and yeast cells, the TOR kinase is incorporated in two functionally divergent complexes, called TORc1 and TORc2, whereas homology searches in the plant genome only found orthologues for TORc1 components. During the past few years progress has been made in the plant TOR research field combining specific TOR inhibitors, RNAi and transcriptomics which resulted in the confirmation of known substrates such as S6K1 and Tap46, and the functional involvement of TOR in growth stimulating processes. Therefore the TOR pathway seems largely conserved in plants. Nevertheless, many upstream regulators of TOR kinase activity are missing when compared to mammalian and yeast cells. This suggests that plants have evolved regulatory mechanisms adjusted to an autotrophic life and the presence of plant-specific hormones like auxin, cytokinin and abscisic acid which are known to be influenced by N and C nutrient levels. Recently, the Functional Interactomics group led by Prof. Geert De Jaeger succeeded in the isolation of TOR kinase protein complexes from *Arabidopsis thaliana* cell suspension using tandem affinity purifications (TAP), thereby confirming the existence of TORc1 in plants. Conserved TOR interactions were found as well, for instance the well-studied substrate S6K1 and several components of the SNF1-related protein kinase 1 (SnRK1) complex, which acts as an antagonist of the TOR kinase in low-energy conditions. Besides conserved interactions, we isolated the plant eIF2B complex for the first time and thus identified a plant-specific link between the TOR pathway and translation initiation. In parallel, our research group established a reliable TOR kinase activity assay based on the phosphorylation of S6K1 in *Arabidopsis* cell cultures. We obtained proof-of-concept of the S6K1 phosphorylation assay when implemented for a phosphoproteomics analysis on S6K1 expressing cells upon sucrose starvation and TOR inhibition, which resulted in the identification of known and novel candidate TOR substrates. Analogous, this master project aims to establish a regulatory link between nutrient sensing, translation initiation and concomitant growth based on nitrogen availability. First, the S6K1 phosphorylation assay will be optimized as a read-out for TOR kinase activity under low nitrogen conditions in *Arabidopsis* cell suspension. This will be followed by a phosphoproteomics analysis to identify potential substrates with an important function in nitrogen sensing. Candidate substrates have to be validated by additional kinase assays and through genetics using mutants based on T-DNA insertions, RNAi or CRISPR/Cas9. Finally, our findings will be translated into wheat, a crop of which the yield depends heavily on nitrogen fertilization. Eventually, our goal is to optimize protein translation in crops through manipulation of the TOR/SnRK1 cross-talk or via the promotion of protein translation under low nitrogen availability, reduce the need for excessive nitrogen fertilization on the field and hence decrease agricultural pressure on the environment.

onderzoeksgroep: Vakgroep Plantenbiotechnologie en Bio-informatica, groep Functional Interactomics

Copromotor(en):

Gadeyne Astrid

Begeleider(s):

Gadeyne Astrid

opmerking

voorbehouden: Ruben Lacombe

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 know how these factors trigger this specific type of divisions. In this Msc. project, we aim to understand how specific cell division orientations are controlled by identifying and characterizing the downstream signaling cascades that lead to periclinal cell divisions. By inducible activation of the two transcription factors, we will determine the genome wide transcriptional changes that occur during the switch to periclinal cell divisions. Genes that are significantly induced or repressed will be characterized into detail by studying gene expression and protein localization using confocal microscopy. Loss- and gain- of function phenotypes will be analyzed to understand the function of these genes. Finally, we will determine if these target genes have interaction partners using immuno-precipitation followed by tandem mass spectrometry (IP-MS/MS). The combination of genetic, molecular and biochemical experiments will provide a solid basis to understand how the orientation of cell divisions is controlled during early vascular development. References: De Rybel B, Adibi M et al., (2014) Science 345(6197): 1255215 De Rybel B, Möller B et al., (2013) Developmental Cell 24(4): 426-37 Smet W and De Rybel B., (2015) Current Opinion in Plant Biology (accepted) De Rybel B, Mähönen AP, Helariutta Y and Weijers D., (2015) Nature Reviews (accepted)

onderzoeksgroep: Moleculaire Genetica (WE09)

Begeleider(s):

Smet Wouter

opmerking Aim To identify and characterize new factors involved in controlling oriented cell divisions. Techniques - Cloning and other basic molecular biotechnological techniques - Confocal microscopy - DNA extraction and PCR based genotyping - RNA extraction and qRT-PCR - IP-MS/MS Category : III : no use of laboratory animals FOCUS : PLB

voorbehouden:

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 by activating the plant hormone cytokinin (CK). Although CK is well known for its role in controlling cell division, it is completely unclear how it is able to trigger this specific type of divisions. In this Msc. project, we aim to unravel what part of the CK signaling pathway controls periclinal cell divisions during early vascular development. In order to do so, we will first systematically study the expression patterns and protein localization of all CK response factors (ARR type transcription factors) and select those that overlap in the young vascular tissues. Next, loss-of-function mutations in the selected ARR genes will be combined in higher order mutants. Together with the creation of misexpression or overexpression lines of the candidate ARRs; these loss- and gain of function experiments will allow us to pinpoint the exact function of these genes during early vascular development. If possible, we will also determine if these ARRs function in protein complexes by using immuno-precipitation followed by tandem mass spectrometry (IP-MS/MS). The combination of these genetic, molecular and biochemical experiments will serve as a starting point to understand how CK can specifically control the orientation of cell divisions within the vascular tissues, which are crucial for normal development. References: De Rybel B, Adibi M et al., (2014) Science 345(6197): 1255-1261 De Rybel B, Möller B et al., (2013) Developmental Cell 24(4): 426-437 Smet W and De Rybel B., (2015) Current Opinion in Plant Biology (accepted) De Rybel B, Mähönen AP, Helariutta Y and Weijers D., (2015) Nature Reviews (accepted)

onderzoeksgroep: Moleculaire Genetica (WE09)

Begeleider(s):

Wybouw

Brecht

opmerking Aim To understand how cytokinin signaling is involved in controlling oriented cell divisions. Techniques - Cloning and other basic molecular biotechnological techniques - Confocal microscopy - DNA extraction and PCR based genotyping - RNA extraction and qRT-PCR - IP-MS/MS Category : III : no use of laboratory animals FOCUS : PLB

voorbehouden:

abstract There is a growing concern about the ability to produce enough nutritious food to feed the global human population by the end of this century ('9 billion people question', UN 2015). Nevertheless, hope goes to marine resources like aquaculture as a protein source for humans. A sustainable exploitation of these marine resources is needed and it should be taken into account that the overall functioning of marine ecosystems and the energy transfer efficiency from primary producers to top consumers is expected to be impacted by global change. Marine fish larvae have a nutritional requirement for live food with high concentrations of so-called essential fatty acids (EFAs), being fatty acids (FA) that they can't produce themselves and need to be obtained through their diet. Copepods (Crustacea), which constitute the principal food of many marine fish larvae, have high amounts of these EFAs, however, how they assimilate and modify these fatty acids remains unknown. In this light, the master thesis will focus on the biosynthesis and bioconversion of FA by copepods at the basis of marine food webs. This thesis will contribute to a PhD research with the following 2 objectives: (1) to determine the efficiency of transfer of FAs from primary producers (diatoms) to consumers (copepods) under different temperature, food and stress regimes and (2) to study the molecular pathways of FA biosynthesis and metabolism under these regimes. The practical work will range from fieldwork to short-term lab experiments with live copepods and their food sources, followed by FA analyses and RNA analyses. Depending on the interest of the student, the focus of this study can be directed to experimental work or molecular work. This master thesis will be conducted at the Marine Biology Research group (UGent).

onderzoeksgroep: Marine Biology

Begeleider(s):

Sannen

Laurien

opmerking

voorbehouden:

abstract Water level changes in Lake Tanganyika have led to episodes of population contractions during which geographic separation is enhanced, followed by population expansions during which secondary contact and hybridisation between previously separated populations can occur. These processes are thought to be a major driver of the immense diversity of cichlids. However, the genetic drivers of speciation remain poorly studied, and understanding the impact of geographic barriers to speciation requires the study of recently formed species with different degrees of geographic overlap. The genus *Ophthalmotilapia* comprises four closely related species which have comparable ecological preferences, but show different degrees of allopatric and sympatric populations in Lake Tanganyika. The aim of this thesis is to characterize the genetic diversity within each of the four species and investigate whether the genetic patterns can be linked with geography and historical water level fluctuations. To investigate the historical processes that have affected populations of the four species, we selected 411 specimens originating from within their complete distribution range in lake Tanganyika. Phylogeographic structure will be investigated by analyses of mitochondrial D-loop sequences. Moreover, recent advances in next generation sequencing techniques now allow to look at genetic differentiation at a genome wide level, thereby allowing to detect signals of gene flow between species (introgression). Using a genotype-by-sequencing approach will yield thousands of SNP's that are distributed throughout the genome. The genomic regions that are differentiated between the species will form a starting point to unravel the genetic basis of speciation.

onderzoeksgroep: KBIN, OD Taxonomy&Phylogeny,Vertebrates

Copromotor(en):

Verheyen Erik

Begeleider(s):

Derycke Sofie

opmerking

voorbehouden:

abstract Microorganisms in the digestive tract of animals can influence the health, physiology and behaviour of the host. Gut symbionts can supplement the host genome with functional genes that can extend the host niche (for example through the exploitation of nutrients that cannot be exploited by the host genome) and can provide opportunities to adapt to new environmental conditions. In turn, the host genome can alter the gut microbiome. Recent studies in a variety of animals, including cichlids, have shown species-specific gut microbiomes. This, together with the frequently observed high intraspecific variability in the gut microbiome, suggests that the host genome is an important factor affecting the gut microbiome composition. Yet, only few studies have investigated genome-microbiome interactions in non-model organisms. The genus *Ophthalmotilapia* is endemic to Lake Tanganyika and comprises four closely related species with comparable ecological preferences and very similar morphology. The four species are relatively young, and occasional gene flow between species occurs indicating that the speciation process has not yet reached the phase of reproductive isolation. Three of these species are available at RBINS for behavioural and reproductive experiments. So far, nothing is known on the differences in gut microbiome between these species. We have performed a controlled experiment in which three *Ophthalmotilapia* species have been reared together in the same tank for three months. In addition, the three species were also reared in separate tanks. Microbiome analysis of the gut will reveal whether bacterial composition is different between the three species and whether the presence of other species affects the microbial composition. If species-specific microbiomes exist, gene expression in the gut of the host can reveal which pathways are differentially activated in the hosts. To this end, gut tissue was also preserved in RNA later to allow gene expression analysis. This thesis provides experience in 16S amplicon-based NGS and RNAseq wet lab hands-on experience and requires interest in bioinformatics.

onderzoeksgroep: KBIN, OD Taxonomy&Phylogeny,Vertebrates

Copromotor(en):

Verheyen Erik

Begeleider(s):

Derycke Sofie

opmerking

voorbehouden:

Goetghebeur Paul

abstract While being amongst the most popular and common houseplants, the genus *Sansevieria* (Asparagaceae) is little studied from an evolutionary point of view. Recent research has confirmed its nested position in *Dracaena*. Furthermore, there are few morphological characters to clearly separate the ca. 60 species. This thesis aims to review the infrageneric classification of the genus and its nested position in *Dracaena* and to find morphological and anatomical characters to clearly identify and separate species. With leaf material from the extensive *Sansevieria* collection of the Ghent University Botanic Garden and sequences from previous studies, a phylogenetic hypothesis will be constructed. This hypothesis will be used to plot those morphological and anatomical characters to assess if they hold any evolutionary value.

onderzoeksgroep: Spermatophytes

Copromotor(en):

Leroux Olivier

Begeleider(s):

Bauters Kenneth

Veltjen Emily

opmerking

voorbehouden: Catharina van Kleinwee

1404

Analysis of maize and wheat roots in transparent pots as a proxy for overall root structure architecture.

abstract Recently, a new robotized plant phenotyping platform was installed at VIB to monitor shoot and root growth of young maize and wheat seedlings combined with automated irrigation to control soil water humidity levels. The plants are growing in transparent pots which are positioned in a closed frame to protect them from the light. During the treatment pots are taken out of the frame and a line scanner camera images the side of the pot while the pot makes a rotation of 360 degrees. This allows producing a picture that projects the roots touching the transparent pot into a 2D plane. From these images one can analyze the number and diameter of roots present at a specific depth. In this master thesis project, maize and wheat seedlings will be analyzed during development both under well-watered and mild drought stress conditions. Furthermore, soil types with different levels nutrients will be tested. The question however remains how the roots at the side of the pot represent the overall root structure architecture. To study this, the analysis from the images will be compared to the overall root structure using methodologies developed at ILVO Vlaanderen after the roots have been washed out from the soil.

onderzoeksgroep: VIB-UGent Plant Systems Biology Rhizosphere Group

Copromotor(en):

Lootens Peter

Begeleider(s):

Dhondt Stijn

opmerking**voorbehouden:****1405**

The use of plant growth promoting soil bacteria to alleviate salt stress in plants

abstract Plants are surrounded by countless species of microorganisms that can be either beneficial, neutral or harmful. The main site for the interaction between these microorganisms and land plants occurs on the roots, between the root cells, are in the soil, in close proximity to the roots. Beneficial rhizobacteria (plant growth promoting rhizobacteria (PGPR)) can contribute to plant health via promotion of plant growth, by ameliorating nutrient access or alleviating biotic and abiotic stresses. One of the major environmental factors limiting crop productivity in the world is soil salinity. It can affect almost all aspects of the plant development, from germination to reproductive development. Because soil desalination is very complex, the affected areas are usually abandoned. However, the use of PGPRs might bring a solution as a few of these have been shown to protect plants against salt stress. The aim of this project is to identify *Streptomyces* sp. strains that can promote growth in the plant model *Arabidopsis thaliana* and tomato plants under saline stress conditions and understand the molecular mechanisms that leads to the activation of salt resistance in plants. TechniquesThe screening of bacterial strains will be done by analysing the growth of plants in various plant bioassays. To visualize how the resistance pathways are activated by the PGPRs, we will use reverse genetics approaches with *Arabidopsis* and tomato mutants for already known salt resistance pathways in plants. Additionally qRT-PCR as well as marker gene analysis will be done in order to compare the expression profiles between control plants and plants inoculated with PGPR.

onderzoeksgroep: VIB-UGent Plant Systems Biology Rhizosphere Group

Begeleider(s):

Saito Suzane

opmerking**voorbehouden:**

1407 Influence of decaying coarse woody debris (CWD) on nutrient status of soil and regenerating trees in two unmanaged beech forests with contrasting nitrogen-deposition load.

abstract Forests in Flanders are subject to increased nitrogen deposition, that may lead to acidification and subsequent deterioration of the forest habitat. One of the mitigating measures that is being proposed in the framework of the Programmatic Approach Nitrogen (PAS) is the conservation of dead wood. This appears contradictory at first sight, as the nitrogen stored in the dead wood remains in the system, whereas it would be removed when harvested. However, it appears that the removal of biomass can cause a depletion of base cations (calcium, magnesium, potassium), that are essential to the forest ecosystem. Therefore, the reduced removal of biomass, that results into a higher amount of dead wood, could mitigate acidification caused by nitrogen deposition. We want to test this hypothesis in two unmanaged forest reserves with a contrasting level of nitrogen deposition. The nutrient concentration in the decaying dead wood is determined and the effect of nutrient release by decomposition, on the forest soil and the nutrient status of regenerating beech trees is studied. For this purpose, 15 large decaying beech trees are selected in the strict forest reserves of Wijnendalebos en Zoniënwood (totaling 30 trees), both unmanaged for more than 30 years. Wood samples of each decaying log are collected for analysis. The forest soil is sampled at fixed locations, on linear transects perpendicular to the decaying trunks. Leaves of beech saplings at contrasting positions to the decaying logs are analysed as well, to determine the nutrient status of the juvenile trees. These results can clarify up to which distance soil conditions are affected by decomposing CWD and if the nutrient status of regenerating trees is influenced as well.

onderzoeksgroep: Terrestrial Ecology & INBO Geraardsbergen

Copromotor(en):

De Keersmaecker Luc

Begeleider(s):

nog te bepalen

opmerking Support : sampling set-up and chemical analysis of the samples is done at INBO; logistics and support for field sampling also by INBO

voorbehouden:

1273 The role of BIG BROTHER and its targets in controlling leaf growth.

abstract Leaves are the solar panels of plants, providing the essential energy to successfully complete their lifecycle. These organs emerge from the shoot apical meristem and initially grow through cell proliferation, followed by cell expansion. The duration of the cell division period therefore largely determines final leaf size. The E3-ligase BIG BROTHER (BB) has been identified as a central regulator of leaf growth, restricting the period of cell proliferation (Disch et al., 2006) in concert with DA1 (Li et al., 2008). Mutants of both genes produce much larger leaf organs that contain more cells, whereas overexpression reduces plant growth and even leads to dwarfism and growth arrest. The molecular mechanisms underlying this growth-regulation are now starting to emerge. Recently, it was found that overexpression of DA1 rescues the dwarfed 35S::BB phenotype, most likely by degrading the BB protein. In addition, DA1 and several DA-related genes are highly upregulated upon induction of BB, indicating an additional layer of transcriptional control in this growth-regulatory network. Through various proteomic, transcriptional and phenotypical approaches we will identify potential targets of BB and characterize their role in cell division, hereby further elucidating the complex genetic network that regulates leaf growth.

onderzoeksgroep: Plant Systems Biology, Vlaams Instituut voor Biotechnologie

Copromotor(en):

Vanhaeren Hannes

Begeleider(s):

Vanhaeren Hannes

opmerking

voorbehouden:

1408 Enhancing yield in maize

abstract Global warming and population growth severely impact agricultural production and agricultural adaptation should occur sustainably without affecting ecosystems. One way to address this is by understanding processes that determine plant productivity. In our research team we study how leaves grow and how we can expand the area with which they harness solar energy and convert CO₂ to chemical energy that can be used by the plant to grow. Maize is one of the most economically important crops that can be grown in distinct geographical regions around the world. In addition, maize has both cereal and fodder value, making it an extremely versatile crop. Over the past years, we gained information on the molecular and cellular mechanisms of how the maize leaf grows in the length direction. However, we noticed that an increased growth in the length direction is not linearly correlated to an increase in lamina width and area. In this project, the student will study the relationship between proximo-distal and mediolateral regulation of maize leaf growth, starting from leaf size mutants. Aim: The student will be actively involved in investigating the mechanisms underlying the correlation between proximo-distal and mediolateral leaf growth in maize. Techniques and methods: microscopy, maize genetics, DNA- and RNA-based technologies, growth analyses

onderzoeksgroep: Vakgroep Plantenbiotechnologie en Bio-informatica - onderzoeksgroep Systems Bioloav of Yield

Copromotor(en):

Nelissen Hilde

Begeleider(s):

nog te bepalen

opmerking

voorbehouden:

1409 Plants are thirsty too: water use behaviour in maize

abstract Water is unmistakably a critical component of any form of life on earth. Plants are major consumers of water for growth and development, either directly in the maintenance of cell turgor for growth, or indirectly by a flow of mineral nutrients from the soil to developing and functional organs through transpiration. Both developing and mature organs respond to water deficits caused by low soil humidity and/or atmospheric conditions that increase transpiration rates above crucial thresholds. In first instance, growth is slowed down, but this can be followed by permanent wilting and organ loss. Both processes have potentially large consequences for biomass production and yield. Plants have developed various mechanisms to remain in a 'water-deficit-tolerant' state which may allow them to recover growth and development quickly upon rehydration. In this Master thesis, you will develop methods to determine the water use behaviour of maize plants during leaf growth and in response to water deficit and rehydration. You will apply these methods on maize genotypes that show differences in both leaf growth and the usage of the available water during growth. Your findings will contribute to the understanding, on a mechanistic level, of the mode-of-action of growth regulatory network components, and provide methods to screen existing and future genotypes for drought tolerance traits. The latter is of great importance with regard to climate change and its consequences for agricultural production.

onderzoeksgroep: Plant Systems Biology, Vlaams Instituut voor Biotechnologie

Copromotor(en):

Wuyts Nathalie

Begeleider(s):

nog te bepalen

opmerking

voorbehouden:

abstract Because of climate change, population pressure and political and public awareness about sustainability, agriculture faces major challenges: increasing productivity in a sustainable manner, while adapting production systems to overcome fluctuating weather conditions, optimally managing nutrient and water resources, maintaining biodiversity, and fulfilling the increasing demands from food chains and consumer. Precision agriculture is based on the 'speaking plant' concept in which the supply of resources is controlled by the plant's actual requirements. To determine these requirements, methods for the nondestructive monitoring of plant physiology need to be developed. One of the most promising tools for physiology monitoring, is image-based sensing of plants. Hyperspectral imaging systems divide the light spectrum in many small wavelength bands and collect an image for each band. This allows the detection of plant stress before it is even visible to the naked eye. New indices for maize, that can detect changes in photosynthetic light use efficiency and leaf water potential, have been developed in our lab. But currently it is still unknown how well these indices perform for different maize genotypes that differ in their physiological responses to stress. During this master thesis you will investigate the effect of drought on the physiology and light reflectance of different maize genotypes. You will perform a drought experiment on the PHENOVISION platform (www.psb.ugent.be/phenotyping/phenovision), which allows the automatization of the drought treatments and the hyperspectral image collection. During the experiment, different maize genotypes will be grown from seedling until reproductive stage and traditional physiological measurements (portable photosynthesis system, pressure chamber) will be collected on a regular basis. You will use the images and measurements of the drought experiment to understand how drought influences the different maize genotypes and to validate the new indices. You will also have the opportunity to create new imaging proxies for nutrient deficiency by using your gathered data and data of former experiments. The image analysis will be performed using R software by means of scripts developed in our lab. During this thesis, you will thus get the unique opportunity to work with state-of-the-art equipment, to develop your skills in both the traditional and novel methods for plant physiology measurements, and to work with both plants and pc.

onderzoeksgroep: Plant Systems Biology, Vlaams Instituut voor Biotechnologie

Copromotor(en):

Wuyts Nathalie

Begeleider(s):

Mertens Stien

opmerking

voorbehouden:

Lens

Luc

1411 Conservation genetics of the critically-endangered Taita thrush (*Turdus helleri*) in SE Kenya

abstract The critically-endangered Taita thrush is an endemic species to the Taita Hills biodiversity hotspot of south-east Kenya. The species currently only survives in three indigenous forest fragments that vary in size and quality. During 2008, 9 individuals were translocated from the largest and most pristine forest fragment to the smallest, most disturbed one (where the species then was close to extinction). A first objective of this thesis is to assess current genetic effects of this past translocation. A second objective is to compare census (N_c) and effective (N_e) population sizes between the Taita thrush and an ecologically-related, sympatric (but more common) species that underwent a different population history. N_c and N_e are two crucial parameters that influence population viability and of which the N_e/N_c ratio may indicate effects of genetic compensation. Together, these two objectives will help to provide more effective conservation guidelines for the endangered Taita thrush. Practical work will include DNA purification, genotyping and population genetic analyses.

onderzoeksgroep: Terrestrial Ecology

Begeleider(s):

Cousseau Laurence

opmerking

voorbehouden: Pieter Sanczuk

abstract In 2001, the Research Institute for Nature and Forest initiated a monitoring and research programme on the breeding and feeding ecology of Sandwich Terns in Belgium. From 2009, a similar study was started in the Dutch Delta-area. In 2016, a pilot study on the adult diet of Sandwich Terns on a European scale was initiated which will be extended in 2017. For this study, diet samples were collected in various European countries, ranging from France to Poland. This master thesis consists of two parts. The student is responsible for the identification of the diet of adult Sandwich Terns in Europe which is new research and has never been conducted before. The second part is to look into the relationships between the diet composition of both adult and juvenile Sandwich Terns, the body-condition of the chicks and the breeding success. We are also interested in the influence of abiotic conditions (wind speed, tidal cycles, seawater temperatures) on variation of the diet of adults and chicks during the breeding season. In order to identify the diet of adult terns, faecal samples that will be collected in 2017 have to be processed. This is lab-work consisting of selecting, photographing, identifying and measuring fish remains (mainly otoliths). The cleaning of the samples has been done already. For the second part, the student will have access to all data collected by the INBO between 2001 and 2016. There is also the possibility of assisting with the fieldwork (collecting samples, making observations from a hide, measuring chick condition during the breeding season etc). This is not mandatory because the fieldwork starts at the beginning of May and goes on till mid-July, but very interesting nevertheless. Arrangements can be made with the student applying for this master thesis. Both during fieldwork and analysis of the data you'll be assisted by INBO-coworkers.

onderzoeksgroep: Terrestrial Ecology & INBO Brussel

Copromotor(en):

Stienen Eric

Begeleider(s):

Courtens Wouter

opmerking

voorbehouden:

abstract Anthropogenic habitat fragmentation is increasingly recognized as one of the major drivers of biodiversity loss. However, habitat fragmentation can also have more subtle effects on species, such as changes in their mobility and habitat use. As such behavioural changes can ultimately alter fitness, a better understanding of the underlying mechanisms is important to plan adequate conservation measures. In this thesis, you will assess effects of foraging outside forests during winter on nutritional stress and breeding performance of a common forest bird (great tit, *Parus major*). Individuals that leave the forest to visit winter feeders near houses can be expected to be subject to a higher (perceived) predation risk (eg. from house cats, sparrowhawks), which could lead to chronic stress. Through carry-over effects, this may reduce their breeding performance during the consecutive spring. To test these predictions, great tits residing in the Aelmoezenijde forest (Melle) will be fitted with PIT (Passive integrated Transmitter) tags to automatically register their feeder visits, and two (homologous) tail feathers of each tagged individual will be sampled before and after winter. Measurements of the growth bars on these feathers (so-called ptilochronology) can be used as a proxy for the nutritional condition of each individual. The student will assist in mist-net captures of birds and will measure and analyse growth bars on sampled tail feathers in relation to winter mobility. Furthermore, she/he will also analyse available data collected during the previous year.

onderzoeksgroep: Terrestrial Ecology

Copromotor(en):

De Neve Liesbeth

Begeleider(s):

De Keukeleire Daan

opmerking

voorbehouden:

Mees

Jan

1418

Seasonal presence and distribution of harbour porpoises in the Belgian part of the North Sea

abstract Harbour porpoises (*Phocoena phocoena*) are the most common cetacean in the North Sea and use echolocation to extract information from their surroundings. Porpoises are producing clicks which are recorded by passive acoustic C-pods. Eight c-pods are installed in the Belgian part of the North Sea along an east-west gradient covering coastal, midshore and offshore zones and recordings are made from 2015 onwards. The echolocation clicks of porpoises are an expression of their behaviour, such as foraging and swimming and can be studied in detail using the cpod.exe software. This master thesis will determine the seasonal distribution of harbour porpoises in the Belgian part of the North Sea. Secondly, the foraging behaviour of harbour porpoise will be investigated and linked to (a)biotic factors (time before sunrise, after sunset, presence of artificial structures,...). More information can be found at <http://lifewatch.be/en/cetacean-passive-acoustic-network>.

onderzoeksgroep: Marine Biology

Copromotor(en):

Deneudt Klaas

Begeleider(s):

Debusschere Elisabeth

opmerking

voorbehouden:

Moens

Tom

1419

Impact of offshore wind farms on the soft-sediment macrobenthos

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. A monitoring programme was set up to determine the ecological effects of this anthropogenic disruption on the soft-sediment macrobenthos (organisms living in the sediment and larger than 1mm) applying a BACI (Before After Control Impact) strategy. In October 2017, a monitoring campaign will be organised to sample the soft-sediment macrobenthos around the offshore wind farms and selected reference stations. The student involved has the opportunity to join the sampling campaign (one week) and will analyse the samples during the end of 2017 and beginning of 2018. All species will be identified until species level and possible changes in the environment will be evaluated using biotic (biomass, abundance, diversity) and abiotic variables (sediment grain size, organic material).

onderzoeksgroep: Marine Biology

Begeleider(s):

Colson Liesbet

opmerking

voorbehouden:

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

onderzoeksgroep: Marine Biology

Copromotor(en):

De Meester Nele

Derycke Sofie

Begeleider(s):

De Meester Nele

opmerking

voorbehouden:

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

onderzoeksgroep: Marine Biology

Copromotor(en):

De Meester Nele

Begeleider(s):

De Meester Nele

opmerking

voorbehouden:

1424 Bone histological diversity in the evolutionary context of dinosaurian-avian flight

abstract The evolutionary transition of theropod dinosaurs into birds is not a myth anymore but a scientifically established fact. However, a lot of aspects of this transition are still debated or unknown. The increasing number of discoveries of dinosaur-bird transitional forms ("dinobirds") allows us to address issues such as how many times powered flight has evolved or got secondarily lost in different lineages and what exactly defines a theropod dinosaur as a bird. So far, these questions have largely been investigated by comparative skeletal morphology of birds and "dinobirds", whereas bone histological studies, even though widely used to answer other paleobiological questions, are underrepresented in this area of research. In this project we aim to use comparative bone histology of birds related to flight capabilities by quantifying intraspecific and interspecific osteohistovariability in the context of different flight styles. For this, limb bones of species of similar body mass and life style but differing flight modes and phylogenetic interrelationships will be sampled and histological sections prepared. Bone histological characters will be investigated under polarized light microscope, quantified by histomorphometric measurements (ImageJ) and intra- and interspecific histovariability of homologous elements analyzed in R with diverse univariate & multivariate methods (PCA, PCoA, variation partitioning, PCM regressions, etc.). The outcome of this study will represent an important input in an ongoing research in which these findings in birds will be used as one of the baseline data to infer similar features in dinobirds to gain more insight in the evolution of avian flight.

onderzoeksgroep: Evolutionary Morphology of Vertebrates

Begeleider(s):

Prondvai

Edina

opmerking**voorbehouden:****1425** Climbing about, flying around: effects of precocial forelimb usage on the bone histology of hoatzin

abstract Hoatzin (*Opisthocomus hoazin*) is an enigmatic bird living in the tropical forests of South America and having still debated phylogenetic interrelationships. The unsettled phylogeny largely originates from hoatzin hatchlings showing an apparently ancestral feature throughout their juvenile ontogeny: they bear two pairs of claws on their wings which enables them to climb about in trees and flee from the nest in case of a predatory attack. These claws are present already in embryos and disappear by adulthood, i.e. by the time the animal starts flying. Climbing trees requires strong, functionally developed forelimbs already in early ontogeny, and is expected to have a profound influence on, among others, the bone histological features of the wings. This project aims to trace back the bone histological characters that may reflect this unusual precocial climbing behavior of the hoatzin chicks by sampling forelimbs of hoatzin specimens representing different ontogenetic stages from hatchlings to adults. Here, the major question is whether there is any osteohistological correlate of the onset of climbing and thereafter the onset of flight. For this, histological sections of the forelimb will be prepared and bone histological characters will be investigated under polarized light microscope, quantified by histomorphometric measurements (ImageJ) and analyzed in R with diverse univariate & multivariate methods (PCA, PCoA, variation partitioning, PCM regressions, etc.). If applicable, CT scanning data may also be included in the overall analysis to get insight into the 3D vascular architecture and its potential changes related to the developing locomotor abilities during posthatching ontogeny. This will increase our understanding of the extent to which such functional factors shape the bone histological characteristics of hoatzin and will provide a starting point for inferences on the evolution of grasping and/or flight-related forelimb functions in the dinosaur-bird transition; the focus of an ongoing project on the evolution of avian flight.

onderzoeksgroep: Evolutionary Morphology of Vertebrates

Begeleider(s):

Prondvai

Edina

opmerking**voorbehouden:**

1426 Algal bloom diversity and dynamics in the Belgian coastal zone

abstract Planktonic microalgae play a crucial role in the cycling of nutrients and energy in marine ecosystems: their photosynthesis drives fluxes of C, N, P and other nutrients and fuels marine food webs. The dynamics of the phytoplankton is in itself affected by numerous environmental factors, ranging from nutrient concentrations, light and temperature to grazing by zooplankton. In collaboration with the Flanders Marine Institute (VLIZ), the Protistology & Aquatic Ecology (PAE) lab is involved in the seasonal monitoring of phytoplankton diversity and biomass in the Belgian coastal zone. Such multi-annual monitoring campaigns are crucial to obtain a deeper understanding of the factors driving the spatial and temporal dynamics of phytoplankton in this dynamic area. During biweekly-monthly monitoring cruises with the VLIZ research vessel 'Simon Stevin', 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 analysed using appropriate multivariate and statistical tools. The results of these analyses will be compared with DNA sequencing-based and flow-cytometric diversity inventories and long-term data sets available for the Belgian coastal zone.

onderzoeksgroep: Protistology & Aquatic Ecology

Copromotor(en):

Vyverman Wim

Begeleider(s):

De Blok Reinhoud

opmerking**voorbehouden:****1427** Do diatoms display Gondwanan distributions? A taxonomic and 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 unspoilt, 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. Diatom identification will be done using state-of-the-art microscopic techniques (light and scanning electron microscopy) at UGent and the Botanic Garden in Meise.

onderzoeksgroep: Protistology & Aquatic Ecology & Nationale Plantentuin Meise

Copromotor(en):

Van De Vijver Bart

Verleyen Elie

Vyverman Wim

Begeleider(s):

Pinseel Eveline

opmerking**voorbehouden:**

1428 Does taxonomic and functional biodiversity affect carbon flows in intertidal sediment biofilms?

abstract In shallow coastal and estuarine waters, food webs are not only fueled by phytoplankton, but also rely on the primary production of microalgal biofilms which inhabit sub- and intertidal sand- and mudflats. These biofilms are complex and highly diverse, both from a taxonomic and functional point of view (e.g. with respect to growth form, photophysiology and mixotrophic capacity). How this diversity relates to the functioning of these microbial biofilms however is as yet unclear. Primary production by diatoms, the dominant microalgae in such biofilms, not only builds biofilm biomass, but also releases large amounts of carbohydrate-rich extracellular polymers (EPS) which are an ideal substrate for bacterial growth and can also be used by the microalgae themselves (mixotrophy). Both bacteria and microalgae are grazed upon by protozoa and zoobenthos. In this thesis we will investigate how diatom diversity affects carbon flows in these sediments. Experiments will be set up in which diatom taxonomic and functional diversity will be manipulated. Stable isotope probing (SIP) of organic compounds and biomarkers (including fatty and nucleic acids) will be used to trace the flow of carbon between these diatom assemblages and EPS, bacteria, protozoa and meiofauna. These experiments will allow evaluating to what extent diatom diversity determines EPS composition and complexity, and whether this will affect the carbon flow to higher trophic levels. If more than one student would select this topic, additional experiments will focus on the impact of light stress, nutrient limitation or top-down effects of nematodes on these carbon flows.

onderzoeksgroep: Protistology & Aquatic Ecology, Marine Biology

Copromotor(en):

Moens Tom

Begeleider(s):

D'Hondt An-Sofie

opmerking**voorbehouden:****1429** Remote sensing of coastal algal blooms using hyperspectral imaging

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 dominant. Algal blooms are very important as they form the basis of marine food webs. However, they can also be a nuisance through undesirable accumulation of foams (Phaeocystis) or green tides (Ulva), or even harmful through the production of toxins (dinoflagellates and diatoms). Monitoring such blooms is crucial for understanding and predicting their occurrence. Because the blooms are spatially complex and highly dynamic, optical remote sensing, with its high spatial and temporal resolution, is ideally suited for monitoring purposes. While current satellites carry sensors with low spectral resolution (allowing only a very general description of algal biomass), future sensors will be hyperspectral. Detailed spectral information will open up new perspectives for discriminating algal taxonomic and functional groups on the basis of differences in light absorption (~pigment composition), fluorescence, but also size and shape. In the thesis, which forms part of the Belgian project HYPERMAQ, we will analyze absorption and reflectance spectra of micro- and macroalgae from both cultures and field samples, in order to explore the development of new algorithms for discriminating algal groups in turbid coastal waters using hyperspectral remote sensing. The thesis will involve bio-optical analysis (spectrophotometry, spectrofluorometry), pigment analysis and hyperspectral imaging of both algal cultures and field samples obtained during field work in the Spuikom and the North Sea.

onderzoeksgroep: Protistology & Aquatic Ecology

Copromotor(en):

De Clerck Olivier

Ruddick Kevin

Begeleider(s):

nog te bepalen

opmerking**voorbehouden:**

Below-ground changes under carbon farming: using nematodes to understand biological shifts.

abstract Improving the biological health of our agricultural soils is now seen as one of the best hopes towards achieving sustainable agricultural production, and there is a greater cognizance of the role soil biological diversity plays in soil health. Application of compost is a common method to increase the organic matter in soil, provide fertility, and possibly to introduce micro-organisms. Nematodes are present in large numbers in both soils and composts, and indices have been developed to use nematode feeding types to give a measure of the complexity and stability of the soil food web, as well as the maturity of composts. Compost additions to managed rangelands (where livestock are intensively managed in rotational grazing) have been shown to stimulate the production of forage and lead to improvements in soil quality. In both short (0-5 yrs) and longer term (5-14 yrs) studies, compost application on temperate grasslands as a management strategy has been shown to enhance carbon storage in the soil. In some of these studies, changes in microbial communities have been investigated, and show shifts towards greater fungal biomass under compost amendment and managed grazing. The ability of soils to successfully build carbon stocks and increase biological functions is likely to be at least partially the result of particular biological processes being altered. However little information on the changes that occur in the soil biota from the combination of compost amendment and grazing management strategies is known or available. We are currently collaborating with researchers at UC Berkeley in California to measure the carbon sequestration potential of applying compost to rangelands in a new experiment started in October 2016 - to test compost application effects across a wider range of soil and climate zones of California. For this project the student will use baseline soil samples collected in 2016 before the addition of compost, samples taken 6 months after compost addition, and samples taken one year after compost addition (ideally the samples at the one year point should be collected together with the Masters student in California) at several sites to evaluate how the nematode community changes with the addition of compost over time, compared to the control plots, using both light microscopy and next generation sequencing techniques. Through our collaborations we will also have data on the soil carbon increase and microbial community changes over that time.

onderzoeksgroep: Nematology

Copromotor(en):

Bert Wim

Begeleider(s):

Herren Gisele

opmerking Sampling trip in California in September/October for 3 weeks approximately (date not confirmed yet).

voorbehouden:

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):

Ee Zin Ong

opmerking**voorbehouden:****1432** Microplastic Transfer in Marine Food Webs

abstract Plastic debris, a large component of marine litter, is ubiquitous in the marine environment and internationally recognized as a matter of increasing concern. There is potential for microplastic and its associated contaminants to enter marine food webs via a variety of pathways. Both planktonic and benthic marine invertebrates with a range of feeding methods have been shown to be able to ingest microplastics including: filter feeders (copepods, mussels and barnacles), deposit feeders (lugworms) and detritivores (amphipods, sea cucumbers). In situ work has also discovered microplastic ingestion in several vertebrate species. More and more species are now known to be affected, including some considered threatened. Further, MPs have demonstrated a capacity to adsorb to organisms such as marine algal cells. However, at present we know little about what affects the uptake of microplastics by marine organisms, and there are uncertainties about whether the plastics ingested at one trophic level can be transferred to higher trophic levels. Most knowledge is based on laboratory work, and field empirical data on the distribution and accumulation of microplastics in the food webs are limited. In this thesis, you will execute experiments that quantify accumulation of microplastics in food webs and determine the factors affecting the ingestion of microplastics in marine organisms, e.g. size, shape, colour and colonization of microbial communities.

onderzoeksgroep: Marine Biology

Copromotor(en):

Moens Tom

Begeleider(s):

Van Colen Carl

opmerking**voorbehouden:**

abstract The enhanced emission of greenhouse gasses (e.g. CO₂) have raised global sea surface temperatures (SST) at approximately 0.13 °C per decade since the current period of climate warming started in the mid 1980s. Climate models suggest that patterns of mean and extreme SST will alter across the globe. In addition, ocean CO₂ absorption alters sea water carbonate chemistry and pH, with temperate shallow marine ecosystems currently experiencing a one order of magnitude faster decrease in pH (i.e. ocean acidification) as compared to global estimates. This unprecedented fast rate of acidification likely has consequences for marine biodiversity as resident species of different taxonomic and functional groups have already been shown vulnerable to scenarios of ocean acidification as projected by climate change models to occur in the next century. Consequently, the investigation of the combined effects of concurrent ocean warming and acidification on the physiology, condition and survival of marine benthos has been put forth to improve our understanding of the mechanisms that underpin resilience of coastal soft-sediment ecosystems to climate change. In addition to the examination of such stressor effects on the performance of organisms, the likelihood to adapt to these stressors should be assessed. For example, phenotypic plasticity may facilitate the persistence of populations at the short term, i.e. the rate at which environmental changes currently take place, while evolutionary genetic adaptation will likely be required to persist at the long-term. During this thesis you will experimentally investigate the response and potential for evolutionary adaptation of different species of benthic invertebrates (clams and polychaetes) by quantifying phenotypic variability and response to combined effects of ocean acidification and warming (i.e. high pCO₂ conditions). Therefore adults will be incubated under high and ambient pCO₂ conditions and genetic variation in tolerance of their offspring will be quantified in a full-factorial breeding design including multiple seawater temperature and pH levels.

onderzoeksgroep: Marine Biology

Copromotor(en):

Moens Tom

Begeleider(s):

Van Colen Carl

opmerking

voorbehouden:

abstract Seeds often germinate below ground, either in nature or in the field. In nature, successful germination and seedling growth is essential to sustain or establish species within plant communities. Moreover, a main agricultural goal is to obtain rapid and uniform germination and seedling emergence after sowing. Because the topsoil is a stressful environment for developing seedlings losses are often substantial at this early stage and are generally not recovered. Hence, there is a great impact on crop yield, as there is on survival of seedlings buried under ground in nature. Rapid elongation of the seedling stem provides a means for the seedlings to advance the emergence from the soil and exposure to light. However, the overlying soil hinders growth with possible mechanical wounding as a result. In glaring contrast with dark-induced hypocotyl elongation, mechanical stress inhibits elongation and induces radial expansion. Hence, development must be tuned to both stress responses. However, factors regulating below-ground development of seedlings subjected to mechanical stress remain obscure. A regulatory role for jasmonates is suggested by several findings. Ethylene has been shown to be involved in the regulation of the response of etiolated seedlings to soil cover. The role of jasmonates in seedling development upon underground germination remains obscure. To protect the seedling cotyledons and the apical meristem from damage, dicotyledonous seedlings develop a hook-like structure shortly after germination. The apical hook is maintained until seedling exposure to light upon emergence from the soil. The indispensability of hook development for seedling survival demonstrates the impact of mechanical stress associated with development upon underground germination and suggests hook opening will not proceed under mechanical impedance. The hormonal regulation of apical hook development under mechanical stress remains enigmatic. When seedlings emerge from the soil, and become exposed to sunlight, the mechanical impedance of the covering soil on the apical part of the hypocotyl disappears. The apical hook opens, but hypocotyl elongation is, as under mechanical stress, inhibited by light. With this master thesis we aim to further unravel the role of jasmonates in the development of etiolated Arabidopsis seedlings and the effect of mechanical stress and light thereupon, focusing on hypocotyl elongation and expansion, and the development of the apical hook. In addition, the interaction with ethylene and other plant hormones will be investigated. Therefore, different mutants, transgenic lines as well as agonist and antagonist treatments will be employed. Both hypocotyl elongation and apical hook development are utmost dynamic processes, regulated in response to the prevailing environmental conditions. Therefore, to kinetically study Arabidopsis' skotomorphogenesis an automatic, computer-controlled infrared imaging system was developed in the laboratory of Functional Plant Biology (Smet et al. 2014). The system allows dynamic, high-throughput imaging of etiolated seedlings. Using these methods, we will acquire insights in the dynamics and regulation of underground development and the subsequent photomorphogenesis after emergence, allowing us to build a model on hormone interactions therein.

onderzoeksgroep: Functional Plant Biology (FPB)

Begeleider(s):

Smet Dajo

opmerking

voorbehouden:

abstract Ethylene is a small volatile phytohormone regulating a myriad of plant developmental processes, such as vegetative growth, fruit ripening, abscission and senescence. Furthermore, ethylene is part of an intricate network that drives abiotic stress and pathogen responses. A thorough fundamental knowledge on the metabolism of ethylene therefore does not only enhance our understanding of plant development in general, but is also valuable for the agri- and horticultural industry where control of endogenous ethylene levels is highly valuable. Classical mutant analysis complemented with molecular cloning of the corresponding genes has led to a comprehensive understanding of the molecular components of the ethylene signaling network. However, this approach is subjected to several drawbacks such as gene lethality and functional redundancy. Furthermore, the majority of these ethylene effects are the result of crosstalk with internal (eg. hormones) and external signals (eg. abiotic). Chemical genetics approaches have provided new tools in plant hormone biology that overcome these drawbacks. It involves the use of small bioactive chemicals to perturb biological processes and screen for desired phenotypes. The discovery of new ethylene agonists or antagonists will not only complement conventional genetics strategies to study ethylene biology, but their potential use in pre- and postharvest practices and crop management is of great value to the agri- and horticultural field. Previously, a chemical genetics screen was conducted based on a library that contains 12,000 small molecule compounds, while maintaining maximum structural and chemical diversity. This screen was specifically aiming at the identification of compounds that alter the triple response in dark-grown wild-type (WT) Arabidopsis seedlings grown in the presence of the ethylene precursor 1-aminocyclopropane-1-carboxylic acid (ACC) (Hu et al., 2014). Two compounds were retained based on their ethylene-enhancing effects. This thesis will focus on the elucidation of the mode of action of ethylene-enhancer compound C1. Previous work has linked C1 to both ethylene/auxin crosstalk and the generation of reactive oxygen species. Mutant analysis, pharmacological treatments, analysis of transgenic reporter lines and transcriptomic analysis will be employed to shed light on the mode of action of C1. Furthermore, a forwards genetics screen was initiated to search for putative C1-resistant mutants. Follow-up work with selected resistant candidates and subsequent next-generation sequencing will identify C1 molecular target(s). In parallel, biochemical approaches (e.g. affinity purification) will be exploited to corroborate the genetic screen.

onderzoeksgroep: Functional Plant Biology (FPB)

Begeleider(s):

Depaepe

Thomas

opmerking

voorbehouden:

abstract Rice is a massively consumed staple crop, serving as the main food source for about half of the human population. Unfortunately, the aleurone layer, containing many micronutrients, is often removed, leaving the polished starchy white rice. When consumed as main food source this polished rice, though being a good source of calories, can provoke insufficient intake of micronutrients, causing micronutrient malnutrition known as the 'hidden hunger'. Micronutrient malnutrition is estimated to affect 2 to 3 billion people on a global scale. Biofortification of staple crops is advocated as a cost-effective method to alleviate this global burden, complementary to other strategies, such as dietary diversification, supplementation and fortification. Polished rice, which is the main food source of the rural population in Asia, contains very low amounts of thiamin (vitamin B1). Implications of thiamin deficiency, such as cardiac failure, sudden infant death syndrome, encephalopathy and peripheral neuropathy are responsible for a considerable mortality in Asian countries, affecting mostly children. Biofortification of staple crops such as rice holds great promises to eradicate vitamin deficiencies. Via metabolic engineering, folate levels were augmented 150-fold in rice endosperm, with 100g of cooked grains containing enough folate to fulfill the adult daily requirement of 400 µg [Blancquaert et al., 2015]. Similar metabolic engineering strategies in rice have led to the successful enhancement of beta-carotene A and iron. The strong regulation of thiamin synthesis advocates a potential important role in plant metabolism. Indeed, its pyrophosphorylated form thiamin pyrophosphate (TPP) seems to be a major regulator of central carbon catabolism. TPP is the active vitamers, as it serves as a cofactor for different crucial reactions in sugar catabolism. Furthermore, the thiamin biosynthesis gene *THI1* might play a dual role, knowing it is upregulated upon abiotic stresses and able to improve drought resistance. Thus, influences of enhanced thiamin levels on plant physiology need to be evaluated and their implications on biofortification strategies should be considered. The goal of this research is to create a better understanding of thiamin metabolism in plants, while assessing different metabolic engineering approaches in *Arabidopsis* as well as rice. These engineering strategies will be examined for their ability to augment levels of thiamin along with unraveling the complex and tight regulation of thiamin metabolism. By constitutive overexpression of different combinations of three thiamin biosynthesis genes (*THIC*, *THI1*, *TH1*) in *Arabidopsis*, their ability to affect thiamin metabolism will be examined, allowing to pinpoint the different bottlenecks in the flux through thiamin biosynthesis. Homozygous lines will analyzed for their transgene expression as well as vitamin content. In order to obtain a better understanding of thiamin regulation of the central metabolism the lines will also be analyzed phenotypically, as well as at the level of the transcriptome and metabolite content, in varying stress conditions. Successful engineering strategies tested in *Arabidopsis* will be implemented in rice endosperm, serving as a 'proof of concept' towards creation of vitamin B1 rich rice variants. Homozygous elite events, harboring high transgene expression as well as vitamin levels, will be selected. Blancquaert D, Van Daele J, Strobbe S, Kiekens F, Storozhenko S, De Steur H, Gellynck X, Lambert W, Stove C, Van Der Straeten D (2015). Improving folate (vitamin B9) stability in biofortified rice through metabolic engineering. *Nature Biotechnology*, 33: 1076–1078.

onderzoeksgroep: Functional Plant Biology (FPB)

Begeleider(s):

Strobbe Simon

opmerking

voorbehouden:

1437

A quantification of the effect of fouling fauna in windmill farms on the coastal nitrogen cycling in current and future settings

abstract In order to increase the share of renewable energy, many European countries installed offshore wind farms in their coastal areas. At the moment, about 3200 turbines are in place, at 84 offshore wind farms in 11 European countries. These windmills act as artificial hard substrates in environments that were formerly sandy environments. These artificial hard substrates are colonized by huge amounts of fouling organisms, mainly blue mussels (*Mytilus edulis*) and the colony-forming amphipod *Jassa* sp. Recent evidence suggests that the presence of the blue mussel can have important effects on the local nitrogen cycle, resulting in the production of the important greenhouse gas N₂O. In Belgium, there are plans to combine offshore wind farms with aquaculture activities where the blue mussel is one of the target species. As such, it is of high importance to assess the effect of these abundant fouling organisms on the local nitrogen cycle. Within this thesis, you will investigate the relative contributions of these dominant fouling organisms on the biogeochemical characteristics of the water column, and we will unravel which part of the organisms is responsible for the observed patterns. There is evidence that the biofilm on the outside of the mussel shell contributes largely to the N₂O production, while for *Jassa* there is no current knowledge available. However, *Jassa* is a good candidate for impacting the nitrogen cycle as it inhabits tubes build of organic material that are subjected to slow water currents caused by the feeding movements of the amphipod. You will incubate both species, and their hard structures (mussel shells, *Jassa* tubes) in experimental settings to quantify how oxygen consumption and nitrogen cycling is affected by the presence of the fouling organisms, and to allocate the observed patterns to different parts of the organisms. This will be done in the current oceanographic setting, and in future conditions. These future conditions will take into account predictions made by IPCC with respect to temperature rise and ocean acidification

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

Copromotor(en):

Van Colen

Carl

Begeleider(s):

nog te bepalen

opmerking

voorbehouden:

1438

Predictive modelling of the abundance and biomass of functionally important species

abstract Sea floor sediments are an important component of the marine ecosystem. In coastal areas, about 30% of the pelagic primary production ends up at the sea floor. This organic matter is mineralized, and the resulting products of this mineralization process (inorganic nutrients) are returned to the water column where they are needed for the following phytoplankton bloom. These mineralization processes are affected by the activities of the organisms living in the sediment. They bring organic matter deep in the sediment, provide oxygen to deeper layers and remove toxic substances. All this depends on the functional attributes of the organisms. Two important functional attributes are "mobility" and "sediment reworking mode". These attributes, together with the abundance and biomass of the organisms, is at the base of an index, the Bioturbation Potential of the Community (BPC). Recently, we showed that this index is very important when it comes to modeling important benthic mineralization processes. A next step is the modeling of the components of this index. This can be done by modeling the actual abundances and biomass of those species that contribute largely to the final score of BPC (and hence to the benthic ecosystem functioning). Therefore, we (1) will use existing data, available at ILVO and the Marine Biology Research Group, to model biomass and densities of functionally important species, and (2) we will test the relation with ecosystem functioning with newly available data collected in an ongoing project. By doing so, a first step towards the modeling of the BPC scores is taken, which in the end will lead to the production of an ecosystem functioning map for the Belgian Part of the North Sea. In addition, it will set a procedure for similar exercises in different areas in other European countries.

onderzoeksgroep: Marine Biology & ILVO Oostende

Copromotor(en):

Van Hoey Gert

Begeleider(s):

nog te bepalen

opmerking

voorbehouden:

1439

Spying the seafloor

abstract Sediment Profile Imagery (SPI) provides an in situ view of the sediment-water interface. Typically as much as 15 to 20 cm from the sediment surface is photographed, providing both quantitative and qualitative data on the biological, chemical and physical character of the sediments. This sampling technique minimizes disturbance of the seabed and offers a quick scan method to study biodiversity as well as biological (e.g. animal burrows) and physical (e.g. sediment layering) features. In Belgian waters, this information is classically examined by grab or core sampling, and only quite recently a SPI camera is available to the research community. In this thesis, we want to link the information collected by SPI images to ground truth data collected by a Van Veen grab in different impact areas (sand extraction and dredge disposal) on the Belgian part of the North Sea. As such, we hope to find a quick method to determine the bioturbation potential (an indicator in the MSFD to assess good environmental status) of an impact area by just using a SPI.

onderzoeksgroep: Marine Biology & ILVO Oostende

Copromotor(en):

Van Hoey Gert

Begeleider(s):

nog te bepalen

opmerking

voorbehouden:

abstract In the framework of international legislation (i.e. Marine Strategy Framework Directive), European countries need to assess how healthy the marine ecosystem is in their territories. So far, these assessments are mainly based on indices based on species identity, and abundances of species. However, assessing the quality of an ecosystem component requires that the function of that component is investigated. Benthic ecosystem functioning is largely depending on functional aspects of the communities inhabiting the sediment, and not on the "name" of the organism. Therefore, research turned towards the understanding of how functional attributes of communities reflect the quality of an ecosystem component. A very important functional characteristic of a community is the distribution of body sizes: larger animals usually have a more profound effect than smaller animals. In pelagic component of the ecosystem, the use of indicators based on organism size is well established, while for benthic ecosystems, this research is only emerging. This thesis will contribute to this emerging field of research by investigating size related aspects of macrofaunal communities in relation to anthropogenic disturbance. Macrofaunal communities are considered as ideal monitoring tool, however the bulk of the indicators are derived from structural aspects (i.e. based on species identities). Based on newly collected data (students should be willing to participate to sampling campaigns at sea) and existing data, we will investigate whether size-related aspects of these communities (biomass spectra, size diversity) can be used as a tool to detect environmental disturbance by human activities, and evaluate their usefulness compared to traditional tools. This is a first, but important step towards size based assessments of the status of coastal benthic habitats.

onderzoeksgroep: Marine Biology & ILVO Oostende

Copromotor(en):

Van Hoey

Gert

Begeleider(s):

nog te bepalen

opmerking

voorbehouden:

1441 A century of scientific research on shrimp fisheries along the Belgian Coast.

abstract Since the early 20th century Belgian researchers organize scientific campaigns onboard of commercial vessels to investigate the shrimp fisheries along the Belgian coast. Research focused on the identification of species captured during fishing, determining the impact of shrimp fisheries on the shrimp and fish populations and gear alteration in order to optimize catch and minimize bycatch. Today a century of catch data exists. Most of these data were fragmented in reports or original paper forms and have been made digitally available by VLIZ and ILVO. The possibilities of exploring and analyzing these data are high. During this master thesis the student explores the data series in order to identify research questions that can be tackled with the available data in collaboration with VLIZ and ILVO. This could be: presence or absence of fish and differences in length over time, catch efficiency of different fishing gears, trend analysis including a changing environment or pressure,.. One or several of the research questions will be investigated by the student itself. The main tools will be literature and the existing integrated database but in case more scientific results are needed, experimental fishing campaigns can be organized in order to get insight into the comparability of the fishing gear.

onderzoeksgroep: Marine Biology & VLIZ & ILVO Oostende

Copromotor(en):

Mees Jan

Polet Hans

Begeleider(s):

Dewitte Elien

Goffin Annelies

Torreele Els

Verschueren Bart

opmerking Students will work regularly at Oostende (VLIZ). Most of the older literature is in Dutch/French

voorbehouden:

955 Testing morphology to recognize species among large white russula's

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 in Southern Belgium and Northern France or Germany to see and describe fresh collections.

onderzoeksgroep: Mycology

Copromotor(en):

Eberhardt Ursula

Begeleider(s):

De Lange Ruben

opmerking

voorbehouden:

1308

Changes in species composition of macrofungi in undisturbed forests: monitoring mycological transects in the forest reserves Wijnendalebos and Zoniënwoud.

abstract In order to investigate spontaneous processes in strict forest reserves (unmanaged), in 2003-2004 some mycological transects were lined out and monitored. It concerns plots of 10 x 100 m, divided in 10 subplots of 10x10m, in which all present macrofungi were counted and identified based on at least five visits spread over the seasons (Walley et al., 2005). More than 10 years after the start of the monitoring we want to repeat the inventarisatie and detect eventual changes in species composition. Our hypothesis is that the zero management lead to a decrease of the number of ectomycorrhizal species and an increase of saprotrophic species involved in wood decay. Furthermore we want to find out to which extent the possible changes in species composition are related to changes in nitrogen deposition. For both forests, measurements over a long time interval are available. Effect of succession: what is the effect of spontaneous forest development on fungal species composition, and how can we relate this to changes in forest structure and -composition. The transects are situated in a larger plot where data about forest structure, vegetation and light conditions are available, allowing to link eventual changes in mycoflora to changes in vegetation and microclimate. Effect of changing nitrogen deposition: the last decade an important decrease in nitrogen deposition is observed in Flanders. Question is how this relates to the mycoflora. Do we see signs of recovery for species that are sensitive to nitrogen deposition? For this part of the research long time N-deposition measurement will be involved in the analysis. This thesis is in close collaboration with INBO (Instituut voor Natuur- en Bosonderzoek). Walley, R. et al. (2005). Mycologisch rapport : monitoring en inventarisatie van de paddestoelen van de bosreservaten kersselaerspleyn, everzwijnbad, wijnendalebos, en de heirnisse. Rapporten van het instituut voor bosbouw en wildbeheer - sectie bosbouw, 2005(7). Instituut voor Bosbouw en Wildbeheer: Geraardsbergen : Belgium. 81 pp. (download beschikbaar op ResearchGate)

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

Vandekerckhove Kris

Begeleider(s):

De Lange Ruben

Verbeken Annemieke

opmerking**voorbehouden:****1309**

Creating order out of chaos: species delimitation in webcaps (Cortinarius).

abstract Cortinarius is the most species rich genus of Agaricomycetes and morphologically identifying webcaps is often considered one of the most difficult challenges in mycology. In addition, there are many taxonomic problems within the genus, leading to a nomenclatural chaos. Here in Flanders webcaps are morphologically very well studied by the Cortinarius work group. An explorative molecular study has shown that there are many conflicts between the traditional morphological species and the phylogenetic species. Many existing names are synonyms, but also many species remain unnamed. In addition, many traditional species turn out to represent complexes of species, either cryptic or pseudocryptic. The goal of this thesis is to investigate one or multiple groups of webcaps molecularly with multiple genes, to unravel the true diversity, leading to nomenclatural changes and the description of new species. In this thesis you will collect webcaps in Flanders, perform molecular lab work and phylogenetic analyses, and examine the species macro- and microscopically.

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

Nuytinck Jorinde

Begeleider(s):

Delgat Lynn

opmerking**voorbehouden:**

1310

Milkcaps (Lactarius) in North-America and Europe: testing species concepts

abstract The genus *Lactarius* has an almost cosmopolitan distribution and some continents, like Africa, have their own, endemic *Lactarius* mycoflora. Evidently, the occurrence of a milkcap species strongly depends on the occurrence of its ectomycorrhizal partner, since all milkcaps show host specificity to some degree. Many milkcaps in North-America are look-alikes of European species. However, very few studies have verified whether these milkcaps are actually the same species. The hypothesis is that arctic species have a circum-arctic distribution, while this is true for a much lower number of boreal species. Temperate North-American *Lactarius* species probably are rarely conspecific to European species, while up to a quarter of the names used for those species are European names. On top of that, the mycoflora of Eastern and Western North America differs significantly. This subject focusses on a couple of enigmatic milkcap-groups like the coconut-smelling *Lactarius glycosmus* and relatives. By carefully observing and comparing morphological characters and testing phylogenetic species concepts using multiple markers, conspecificity between both continents can be tested.

onderzoeksgroep: Mycology

Copromotor(en):

Nuytinck Jorinde

Begeleider(s):

Nuytinck Jorinde

opmerking

voorbehouden:

1311

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

Begeleider(s):

Delgat Lynn

opmerking

voorbehouden:

1442 Hatts of to the milkcaps (Lactarius and Lactifluus)!

abstract One of the microscopical characters with high phylogenetic signal in both milkcap genera Lactarius and Lactifluus is the structure of the upper layer of the cap, the so-called pileipellis. Hyphae are arranged in a particular way in this upper layer, and other elements such as rounded cells, clavate elements, thick-walled hairs, pigments, slime-layers etc. might also be present and build a very own microscopical structure. This structure is also translated in the macromorphology of the species: from smooth and very slimy to dry, felty and scaly, from bold to very hairy, etc. The variation of caps is outstanding in the group of the milkcaps and much more variable than in big sister Russula! For these pileipellis structures different typologies and different names have been proposed, but there is no consensus yet between different authors. Furthermore the existing terminology does not cover all capstructures, including some we observed in recently discovered species while studying the genera world-wide. The splitting of the genera Lactarius and Lactifluus is very recent and a pileipellis typology per genus will reveal important differences. The aim of this dissertation is to give an overview of all existing typologies and names and to test them again the real situation, in order to propose a new and complete typology. The different types will be illustrated with microscopical drawings and pictures. An innovating aspect here is that we want to use confocal microscopy in order to obtain a tridimensional view of the structures.

onderzoeksgroep: Mycology

Copromotor(en):

Leroux Olivier

Begeleider(s):

Delgat Lynn

opmerking

voorbehouden:

Verheyen Kris

1312 Morphometry of the dung beetle *Anoplotrupes stercorosus* in European small forest fragments.

abstract Keywords: Morphometrics, *Anoplotrupes stercorosus*, fragmentation, forest Forests in Western-Europe are often very fragmented and surrounded by intensively managed agricultural areas. In this agricultural matrix, forest fragments are islands for forest biodiversity. The dung beetle *Anoplotrupes stercorosus* is widespread along Europe and a forest specialist. It digs vertical holes up to 30 cm deep to store leaf litter as food for its larvae, making it a very important species for nutrient cycling within forests. By studying the morphometry (measuring certain body characteristics) of this species we can gain information about the species fitness and dispersal ability. This data can give us inside in the effects of forest fragmentation and habitat quality on this important forest species. Beetles have been trapped with pitfall traps in Belgium, Germany and Sweden and will be measured in the lab during this master thesis.

onderzoeksgroep: Terrestrial Ecology & Forest & Nature Lab

Copromotor(en):

Bonte Dries

Begeleider(s):

De Smedt Pallieter

opmerking

voorbehouden:

abstract Recent warming of the Antarctic Peninsula and the Sub-Antarctic Islands has led to reduced sea-ice cover, which has significantly altered ocean primary productivity and Adélie, Gentoo and Chinstrap penguin populations. Ongoing and previous studies from abandoned penguin rookeries using biogeochemical compounds extracted from lake sediment records showed that a longer-term relationship exists between climate, sea ice distribution and penguin population size, but also that penguin response to climate change is complex and site and species specific. For example, Adelie penguins are currently thought to be reacting negatively to warming across the Peninsula region where sea ice loss is greatest, but more positively in some areas of East Antarctica where sea ice is increasing. There is however a lack of long-term records examining different species responses and the past spatial distribution of penguin populations. This limits our ability to: 1) identify what the 'baseline' or 'natural' penguin population level might have been on centennial-millennial timescales, and 2) predict how penguin populations might change with future climate change scenarios. To address this, we will develop a paleolimnological toolkit based on fossil DNA to identify the presence and abundance of penguins and penguin-derived products preserved in guano and guano-influenced lake sediment records. More in particular, we will assess the efficiency of different DNA primers and extraction techniques to be used in combination with high throughput sequencing of samples from the dated lake records. When combined on a regional scale with marine records of past changes in relative sea level and sea ice distribution, it will be possible to provide a better understanding of the key drivers of past changes in penguin population in the Antarctic Peninsula.

onderzoeksgroep: Protistology & Aquatic Ecology

Copromotor(en):

Vyverman Wim

Begeleider(s):

Tytgat Bjorn

opmerking

voorbehouden:

abstract Precipitation patterns at the mid latitudes of the Southern Hemisphere are highly influenced by the Southern Hemisphere westerly winds (SWW), which are also one of the main drivers of the global climate system through influencing the ventilation and uptake of CO₂ by the Southern Ocean via wind-driven up or down welling of carbon rich waters. More in particular, recent observational data revealed that a weakening of the Southern Ocean as a sink for CO₂ coincided with an intensification and southward shift of the SWW. A better understanding of the relation between past atmospheric CO₂ concentrations and the long-term variability of the SWW is key for predicting the consequences of future changes and their impact on the global climate system. Despite this, the variation in the latitudinal position and intensity of the SWW and hence precipitation patterns at the mid latitudes in the Southern Hemisphere during the Holocene are still a matter of debate. Moreover, the reconstructions that do exist show inconsistent or partly opposite patterns. The Sub-Antarctic islands are key sites for studying past changes in SWW strength as they are located in their core belt in the Southern Ocean. On the Sub-Antarctic islands the SWW entrain sea spray into the air and deposit the salts directly into the catchment and water of the numerous small lakes and ponds through precipitation and sea-salt scavenging, or indirectly as washout from the catchment area. As a result, lakes on the western side of these islands are generally more brackish than those lying on the other shorelines. Moreover, their lake water salinity increases with increased salt deposition during periods of enhanced SWW strength. In this project a diatom-based transfer function to reconstruct lake water salinity will be developed using existing calibration datasets for the Sub-Antarctic islands. This model will be subsequently applied to reconstruct changes in salinity in a sediment core from a lake in South Georgia (South Atlantic Ocean). Combined with other proxies for sea spray such as the concentration of halogens, this will result in the first quantitative reconstruction of past changes in SWW strength during the Holocene in the region.

onderzoeksgroep: Protistology & Aquatic Ecology

Copromotor(en):

Sabbe Koen

Vyverman Wim

Begeleider(s):

Pinseel Eveline

opmerking

voorbehouden:

abstract Polar lakes are localized hotspots for both biodiversity and primary production compared to their surrounding cold desert ecosystems. Long-term monitoring studies in the Arctic and Maritime Antarctica, where global warming is particularly amplified, revealed that the recent temperature rise has resulted in enhanced primary production and a negative precipitation-evaporation balance in lakes. High latitude lakes therefore appear to act as 'early warning systems' because they respond quickly to climate-induced environmental changes. High-throughput sequencing using parts of the 16S and 18S rRNA genes in microbial mat communities from over 120 polar lakes revealed marked differences in the taxonomic structure and biodiversity between Arctic and Antarctic lakes. However, their functional diversity and food-web structure largely remain unstudied. This student project is aimed at studying the functional genetic make-up of 15 lakes from Antarctica, the Sub-Antarctic islands and the Arctic region by using a shotgun metagenome sequencing approach. The sequencing data will be analysed using bioinformatics pipelines and will form the base for developing conceptual food-web models for polar lakes.

onderzoeksgroep: Protistology & Aquatic Ecology

Copromotor(en):

Vyverman Wim

Begeleider(s):

Tytgat Bjorn

opmerking

voorbehouden:

1446

Climate-driven ecosystem dynamics of oasis lakes in the Sahara desert, based on analysis of aquatic invertebrate fossils in lake-sediment cores covering the last 2000-3000 years

abstract The Ounianga region of northeastern Chad is home to the largest permanent aquatic ecosystems in the hyperarid Sahara desert. Protected as a UNESCO World Heritage site, the lakes and swamps of Ounianga owe their paradoxical existence to a significant inflow of fossil groundwater which was last recharged in the early Holocene, under the wetter climate conditions of the so-called African Humid Period. The lakes lie in two clusters, Ounianga Kebir and Ounianga Serir, and range from shallow to deep (0.4 to 26 m) and from fresh to hypersaline (330 to 157,000 $\mu\text{S cm}^{-1}$). Most of them are surrounded by reed swamp (Phragmites) as is typical for desert oases. Because of their unique hydrological permanence and habitat diversity, these lakes represent a desert refuge for water-dependent biota which is unmatched in the central Sahara. The freshwater lakes also represent key ecosystem services for the resident human population. The mid-Holocene environmental transition towards the present Sahara desert landscape can be traced in numerous rock paintings across the region, and was recently also documented from the sediment record of Lake Yoa in Ounianga Kebir. However, the region's environmental (and human) history during the last few millennia is much less well known. For this purpose, we recovered new sediment cores from various lakes in Ounianga Serir, which presumably contain a detailed record of lake-level and water-chemistry fluctuations resulting from climate change in the last 2000-3000 years. This thesis research will focus on analysis of the fossil remains of aquatic invertebrates preserved in the sediment record (molluscs, ostracods, cladocerans, chironomid larvae, bryozoans), which at the species or genus level each have their own habitat requirements and tolerance for water-chemistry variation, and thus represent sensitive indicators of climate-driven changes in their aquatic habitat through time. A reconstruction of such changes will promote understanding of the long-term ecological resilience of these isolated desert lakes and the suitability of diverse water-use and lake-management strategies. It will also help produce a robust paleoecological framework to link the history of these lake ecosystems with dated archeological evidence on the occupation (and abandonment) of ancient lakeshore sites. The practical work for this thesis involves the processing and sieving of sediment samples, and identification of the remains of aquatic invertebrates at the appropriate magnification (25-200x) using taxonomic literature, identification guides and reference collections; followed by analysis of variation in their (relative) abundance through the sediment sequence. Depending of the nature of the fossil assemblages, the work will focus either on the calcitic/aragonitic fossils (molluscs, ostracods) or chitinous fossils (cladocerans, chironomid larvae, bryozoans).

onderzoeksgroep: Limnology

Copromotor(en):

Van Bocxlaer Bert

Van der Meeren Thijs

Begeleider(s):

Ryken Els

opmerking

voorbehouden:

1447 Defining the niche of phytoplankton functional types in coastal seas

abstract Coastal regions worldwide have been strongly altered as a result of climate change and changes in land use, over the past decades. The changing fluxes of nutrients, organic matter and sediment to coastal seas resulted in an altered resource availability and growing conditions for coastal plankton. As phytoplankton is the basis of the marine foodweb and accountable for 50 % of the global primary production, and is responding very fast to environmental change, it is important to monitor the ongoing effects of climate change and eutrophication on the phytoplankton community. The Flanders Marine Institute (VLIZ) in close collaboration with the research group of Protistology & Aquatic Ecology (PAE) initiated high resolution monitoring of phytoplankton functional diversity in the Belgian coastal zone (BCZ) within the framework of the EU LifeWatch program. Using a Cytosense flow cytometer (FCM) and a fast repetition rate fluorometer (FRRF), automated collection and analysis of marine plankton samples allows identification and quantification of functional types based on size, shape and fluorescence characteristics. In parallel, the FRRF is a device that nearly continuously photosynthetic rates in the plankton based on measuring the variability of light emission from chlorophyll a. In this project both monitoring tools will be combined to get insight into the physiological status and growth performance of key functional groups in the North Sea, including Phaeocystis, diatoms and a hitherto largely unrecognized but important group of picoeukaryote phytoplankton. Given the high spatial and temporal resolution of the in situ data, it will be possible to generate a fine-scale view of the niche requirements of the studied functional phytoplankton classes and more broadly to better understand the causes underlying the spatio-temporal dynamics of coastal phytoplankton. Research for this subject includes of fieldwork aboard the research vessel the Simon Stevin to operate both devices, used of dedicated software to analyse data and, when time permitting, mesocosm experiments to test hypotheses generated from the field data.

onderzoeksgroep: Protistology & Aquatic Ecology & VLIZ & NIOZ

Copromotor(en):

Deneudt Klaas

Kromkamp Jacco

Begeleider(s):

De Blok Reinhoud

opmerking**voorbehouden:**

abstract Diatoms and bacteria form the basis of complex patches of microorganisms which are known as biofilms. In bacteria as well as in diatoms group behavior is often regulated by the release of small molecules such as Quorum sensing molecules and hormones, respectively. Interestingly it has been shown in several examples that different signalling molecules cannot only be received by members of the same species but also across kingdoms, meaning diatoms can recognize bacterial signals and vice versa. Such interactions imply a previously unrecognised way by which both groups can influence each others growth, spatial distribution and ecological function within local communities. This thesis will focus on response of diatoms to N-acyl homoserine lactones (AHLs) - the most prominent group of QS molecules. Recently we established that several of these signaling molecules have a growth-suppressing or growth-promoting effect on marine biofilm diatoms and that these effects are partly conserved, partly specific among the species tested. To study the nature of these positive and negative effects we will make of a panel of genotyped strains which will permit to identify genomic regions associated with the response to AHLs and, based on their composition, to locate genes that can be expected to respond to such signals. Gene expression studies will then be used to validate the response of selected genes. The tasks in this project include a combination of laboratory assays, PAM fluorescence and automated imaging analysis, bio-informatics and molecular work.

onderzoeksgroep: Protistology&Aquatic Ecology & Labo Microbiology (WE10) & Dept. Sustainable Ora.Chemistry&Techn. (BW11) & Dept.Appl.Math.Comp.Sc.(WE02)

Copromotor(en):

Clement Lieven

Mangelincx Sven

Willems Anne

Begeleider(s):

Sefbom Josefin

Stock Frederike

Van den Berge Koen

opmerking

voorbehouden:

abstract Diatoms are micro-algae that live in a glass-like shell and have a fascinating life cycle. In this so-called cell size reduction-restitution cycle, every cell division results in a small decrease in size of each of the daughter cells, resulting in a gradually declining average cell size of diatom population. Below a species-specific cells size, however, sexual reproduction becomes possible, resulting in recombination of parental genomes and the establishment of the original larger cell size. The diatom *Seminavis robusta* is the current model system for studies of the life cycle and sexual reproduction in pennate diatoms. This species has two mating types ('sexes'), which are morphologically identical, but behave differently during sexual reproduction. During the mating process, these two mating types were shown to communicate through the action of multiple pheromones. During this master thesis, we will attempt to determine the effect of light intensity, spectral composition and photoperiod on the mating process. In order to quantify 'mating', different steps in the mating process will be analysed: pheromone production, sensitivity to pheromones from the other mating type, mitotic cell division and sexual reproduction (zygote formation). First of all, we will test whether mating is light dependent and which light intensities allow sexual reproduction. Secondly, we will test which light spectra/wavelength bands (red, green, blue) are able to induce a sexual response. This may give us a hint about which photoreceptor(s) are upstream in the mating process. Depending on initial results and the time available, follow-up studies might be set up to compare expression levels of certain photoreceptors in sexual versus non-sexual cultures which have been identified in *Seminavis robusta*.

onderzoeksgroep: Protistology & Aquatic Ecology & Plant Systems Biology (PSB-VIB)

Copromotor(en):

De Veylder Lieven

Begeleider(s):

Bilcke Gust

opmerking

voorbehouden:

abstract Microalgae do not only constitute the basis for aquatic food webs, but are also important drivers of elemental cycling. Thus, understanding the ecology and evolution of these key players is of great interest. A particular feature of microalgae is the enormous genetic diversity as well as phenotypic plasticity of co-existing genotypes in natural populations. Vital step in furthering our understanding of the eco-evolutionary significance of this diversity is being able to link genetic information (genotypes) to environmentally important traits (phenotypes) and their expression in individual genotypes. The marine benthic diatom *Seminavis robusta*, has within recent years emerged as a model organism for studying reproductive barriers in diatoms. It has been recognized that within the *S. robusta* species complex there exists three closely related incipient species (mating groups) that co-exist in nature. Previous laboratory studies show that sexual reproduction mainly occurs within the same mating group, and is more rare between mating groups meaning reduced intraspecific gene flow. In comparison, several other diatom species instead indicate reduced gene flow between populations adapted to different local environmental conditions. Ultimately, *S. robusta* provides a unique system for studying phenotypic variation and genetic diversity in the presence and absence of reproductive, physical and environmental barriers to gene flow. In this project we wish to phenotypically characterize a set of *S. robusta* strains, belonging to the three different mating groups that have been collected from various locations along the coast of Belgium and the Netherlands. Currently these strains are in the process of whole-genome sequencing, which will then allow for comparison of phenotypic characterization with genome data. Phenotyping will be done by subjecting the strains to a series of different environmental stressors during which growth will be monitored using PAM fluorescence as well as semi-automated image and video-processing. In addition, crossing experiments will be carried out in order to find out the reproductive success under various culturing conditions. The data generated from this thesis will ultimately provide a better understanding of i) the coupling between genetic diversity and phenotypic variation, ii) identifying environmental parameters that pose strong selective pressure on *S. robusta* and finally iii) if and how phenotypic variation occurs in the presence and absence of barriers to gene flow.

onderzoeksgroep: Protistology&Aquatic Ecology & Dept.Appl.Math.Comp.Sc.(WE02)

Copromotor(en):

Clement Lieven

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opmerking

voorbehouden:
