

22398: 1. The effect of species-area relation on local conservation status indicators: case study on indicator forest herbs

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

Probleemstelling:

The European habitats directive mandates the monitoring of the habitat types and species it protects. In a six yearly report, each member state has to give figures on the percentage of each habitat type that is in a favourable conservation status. This favourable status is based on the evaluation of a set of indicators which determine the local conservation status. For Flanders (and most other regions and countries), these indicators are defined as stand wide or patch wide indicators. For example, to have a favourable status of the habitat type *Asperulo-Fagetum* (9130) more than 5 key herb species should be present at the stand scale. In order to monitor the quality of the Flemish network of habitat types, a set of plots is followed up. This for the simple reason that plots can be revisited and re-evaluated more easily than a stand or patch of habitat. However, some indicators (e.g. the number of key forest herbs) are difficult to evaluate at plot scale as they are originally defined at stand scale. In order to have better insight in this problem, we want to study the effect of the species-area relation on the number of key forest herbs. Based on this relation, we can indicate how many plots are needed from a certain stand or forest before we can evaluate the key herb species indicator.

Doelstelling:

To study the species-area curves, we will first explore the available data. Both the Flemish forest inventory, as well as the monitoring of the Flemish forest reserves and the inventories for forest management plans all use the same 16x16m vegetation plots. From these, we can extract plots that are grouped within a similar forest stand of a certain forest habitat type. Preferably, a species poor habitat (likely *Fago-Quercetum*, 9120) and a more species rich one (e.g. *Stellario-Carpinetum*, 9160) will be selected. Based on the available data, we will select a study area (e.g. Meerdaal forest) to gather additional data. In this study area we will map the presence of key herb and tree species in stands of the selected habitat types (for example 9120, 9160). This field work will mainly take place in March and April. Based on the number of species at stand level, we will evaluate whether the stand is in a favourable condition for this indicator. Secondly, we will evaluate the area needed to significantly discriminate the group of favourable and unfavourable stands and the threshold (number of herb or tree species for this number of plots) that needs to be used to distinguish both groups.

Locatie:

INBO, Brussel

Website:

Meer informatie op: www.inbo.be (from January 2020 onwards)

Opmerkingen:

Useful references: Storch 2016. The theory of the nested species-area relationship: geometric foundations of biodiversity scaling. *JVS*, 27: 880-891 <http://onlinelibrary.wiley.com/doi/10.1111/jvs.12428/abstract> Van Calster & Damgaard 2017. Integral occurrence probability: combining cover and relative shoot frequencies based on bounded point-to-plant distances. *JVS*, 28: 824-837 <http://onlinelibrary.wiley.com/doi/10.1111/jvs.12527/full>

Onderwerp voorbehouden voor nvt

22378: 250,000 years of ecosystem dynamics in a crater lake near Kilimanjaro (East Africa) using fossil aquatic insects, ostracods, mollusks and fish

Promotor(en): Dirk Verschuren, Thijs Van der Meeren
Begeleider(s):

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

Probleemstelling:

The ICDP project DeepCHALLA aims to reconstruct climate and landscape history in equatorial East Africa over the past 250,000 years, through multi-disciplinary investigation of the uniquely long and continuous sediment record of Lake Chala, a 90-meter deep crater lake near Mt. Kilimanjaro. As this period encompasses (almost) the entire known history of our own species, *Homo sapiens*, this research has the potential to reveal how climate change has influenced human cultural and technological progress, and also how and when our ancestors started to impact their environment. An important indicator of past climate change is the succession of lake high-stands and low-stands through time, since this reflects episodes when rainfall was higher or lower than today. These lake-level fluctuations can be traced by analyzing changes in fossil zoobenthos assemblages, because their composition reflects the proximity of near-shore habitat and whether the offshore lake bottom was adequately oxygenated. When water level in Lake Chala dropped 50 m or more, benthic habitat expanded from its steep-sided rocky margins to the soft mud bottom in the center of the lake. Therefore, zoobenthos fossils (aquatic insects, ostracods, mollusks, etc.) may be particularly effective indicators to determine the timing and magnitude of climate change in East Africa during the so-called African Megadrought period (~115,000-90,000 years ago), when severe drought is believed to have stimulated the 'Out-of-Africa II' migration of ancient modern humans out of Africa, first towards the Middle East and then to Europe.

The research material available for this study are sediment samples from turbidites: layers of mud sandwiched between the regular sediment matrix and containing a greater diversity and abundance of zoobenthos fossils. The most important 'by-catch' will be fish remains: scales, vertebrae and teeth of the tilapia *Oreochromis hunteri* living in Lake Chala today. Consequently this study will also reveal precisely when the ancestor of this endemic fish species first colonized the isolated crater lake (presumably a mouth-brooding female cichlid fish was brought in by a fish eagle), and whether these early immigrant fish have maintained a local population continuously until the present.

Doelstelling:

This thesis project involves the sieving of sediment samples, after which the residue is scanned under a binocular microscope (20-80x magnification) to identify and count the fish and zoobenthos fossils. Not much taxonomic difficulty will be encountered, therefore time spent on each sample will be relatively low, and the number of samples can be high enough to cover the lake's entire 250,000-year history with good time resolution. Interpretation of the results will involve uni- and multivariate statistical analysis, and comparison with data sets on other indicators of the lake's environmental history produced by UGent and international project partners.

Locatie:

Campus Ledeganck 9de verdieping hoofdbouw

Website:

Meer informatie op: https://www.belspo.be/belspo/organisation/actua/20161223_DeepCHALLA_nl.pdf

22381: Linking solitary wasp and brood parasite metapopulations

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

Probleemstelling:

Brood parasitism is a specific type of parasitism in which the parasite's offspring feed on the host's nest provisions. The cuckoo might be the best known example, but brood parasites of arthropods are very interesting, less-known study systems. For the solitary, aggregating digger wasp *Bembix rostrata*, the brood parasitic fly *Senotainia albifrons* lays its larvae on the prey provisioned by the female digger wasp at her nest. The impact of such a brood parasite and the dynamics it can create on a metapopulation level are not well understood.

Doelstelling:

This master thesis topic will investigate the link between the metapopulations of *Bembix rostrata* and its brood parasitic fly. Several populations of *Bembix rostrata* will be sampled that differ in colonisation-history, populations size, isolation, and parasite abundance. This to link characteristics of the digger wasp populations with parasite presence and abundance. Genetic analyses with microsatellites will be used to link the genetic diversity and isolation of both the wasp and brood parasite metapopulations.

The student will do fieldwork, mainly at the Belgian coast in July and August, visiting several sites with known populations of *Bembix rostrata*. The student will measure individual digger wasps, take genetic samples by cutting off wing tips, make censuses for presence and abundance of the brood-parasite, and take genetic samples as well.

Locatie:

campus Ledeganck

Onderwerp voorbehouden voor Matthieu Gallin

22455: A possible role of fungal colacosomes in biocontrol?

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

Probleemstelling:

Fungi are an extremely diverse and species rich group of organisms with many ecological interactions. Mycoparasitism, where one fungus parasites on another fungus, is one such relationships. Among the Basidiomycota, one of the main lineages of fungi that comprise important groups such as the smuts, rusts and mushrooms, mycoparasitism is widely spread. In the class Microbotromycetes (rust lineage; Pucciniomycotina) a special submicroscopic structure occurs, the lenticular bodies (lb) or colacosomes. They seem to play an important role in mycoparasitic behavior and were first observed in some red yeasts in the 1970s when the first ultrastructural studies on fungi were done. Later they were found also in hyphally growing fungi, e.g. *Colacogloea peniophorae* (Fig. 1). Figure 1 shows that the lb's contain a globular electron dense nucleus that is surrounded by an electron translucent outside. It is known that the outside contains chitin, but the contents of the core are unknown. We hypothesize that this core contains lytic enzymes that are able to degrade fungal cell walls. Another hypothesis is that the lb's are not organelles as suggested in the literature, but another organism, e.g. a mycovirus, or a growth response by the host cell towards infection by this organism. The target of this master thesis is to explore if the lb's can have a role in biocontrol of specific fungi that cause spoilage of food or plant diseases.

Doelstelling:

In this project we aim: 1. To grow lb-forming fungi, including yeasts, in culture, with and without the host species, assuming that the lytic enzymes will be secreted; 2. To investigate the lytic capability of the growth medium towards an array of fungi. If positive as a second approach lb's can be isolated from the most promising fungi by differential centrifugation. The proteins will be isolated and investigated whether they show lytic activity towards fungi and characterize the most promising enzymes biochemically.

For this project a pioneering spirit is required. The project will be executed in a collaboration between UGent (Nathan Schoutteten, Annemieke Verbeken) and the Westerdijk Fungal Biodiversity Institute (Prof. Teun Boekhout Utrecht, The Netherlands).

Locatie:**22452: A search for the perfect match: host specificity as a character in *Russula* phylogeny**

Promotor(en): Annemieke Verbeken
Begeleider(s): Ruben De lange
Contactpersoon:

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

Probleemstelling:

The genus *Russula* is a large genus within the Russulaceae (Basidiomycota), easily recognised by the white stipe, pale gills and usually bright cap colours. Within the genus new species are still found regularly, even in Belgium. But the search for good characters to distinguish species can be challenging. As *Russula* is an ectomycorrhizal genus, host species relationship is seen as an important character. Most species within the genus are host specific, occurring with only a narrow range of host trees.

Doelstelling:

This thesis will focus on two points: microscopical characters for species distinction and host species relationship of some groups within *Russula*. One of the main groups of this study will be *Russula* subgenus *Compactae*. Species from subg. *Compactae* are easily recognised by the presence of lamellulae and are rather atypical for the genus. The existing phylogeny of this group show there are a lot more species than described until now. The need for good microscopical characters is high and host species relationships are considered to be very important. Field work will be a key factor for the study. Ectomycorrhizal root tips will be collected as well as fruitbodies. One of the main collecting sites will be Jongenbos (Kortesseem), a *Russula* hotspot where in recent years some very rare species and even new species were found.

Locatie:

22489: African fungal communities, diversity of three vegetation types compared

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

Probleemstelling:

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

Doelstelling:

Locatie:

22415: Analysis of future ecosystem services of floodplains in Flanders

Promotor(en): Maurice Hoffmann, Francis Turkelboom
Begeleider(s): Francis Turkelboom, RaÅsa Carmen
Contactpersoon: Francis Turkelboom
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie

Niet behouden voor:

Nog onbeslist voor:

Aantal studenten: 1

Aantal masterproeven: 1

Motivering voor deze opleiding:

Probleemstelling:

The Future Floodplains (<https://www.futurefloodplains.be/>) aims at providing fundamental insights into the mid- to long-term geoechydrological dynamics of rivers and floodplains under changing socio-ecological conditions. This will allow evaluating the sustainability of present-day integrated management and policies in river floodplains and provide a framework to revise environmental decision support systems for the future that takes into account the dynamic nature of floodplain systems.

The project results will be evaluated in a wider ecosystem services framework. Throughout the discussions with the various social users active within river floodplains, the conflicting nature of many ecosystem services in floodplains became apparent. For instance, many floodplains are nowadays nature reserves and are managed in a way to obtain a specific ecological status. On the other hand, floodplains are becoming more and more (again) a tool within flood control management plans. However, both flooding frequency as well as the quality of the flood water may be detrimental for the ecology of the floodplains. In order to balance both potentially contrasting objectives in management plans, it is important that local nature conservation managers and regional flood control managers know not only how both ecosystem services (flood prevention and ecological status) will evolve under future socio-ecological changes (e.g. climate change), but also how these would interact in a changing floodplain. Other desired ecosystem services which are dependent on the status of the floodplains include –among others - recreation, carbon sequestration, agricultural production.

Doelstelling:

The proposed research aims to assess the changes in ecosystem services in 3 focus floodplains of the project and assess the possible friction points. This research will require use of existing ESD assessment tools (natuurwaardeverkenner and ECOPLAN-SE -which require Q-GIS skills) and interviews with water managers. Based on these assessments the major future demand for floodplain ES and their trends will be assessed, and expected friction points (trade-offs) will be analysed.

Locatie:

INBO, Brussel, campus Ledeganck

Website:

Meer informatie op: www.inbo.be (from January 2020 onwards)

Opmerkingen:

Useful references: De Ryck J. (2019). Toetsen van methoden voor het bepalen van ecosysteemdiensten in valleigebeden in het kader van het future floodplains project (stagerapport). INBO & KULeuven. Liekens, I., Smeets, N., Staes, J., Van der Biest, K., De Nocker, L., Broekx, S. (2018). Waardering van ecosysteemdiensten, een handleiding. https://www.natuurwaardeverkenner.be/download/manual_NL.pdf Tomscha, S. A., Gergel, S. E., Tomlinson, M. J.. (2017) The spatial organization of ecosystem services in river-floodplains. *Ecosphere* 8(3). Vrebos, D., Staes, J., Bennetsen, E., Steven, B., Gabriels, K., Goethals, P., Martin, H., Liekens, I., Marsboom, C., Ottoy, S., Vanderbiest, K., van Orshoven, J., Meire, P. (2017). ECOPLAN-SE: Ruimtelijke analyse van ecosysteemdiensten in Vlaanderen, een Q-GIS plugin. <https://www.uantwerpen.be/images/uantwerpen/container25746/files/Handleiding%20>

Onderwerp voorbehouden voor nvt

22473: Antarctic shallow water benthos from the Belgica 121 expedition

Promotor(en): Francesca Pasotti, Ann Vanreusel

Begeleider(s):

Contactpersoon: Francesca Pasotti

Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie

Niet behouden voor:

Nog onbeslist voor:

Aantal studenten: 1

Aantal masterproeven: 1

Motivering voor deze opleiding:

Probleemstelling:

In February-March 2019, a crew of 9 scientists from different institutes boarded a 23 m sailing vessel heading to the Gerlache Strait, in the fast changing West Antarctic Peninsula. For the first time since the venture of Commander Adrien de Gerlache (in 1898) a fully Belgian funded expedition of purely marine scope

was happening again in the Antarctic region. The use of a very mobile platform such as the RV Australis of Oceans Expeditions, allowed the researchers to reach location of the shallow water Antarctic otherwise largely unexplored by science. As Marine Biology Laboratory we focused on the sampling of soft sediment communities and we collected samples for meiofauna (tiny creatures living in the sand which pass through a sieve of 1mm and are retained on a 32µm sieve mesh size), macrofauna and sediment biogeochemistry.

Doelstelling:

You will have the chance to learn about these type of sample processing (storage, extraction, fixation, slide preparation), you will be taught how to count and identify these organisms, and depending on your interest, you will collaborate in describing the assemblage structures and their local food webs ($\delta^{13}C$ and $\delta^{15}N$ stable isotope approaches) in relation to the different glacial conditions by which the various coves we sampled were affected by. You will learn how to keep your data in order and how to process ecological results carrying out relevant statistical analysis in R. You will learn how to produce a scientific paper and finally you will collaborate in producing the first results of this historical scientific expedition: check it out at www.belgica120.be.

Locatie:

sterrecampus S8

Website:

Meer informatie op: www.belgica120.be.

22481: Aquatic ecosystem dynamics in contrasting freshwater and saline lakes in equatorial East-Africa

Promotor(en): Gijs De Cort, Thijs Van der Meeren
Begeleider(s): Thijs Van der Meeren
Contactpersoon: Gijs De Cort
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Pronounced climate variability in East Africa represents an important constraint for socio-economic development in the region, because quantity and quality of available water resources respond strongly to inter-annual and longer-term climate change. The region is characterized by marked natural climate variability at time scales from seasons to multiple millennia and longer. These play a major role in shaping the naturally dynamic ecosystems of East Africa, among which its lakes and other inland aquatic environments. Lake sediments provide an important tool in studying the history and evolution of aquatic ecosystems, because they preserve information on surrounding climate and environment as well as fossil remains from diverse aquatic biota that get deposited on the bottom of the lake through time. As such, the study of lake-sediments as paleo-ecological archives can shed light on ecological processes that act on much longer time scales than can be revealed by studies focusing on experimental or observational ecology. Aquatic communities adapted to fresh or saline lakes develop different tolerances to environmental disturbances, and hence dissimilar ecological responses are expected to overall similar long-term climate change in fresh and saline lakes.

This master-thesis research aims to contribute to knowledge of lake ecosystem response to natural climate change that has taken place in equatorial East Africa during the Holocene (i.e. the last ca. 11,700 years, or the current geological era). This natural climatic variability is relevant in light of the still highly uncertain effects that 21st-century anthropogenic climate change and other human impacts (e.g. water extraction, intensification of land-use changes) will have on the region's aquatic ecosystems and water resources. The Holocene presents a suitable study target because climatic events of durations and magnitudes relevant to human societies during this era have been relatively well described.

More specifically, the student will investigate temporal changes in the assemblages of key groups of aquatic invertebrates in the sediment record of at least two contrasting lake systems from equatorial East Africa. Lake Naivasha is a freshwater rift lake situated in the Kenya Rift Valley. Sediment cores from its deepest point, a submerged volcanic explosion crater, have previously revealed that the lake's water level is extremely responsive to climatic change. Lake Simbi is a small, hypersaline crater lake in western Kenya. Located only a few kilometers from Lake Victoria, it is hypothesized to be a key site for deciphering the environmental history of its enormous neighbour. New sediment cores from both of these lakes will be taken in January 2020 and will provide the study material for this thesis research.

Doelstelling:

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 (e.g., amplitude of ecological response, response time) of different lake ecosystems. 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. Ecologically meaningful interpretations will be aided by multivariate statistical analysis. 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).

Locatie:

Campus Ledeganck

22410: Are insect communities of agricultural crops impoverished beyond repair?

Promotor(en): Maurice Hoffmann, Marc Pollet
Begeleider(s): Marc Pollet, Luc De Bruyn
Contactpersoon: Marc Pollet
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Recently, a German study (Hallmann et al. 2017) suggests that insect communities in nature reserves in western Germany declined with over 75% in the past three decades. And a similar phenomenon has been observed in certain insect taxa in the Netherlands as well (Kleijn et al. 2018). The authors do not exclude that the intensification of agricultural practices might be an important factor, but there is no hard evidence for this assumption. And thus far, no attempts have been made to assess the current insect diversity nor its recent trends in Flanders. As a result, we have no idea about the insect biodiversity in agricultural land (versus semi-natural habitats) nor whether crucial ecosystem services (pollination, crop protection, food supply, ...) are still provided. Trying to get a grip on this system is what this project is all about.

Doelstelling:

Apart from various but often detailed datasets on a number of insect families from the past, most samples and data will be gathered during the project itself. A representative number of sites in agricultural land (arable crops, pastures, meadows) and in adjacent semi-natural habitats will be investigated with an array of collecting methods that should provide us with a first indication on both the species richness and abundances. Though identification until species level is not excluded per se, in a first step we will rather focus on functional groups and other higher level taxonomic traits. In a second step the natural history of these functional groups will be screened (via literature research) in order to establish their role in the respective ecosystems and potential ecosystem services for mankind. In a final step an attempt will be made to construct an ecosystem model, focusing on the insect component.

Profile: we seek a biologist with a pronounced interest in entomology, who likes fieldwork, is both accurate with data and material, creative, thinks out-of-the-box and is not afraid of modelling, i.e., a can-it-all. (S)he knows the different insect orders, and might be willing to extend her/his taxonomic knowledge.

Locatie:

INBO, Brussel, campus Ledeganck

Website:

Meer informatie op: www.inbo.be (from January 2020 onwards)

Onderwerp voorbehouden voor nvt

22443: Auxin immunolocalisation and chemical screening in macroalgae

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

Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Macroalgae attach the substrate by means of (i) adhesive secretion; (ii) rhizoids differentiation which differentiate into (iii) hapters upon contact with the substrate. Zygotes of *Dictyota* are being used to study cell polarisation and asymmetric cell division in plant systems because of some practical advantages of broadcast spawning algae (Bogaert et al. 2017). The cell normally polarizes and one pole differentiates into the basal cell fate (developing the rhizoid or attachment structure) and the other into the apical cell fate (becoming the thallus). The rhizoids will attach the embryos to the substrate and mature into branched discoid hapters that may develop a large physical attachment surface.

In chemical biology, molecules are applied as conditional tools to reveal the underlying mechanisms of growth and development. For example exogenous application of auxin analogs interferes with the process of apical-basal patterning by inducing embryos with two cell poles with a basal cell fate: embryos with two rhizoids instead of one (Bogaert et al. 2018). The hypothesis is that exogenous application of auxins interferes with the establishment of an intercellular gradient of auxin. While preliminary evidence suggests such a gradient, the existence of intercellular auxin gradients is controversial.

Doelstelling:

The first projects objective, is to test this hypothesis by means of auxin immunolocalisation of developing cells of algae. Secondly, the master student will deliver pioneering work in establishing a protocol for an automated chemical screening protocol that will be used to discover new molecules affecting asymmetric cell division, rhizoid emergence and rhizoid maturation into hapters. Although pre-plated compound collections are commercially available, the challenge is in developing a proper and robust screening assay: (I) screening protocols of *Arabidopsis* protoplasts and tobacco BY-2 cells need to be modified for *Dictyota* zygotes or spores. (II) Using imaging software we will make first steps to automate the read-out using cell shape and hyalinity of the rhizoid cells. Using chemical screening we envisage to develop compounds that (i) provide a powerful tool to study early algal development and (ii) may result in an applications as anti-biofouling agents or attachment promoting components in seeding lines and canvasses.

Locatie:

De Sterre, VIB Zwijnaarde

22354: BREEDIT combining breeding with genome editing to improve plant yield

Promotor(en): Dirk Inzé, Hilde Nelissen
Begeleider(s): Denia Herwegh
Contactpersoon:
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Feeding the growing world population under changing climate conditions poses an unprecedented challenge on global agriculture and our current pace to breed new high yielding crop varieties is too low to face the imminent threats on food security. In the BREEDIT project, a novel crossing scheme is being developed that allows for an expeditious evaluation of combinations of potential yield contributing alleles by unifying 'classical' breeding with gene-centric molecular biology. The acronym BREEDIT, a word fusion of breeding and editing, reflects the basic concept of combining breeding with multiplex genome editing of yield related genes. By introducing plants with distinct combinations of genome edited variations in more than 80 known yield related genes into a crossing scheme, the combinatorial effect of these mutations on plant growth and yield will be evaluated.

Subsequent rounds of crossings will increase the number of stacked gene-edits per plant, thus increasing the combinatorial complexity. Phenotypic evaluations throughout plant development will be done on our in-house automated image-analysis based phenotyping platform.

The nature and frequency of Cas9-mediated variations in the entire plant collection will be characterized by multiplex amplicon sequencing to follow the efficiency of CRISPR-cas9 genome editing and to identify the underlying combinations of genes that cause beneficial phenotypes (genetic gain). The obtained knowledge on yield regulatory networks can be directly implemented into current molecular breeding programs and the project will provide the basis to develop targeted breeding schemes implementing the optimal combinations of beneficial alleles into elite material. BREEDIT will be a major step forward in integrating basic knowledge on genes with plant breeding and has the potential to provoke a paradigm shift in improving crop yield.

Doelstelling:

The aim of the master thesis is to genotype and phenotype the first generation of edited plants and to initiate the crossing scheme. The student will be involved in DNA, RNA and protein analysis techniques to understand the nature of the combinatorial mutations. Particular attention will be given to data management to link the genotypic and phenotypic data to each individual plant. Overall, the student will be involved in all different steps of the pipeline.

Locatie:

FSVM building Campus Ardoyen - Tech Lane

Onderwerp voorbehouden voor Yara De Boe

22401: Can trees cope with a changing climate? The Lombardy poplar (*Populus nigra* cv. *Italica*) as model system

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

Probleemstelling:

In the absence of genetic diversity, plants rely on the capacity of phenotypic plasticity to cope with shifts in environmental conditions. Understanding the mechanisms behind phenotypic plasticity and how local phenotypic adjustments are transferred to clonal offspring, will provide insight into its ecological and evolutionary significance. Epigenetic changes has recently been proposed to play a crucial role in rapid environmental adaptation.

This project investigates the epigenetic and phenotypic variation (in terms of bud flush and bud set) of the Lombardy poplar, a single clone of *P. nigra* L. that is distributed worldwide since the beginning of the 18th century. Its clonal origin in combination with its widespread distribution in space and time, makes the Lombardy poplar an excellent study system to investigate how long-lived plant species with a prevailing vegetative reproduction can cope with widely contrasting environmental conditions, without variation at the genetic level.

Doelstelling:

Cuttings were collected across Europe in winter 2016-2017 from 60 adult Lombardy poplars grown across Europe in different environments. The plants are grown in the greenhouse. This study includes bud flush and bud set observations in the greenhouse and the study of epigenetic variation (data-analysis) on vegetative offspring grown in a common greenhouse environment. Using statistical models, we investigate correlations among epigenetics, bud phenology and the climate at the home site of the Lombardy poplar trees.

This project combines spring bud flush and fall bud set observations in the greenhouse (ILVO - Melle), with statistical data-analysis analysis of the greenhouse observations and genetic data analysis of epigenetic profiles (methylation sensitive AFLPs).

Locatie:

INBO, Geraardsbergen, Melle; Ledeganckcampus

Website:

Meer informatie op: www.inbo.be (from January 2020 onwards)

Opmerkingen:

Useful references: Vanden Broeck A, Cox K, Brys R, Castiglione S, Ciatelli A, Guarino F, Heinze B, Steenackers M, Vander Mijnsbrugge K. (2018). Variability in DNA Methylation and Generational Plasticity in the Lombardy Poplar, a Single Genotype Worldwide Distributed Since the Eighteenth Century. *Frontiers in Plant Science* 9(1635). <https://doi.org/10.3389/fpls.2018.01635> Dewan S, De Frenne P, Vanden Broeck A, Steenackers M, Vander Mijnsbrugge K, Verheyen K. (2018). Transgenerational effects in asexually reproduced offspring of *Populus*. *PLOS ONE* 13(12):e0208591. <https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0208591>

22421: Carbon flow in the pelagic food webs of contrasting fjord systems in SW Greenland

Promotor(en): Koen Sabbe, Lorenz Meire
Begeleider(s):
Contactpersoon:

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

Probleemstelling:

Fjords around Greenland are characterized by highly productive and diverse food webs. As such, they act as globally important carbon sinks, and support rich fishing grounds. Global warming however significantly impacts these systems through the accelerated melting of the Greenland Ice Sheet. This leads to an accelerated retreat of coastal glaciers. Between 2000 and 2010, 90 % of the glaciers currently terminating in the sea (= marine-terminating glaciers, MTG) showed an accelerated retreat, and in many parts of Greenland these glaciers will retreat above sea level in the near future to become land-terminating (LTG). Both glacier types cause major differences in the physical, biogeochemical and ecological processes in the associated fjord systems, but the consequences for the pelagic and especially the benthic components of the changing fjord systems remain a major gap in our understanding. Consequently, the impacts of further warming on ecosystems services of Arctic fjords such as their importance as carbon sink and fishing grounds remains unknown.

Doelstelling:

In this dissertation, the hypothesis will be tested that MTG dominated fjord systems will be characterized by more productive pelagic microphytoplankton, whereas LTG dominated fjords will be less productive and dominated by pico- and nano-sized phytoplankton. In addition, transparent exopolymeric particles (TEP) production is also hypothesized to be higher in the MTG fjords. As a result of higher productivity and increased TEP production, vertical export of organic material is hypothesized to be more intense in MTG fjords. During 2020, samples will be collected to quantify the carbon flow in the pelagic compartment of two contrasting fjord systems in SW Greenland (Godthåbsfjord with a MTG, Ameralik fjord with a LTG). The following parameters will be measured: photosynthetic pigments; viral, bacterial, phytoplankton and microzooplankton counts using flow cytometry and/or microscopic counts; 16S and 18S rRNA amplicon sequencing; primary production; community respiration and microzooplankton grazing.

Locatie:

22285: Cell-type specificity of ethylene responses: the role of ethylene during abiotic stress

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

Probleemstelling:

The gaseous molecule ethylene is known to regulate a wide variety of plant physiological and developmental processes (Depaepe and Van Der Straeten, 2019). For instance, the action of ethylene is vital in processes such as vegetative growth, fruit ripening, senescence, and abscission, among many more. Furthermore, ethylene has an important signaling function upon both abiotic and biotic stress. The molecular framework driving these ethylene responses have been extensively studied and characterized using classical genetic and pharmacological approaches. However, stimulating or blocking the ethylene response in whole plants ignores crucial differences between tissue- and cell-types. Previously, tissue-specific expression of two negative regulators of the signaling cascade was carried out, to selectively disrupt the ethylene signal in different cell types. With this strategy, we successfully identified the epidermis as the primary site of action for ethylene responses in root growth inhibition (Vaseva et al., 2018). However, until now, no studies have reported on tissue- and cell-type specific ethylene responses during abiotic stress. Furthermore, novel research has demonstrated that the immediate biosynthetic precursor of ethylene, 1-aminocyclopropane-1-carboxylate (ACC) can influence growth independently of ethylene, which adds an additional layer of complexity to the field of ethylene biology (Vanderstraeten, Depaepe et al., 2019).

References:

T. Depaepe and D. Van Der Straeten (2019). Tools of the ethylene trade: a chemical kit to influence ethylene responses in plants and its use in agriculture. *Small Methods* 190267.

I.I. Vaseva, E. Qudeimat, T. Potuschak, Y. Du, P. Genschik, F. Vandenbussche and D. Van Der Straeten (2018). The plant hormone ethylene restricts Arabidopsis growth via the epidermis. *PNAS* 115: E4130-E4139.

L. Vanderstraeten, T. Depaepe, S. Bertrand, D. Van Der Straeten (2019). The ethylene precursor ACC affects early vegetative development independently of ethylene signaling. *Frontiers in Plant Science* (in review).

Doelstelling:

In this thesis we will determine the cell-type(s) that are essential for ethylene signaling in response to different types of abiotic stress (e.g. flooding, salt stress). In addition, we will examine putative ACC- and/or ethylene-specific responses. In the first part of the project, several of these ethylene-insensitive lines (with cell-type specific action) will be analyzed, using an in house developed high-throughput phenotyping platform capable of assessing 'plant health' as measured –amongst others- by several growth-related parameters as well as photosynthetic activity, and plant temperature. Secondly, we will study the molecular basis of the ethylene response and its interaction with other hormones in a cell type- and tissue-specific manner. The techniques that will be used here include plant tissue culturing, plant genotyping, plant phenotyping, GUS staining, confocal analysis of fluorescent reporter lines, ethylene measurements by means of photo-acoustic laser-based spectroscopy, and gene expression analysis (qPCR).

Locatie:

Campus Ledeganck, Laboratory of Functional Plant Biology

22419: Change in North Sea benthos communities in the Anthropocene

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

Probleemstelling:

Regime shifts are rapid reorganizations of ecosystems from one relatively stable state to another. Because the system state after the regime shift can be functionally different from that before the shift the occurrence of such shifts has considerable implications for the management of the marine environment and the provision of ecosystem services, particularly fisheries. Regime shifts can have a number of causes. Probably the best well studied are those caused by climatic oscillations which often occur on (very) large scales. Additionally, ecosystem state shifts can also occur on much smaller scales e.g. as the result of eutrophication, change in resource availability, overfishing or the introduction of alien species. Regime shifts driven by climate change and anthropogenic disturbances have been reported from many geographical areas for diverse groups of marine organisms such as fish, phyto- and zooplankton. However, our knowledge of whether such regime shifts also occur in marine benthic soft-sediment ecosystem is far less detailed.

Doelstelling:

Through analysis of historic time series from different locations, this thesis will reveal insights in the stability of benthic communities in the Belgian Part of the North Sea (BPNS) and identify the role of climatic oscillations and/or historic and ongoing anthropogenic activities (e.g. fisheries, sand extraction and dumping of dredge materials) for community change. Such knowledge is currently lacking and these insights will assist in the management of coastal ecosystems in the current Anthropocene era.

Potential topics include (1) a large-scale study of the distribution patterns of communities in the BPNS between 1970-1976 (i.e. the oldest sample series present for the area); (2) the analysis of long-term (1970-2015) benthic community change at selected stations of known anthropogenic pressure; and (3) the analysis of community biotic properties as early warning indicators of community change.

Locatie:

22467: Change of colour of a house sparrow/pigeon through time

Promotor(en): Matthew Shawkey
Begeleider(s): Michaël Nicolai
Contactpersoon:
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1

Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Since the industrial revolution both the number of cities, and the global temperatures have risen. According to multiple thermoregulation studies animals change colour in function of climate change and/or urban heat islands. Sparrows might thus change their colours both spatially and temporally.

Doelstelling:

The RBINS (Royal Belgian Institute of Natural Sciences) has a large collection of sparrows (*Passer domesticus*), sampled through time and space, and thus provides multiple snapshots of sparrow colour through time. As such it provides an excellent resource to study colouration through time and space. In this thesis the student would visit the collection of the RBINS (and potentially the Royal Museum for Central Africa) to measure the darkness of sparrows that differ in geographical scale (e.g. latitude dependend – see Gloger's rule), habitat (e.g. rural vs urban) and temporal time (e.g. present vs past) to see whether sparrows have, or are, adapted to different biotic and abiotic factors. If time permits, the student might join bird-ringers to see whether there currently is a difference in live birds between urban and rural birds.

Locatie:

campus Ledeganck

22439: Characterization of wild legume-rhizobia combinations from Northeast Thailand: isolate authentication and assessment of nitrogen-fixing efficiency

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

Probleemstelling:

Food self-insufficiency remains a real challenge in Northeast Thailand causing widespread malnutrition and extreme poverty. The Northeast experiences the lowest levels of agricultural productivity despite being Thailand's largest region with more than 80% of its population being engaged in agriculture. There, farmers have limited resources and lack sufficient guidelines to cropping and management strategies which are needed to cope with their region's recurring issues of soil nutrient depletion as well as the severe and prolonged periods of drought. Targeting such restraints to farming in the Northeast, the current research acknowledges the potential benefits to agricultural output through the use of wild and native legume species. Northeast Thailand's Tropical Savannah climate boosts a vast array of wild legumes that are currently underutilised. Besides being extremely vigorous during the dry season, many legume species that engage in symbiosis with rhizobia bacteria can perform Biological Nitrogen Fixation (BNF); a process that converts highly inert atmospheric Nitrogen (N₂) to plant usable forms. Given that N is required for plant growth in large quantities and yet it is almost invariably the most limiting nutrient in farming systems, BNF is vital to productive agriculture, offering an alternative to the financially and environmentally costly synthetic fertiliser-N. This thesis topic is embedded in a PhD project that aims 1) to exploit the genetic biodiversity among wild legumes and their effective rhizobia pairs which exhibit drought-tolerance and BNF traits for integration to Northeast Thailand's crop rotation systems and 2) to establish solid guidelines to legume establishment in the dry season during which other crops cannot be grown productively. Work started early in 2019 with the organisation of a questionnaire involving responses from over 500 farmers living in 25 villages across 5 districts of the Khon Kaen province. To identify superior symbionts, whole rhizobia communities are being profiled independent of culturing and also through targeted isolation and identification using MALDI-TOF MS as well as amplicon sequencing of the 16S rRNA, *gyrB* and *nifH* genes.

Doelstelling:

The aim of this thesis project is to verify that isolates already obtained from collected nodules are indeed effective symbionts of their original host plant so that later field tests can be conducted with the most promising bacterial strains. The focus will be on isolate authentication of host plant nodulation and assessment of nitrogen-fixing efficiency. Techniques used will include the preparation of liquid inoculants at a given concentration (for use in the authentication test), surface sterilisation and germination of legume seeds. In addition, the student will be involved in designing an optimal growth apparatus for legume seedlings under sterile conditions. To confirm isolate identities, rhizobia will be re-isolated from newly formed nodules and identified through 16S rRNA sequencing. Plant performance and isolate effectiveness will be measured through qualitative characteristics linked to N₂-fixation efficiency such as plant vigour and leaf greenness. Additionally, legumes will be harvested and quantitative measurements such as plant fresh/dry weights, nodule number and weight will be made. Finally, the student may be involved in measuring BNF using the ¹⁵N natural abundance method to determine the best performing legume-rhizobia pairs.

Locatie:

campus Ledeganck, VIB-Technologiepark Zwijnaarde

Onderwerp voorbehouden voor Eline Verhelst

22403: Chinese muntjac in Flanders: population genomic reconstruction of a recent invasion of a non-indigenous mammal species

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

Probleemstelling:

Chinese Muntjac (*Muntiacus reevesi*) is a deer species that was introduced to the UK in the 20th century, with a population in England and Wales estimated at more than 100,000 animals. This species is also kept (illegally) in Belgium, and since c. 2006 were also illegally deported in Belgium and the Netherlands and escaped from captivity. In Belgium, specimens have been observed in all provinces except Liège and Luxembourg, with an important concentration N of Antwerp. The species is mentioned on the European black list of invasive species that are of concern to the European Union since 2014. This means that all necessary measures must be taken to prevent further spread and to prevent new fires. In 2018, Flanders breeding aimed at hunting was registered, whereby a nursery was "rolled up". Many animals were seized and killed. A tissue sample was taken from all of these animals for DNA research to learn about their origin and their relationship with individuals in the wild. In the meantime, this species is actively being controlled on behalf of the Agency for Nature and Forest (ANB), and a DNA sample is taken from each animal. Droppings can also be used to genotype animals.

Doelstelling:

In this project the intention is to

- 1) Develop a panel of SNP markers to determine genetic relationships between individuals in the first and second degree. We first do an SNP discovery with rad sequencing, map the SNPs on the published genome of Chinese Muntjac. We then select a set of 356 suitable markers, and use multiplexed amplicon sequencing (GT-seq) to determine genotypes on all samples.
- 2) Determine genetic relationships between all Flemish samples, to determine how many independent sources of introduction there are. We compare the data with DNA from Chinese Muntjac from official collections (e.g. zoo's- and British and Dutch samples).

Locatie:

INBO, Geraardsbergen, Melle; Ledeganckcampus

Website:

Meer informatie op: www.inbo.be (from January 2020 onwards)

22449: Clarifying the role of BLI-4 isoforms in ADR longevity

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

Probleemstelling:

Lifespan extension by means of dietary restriction (DR), a regimen of restricting nutrients without malnutrition, is evolutionary conserved yet we do not fully understand its molecular mechanisms. *C. elegans*, a small nematode, is a valuable model organism to study the regulatory pathways underlying longevity. Worms raised in axenic media, a sterile nutrient-rich liquid medium lacking bacteria (the standard food source of *C. elegans*), show a spectacular lifespan doubling. Still, the underlying mechanisms of this impressive phenotype are not well understood. We have recently found that the lifespan doubling of axenic dietary restriction depends on the activity of the proprotein convertase BLI-4.

Doelstelling:

In this thesis, we aim to study the cellular localization of the three prime bli-4 isoform candidates (BLI-4B, BLI-4C and BLI-4D). Therefore, we will generate translational reporter lines in which GFP is fused to these specific isoforms. Plasmids will be created using an in-house cloning technique (e.g. Gateway cloning, CRISPR-Cas9,...) and delivered to the worms by microinjection or biolistic bombardment. In case transgenic reporter lines are successfully made, we will explore the cellular localization using confocal microscopy.

Locatie:

campus Ledeganck - 2e fase - 4e verdieping

22423: Climate change effects on germination success of marram grass, a key dune-forming species

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

Probleemstelling:

Coastal foredunes form the first line of defense against storm surges and flooding along much of the European coastline. In comparison with hard defense structures such as dikes, dunes have the advantage that they can reform after disturbance and grow along with rises in sea level. Moreover, they are much more cost-effective. Dunes are therefore likely to increase in importance as a nature-based solution for the problem of rising sea levels and increasing storm frequencies and intensities predicted under climate change. The main dune-forming plant species in Europe is marram grass (*Ammophila arenaria*). Marram grass can survive up to one meter of sand burial per year and can produce rhizomes both vertically and laterally, stabilizing the newly deposited sand layer. Moreover, the aboveground marram tussocks lower wind speeds, so that sand carried by the wind gets deposited around these plants. The ecology of marram grass and its capacity for dune formation via vegetative growth have been studied extensively. However, marram grass also reproduces via seeds. These seeds are thought to germinate mainly in moist places where the wind has scoured out the sand to the ground water table or after intense rain events. As climate change is predicted to increase both temperature and precipitation levels, this could cause large changes in the germination of marram and thus the formation, growth, and maintenance of our coastal dunes.

Doelstelling:

The aim of this project is to test how changes in precipitation and temperature alter the germination success of marram grass. We will combine laboratory experiments with field observations to address this question. In the lab, seeds of marram grass will be germinated under different soil moisture and temperature levels and germination success monitored. In the field, areas with new marram seedlings will be mapped, and correlated with data on temperature and precipitation, to infer whether predictions based on lab results translate into distributions in the field, or whether –and if so, which– other factors determine germination success in the wild.

Locatie:

22444: Comparative genomics of multicellularity

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

Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

An increasing number of protist and algal genomes from a diverse range of evolutionary clades is becoming available. This opens up the question to what extent convergent evolution of particular traits (e.g. multicellularity, habitat, trophic strategy) lead to similar solutions at the genomic level. This thesis aims to explore the genomic underpinning of multicellularity by comparing genome content (protein coding genes, protein domains) of organisms which evolved multicellularity independently.

Doelstelling:

More specifically, we will compare genomes of green, brown and red seaweeds with those of plants and animals. Using Python and R programming, the student will build further on the development of a pipeline to test diverse hypotheses on protein domain combinations (Interpro) enriched in multicellular organisms (or organisms with a different trait) in using both phylogenetic explicit and implicit methods. Some basic experience in Python and especially a good motivation for bioinformatics is required for this thesis.

Locatie:

campus Sterre, S8

22461: Conservation of Magnolias from the Dominican Republic

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

Probleemstelling:

The Dominican Republic, located on the eastern part of the Caribbean island of Hispaniola, boasts an astounding 6,000 species of plants. Over a third of them, 2,050 species, are endemic – only found in the Dominican Republic. The endemic plant species include three Magnolia species: *Magnolia pallescens*, *M. hamorii* and *M. domingensis*. All three species are threatened according to the IUCN (International Union for Conservation of Nature) Red List. Information on the genetic makeup of populations, and on the reproductive biology is currently lacking. This data shortage hampers effective conservation work by our local partner organization, Fundacion Progressio. In 2015, we conducted an expedition and collected plant samples and GPS data of 30+ trees from two populations per species. We extracted DNA from the samples and we developed and tested microsatellite (SSR) markers on these species.

Doelstelling:

The aim is to investigate and compare the genetic diversity of the six populations and calculate different diversity indices (e.g. HO, HE, AR, FST, FIS). This will allow us to assess the genetic makeup and viability of these populations. The student will need to optimize the SSR multiplexes and genotype the different collected populations. The resulting data will provide interesting information to analyse using conservation genetic software (e.g. Arlequin, FSTAT, GenAlEx, STRUCTURE). Even more so, using predictive species distribution modelling we can model where to search for more Magnolia populations. Though not compulsory, we highly encourage the student to join in on a field expedition that we plan to undertake in the course of 2020-2021. During this expedition more population genetic and ecological data on the species will be collected, directed by the results of the species distribution modeling. The newly collected samples their DNA will be extracted in the lab at Ghent University. Once genotyped, the results can be added to the those based on the samples collected in 2015. We highly encourage students at the Systematic and Evolutionary Botany Lab to publish their MSc thesis as an A1 paper.

This thesis will give opportunity for the student to:

1. Execute lab work: DNA extractions & SSR PCRs.
2. Genotype the SSR data using Geneious.
3. Conduct conservation genetic analyses.
4. Analyse location and climatic data to model where to go to on our next expedition with the R packages 'sdm' and 'humboldt'.
5. If interested: join an expedition to the Dominican Republic to
 - Search & sample more Magnolia populations.
 - Collect ecological data. Depending on the timing and amount of days of the expedition this can be any of the given options, depending on the

students' interest and availability in terms of time:

- Comparative study between the species their seed dispersers (birds).
- Floral scent collection & comparison.
- Study of self- and cross-pollination within the tree species by supplementary pollination, emasculation and bagging experiments.
- Phenology observations and comparisons between the three species.
- Placing pollinator sticky traps around the flowers to catch the pollinators, identify them and compare within and between the species.

6. Compile the comparative genetic and ecological data of the Dominican Magnolias in an A1 publication.

Locatie:

Ledeganck, possibly with fieldwork in the Dominican Republic

Onderwerp voorbehouden voor Tim Claerhout

22445: Controlling the life cycle of nori and dulse

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

Probleemstelling:

In Asia seaweed make up an important part of the diet. In Europe interest in cultivating seaweed for human consumption is steadily increasing. Two of the prime species are Porphyra (nori used in sushi) and Palmaria (dulse). While good control over the life cycle and abiotic growth of local nori species (mainly Porphyra) has been achieved in Asia, for mariculture at European coasts local varieties need to be isolated to comply with legislation and checked for their suitability for mariculture.

Doelstelling:

In this master dissertation the student will isolate and culture additional strains of Porphyra (nori) and Palmaria (dulse) and apply different methods to control the life cycle and to achieve optimal conditions for abiotic growth and reproduction. This thesis will involve field work (sampling), wet lab experiments (isolation and culture) and the molecular lab (identification).

Locatie:

campus Sterre, S8

22416: Cross-casus analysis of desirability of ecosystem services in Flanders rural area

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

Probleemstelling:

While human well-being depends upon the conservation and sustainable use of biodiversity and ecosystem services, global changes and unsustainable human activities increasingly threaten the world's capacity to deliver those services over the long term. In Europe and beyond, a solution to such challenges can be found by merging landscape planning with ecosystem services concepts. Landscape planning has strengths in recognition of public benefits and implementation mechanisms, while the ecosystem services approach makes the connection between the status of natural assets and human well-being more explicit. It can also provide an economic perspective, focused on individual preferences and benefits, which helps validate the acceptability of environmental planning goals.

Thus linking landscape planning and ecosystem services provides a two-way benefit, creating a usable science to meet the needs of local and regional decision making.

Doelstelling:

Within the Flemish context, the INBO team has participated in several planning process of specific rural areas. To support this we assessed the demand side of ecosystem services via a multistakeholder questionnaire. These results indicate the high importance of cultural ecosystem services and biodiversity, while some type of agriculture, high-dynamic recreation and hunting are often controversial. The proposed study will look for general trends in the results of 5 case studies, and identify major conflicting uses. Via literature research and interviews of key informants, these friction points will be analysed.

Locatie:

INBO, Brussel, campus Ledeganck

Website:

Meer informatie op: www.inbo.be (from January 2020 onwards)

Opmerkingen:

Useful references: Boeraeve, Fanny; Dufrene, Marc; De Vreese, Rik; et al. (2018). Participatory identification and selection of ecosystem services: building on field experiences. *ECOLOGY AND SOCIETY*, Volume: 23, Issue: 2. Ryckebusch, Maura; Jacobs, Sander; Van Winkel, Jos; Broekx, Steven; Verheyden, Wim; Turkelboom, Francis; Van der Biest, Katrien; Staes, Jan; De Palmaer, Davina; Dewart, Sylvie; Leone, Michael Plannen met ecosysteemdiensten in de Maarkebeekvallei. (2018). Instituut voor Natuur- en Bosonderzoek (INBO), 2018. (Rapporten van het Instituut voor Natuur- en Bosonderzoek; No. 73). Turkelboom, Francis; Leone, Michael; Jacobs, Sander; et al. (2018). When we cannot have it all: Ecosystem services trade-offs in the context of spatial planning. *ECOSYSTEM SERVICES* Volume: 29 Pages: 566-578. von Haaren, C., Lovett, A., Albert, C. (Eds.) (2019). *Landscape Planning with Ecosystem Services: Theories and Methods for Application in Europe*. Springer.

Onderwerp voorbehouden voor nvt

22477: Deciphering the genomic basis underlying rapid, in situ evolution in a wing-polymorphic beetle

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

Probleemstelling:

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

Doelstelling:

The aims of this project are (i) to identify the alleles involved in rapid ecological adaptation; (ii) to quantify the presence and frequency of adaptive alleles in the founding population; (iii) to follow frequency changes in these alleles through time and (vi) to decipher the evolutionary origin of the alleles. Students will have the opportunity to be involved in all steps of this research i.e. sampling of beetles in the core populations, measuring of wing sizes, DNA extraction, preparation of Restriction-site Associated DNA libraries (RADseq) and bioinformatic analysis of the data. No prior knowledge on the bioinformatic and programming tools is required.

Locatie:

Koninklijk Belgisch Instituut voor Natuurwetenschappen en campus Ledeganck

22437: Deep time conflicts: tracing an ancient hybridization in tropical trees using phylogenomics

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

Probleemstelling:

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

Doelstelling:

See above.

Locatie:

Ledeganck

22356: Detection of commercially exploited marine fishes through eDNA

Promotor(en): Sofie Derycke
Begeleider(s):
Contactpersoon: Sofie Derycke
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1

Motivering voor deze opleiding:

Probleemstelling:

The distribution and occurrence of fishes in the marine environment can be accurately monitored through sequencing of DNA that is present in the water column. This eDNA contains DNA molecules that have been released by living animals through scales, faeces and/or slime or by decaying dead animals. The DNA molecules are obtained by filtering large amounts of seawater, which are then sequenced using DNA metabarcoding of the mitochondrial genes. In fresh water systems and harbours, the detection of fish species through eDNA has proven to be very accurate in comparison with traditional fishery methods. At ILVO, we explore the use of eDNA to identify fishing, nursery and spawning grounds in the North Sea to understand better the population structure of commercially important fishes such as sole.

Doelstelling:

The aim of the master thesis is to investigate whether eDNA from the water column reflects the whereabouts and abundances of fishes in the North Sea. Water samples will be collected during fish surveys, so that the eDNA approach can be compared to fish catches. In addition, eDNA will be used to investigate whether spawning grounds of commercially important fishes can be accurately identified. If so, this would greatly improve fisheries management.

Locatie:

ILVO, Ankerstraat 1, 8400 Oostende

Opmerkingen:

accurate and organised laboratory skills are required, interest in bioinformatics, good skills in R

22462: Dipping below the Equator: disentangling a complex Magnolia species complex

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

Probleemstelling:

This project will be done in cooperation with EcoMinga, and Ecuadorian foundation dedicated to the conservation of Andean ecosystems. EcoMinga has seven reserves in the centre of Ecuador with unique environmental conditions. All of these reserves are home to a remarkably high number of plant and animal species. Two species of Magnolia occurs in these reserves: *M. vargasiana* and *M. llangtanensis*. Some trees have been found in the reserve, however, the identification of which is uncertain. These trees are either hybrids of the two species known to occur in the area, or represent a new species.

Doelstelling:

This main aim of this project is to clarify the status of the Magnolia species in the reserve using morphological, ecological and genetic data. Some morphological and location data is already available due to sampling efforts in 2018. Moreover, HybSeq sequence data is also available of eight reference samples from this reserve, including trees that belong to the two known Magnolia species as well as the putative hybrids / new species. The existing data can provide a quick start for the extraction of discriminating genetic sites or "barcodes". The student will mine the HybSeq data to design primers for Sanger sequencing. During fieldwork in the course of 2019-2020, the student will screen more trees, and collect morphological data and samples for further genetic analysis when back in Ghent. We highly encourage students at the Systematic and Evolutionary Botany Lab to publish their MSc thesis as an AI paper.

This thesis will give opportunity for the student to:

1. Mine HybSeq data of the species under question and search for DNA barcodes to discriminate the species.
2. Join an expedition to the Ecuador to collect genetic, morphological and ecological data.
3. Execute lab work: DNA extractions & Sanger sequencing.
4. Test the DNA barcodes on newly collected individuals.
5. Work on a report for the EcoMinga website whereby you bring the results to a broader audience.
6. Compile the genetic and ecological data of the Ecuadorian Magnolias in an AI publication.

Locatie:

22454: Diversity and succession of fungi on dead beech wood in Wijnendalebos.

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

Probleemstelling:

Unmanaged forest reserves have an important scientific function. They can be considered as field laboratories where spontaneous processes and their effects on biodiversity can be studied. Wijnendalebos (Torhout) is one of the oldest forest reserves in Flanders: the reserve has been left unmanaged since 1983 and developed a large amount of dead wood in various stages of decay. The forest is located in a region with a high historical and current nitrogen deposition.

In 2016-2017, herb layer and moss layer on dead beech trunks were studied in the forest reserves of Wijnendale and Zoniënwood (Van Landuyt & De Beer, 2016; Van Parys, 2018). The nutrient status in the dead trees was also extensively studied (Dhiedt, 2018; Dhiedt et al. 2019). More than 100 trees in the Sonian Forest and about fifty beech trunks in Wijnendalebos were selected for this purpose. The deadwood fungi were also investigated in the Sonian Forest (Schoutteten, 2018; Goes, in prep.) This was not done yet in the Wijnendale forest.

Doelstelling:

The aim of this thesis is to fill this gap and to study the fungal succession on decaying beech wood, by comparing trees in different stages of decay. In addition, a comparison can also be made with the moss and vascular plant diversity on the same stems, and with the diversity on comparable stems in the Sonian Forest. The latter comparison can also be used to determine whether there is an effect of nitrogen deposition, directly or via the chemical composition of the wood that is the substrate of the wood decaying fungi (deposition data and wood analyzes are already available).

In addition, there is also the possibility to make an inventory and report on the species diversity of deadwood fungi in the Blauwe Torenbos (Bruges), and to compare this with the species diversity in Wijnendalebos.

Locatie:

Opmerkingen:

Support : data on nitrogen deposits, wood analyzes, other inventories and digital maps material with positioning and measurements on the lying trees (diameter, volume, etc.) are made available by INBO. Staff of INBO can also help in the field to locate the logs.

Onderwerp voorbehouden voor Noga Abecassis

22343: Diversity and succession of nematode fauna in ant nests

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

Probleemstelling:

Ants are well-known ecosystem engineers that significantly affect soil processes and the distribution of other organisms. The large, conspicuous, dome-shaped nests of red wood ants are thermoregulated and are constantly supplied with food resources. These unique conditions make red wood ant nests biodiversity hubs for a diverse fauna of commensalistic and parasitic arthropods, including beetles, mites and spiders. A hitherto unexplored group in ant nests are

nematodes. Given the unique microconditions in red wood ant nests, we expect that they house a rich and distinctive nematode fauna as well. The aim of this thesis is to characterize the nematode diversity in different niches (underground earth nest and organic mound) of red wood ant nests. As nematodes are ideal organisms to test succession patterns, we will compare the fauna between recently founded red wood ant nests and nests established for more than 10 years. This thesis starts with sampling in the field during the summer of 2019 followed by characterization of the nematode fauna in the lab. Subsequently, next-generation sequencing will be applied to assess nematode diversity in high-resolution.

Doelstelling:

Locatie:

22460: Diversity, DNA barcoding and phylogeography of plant-parasitic nematodes of Banana in East Africa

Promotor(en): Wim Bert
Begeleider(s): Emmanuel Olorunfemi Olajide, Huu Tien Nguyen, Marjolein Couvreur
Contactpersoon: Emmanuel Olorunfemi Olajide
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Banana including plantain (*Musa* spp.) is a staple food in Africa providing a valuable source of carbohydrates and income, feeding millions of Africans. However, plant-parasitic nematodes of banana are a significant pest causing significant crop losses. After a survey and visual assessment of banana farms in Kenya (these data will be available) the plant-parasitic nematodes associated with banana will be morphologically and molecularly characterised. The relative importance of each nematode will be computed based on the frequency of occurrence and prominence value for each species. For the morphological analyses, new fixation techniques will be compared and further developed in order to establish an improved and more save fixation technique for nematodes. For the molecular analyses routinely used molecular barcodes will be sequenced in order to allow comparison with known populations (D2D3 of LSU rDNA and COI mitochondrial DNA). Next to routine identification, new molecular markers will be developed in order to reveal intraspecific differences, with a focus on *Pratylenchus goodeyi*. DNA samples of multiple populations of *P. goodeyi* are already available in the lab in order to allow a phylogeographical study and/or investigate a possible correlation with variation in the pathogenicity of *Pratylenchus* spp population on bananas.

Doelstelling:

The most important goals of this thesis project are:

- gain insight into a range of and combination of research methods, including microscopy and a wide range of molecular techniques.
- describe the diversity of plant-parasitic nematodes associated with banana in Africa
- develop new DNA barcodes to identify plant-parasitic nematodes
- adapt and develop new microscopy techniques

Locatie:

campus ledeganck

Website:

Meer informatie op: www.nematology.UGent.be

22411: Do shape and colour really matter? Assessing the effectiveness of pan traps to collect flying insects

Promotor(en): Maurice Hoffmann, Marc Pollet
Begeleider(s): Marc Pollet, Luc De Bruyn
Contactpersoon: Marc Pollet
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1

Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Assessing insect species richness and diversity, even in one single site, remains quite a challenging undertaking. For flying species, the most widely employed collecting methods are Malaise traps, pan traps and sweep nets, each with their specific benefits and restrictions. Contrary to Malaise traps, pan traps are far less frequently used despite their high effectivity and their standardized application. They come in all kind of shapes, sizes and colours, which has an effect on both the numbers and species obtained. At present, no unequivocal data are present on which trap types are best used in local or large scale surveys. Finding an answer to that question and turning this into a clear advice for future research is the goal of this project.

Doelstelling:

We do not start from scratch, on the contrary: extensive datasets from surveys in both the Palaearctic realm and the Neotropics (e.g., Chile, Ecuador, Martinique) are available, as well as sample sets from two field experiments conducted in two different marshland habitats in 2017 and 2018. Additional field work is most desirable and might a.o. entail assessing the proportion of species and specimens effectively being trapped. Indeed, the collected samples are merely the final product of possibly intricate processes that are not yet known or understood. The available datasets alone guarantee a number of peer-reviewed papers, and additional sample processing and field experiments only add more potential research outputs.

Profile: we seek an allround biologist with a pronounced interest in entomology, who is both accurate with data and material, creative and thinks out-of-the-box. (S)he knows the different insect orders, and it is considered an asset to be into flying insects or to excited to gain knowledge on these taxa during the project. (S)he is expected to take charge of one or a few smaller fly families.

Locatie:

INBO, Brussel, campus Ledeganck

Website:

Meer informatie op: www.inbo.be (from January 2020 onwards)

Onderwerp voorbehouden voor nvt

22457: Does intraspecific niche variation affect the performance of predictive models of species invasion risk

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

Probleemstelling:

Invasive species rank among the main threats to biodiversity, and understanding why some species succeed to invade whereas others fail is paramount for formulating effective management and conservation strategies. Risk assessment protocols based on either life-history characteristics or climatic niche profiles can be used to predict the likelihood that introduced species will establish, but these methods often fail when applied to (sub)tropical species introduced to temperate areas. It has been suggested that existing protocols may fail because they do not account for intraspecific niche variation. Intraspecific niche variation may lead some native range populations to have niches that are closer to the conditions in invasive areas, but when species are modelled as a whole; such differences likely are inadequately characterized. The overarching goal of this thesis is to make use of the successful invasion of Europe by ring-necked parakeets (*Psittacula krameri*), a species native to the African Sahel zone and parts of south-east Asia, to test whether incorporating within-taxon niche variation into predictive modelling techniques improves forecasts of invasion risk.

Doelstelling:

Ring-necked parakeets have established numerous populations in Europe; covering a climatic gradient from cold German cities (e.g. Heidelberg) to the Mediterranean (e.g. Seville), with a total population size likely exceeding 100.000 individuals. In its native range; it occurs from the cooler foothills of the Himalaya to the tropical lowlands of Sri Lanka. Existing distribution models show that in Europe; the species occupies areas significantly colder than in its native range; and subsequently, traditional species-level predictive models fail to accurately characterize its invasive distribution in Europe. Four subspecies are

currently recognized (two African and two Asian), but it is unclear how robust these classifications are. Therefore, the student will (a) take morphological measurements on a large number of ring-necked parakeets held at natural history museums (KBIN, Africa museum, possible too Naturalis (Netherlands); MNHN (France) and Tring (UK), characterizing beak, wing, tarsus and whole-body morphology plus aspects of the feathers (feather depth, length and solar reflectivity), (b) assess whether morphological variation found is related to relevant climatic and habitat variables, (c) delineate morphological clusters ('groups') in the native range, create species distribution models based on these groups and assess whether accounting for native range-within taxon niche variation improves forecasts of parakeet invasion risk across Europe.

Locatie:

Ledeganck; KBIN, Africa museum, other (nearby) natural history museums

Onderwerp voorbehouden voor Fleur Petersen

22456: Does microclimate and spring phenology influence ring-necked parakeet (*Psittacula krameri*) timing of breeding and breeding success?

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

Probleemstelling:

Invasive species rank among the main threats to biodiversity, and understanding why some species succeed to invade whereas others fail is paramount for formulating effective management and conservation strategies. Risk assessment protocols based on either life-history characteristics or climatic niche profiles can be used to predict the likelihood that introduced species will establish, but these methods often fail when applied to (sub)tropical species introduced to temperate areas. It has been suggested that existing protocols may fail because they do not account for microclimate conditions nor do they consider temporal niche aspect such as breeding phenology. The overarching goal of this thesis is to make use of the successful invasion of Europe by ring-necked parakeets (*Psittacula krameri*), a species native to the African Sahel zone and parts of south-east Asia, to test whether microclimate conditions influence its timing of breeding and breeding success along an urban to rural gradient.

Doelstelling:

Ring-necked parakeets have spread considerable from the Brussels area where they were first released in the 1970ties; and now have growing populations in many urban centres (e.g. > 1.000 birds across Antwerp, +10.000 birds in Brussels). While the bulk of the population occurs in urban centres, parakeets can be found breeding in forest fragments in rural areas adjacent to cities as well. Yet, currently it is unknown what the breeding success of these parakeets is in Belgium, and whether timing of breeding and breeding success varies between urban and rural areas. This is an important knowledge gap as it is currently unclear whether parakeets can establish self-sustaining populations in rural areas or whether they are dependent on immigration from urban centres. Therefore the student will (1) survey forest fragments along an urban-to-rural gradient (Brussels area) for breeding parakeets, (2) determine breeding phenology in these areas through behavioural observations, (3) monitor breeding success using a mobile camera attached to a telescopic pole (clutch size, hatching success, fledging success), (4) quantify microclimates by installing iButton microclimate loggers in- and outside a selected set of parakeet breeding cavities. Data analysis will consist of relating the breeding phenology and breeding success data to degree of urbanization, microclimate, and characteristics of breeding trees. The main hypothesis is that in cities, a warmer microclimate will allow parakeets to breed earlier and more successfully.

Locatie:

Ledeganck; Brussels area for fieldwork

Onderwerp voorbehouden voor Yahya Ghalayini

22448: Does mommy know best? Transgenerational plasticity in the brown macroalga *Dictyota dichotoma* in response to climate change.

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

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

Probleemstelling:

Global climate change represents a major threat to marine ecosystems and species worldwide. Continuously increasing greenhouse gas emissions cause changes in oceanographic conditions such as temperature and pH, which in turn affect biological systems at levels ranging from individuals to entire communities. Understanding the response of marine organisms to a changing environment as a consequence of global change is therefore crucial.

One of the mechanisms through which organisms can respond to fast environmental changes is transgenerational plasticity (TGP). TGP occurs when environmental conditions experienced by the parents influence the phenotype of the offspring. If the parental environment is a good predictor of the offspring environment, TGP can be adaptive and may buffer populations against rapid environmental change, providing time for genetic adaptation to catch up.

Doelstelling:

In this master thesis, we will study the transgenerational impact of ocean warming on the brown macroalga *Dictyota dichotoma*, a key component of European coasts. Specifically, we will test how the thermal environment experienced by the parents can affect the transgenerational response observed in offspring. To this end, we will use algae from our culture collection to conduct parents-to-offspring experiments, in which part of the parental generation will be conditioned to ocean warming while another part will be exposed to ambient conditions. Differences in fitness of the offspring when subjected to the same stressor conditions will yield information on the importance of TGP.

Locatie:

campus Sterre, S8

22483: Does resilience of marine invertebrates to environmental stress depend on their population-genetic diversity?

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

Probleemstelling:

Marine environments are being threatened by a broad range of anthropogenic stressors, from climate change to various kinds of pollution. Such stressors affect species and communities through interference with life-history traits, physiology and species interactions, among others.

The importance of population-genetic diversity to the long-term persistence of populations is well-known and is key in many conservation programmes of endangered species at local to global scales. A low population-genetic diversity – often coinciding with a small effective population size and/or a limited geographic range – increases the risk of inbreeding as well as a population's vulnerability to disease. One may similarly expect that populations with a higher standing diversity would be more resistant or resilient to various kinds of anthropogenic stressors, because the probability of having tolerant phenotypes increases with genotypic diversity. However, surprisingly little empirical evidence exists on whether and to what extent population-genetic diversity conveys more tolerance to human-induced stressors in populations of marine animals. This information is crucial for a proper understanding of how marine organisms will respond to a changing environment.

The nematode *Litoditis marina* is a common inhabitant of coastal environments worldwide. It is one of few marine representatives of the nematode family Rhabditidae to which also the well-known model organism *Caenorhabditis elegans* belongs. Like *C. elegans*, it is easy to maintain in laboratory culture under controlled conditions and has a short generation time (< 1 week), rendering it an excellent model organism in experimental ecology. Since laboratory cultures can be raised from a single gravid female, one can rapidly establish strongly inbred cultures with a very low genetic diversity. At the same time, it is possible to establish a multitude of such inbred culture lineages, which can then be used to establish populations comprising different levels of population-genetic diversity by pooling individuals from fewer or more different lineages.

Doelstelling:

In this thesis we will experimentally assess the impacts of anthropogenic stressors on the fitness of populations (measured as rate of increase, total abundance, generation time, mortality...) of *Litoditis marina* populations composed of different levels of genotypic diversity. Depending on the student's interest, the focus can be on different kinds of anthropogenic stressors, for instance shifts in temperature regime or exposure to pollutants. The practical work will entail a combination of laboratory manipulations (setting up lab experiments, maintaining cultures, ...) and microscopy (mostly binocular for observations and counts).

Locatie:

Campus Sterre en campus Ledeganck.

22399: Effect of forest edge dynamics and canopy closure on the survival of forest edge species: a case study on the European stag beetle

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

Probleemstelling:

Natural forest have wide forest edges and gradients in canopy closure. The canopy closure and the linked light and climatic conditions are not fixed in time but can be quite dynamic, especially young trees can restore canopy closure within a few years in small to medium sized gaps.

Many species are known to be specifically adapted to these forest edges and gradient canopy closures. However, little is known if and how these species cope with the dynamics of this system. The plasticity required from species might be particularly important for immobile species.

The European stag beetle (*Lucanus cervus*) is a typical forest edge species with a long larval phase that can take up to four years. Previous research revealed that females actively fly to the forest edge when placed in closed canopy forest in search for egg deposition sites. However, little is known about the larval development and their plasticity to cope with canopy closure and associated effects on soil temperatures.

Doelstelling:

In the provincial domain of Huizingen, a study was set up with 75 larvae of the European stag beetle that will be followed up during four years (spring 2016 to spring 2020). The larvae were placed in 20l plastic containers and kept in natural conditions along a gradient from closed canopy forest to open sites. Data loggers were used to follow up the temperature and larvae were weighted every 6 months. Furthermore, data is available from a common garden experiment in the Netherlands and UK where larvae were kept under two temperature regimes, closed canopy forest and a warm exposed side. Aim of this study is to analyse the effect of canopy closure and other relevant parameters on the larval development of the European stag beetle.

Locatie:

INBO, Brussel, campus Ledeganck

Website:

Meer informatie op: www.inbo.be (from January 2020 onwards)

Opmerkingen:

Useful references: Thorn S, Forster B, Heibl C, Muller J, Bassler C 2018. Influence of macroclimate and local conservation measures on taxonomic, functional, and phylogenetic diversities of saproxylic beetles and wood-inhabiting fungi. *Biodiversity and Conservation*, 27: 3119-3135
<https://link.springer.com/article/10.1007/s10531-018-1592-0> (abstract) Thomaes A, Dhont P, Dekeukeleire D & Vandekerckhove K 2018. Dispersal behaviour of female stag beetles (*Lucanus cervus*) in a mosaic landscape: when should I stay and where should I go. *Insect Conservation & Diversity*, 11: 523-533
<https://lib.ugent.be/catalog/pug01:8574422>

Onderwerp voorbehouden voor nvt

22474: Effect of urbanisation on *Araneus diadematus*.

Promotor(en): Bram Vanthournout, Dries Bonte
Begeleider(s): Bram Vanthournout, Matthew Shawkey

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

Probleemstelling:

Cities are anthropogenic areas that differ markedly in (a)biotic characteristics compared to more natural systems. In this way, cities can be viewed as "living labs" due to the strong selection pressures they exert on affected species and provide unique opportunities to investigate evolution in real-time. Urban areas are characterised by a higher environmental temperature, caused by the heat island effect, and by smaller body sizes in prey populations. It is expected that the increased temperature selects for lighter individuals in urban areas as these could thermoregulate more efficiently. The smaller body size of insect species requires a higher capture success for insect predators. Using the model system *Araneus diadematus*, it was indeed found that city spiders weave webs with smaller mesh sizes to increase capture efficiency and first results on spider colour indeed demonstrate that city spiders have a more lighter colour compared to rural ones. However, densities of Cross spiders are lower in cities than in the surrounding countryside.

Doelstelling:

In this thesis we develop these research lines further. Depending on the interest of the student, there is a possibility to investigate the effect of spider colour on prey attractance using field and/or lab observations, determine in detail the prey consumption and, hence, to pinpoint the importance of spiders in controlling insect populations in urban and rural areas.

Locatie:

Campus Ledeganck

22417: Effecten op de gezondheid van contact met de natuur

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

Probleemstelling:

De relatie tussen natuur en gezondheidszorg krijgt steeds meer aandacht in onze maatschappij. We hebben nood aan meer kennis over de gezondheidseffecten van contact met de natuur. We willen hierbij aandacht hebben voor de gezondheidswinst die geboekt kan worden met de natuurlijke oplossingen (nature-based solutions), zoals bv herstel van stress, versterking van het immuunsysteem van kinderen of vermindering van de impact milieuvuiling of klimaatverandering. We willen hierbij ook aandacht hebben voor gezondheidsrisico's in relatie tot natuur, zoals bv pollenallergie of infectieziekten die overgebracht kunnen worden door bv teken of muggen.

Rond beide invalshoeken wordt steeds meer kennis opgebouwd en verzameld, zoals bv in '[Connecting Global Priorities: Biodiversity and Human Health, a State of Knowledge Review](#)' (2015) van de Convention on Biological Diversity (CBD) and the World Health Organization (WHO) of in het kader van Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services '[Contributions to physical, mental and social dimensions of health section](#)' (2018). Eén van de belangrijkste nog voorliggende uitdagingen is het verbinden van kennisontwikkeling en praktische toepassing. In het veld van de gezondheidszorg staat dit nog slechts in de kinderschoenen.

Doelstelling:

We stellen al een flinke hoeveelheid literatuur ter beschikking om een start te maken. Onderzoek kan plaatsvinden in een woonomgeving, werkomgeving, schoolomgeving of een gezondheidszorgsetting (in een zorginstelling of in het kader van een therapie) om te kijken hoe we gezondheidseffecten in kaart kunnen brengen. We kiezen samen met jullie een doelgroep (bv kinderen, werknemers, psychiatrisch patiënten, ouderen) en een type natuur-contact (natuur zien, in de natuur verblijven, in de natuur actief zijn, in de natuur werken)?

Er is eventueel de mogelijkheid om in het kader van je thesis samen te werken met thesisstudenten van de Faculteit Geneeskunde en Gezondheidswetenschappen van de Universiteit Antwerpen (via de [Leerstoel Zorg & Natuurlijke Leefomgeving UAntwerpen](#)).

Deze thesis kadert in een samenwerking tussen Prof. Maurice Hoffmann (UGent - Ecosystem Management & Services) en Prof. [Hans Keune](#) ([Leerstoel Zorg & Natuurlijke Leefomgeving UAntwerpen](#) – INBO).

Locatie:

INBO, Brussel, campus Ledeganck

Website:

Meer informatie op: www.inbo.be (from January 2020 onwards)

Onderwerp voorbehouden voor nvt

22422: Effects of climate change and insect herbivore communities on the evolution of plant resistance

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

Probleemstelling:

Most plants have to cope with multiple herbivores simultaneously attacking them. However, not all herbivores occur everywhere. Different plant populations can thus be exposed to more or less complex herbivore communities. Recent theoretical insights have suggested that interfering selection pressures exerted by different herbivore species on defense traits may hinder the directional evolution of increased herbivore resistance. This could explain why, somewhat counterintuitively, certain plant species evolve higher defense levels as herbivore species become less numerous, yet this hypothesis remains largely untested outside the theoretical realm. How climate change will alter selection by herbivore communities on plant defenses is even more of an open question. One of the most dramatic consequences of climate change for plants in temperate regions is the increased frequency and intensity of drought events. Drought is therefore anticipated to have a strong impact not only on plant performance but also the interactions between plants and other community members.

Doelstelling:

The aim of this project is to test how insect herbivore communities varying in complexity and drought interact with plant genotype to affect plant performance, including resistance and tolerance against insect herbivory. We will use wild cabbage (*Brassica oleracea*) from along the southern coast of England where naturally occurring populations differ in insect communities and defense traits. From each of four populations, ten mother plants were selected and of each mother forty seed pods were harvested. We will perform a laboratory common garden experiment, exposing half-sibs of each mother plant to either simple or complex herbivore communities, in either drought or control conditions. Plant growth and fitness will be determined, and measures of herbivore tolerance and resistance quantified.

Locatie:

22479: Environmental impact assessment in deep-sea nodule fields in the Pacific Ocean

Promotor(en): Ann Vanreusel, Ellen Pape
Begeleider(s): Nene Lefaible, Lara Macheriotou
Contactpersoon: Nene Lefaible
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

The growing demand for metals and recent developments in technology have stimulated the interest in mining polymetallic nodules in the deep sea. The largest, and hence commercially most attractive, nodule fields lie in the deep Pacific Ocean (Clarion-Clipperton zone), between 4000 and 6000 m water depth. These abyssal nodule fields have been explored during the last years and results show that the CCZ harbors highly diverse benthic (seafloor-associated) communities. However, a lack of comprehensive data (patchy- and under sampling) has led to a poor understanding of important ecologic aspects within this ecosystem. As a result, it is crucial to collect sufficient data for the characterization of the currently untouched ecosystem allowing for an environmental impact assessment before commercial mining operations start.

Doelstelling:

In 2019, several types of studies were performed in the Belgian and German license area in order to i) increase the environmental –and biological baseline data, ii) assess the potential impacts (disturbance tests) of the proposed mining activities and iii) provide valuable information for future decisions in terms of mitigation and restoration. Biological samples taken during this campaign mostly constitute meiofauna (0.032-0.063 mm sieve), which can be considered as an important size class in these soft-sediment benthic communities in terms of density, biomass and diversity. Analysis can be both based on metabarcoding as well as morphological analysis

Locatie:

sterrecampus S8

Website:

Meer informatie op: <https://miningimpact.geomar.de/>

22337: European sea bass assessment in the Belgian Part of the North Sea

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

Probleemstelling:

The poor state of the European sea bass (*Dicentrarchus labrax* L.) in the southern North Sea calls for a better understanding of its spatial ecology. The highly mobile sea bass is known to move from shallow, inshore feeding grounds in summer to deeper waters offshore in search of warmer temperatures in winter for spawning. Knowledge of these spatiotemporal changes in movement behaviour and distribution is critically limited in the southern North Sea. These spatial dynamics of sea bass in Belgian waters and the southern North Sea are investigated in a collaboration between Ghent University, the Flanders Marine Institute (VLIZ) and the Institute for Agricultural and Fisheries Research (ILVO).

Doelstelling:

The objective of this master thesis will be to investigate spatiotemporal patterns in the distribution and exploitation of sea bass. For this purpose, data from different sources are available: official catch statistics of professional fisheries, spatially explicit catch data from recreational fisheries, fishery-independent survey data and mark-recapture data.

Locatie:

Campus Sterre + ILVO Oostende

Opmerkingen:

The majority of the work will consist of data analysis in R. The student will also be involved in fieldwork, related to telemetry: tagging of fish and deployment of acoustic receivers at sea.

22420: Evolutie van zijwortel stamcelcompetentie in varen

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

Probleemstelling:

Het vormen van een wortel heeft minstens twee onafhankelijke evolutionaire oorsprongen, eenmaal bij de Lycophyta, en een tweede keer bij de gezamenlijke voorouder van de varens en zaadplanten. Zowel de varens als de zaadplanten vertonen monopodale wortelvertakking, wat suggereert dat hun wortelvertakkingssysteem een gemeenschappelijke evolutionaire oorsprong heeft. Ondanks de evolutionaire afstand blijkt zijwortelinitiatie vooral door te gaan in weefsels thv de xylempolen (met uitzondering van de grassen). Er zijn echter ook enorme verschillen. Zo is er een heel groot verschil in de ontogenie van de wortelweefsels in varens en zaadplanten. In zaadplanten worden zijn de weefsels opgebouwd uit clonale cellijnen die afgeleid zijn uit een beperkt aantal stamcellen in de worteltop die georganiseerd zitten rond een niet delend 'quiescent center'. Varens, daarentegen, hebben een actief delende apicale cel waarvan de dochtercellen stamcellen vormen die na een reeks gecoördineerde celdelingen differentieren tot de weefsels die de wortel opmaken. In angiospermen is de competentie tot zijwortelinitiatie beperkt tot de pericyclus, terwijl die competentie tot zijwortelinitiatie in varens varieert van de pericyclus in primitieve varens (zoals Equisetaceae en Osmundaceae), tot de endodermis in moderne varens (vooral polypod varens). Een laatste goed bestudeerde parameter van zijwortelinitiatie in angiospermen is de auxine gevoeligheid van het proces. In varens daarentegen is weinig gekend over de auxine-gevoeligheid van zijwortelinitiatie. De gekende rapporten in Ceratopteris en Marsilea suggereren een auxine-onafhankelijkheid van het proces.

Doelstelling:

In deze thesis is het de bedoeling om de de evolutie van zijwortelvorming binnen de varens na te gaan. Hierbij zullen we ons voornamelijk focussen op 4 species die samen evolutionair en ontwikkelingsbiologische interessante posities vertegenwoordigen. Om onze hoofdoelstelling te kunnen bereiken is het essentieel om morfologisch/anatomische verschillen van het zijwortelvormingsproces gedetailleerd in kaart te kunnen brengen. Hiervoor zullen we de laatste nieuwe methodologieën aanpassen voor gebruik in wortels van deze varens. Daarnaast zullen we bestaande protocols evalueren/optimaliseren om snel transgene planten te maken voor elk van deze varens, waarmee we dan mutanten (genome editing), overexpressielijnen en promotor-reporter lijnen zullen maken. Voor dit uitdagende project zoeken we een gemotiveerde student. We verwachten een belangrijke eigen, creatieve inbreng van de student in het project.

Locatie:

campus Technologiepark (VIB-PSB)

22469: Evolution of structure and function of reptile eggs

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

Probleemstelling:

Eggs are multifunctional structures that enabled early tetrapods to colonize the land millions of years ago, and are now the reproductive mode of over 70% of

land vertebrates. Eggshell morphology is at the core of animal survival, mediating the interactions between embryos and their environment, and has evolved into a massive diversity of forms and functions in modern reptiles. However, we still lack critical data on the basic properties of eggs, including their ultrastructure and functional properties. In this project the student will use electron microscopy, morphological analyses, functional tests (antimicrobial tests and optical properties) and phylogenetic comparative methods to test hypotheses on form-function relationships in eggs as well as the effect of the environment on their evolution. Specifically, the project will address the following questions: 1) How does eggshell morphology affect function? In particular, their reflectance properties and antimicrobial efficiency, and 2) Do nesting ecology and life history drive the evolution of eggshell architecture?. The results of this project will contribute to a larger project whose ultimate goal is to understanding how reptile eggs have evolved and how their morphology and functional properties affect the diversity of lineages we see today. Students with an interest in evolution, ecology, physiology, biomimicry and any combination thereof, are strongly encouraged to apply.

Doelstelling:

The Objectives of this study are:

1. To Design experiments to test the antimicrobial efficiency and to measure optical properties of reptile eggshells.
2. To build a database of nesting ecology of selected reptile species
3. To perform comparative phylogenetic analyses to test the relationship between ecology and functional morphology of reptile eggshells.

Locatie:

campus Ledeganck

22463: Evolution of the musculoskeletal cranial system in relation with the burrowing performances in amphisbaenians.

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

Probleemstelling:

Mostly due to their hidden life style, limbless burrowing vertebrates have received only little scientific attention since the beginning of the 20th century. However, although they have no legs, they show many specializations and occupy a wide range of different habitats. Amphisbaenians are a group of highly specialized burrowing squamates. Most of them are limbless and possess a strongly ossified and compacted skull with different cranial shapes to dig permanent galleries into the ground. However, despite good descriptions of the skull anatomy in the literature, no studies dealt with functional morphology including in vivo burrowing forces and quantitative data on the musculoskeletal system. By combining musculoskeletal morphology and in vivo performances, this thesis aims to give new insights into the function of such specialized morphology and determine what are the exact anatomical structures and biomechanics underlying high burrowing performances.

Doelstelling:

During this thesis, μ CT-scans of five species will be reconstructed in 3D using Amira software and then landmarked to compare the 3D shape of the skull. Dissections and reconstruction of stained μ CT-scans will allow us to qualify and quantify the muscular morphology of the head with emphasis on the muscles stabilizing the head such as the jaw joints. Then, the analysis of force plate data will give us information about the maximum burrowing force that amphisbaenians can perform. Statistical analyses will then be conducted within a well resolved phylogenetic framework and should allow us to understand the relation between the burrowing performance, the modification of the skull shape and the head musculature. These results will give new insights into the organization and adaptive evolution of the cranial system in fossorial taxa.

Locatie:

Campus Ledeganck

Website:

Meer informatie op: www.ugent.be/we/biology/evo-morph/en/research/projects/project-limbless-tetrapods

22465: Evolution of the musculoskeletal cranial system in relation with the burrowing performances in snakes

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

Probleemstelling:

Mostly due to their hidden life style, limbless burrowing vertebrates have received only little scientific attention since the beginning of the 20th century. However, although they have no legs, they show many specializations and occupy a wide range of different habitats. Among these vertebrates, a lot of snakes have been described as fossorial species. Assessments of fossoriality are usually based on simple observations of the species on the field. Moreover, with the exception of the fossorial uropeltids, knowledge about the morphological variations underlying the burrowing behavior remain scarce. Considering that fossorial species are distributed across most major radiations of snakes: from the small scolecophidians, through basal alethinophidians, snakes form a perfect group to study the evolution of the anatomical structures and biomechanics underlying burrowing performance.

Doelstelling:

During this thesis, μ CT-scans of five species will be reconstructed in 3D using Amira software and then landmarked to compare the 3D shape of the skull. Dissections and reconstruction of stained μ CT-scans will allow us to qualify and quantify the muscular morphology of the head with emphasis on the muscles stabilizing the head such as the jaw joints. Then, the analysis of force plate data will give us information about the maximum burrowing force that the different snakes can perform. Statistical analyses will then be conducted within a well resolved phylogenetic framework and should allow us to understand the relation between the burrowing performance, the modification of the skull shape and the head musculature. These results will give new insights into the organization and adaptive evolution of the cranial system in fossorial taxa.

Locatie:

Campus Ledeganck

Website:

Meer informatie op: www.ugent.be/we/biology/evo-morph/en/research/projects/project-limbless-tetrapods

22464: Evolution of the musculoskeletal postcranial system in relation with the burrowing performances in amphisbaenians.

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

Probleemstelling:

Mostly due to their hidden life style, limbless burrowing vertebrates have received only little scientific attention since the beginning of the 20th century. However, although they have no legs, they show many specializations and occupy a wide range of different habitats. Amphisbaenians are a group of highly specialized burrowing squamates. Most of them are limbless and possess a strongly ossified and compacted skull with different cranial shapes to dig permanent galleries into the ground. Moreover, some studies pointed out that amphisbaenians could use the internal concertina locomotor mode like uropletids to move underground. Despite good descriptions of the skull anatomy in the literature, only a few studies have dealt with the musculoskeletal postcranial system. However, some preliminary data show that they can produce really high burrowing forces using their body. To better understand the exact anatomical structures and biomechanics of efficient burrowing in amphisbaenians, more qualitative and quantitative data on the postcranial system are thus needed.

Doelstelling:

During this thesis, μ CT-scans of six vertebrae for five species of amphisbaenians will be reconstructed in 3D using Amira software and then landmarked to compare the 3D shape of the vertebrae. Dissections and reconstruction of stained μ CT-scans will allow us to qualify and quantify the axial musculature. Then, the analysis of force plate data will give us information about the maximum pushing force that amphisbaenians can perform. Statistical analyses will then be conducted within a well resolved phylogenetic framework and should allow us to understand the relation between the burrowing performance and the modification of the postcranial musculoskeletal system. These results will give new insights into the organization and adaptive evolution of the postcranial musculoskeletal system in fossorial taxa.

Locatie:

Campus Ledeganck

Website:

Meer informatie op: www.ugent.be/we/biology/evo-morph/en/research/projects/project-limbless-tetrapods

Onderwerp voorbehouden voor Ditte De Waele

22466: Evolution of the musculoskeletal postcranial system in relation with the burrowing performances in snakes.

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

Probleemstelling:

Mostly due to their hidden life style, limbless burrowing vertebrates have received only little scientific attention since the beginning of the 20th century. However, although they have no legs, they show many specializations and occupy a wide range of different habitats. Among these vertebrates, a lot of snakes have been described as fossorial species. Assessments of fossoriality are usually based on simple observations of the species on the field. Moreover, with the exception of the fossorial uropeltids, knowledge about the morphological variations underlying the burrowing behavior remain scarce. Considering that fossorial species are distributed across most major radiations of snakes: from the small scolecophidians, through basal alethinophidians, snakes form a perfect group to study the evolution of the anatomical structures and biomechanics underlying burrowing performance.

Doelstelling:

During this thesis, μ CT-scans of six vertebrae for five species of snakes will be reconstructed in 3D using Amira software and then landmarked to compare the 3D shape of the vertebrae. Dissections and reconstruction of stained μ CT-scans will allow us to qualify and quantify the axial musculature. Then, the analysis of force plate data will give us information about the maximum pushing force that amphisbaenians can perform. Statistical analyses will then be conducted within a well resolved phylogenetic framework and should allow us to understand the relation between the burrowing performance and the modification of the postcranial musculoskeletal system. These results will give new insights into the organization and adaptive evolution of the postcranial musculoskeletal system in fossorial taxa.

Locatie:

Campus Ledeganck

Website:

Meer informatie op: www.ugent.be/we/biology/evo-morph/en/research/projects/project-limbless-tetrapods

22453: Exclusive for Africa: *Lactifluus* sect. *Pseudogymnocarpi*: creating order in the chaos

Promotor(en):	Annemieke Verbeken, Eske De Crop
Begeleider(s):	
Contactpersoon:	
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	

Nog onbeslist voor:

Aantal studenten: 1

Aantal masterproeven: 1

Motivering voor deze opleiding:

Probleemstelling:

The milkcap genus *Lactifluus* is known for its species complexes and cryptic diversity. Recent studies show a large species diversity within this mainly tropical genus of milkcaps, of which certain lineages still need to be resolved. *Lactifluus* section *Pseudogymnocarpi* is an African species complex containing several cryptic species occurring in woodlands and rain forests of West, East and Central Africa. Current phylogenies show recent species diversification and species are difficult to delimit in the field. This group is in need of an extensive examination that leads to meticulous species descriptions and keys.

Doelstelling:

This project aims to elucidate this complex group of African *Pseudogymnocarpi*, by an extensive study of both herbarium specimens available at Ghent University and fresh basidiocarps collected in Zambia/Zimbabwe. Collections will be carefully described, DNA extractions and PCR's will be performed in order to reconstruct the phylogeny of this section and delimit species using several techniques. The results of these analyses will be combined in keys, that will be tested and adjusted when necessary in the field. This project combines multiple mycological skills/tasks: extensive field work, morphological work in the field and in the lab, molecular study and analyses.

Locatie:

22441: Function and evolution of colour in springtails.

Promotor(en): Bram Vanthournout, Matthew Shawkey

Begeleider(s):

Contactpersoon:

Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie

Niet behouden voor:

Nog onbeslist voor:

Aantal studenten: 1

Aantal masterproeven: 1

Motivering voor deze opleiding:

Probleemstelling:

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

Doelstelling:

Locatie:

22425: Functional analysis of *Caenorhabditis elegans* globin-3.

Promotor(en): Bart Braeckman

Begeleider(s): Tim Loier

Contactpersoon:

Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie

Niet behouden voor:

Nog onbeslist voor:

Aantal studenten: 1

Aantal masterproeven: 1

Motivering voor deze opleiding:

Probleemstelling:

Globins are globular heme-binding proteins that are widely distributed throughout life. Globin diversity is exceptional in nematodes and in the *C. elegans* genome 34 globin genes were discovered. Globin-3 attracted our attention as it is one of the few globins that shows clear phenotypes upon knockout: e.g. reduced fertility, uncoordinated motility, and reduced pharyngeal pumping. This globin is expressed in 20 to 30 neurons, in a specific region in the somatic gonad, and in coelomocytes. It occurs as two isoforms, both predicted to be membrane-bound: one in the plasma membrane and one in the mitochondria.

Doelstelling:

In this project, we will functionally characterize these two GLB-3 isoforms further. Since we know in which particular neurons GLB-3 is expressed, we can try to link GLB-3 with known functions of these neuronal networks. Additionally, we will search for possible GLB-3 interaction partners. As GLB-3 is likely a superoxide generator, we will focus specifically on its interaction with superoxide dismutases, but also guanylate cyclases. *C. elegans* double mutants will be generated by means of classical crossing techniques and verified with PCR. The double mutants will be used to verify the interaction of GLB-3 with these enzymes.

Locatie:

campus Ledeganck - 2e fase - 4e verdieping

22389: Functional characterisation of sexual reproduction in diatoms

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

Probleemstelling:

Diatoms, a successful group of microalgae, are characterised by a unique diplontic life cycle. A dominant vegetative phase, in which cells divide mitotically, precedes a short sexual phase, in which cells undergo meiosis. Vegetative divisions result in an average cell size decrease over the population; without restoration of the original cell size, extreme miniaturisation would eventually cause cell death. Therefore, sexual reproduction is essential for the survival of most diatom species, since the non-silicified zygote can expand and thus restore original size.

In the PAE lab, we study 2 diatom species as model organisms for sexual reproduction: *Cylindrotheca closterium* and *Seminavis robusta*. Both species are heterothallic and can only reproduce when cells of opposite mating types (MT+ and MT-) are present below SST. At first, opposite mates make contact ("cell pairing") before starting meiosis, which results in 4 gametes. Compatible gametes will fuse into 2 zygotes, which can expand into auxospores until the maximal cell size is reached and 2 initial cells are formed. The initial cell will undergo mitosis and the life cycle can start again.

The molecular basis of these events remains largely hypothetical. Gene expression studies have revealed a number of candidate genes involved in different phases of the sexual cycle.

Doelstelling:

The aim of this master thesis is to functionally validate a number of the most promising candidate sex genes. For both model species, an in-house draft genome as well as a list of differentially expressed genes during different stages of sexual reproduction (cell pairing-gametes/zygotes-auxospores) is available. By comparing both data sets, we expect to identify highly conserved genes involved in the regulation of sexual reproduction. We will functionally validate these genes by performing a CRISPR/Cas9 gene KO in *C. closterium*. More specifically, multiple target sites for the same candidate gene will be selected to increase the chance of a successful gene KO. To avoid the disadvantages of the classical 'nuclease-driven' approach (a low transformation efficiency and the stable expression of the Cas9 nuclease), cells will be transformed using a DNA-free approach, in which the Cas9-protein is shot directly into the cells ('proteolistics' approach). After transformation, gene KO mutants will be selected through the growth in selective medium and through gene sequence confirmation. The effect of the KO will be assessed by engaging the mutants in sexual reproduction, of which the progression through the different stages will be followed and evaluated. An aberrant progression of sexual reproduction will provide clues for the functional role of the candidate gene.

Locatie:

22458: Functional traits of fauna associated with offshore wind farms

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

Probleemstelling:

In recent years, many European coastal areas witnessed the installation of offshore wind farms, as the demand for renewable energy is increasing. As a consequence of the European 2030 Energy Strategy, even more offshore wind farms will be constructed in the coming years. While these windfarms indeed provide renewable energy, they induce important physical changes in the marine realm. Constructing offshore wind farms results in the introduction of hard substrate in areas that used to be exclusively sandy. As such, large quantities of new habitat are introduced, which are rapidly colonised by fouling fauna, in huge densities and high diversity, which cascades in the attraction of commercial fish species (i.e. cod) and large crustaceans (edible crab, lobster). Thanks to detailed monitoring programmes, there is detailed information on structural changes in marine fauna (densities, biomass and diversity), but it is still unclear how these new communities affect the functioning of the marine environment, both at the local (turbine – wind farm) or regional (i.e. Southern Bight of the North Sea). On the one hand, this is due to logistic constraints and safety issues related to working in offshore wind farms, on the other hand there is also a lack of well-structured data allowing for an ecosystem-functioning oriented analyses.

Doelstelling:

Within this research, students will assist in filling the data gap by contributing to the first functional trait database compiled for (artificial) hard substrate fauna. The available long-term monitoring data on the fouling fauna of wind turbines in the Belgian Part of the North Sea will be made available to the master student and need to be reorganised and amended with functional trait data. These data will be compiled through a dedicated literature study and added to a relational trait database. The student will then assist and conduct preliminary data-analyses based on the completed data compilation. There will also be opportunities to do practical work in the field and help with ongoing research.

Locatie:

Marine Biology Research Group Ghent University, Campus Sterre S8 Krijgslaan 281 B-9000 Ghent

Opmerkingen:

There will also be opportunities to do practical work in the field and help with ongoing research.

22490: Fungal diversity in a hyperparasitic system of bats, bat flies and Laboulbeniales (Ascomycota)

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

Probleemstelling:

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

Laboulbeniales fungi.

Doelstelling:

Locatie:

22402: Genetic rescue of the threatened butterfly *Hipparchia semele* in Flanders

Promotor(en): Maurice Hoffmann, An Vandenbroeck
Begeleider(s): An Vandenbroeck, Dirk Maes
Contactpersoon:
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

To prevent a further decrease in populations of *Hipparchia semele* in Flanders, a species protection plan is in development by the Agency of Nature and Forest of the Flemish government. This protection plan include the restoration of the habitat and, afterwards, a re-introduction of this butterfly species at specific locations in the Campine region where the species went extinct. In this project, we investigate the genetic structure of populations of the butterfly species *Hipparchia semele* in northeastern (Campine region) and western (coast) Flanders in frame of planned translocation actions. The aim is to define the population genetic structure and genetic diversity of the studied populations and to define the most suitable source populations for a translocation action. Sampling will be done at the coast and the Campine region in August 2020 (together with Natuurpunt).

Doelstelling:

We will use a non-destructive sampling technique by taking wing clips for DNA-extraction of about 300 individuals. After DNA-extraction, we will develop a set of microsatellite nuclear markers to generate individual genetic fingerprints. The labwork and the scoring of the genetic profiles are planned in September – December 2020. Afterwards, the genetic data will be analyzed with different software packages and guidelines for translocation will be provided based on the data. The labwork and the scoring of the genetic profiles need to be done at ILVO Melle – Plant 39 (near Ghent), where INBO has a temporary workplace for the moment. DNA-analysis in the lab will be under assistance of an INBO lab technician. Field work will be in collaboration with an INBO technician or with Natuurpunt

Locatie:

INBO, Geraardsbergen, Melle; Ledeganckcampus

Website:

Meer informatie op: www.inbo.be (from January 2020 onwards)

22429: Global warming and cryptic species: investigating transgenerational effects on the performance and the microbiome of cryptic species.

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

Probleemstelling:

Marine environments are being threatened by global change. Increased atmospheric CO₂ concentrations lead to global warming on the one hand, and on the other hand to a decrease in ocean pH. Such shifts in ocean characteristics act as stressors upon biological communities, e.g. through interference with life-history traits and physiology; or through induction of changes in community composition, functioning, and biodiversity. Understanding the response of marine organisms to a changing environment as a consequence of global change is therefore crucial.

Cryptic species are morphologically indistinguishable, but show consistent genetic and ecological differences and may exhibit species-specific functions in the ecosystem, which makes them an interesting model to study the effect of global change on life-history traits. Besides species-specific differences in reaction to global change, tolerances to environmental change may also be transgenerational: some individuals may be more resistant to environmental changes than others and may pass this on to next generations. This may be caused by differences in the microbiome (bacteria associated with the gut) of different individuals/species.

Doelstelling:

In this thesis we will subject species to changing environmental conditions and check their performance (population growth, behaviour, ...). Moreover effects on the microbiome will be checked with Next Generation Sequencing to test if an effect on their microbiome can be found. Subsequently, we will collect the following generations of these species and raise them in treatments without changed conditions, to investigate if the species' microbiome remains affected. Moreover, we will also subject them to changed conditions, to see if they react differently than organisms from which previous generations have never been in contact with environmental change.

Locatie:

Campus Sterre en campus Ledeganck

22380: Gradients of moth abundance along forest edge-to-interior gradients

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

Probleemstelling:

Moths are a species rich group of invertebrates with an important functional role in deciduous forest. Forest structure can be extremely different between forest patches influencing microclimate, vegetation etc. which again influences moth community composition.

Doelstelling:

This thesis research will investigate moth abundance along forest edge-to-interior gradients using light traps in twelve forests within the [FORMICA-project](#) (four regions in Belgium and northern France x three structural forest types). With this dataset, we investigate the direct and indirect effects of forest structure on moth community composition. The results will give us insight in the biological niches of moths and in the effect of forest management on moth communities.

Locatie:

campus Ledeganck

Onderwerp voorbehouden voor Cyr Mestdagh

22407: Habitat characterization of Atlantic acidophytic beech and oak forest on nutrient poor sandy soils in the Campine region of Flanders

Promotor(en): Maurice Hoffmann, Luc De Keersmaeker
Begeleider(s): Luc De Keersmaeker, Cécile Herr
Contactpersoon: Cécile Herr
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

In this project, we focus on European protected Atlantic acidophytic beech (European habitat 9120) and oak forests (European habitat 9190) on nutrient-poor sands in the Campine region. Reference images of long-term afforestation on sandy soil are scarce in Flanders and throughout NW Europe. It is often assumed that oak forests are the climax on acidic and poor sandy soils, but there are strong indications that further soil development will produce oak-beech forests that are characterized as European habitat 9120. We want to examine how and how fast this secondary succession proceeds and how 9190 and 9120 can be distinguished. Distinction criteria are primarily based on abiotic location characteristics (mainly soil chemistry), historical land use and management characteristics. We study a chronosequence of forests on sand in the Campine region, which are selected a priori with a GIS analysis. The project contributes to the INBO Habnorm project (2015-2020) in which requirements for the sustainable functioning of Natura 2000 habitat (sub) types are determined in relation to the main environmental pressures.

Doelstelling:

The student will be included in an enthusiastic group of experts (forest, soil, statistics) and can also benefit from the data that has already been collected in this project. Additionally, the student will perform vegetation measurements and / or take soil samples. At the laboratory, the student will build up experience with software for data management and processing. A literature study will focus on abiotics of the habitat type at reference and historical locations. The student will be stimulated to organize discussion moments with different experts.

Locatie:

INBO, Brussel, campus Ledeganck

Website:

Meer informatie op: www.inbo.be (from January 2020 onwards)

Onderwerp voorbehouden voor nvt

22424: Hidden diversity of Antarctic soil metagenomes: Exploring Microbial Dark Matter

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

Motivering voor deze opleiding: Onderwerp van vorig jaar werd aangepast aan de actuele stand van het project.

Probleemstelling:

The vast majority of the microbial diversity on Earth has never been characterized in laboratory cultures and is only known from DNA sequence data. A fraction probably has not even been sequenced or detected whatsoever. These unknown microbes (bacteria, archaea, eukaryotes and viruses), sometimes called "microbial dark matter", are numerically dominant in all major environments on Earth, with the exception of the human body, where most bacteria have been characterized. Extreme environments such as polar soils are predicted to contain the highest fraction of these organisms that are new to science. Without genomic data for these organisms, the question remains what their role and significance is in biogeochemical processes that impact Antarctic soils and atmospheric chemistry. Considering that polar regions are shown to be among the most rapidly warming areas of the planet, and that climate change will lead to pronounced shifts in the diversity of soil bacteria, with stronger warming effects on microbial abundances in colder regions, it is vital to incorporate genomic data of Antarctic soils in global ecological analyses.

Doelstelling:

The goal of this study is to analyze metagenomes collected from Antarctic soil samples. This includes assembly and binning of draft genomes from metagenomes, visualization, taxonomic profiling, and functional annotation. Depending on the interest of the student a specific focus (on a particular group of bacteria, archaea or viruses, or on part of the analysis) can be taken. Due to the computational nature of the topic, the student needs to be familiar with linux command line and (bio)informatics.

Locatie:

Campus Ledeganck

22459: Host range, systematics, and geographical distribution in a host-parasite model system

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

Probleemstelling:

Parasitic species are estimated to account for around half of all species worldwide and species discovery rates remain high. Therefore, investigating the ecology and evolution of these organisms can help us understand ecosystems as parasites are a key component of our environment. As part of a larger project on macroevolutionary and ecological drivers of host specificity, we use the parasite-host interaction of monogenean flatworms from cichlid fish as a model system due to the well-known ecology and evolution of the host species. The parasite diversity of cichlids remains biased towards a few economically relevant host species. Therefore, we will investigate understudied host-parasite interactions to address current knowledge gaps.

Doelstelling:

The student will have the opportunity to gain insight into a range of research methods such as microscopy and molecular techniques, and statistical, phylogenetic, and geographical analyses. Furthermore, the student will contribute to a larger research project on parasite ecology and evolution.

Locatie:

onderzoeksgroep Zoology: Biodiversity and Toxicology, Hasselt

Website:

Meer informatie op: <https://www.uhasselt.be/UH/Onderzoeksgroepen/DetOndgr.html?oid=52>

Opmerkingen:

Supervisor: Armando Cruz Laufer +32456054033 armando.cruzlaufer@uhasselt.be co-promotoren Prof Maarten Vanhove maarten.vanhove@uhasselt.be Prof Tom Artois tom.artois@uhasselt.be

Onderwerp voorbehouden voor Tanisha Moons

22412: How different are insect faunas in Flanders nowadays from those two to three decades ago?

Promotor(en): Maurice Hoffmann, Marc Pollet
Begeleider(s): Marc Pollet, Luc De Bruyn
Contactpersoon: Marc Pollet
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

[Sánchez-Bayo & Wyckhuys \(2019\)](#) were the first to report on a global decline in insect faunas. The situation seems most precarious (or at least best documented) in western Europe (see [Hallmann et al. 2017, 2019](#); [Kleijn et al. 2018](#); [Seibold et al. 2019](#)). Most authors do not exclude that the intensification of agricultural practices might be an important factor, but Seibold et al. (2019) also observed considerably poorer insect faunas in forest habitats. Surprisingly enough, thus far no attempts have been made to assess the trend in insect diversity in Flanders, but there are certainly opportunities (see also project proposal no. 8 that focuses on the current insect diversity).

Back in the 80ies and 90'ies, researchers at the Royal Belgian Institute for Natural Sciences (RBINS) conducted a massive Malaise trap sampling campaign all over Belgium, much like the more recent and better known Swedish Malaise Trap Project ([SMTP](#)). Mainly protected sites like nature reserves were investigated in this large scale survey. From the collected samples that mainly consist of flying insects (Diptera and Hymenoptera in particular), a number of dipteran families have been identified; these data are still available. In 2019, i.e. 2 to 3 decades later, we restarted investigating the very same sites in two of these nature reserves (De Gavers, Harelbeke, and De Mandelhoek, Ingelmunster), and during the next years, that initiative will be continued.

Doelstelling:

The comparison of dipteran faunas between both time periods with an interval of 2 to 3 decades might contain clues about factors that affect both their species richness, diversity and even biomass. The more sites are involved, the clearer patterns might arise.

Profile: we are looking for an allround biologist with a pronounced interest in entomology, who is both accurate with data and material, communicative, creative and thinks out-of-the-box. (S)he knows the different insect orders and preferably more, or is willing/capable to extend her/his knowledge.

Locatie:

INBO, Brussel, campus Ledeganck

Website:

Meer informatie op: www.inbo.be (from January 2020 onwards)

Onderwerp voorbehouden voor nvt

22387: How do biological processes influence the flocs flocculation?

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

Probleemstelling:

There has been a growing interest in the transport of fine-grained sediments in estuaries because of both the high dredging costs associated with siltation problems in harbors and navigation channels, and because of environmental problems due to human intervention. The fine-grained sediment particles are important carriers for substances such as trace metals, radio-nuclides and organic micropollutants. Fine-grained sediment is also ecologically important for acting as a substratum for biological processes such as microorganism colonization and biofilm growth, as well as because its role in the transport of nutrients and the organic matter in suspension are important sources of food for many aquatic organisms.

Here sediment coated with biofilms are designated as bio-sediment. The biofilm is a complex structure consisting of living microorganisms and their metabolic products, known as Extracellular Polymeric Substances (EPS). Extensive investigations on the role of biological processes in the Suspended Particulate Matter (SPM) indicated the important role of microorganisms in the formation and degradation of aggregates, which is defined as bioflocculation. The inorganic or organic particles are biologically glued by polymeric fibrils, which are named as Extracellular Polymeric Substance (EPS) or Transparent Exopolymer Particles (TPS). Though many experiments have been done to identify EPS effects on bioflocculation, complex components of EPS, different experimental methods and environments studied resulted in controversial conclusions. A lack of understanding and studies of the contribution and characteristics of EPS on bioflocculation processes thus complicate simulation of sediment distribution along the estuary zones.

Doelstelling:

This master thesis aims to study the nutrient demand and supply under turbulent shear, and bioflocculation processes under different EPS contents or amounts. For this purpose, student(s) will perform flocculation experiments in a mixing chamber to investigate the floc sizes under different EPS contents coupled with shear rate, salinity and sediment concentration. Floc images will be acquired by using a camera system and analyzed by using MATLAB Image Processing Toolbox and ImageJ. This data will also serve as the basis of the understanding of sediment transport pattern in the Scheldt Estuary.

Locatie:

22409: How many insect species occur in a Flemish marshland habitat?

Promotor(en): Maurice Hoffmann, Marc Pollet

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

Probleemstelling:

Recent Red Lists (<https://www.inbo.be/nl/rode-lijsten-vlaanderen>) reveal that a large number of species is currently threatened in Flanders, not in the least insects. But as a German study (Hallmann et al. 2017) suggests, entire insect populations are at stake. Indeed, these authors showed that communities in nature reserves in western Germany declined with over 75% in the past three decades. And there are indications that the same processes are taking place in the Netherlands (Kleijn et al. 2018). So far, no attempts have been made to assess the current insect diversity let alone its recent trends in Flanders. The first aspect is the main goal of this project.

To estimate the number of insect species at one single site alone is already a formidable challenge. Not only the individual species show seasonal activity patterns which requires (semi-) permanent monitoring efforts, but multiple collecting devices are necessary to gather flying, soil surface dwelling and subterranean species. Moreover, there is the issue of the taxonomic impediment: while there might be about 25,000 insect species in Belgium (not all of these occurring at the marshland site under investigation, of course), it is unlikely that a taxonomic expert for each of the collected insect groups can be found. And this knowledge cannot be expected from you individually either.

Doelstelling:

A full year survey has been conducted in a nature reserve in Flanders in 2018 (Wellemeersen, Denderleeuw) including a Malaise trap and pan traps that might provide (part of) the necessary samples for processing. However, other approaches are also possible including additional fieldwork with e.g., the employment of a camera counter (<https://vroegevogels.bnnvara.nl/nieuws/automatisch-insecten-tellen-en-herkennen>). Depending on the approach (after discussion with you), a network of Belgian and foreign taxonomic experts can be involved which would also be part of the project.

Profile: we are looking for an allround biologist with a pronounced interest in entomology, who is both accurate with data and material, communicative, creative and thinks out-of-the-box. (S)he knows the different insect orders and preferably more, or is willing/capable to extend her/his knowledge.

Locatie:

INBO, Brussel

Website:

Meer informatie op: www.inbo.be (from January 2020 onwards)

Onderwerp voorbehouden voor nvt

22384: Impact of offshore wind farms on the soft-sediment benthos and benthic ecosystem functioning

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

Probleemstelling:

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 (BPNS). Currently, several offshore wind farms are already operational in the BPNS and more concession areas are granted for construction. By 2030, all Belgian offshore windfarms together should produce as much renewable energy as windfarms on land. A monitoring program was set up to identify the ecological effects of this anthropogenic disruption on the soft-sediment macrobenthos (organisms living in the sediment and larger than 1mm).

The permanent presence of introduced artificial structures such as wind turbines result in a modification of the habitat, by means of altered local environmental conditions (changes in hydrology, granulometry and food availability) and the associated macrofaunal communities, which is shown in both higher densities and biodiversity in close (<50 m) vicinity to certain types of wind turbine foundations.

In addition, these structures provide surface area for colonizing epifaunal communities, which could intensify these changes by influencing particle -and organic matter fluxes and local biodiversity. It is however expected that the spatial extent of these effects will depend on several factors such local conditions, turbine type and the turbine-specific epifaunal communities.

Therefore, next to the yearly monitoring campaign, a multidisciplinary integrated monitoring campaign will be conducted in August 2020 to investigate the small-scale effects of wind turbine presence on local hydrodynamics, hard substrate fauna colonizing the turbines, geological imprints of locally altered hydrodynamics on the sediment and benthic communities along with the characterization of their habitat.

Doelstelling:

The student will be able to take part in this one week campaign in the offshore windfarms. Back in the home lab, she/he will identify the macrobenthic organisms in the sediment samples until species level and possible changes in the environment will be evaluated using biotic (biomass, abundance, diversity on and around the turbines) and abiotic variables (sediment grain size, organic material, hydrodynamics). Also benthic ecosystem functioning can be assessed by measuring carbon mineralization rates in sediments in a transect along the wind turbines. If interested, the student can also be involved in the large-scale, yearly monitoring campaign during October/November 2020 (1 week at sea with RV Belgica and several days at sea with a small research vessel to access the sites adjacent to the wind turbines). Also macro- and hyperbenthic samples from these monitoring campaigns can possibly be studied in the framework of an IMBRSea master thesis.

Locatie:

campus Sterre

22488: Impact of sand extraction activity on micro- and macrobenthic communities in the North Sea

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

Probleemstelling:

The North Sea is one of the busiest shipping routes in Europe and multiple other activities such as offshore wind energy exploitation and sand extraction take place. All these activities can impact marine biodiversity and to ensure sustainable exploitation of the marine environment, monitoring of marine life is key. Traditionally, environmental impact assessments are mainly based on morphological species identification. However, this method is very time-consuming, labor-intensive and demands specific taxonomic knowledge. Faster and cost-effective monitoring methods use DNA-based characterization of marine life to complement morphology based identification. In addition, DNA signatures of marine sediments can be used as a proxy for good environmental status by applying machine learning models.

Doelstelling:

This research will investigate how sand extraction activity in the Belgian part of the North Sea affects the benthic communities using DNA-based methods. Different sand banks with similar sand extraction activities in the North sea have been sampled. DNA metabarcoding of bacterial and macrobenthic samples will be conducted to investigate whether similar shifts in benthic communities related to sand extraction are occurring in the different sand bank systems. The student will contribute to the implementation of genetic methods for the monitoring of sand extraction. Very good laboratory and programming skills in R are needed for the successful completion of this research.

Locatie:

ILVO, Ostend

22404: Influence of ash dieback-disease on the development of the herb layer: a case study in Muizenbos (Ranst)

Promotor(en): Maurice Hoffmann, Luc De Keersmaecker

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

Probleemstelling:

Since five years, ash dieback (caused by *Hymenoscyphus fraxineus*) has been causing massive dieback and loss of vitality in the common ash. In addition to the important forestry impact, this damage has also led to the fact that a lot of ash forests have suddenly become very bright.

We want to investigate the effect of this sudden opening of the canopy on the development of the herb layer. Quite a lot of research has already been done into the effects of canopy cover on the herb layer. However, this is usually based on the effect of fellings. In such situations there is always a combination of extra light and disturbance of the soil when harvesting the trees. In this case we can examine the effect of additional light without the side effects of harvesting.

The aim of this study is thus to analyze the effects of sudden exposure to light as a result of ash dieback on the herb layer. For this purpose a case study is performed in the core area of the unmanaged forest reserve of Muizenbos. This core area is located in ancient woodland on a base-rich, nutrient-rich soil. So a very rich herb layer of ancient woodland species occurs. A lot of research has already been carried out in this forest, so there is a lot of background information that can be incorporated and used.

The core area of Muizenbos is approximately 1 ha in size. Half of the area is a poplar plantation with an understorey of mainly common ash, and the other half is an old ash stand with a mixed understorey, dominated by hazel. In both parts of the forest, the ash trees suffer heavily from ash dieback, so that the secondary canopy resp. the upper canopy suddenly became much more transparent.

Doelstelling:

Vegetation recordings before and after the attack by *Hymenoscyphus fraxineus* are available for this core area: in 2007 and 2017, 49 subplots of 10 x 10 m were inventoried in each part (full survey of herb layer, estimate of canopy cover). There are also dendrometric measurements of the plots available. In 2017, the vitality of the 150 ash trees in this core area was also assessed, estimating leaf loss (forest vitality inventory method). All trees are also positioned.

Support : data on vegetation relevés, dendrometry, soil chemistry, ... GIS-layer of the sample plots, vitality survey of the ashes in the core area are available. Supplementary support for field survey (relocation of the plots...), background information can be provided by INBO.

Locatie:

INBO, Geraardsbergen, Ledeganckcampus

Website:

Meer informatie op: www.inbo.be (from January 2020 onwards)

Opmerkingen:

Useful references : Bloome & Mitchell, 2017. Ecological impacts of ash dieback and mitigation methods. <https://livingashproject.org.uk/pdfs/FCRN029%202017.%20Ecological%20impacts%20of%20ash%20dieback%20and%20mitigation%20measures.pdf> Mitchell et al., 2014. Ash dieback in the UK: A review of the ecological and conservation implications and potential management options. *Biological Conservation* 175, 95–109. https://www.researchgate.net/publication/262489965_Ash_dieback_in_the_UK_A_review_of_the_ecological_and_conservation_implications_and_potential_managem Mitchell et al., 2016. Potential impacts of the loss of *Fraxinus excelsior* (Oleaceae) due to ash dieback on woodland vegetation in Great Britain. *New Journal of Botany* 6, 2-15. <https://www.tandfonline.com/doi/abs/10.1080/20423489.2016.1171454?journalCode=yjnb20> Vasaitis & Enderle (eds), 2016. Dieback of European Ash (*Fraxinus* spp.) Consequences and Guidelines for Sustainable Management <https://www.slu.se/globalassets/ew/org/inst/mykopat/forskning/stenlid/dieback-of-european-ash.pdf>

Onderwerp voorbehouden voor nvt

22405: Influence of wild boar (*Sus scrofa*) on vegetation development in the Meerdaal forest

Promotor(en): Maurice Hoffmann, Luc De Keersmaecker
Begeleider(s): Luc De Keersmaecker, Kris Vandekerckhove
Contactpersoon: Luc De Keersmaecker
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:

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

Probleemstelling:

After more than 200 years of absence, wild boar have recolonized the Meerdaal forest since about ten years. In the meantime, the population has already grown to over a hundred. These animals have an important impact on the forest ecosystem. Because of their disturbance of the soil they provide extra dynamics and can therefore also have an important influence on the development of the herb layer.

In the forest there are about 100 permanent vegetation plots in the unmanaged forest reserves of 'Everzwijnbad' and 'Pruikenmakers'. Two vegetation surveys have already been carried out in these plots, in 2003-2013 and 2005-2015, so before and after the arrival of wild boar. In the second vegetation survey, wild boar rooting areas were specifically quantified in the vegetation survey.

Doelstelling:

The aim of the thesis is to investigate to what extent the increasing population of wild boar has an impact on the herb layer and how large this impact is. This can be done on the basis of the available datasets supplemented by additional surveys, specifically focusing on wild boar impact in the permanent plots by the thesis student.

Similar studies have already been carried out in Denmark (Brunet et al. 2016) and Italy (Burrascano et al. 2015). On the impact of recolonisation by wild boar on vegetation in Flanders, a master study was performed in the Zwarte Beek (Volckaert, 2013).

Support : data on vegetation, tree layer, soil chemistry, ... GIS-layer of the permanent plots and additional guidance in the field (to retrieve the plots) can be supplied by the staff of the forest ecology research team of INBO. Detailed estimates of the population of wild boar in Meerdaal forest is available from the research team on Fauna Management of INBO.

Locatie:

INBO, Geraardsbergen, Ledeganckcampus

Website:

Meer informatie op: www.inbo.be (from January 2020 onwards)

Opmerkingen:

Useful references: Brunet J. et al. (2016). Disturbance of the herbaceous layer after invasion of an eutrophic temperate forest by wild boar. *Nordic Journal of Botany* 34: 120–128. <https://onlinelibrary.wiley.com/doi/epdf/10.1111/njb.01010> Burrascano S. et al. (2015). Wild boar rooting intensity determines shifts in understorey composition and functional traits. *Community Ecology*, 16 (2). pp. 244-253 <http://real.mtak.hu/38073/> Volckaert M. (2013). Kwantificeren van wroetpatronen van everzwijn (*Sus scrofa*) in waardevolle graslanden in de vallei van de Zwarte Beek. Masterthesis UGent https://lib.ugent.be/fulltxt/RUG01/002/063/419/RUG01-002063419_2013_0001_AC.pdf

Onderwerp voorbehouden voor nvt

22342: Interactions between red wood ants and a facultatively associated isopod

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

Probleemstelling:

Ants are well-known ecosystem engineers that significantly affect soil processes and the distribution of other organisms. The large, conspicuous, dome-shaped nests of red wood ants are thermoregulated and are constantly supplied with food resources. These unique conditions make red wood ant nests biodiversity hubs for a diverse fauna of commensalistic and parasitic arthropods, known as myrmecophiles. Interestingly, these arthropods display a gradient in specialization ranging from species that are facultatively associated with ants to extremely specialized guests that cannot live away from their host. The common free-living isopod *Porcellio scaber* is surprisingly abundant in red wood ant nests and may even outnumber specialized, obligate myrmecophiles.

Paradoxically, this facultatively myrmecophilous isopod is also one of the preferred prey species of red wood ants.

Doelstelling:

The aim of this thesis is to unravel the intriguing relationship between *P. scaber* and red wood ants. The thesis will consist of field work and lab experiments:

- We will characterize the densities of *P. scaber* in red wood nests and along a distance gradient away from the nests. We will compare the spatial distribution of *P. scaber* with these of other species of isopods in the study site.
- We will compare the phenotype of isopods in nests with individuals found in absence of ants.
- We will assess the aggression response of red wood ants towards different species of isopods.
- We will assess the share of *P. scaber* in the red wood ant diet in the field.
- We will compare the fitness (survival, number of offspring ...) of *P. scaber* in a lab setup with and without red wood ants.

Overall, the results of this thesis will unveil the interaction between red wood ants and a facultative associate and will hint how the first steps towards myrmecophily are taken.

Locatie:

campus Ledeganck

Onderwerp voorbehouden voor Jens Zarka

22430: Interference or exploitation competition? Experimental studies on the interspecific interactions of cryptic species and the importance of priority effects

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

Probleemstelling:

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

Doelstelling:

In this master thesis, we will test whether 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 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 larger 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 identification and quantification of nematode species using quantitative PCR, ...).

Locatie:

22432: Interspecific competition and trophic interactions under a climate change scenario

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

Probleemstelling:

Global average temperature, frequency of extremes and temperature fluctuations are expected to rise in the future, with many implications for organisms. Despite the sensitivity of coastal species to climate change, little research has been done on the effects of daily temperature fluctuations and extreme thermal maxima on populations and species interactions. When closely interacting species display divergent responses to change, the outcome of their interactions may be altered. Direct predator-prey interactions are often important in determining the stability of biodiversity and ecosystem functioning. Studies focusing on effects of temperature regime on the outcome of species interactions have hitherto only focused on interspecific interactions of closely related species but not on the predator-prey competition. This project focuses on daily temperature fluctuations and extremes as a single stress factor, and of the synergistic effect of species interactions and temperature regime, comparing two different types of interspecific interactions: horizontal interactions of co-occurring species and vertical interactions of predator-prey species.

Doelstelling:

Specifically, the response of marine nematodes to temperature fluctuations and extreme maxima will be examined at the population level, including prey and predator species. The performance of individual species in monospecific cultures will be compared with that in microcosms with different species together, to assess how trophic web interactions are affected by thermal regime. Adding a predacious nematode to the artificial assemblages will increase complexity, to assess how thermal regime affects top-down controls on assemblages of bacterivorous nematodes. Both the monospecific and 'mixed species' experiments will assess nematode fitness 1) under different constant temperatures and 2) under daily temperature fluctuations. Measurements of population abundance and biomass will provide a link to ecosystem functioning, since nematodes are a food source for higher trophic levels and since they impact microbial community structure and activity and in this way also organic matter mineralisation.

Locatie:

22484: Living in the light during the day or at night? Light preference of *Araneus diadematus* in urban and rural areas.

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

Probleemstelling:

Cities are anthropogenic areas that differ markedly in (a)biotic characteristics compared to more natural systems. In this way, cities can be viewed as "living labs" due to the strong selection pressures they exert on affected species and provide unique opportunities to investigate evolution in real-time. Urban areas are characterised by a higher environmental temperature, caused by the heat island effect, and by drastically different light intensities caused by artificial lighting. It is expected that the increased temperature selects for lighter individuals in urban areas as these could thermoregulate more efficiently. Artificial lighting could shift light preferences of species if it increases prey capture success due to higher densities of light attracted prey. Using the model system *Araneus diadematus*, first results indeed demonstrate that city spiders have a more lighter colour compared to rural ones.

Doelstelling:

In this thesis we build further on these results and investigate the effect of urbanisation on proportion of diurnal/nocturnal individuals of *Araneus diadematus* by field sampling and determine the light preference or aversion of city and country spiders in an experimental lab setup.

Locatie:

22446: Low sex: mechanisms and evolutionary consequences of sporadic sexual reproduction in seaweed

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

Probleemstelling:

Genomic data facilitate to test theoretical predictions of how mating system variation affects genome organization and evolution. The relative degree of sexual or asexual reproduction should reflect on the efficacy of natural selection, both adaptive and purifying. Using a combination of laboratory experiments, genetic data of natural populations and transcriptomic data, this thesis will determine the precise mechanisms of asexual reproduction in a brown seaweed (*Dictyota dichotoma*).

Doelstelling:

To do so the student will sample 4 natural populations, Roscoff (France) and Goes (Netherlands) in the NE Atlantic, and Sormiou and Carry-Le-Rouet both in the Gulf of Lyon, France. Genetic signatures of asexual reproduction will be traced using a combination of lab experiments and genetic data. In addition the student will investigate the role of environmental factors in determining the degree of sexual versus asexual reproduction.

The subject requires field work in summer, wet lab skills (cultivating seaweed) and generating and analysing molecular data.

Locatie:

campus Sterre, S8

22450: Macroalgae-microbiome interactions: testing the holobiont concept in a changing environment

Promotor(en): Olivier De Clerck, Anne Willems
Begeleider(s): Frédéric Leliaert, Luna van der Loos
Contactpersoon: Luna van der Loos
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Microbes colonize a range of eukaryotic organisms, such as seaweeds, corals and sponges. They may be small in size, but they have a huge impact on the functioning of these hosts. Together the host and associated microbiome are often thought to form a holobiont: a functional unit that is based on a symbiotic relation. When studying the effects of environmental change on eukaryotic organisms, the interactions with microbes are often overseen. Especially in relation to human-caused environmental change, the holobiont concept may become increasingly important.

Doelstelling:

To investigate the role of microbes in the reaction of the host to elevated temperature and increased nutrient loadings, the student will focus on the green seaweed *Ulva*, Sea lettuce. These seaweeds are important for the food and biotech industries, but can also have a wide impact on the ecosystem by the formation of huge blooms coined "green tides". In nature, seaweeds never occur without their microbes, so distinguishing between cause and effect is difficult. In a series of field and laboratory experiments, the student will test if and how the response of an axenic host (a sterile seaweed lacking microbial associates)

differs from the response of seaweeds plus their microbes (the holobiont) to climate change and attempt to establish causal relations, as well as testing if the same mechanisms apply to natural systems.

Specifically, the student will characterize host-associated microbiomes of natural populations using a combination of sequencing techniques, isolation of bacteria, and high throughput screening with MALDI-TOF MS. 2) Determine the influence of the microbiome on host performance with changing environmental conditions (laboratory experiment). Next the student will investigate the role of the microbiome in altering the response of the host (*Ulva rigida*) to high nutrient concentrations and elevated temperature. There to he will manipulate host and holobiont by creating axenic hosts (i.e. a culture of a single *Ulva* with a minimal microbiome), and subsequently subjecting these to three "microbiome" treatments by supplying the individuals with 1) sterilized seawater (the axenic host treatment); 2) seawater that contains a synthetic microbial community and 3) non-sterilized seawater that contains a natural microbiome (creating a holobiont resembling in-situ specimens; i.e. the natural microbiome treatment). These treatment will be subjected to a series of growth experiments to determine the fitness of the host and associated microbiome to varying environments.

Locatie:

Onderwerp voorbehouden voor Ruben Algoet

22379: Make your move: how interactions impact movement rules and ecological feedbacks

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

Probleemstelling:

Birth and death numbers, but also movement is pivotal to understanding the fate of populations in spatially structured environments. Individual movements are behaviours that are steered by the environment, more specifically by the availability and distribution of resources and traits. Depending on these conditions, we expect the statistical properties (the rules) behind the movement paths (speed and directionality) to show consistent patterns, but also the occurrence of discontinuities that accompany shifts in movement strategies from for instance routine foraging to dispersal. Despite the recognition of movement as a driver of population dynamics and biodiversity, we lack a general theory on how interactions with the same or other species, or with kin affect these movement rules and eventually lead to different spatial dynamics.

Doelstelling:

To date, most insights on animal movement come from pattern-based research that rely on the tracking of wild animals. This project will take an inverse approach, by developing an experimental movement ecology at scales that allow sufficient control for repetitive observations and, at the same time, a large enough stochastic variation to bring ecological realism. More specifically, the project will search general principles by manipulating population densities and trait variation of soil arthropods under lab conditions, quantifying individual movement tracks by automatized tracking equipment, as well as feedbacks on the distribution of resources. By doing so, insights will be obtained on the relative contribution of environmental heterogeneity, population dynamics and ecological feedbacks on movement rules and movement strategies. This insights are then expected to provide a mechanistic framework to understand animal movement at larger spatial scales.

Locatie:

campus Ledeganck

Onderwerp voorbehouden voor Lisse Goris

22440: Microbiome based selection of plant growth promoting rhizobacteria in lettuce

Promotor(en): Sofie Goormachtig
Begeleider(s): Antoine Persyn
Contactpersoon: Antoine Persyn
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1

Aantal masterproeven: 1

Motivering voor deze opleiding:

Probleemstelling:

In Flanders, Belgium, lettuce farmers create a yearly turnover of 37 million euro, making it the regions second most grown vegetable crop. Lettuce growth is optimal at temperatures ranging between 20°C and 25°C, making it possible for farmers to grow it up to a consumable size in six weeks during spring and summer. During the winter time on the other hand, this process takes up to four months. A promising discipline to promote plant growth under stress conditions is the use of plant growth promoting rhizobacteria (PGPR).

Doelstelling:

Through 16S amplicon sequencing, we aim at comparing the rhizo and endomicrobiome of different lettuce cultivars grown in different soils at low temperature conditions compared to control conditions to detect the enriched rhizosphere and endophytic bacterial genera in the cold. Additionally, differences between anthocyanin producing and non-anthocyanin producing cultivars will be investigated. In parallel we will isolate these PGPR out of the lettuce root and evaluate them for their plant growth promoting potential by adding an overdose of them to the plants. Subsequently, we want to know which plant associated molecular pathways are triggered by these bacteria to promote the plant's growth. The above mentioned experiments will provide us with insights into which bacteria live inside lettuce roots, which of these bacteria can promote lettuce growth and how they influence the plant's molecular pathways to do so. This project will significantly aid lettuce farmers living in temperature climate areas by increasing the crop's turnover rate during the cold season.

Methodologies used:

- Microbiome pipeline: growing plants of interest under desired conditions, DNA extraction, PCR amplification and barcoding, purification, high throughput sequencing, analysis of sequencing data by using bio-informatics pipeline in R
- Fluorescence-Activated Cell Sorting
- Screening of bacterial collection: using Arabidopsis reporter lines, performing antagonism assays

Locatie:

Campus Ardoyen, PSB

Website:

Meer informatie op: www.psb.ugent.be

Onderwerp voorbehouden voor Helena Van den Eynde

22487: Molecular and phenotypic characterization of growth-regulating genes

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

Probleemstelling:

How plants grow from a small seed to their final stature appeals to the imagination of many people. Uncovering the molecular mechanisms that determine plant organ growth and size is therefore a challenging and fascinating research topic. Growth is a complex trait, steered by tightly controlled, interconnected genetic networks. The peptidase DA1 plays a crucial role in restricting the final size of organs in many plant species, such as Arabidopsis, rapeseed, wheat and maize. By limiting its enzymatic activity, the final size of leaves, flowers and seeds can be dramatically enhanced.

Upon multiple mono-ubiquitination by the E3 ligases BIG BROTHER (BB) or DA2, the latent peptidase activity of DA1 and two DA1-RELATED (DAR) proteins is activated to cleave growth regulators. In addition, the activating proteins BB and DA2 are cleaved and BB is subsequently degraded by the proteasome. Single knock-outs in DA1, DAR1 and DAR2 only have very subtle effects on organ size. Plant growth is however strongly enhanced in the double mutant *da1ko_dar1-1*, comparable to *da1-1* mutants, which carry a point mutation (DA1R358K). The latter has a dominant-negative action towards DA1 and DAR1 and causes a reduction

in peptidase activity. A tight balance between active and inactive DA1, DAR1 and DAR2 and a strict coordination of substrate cleaving is hence crucial for normal plant development. However, only few DA1 substrates are described and the precise spatio-temporal circumstances of the substrate cleaving in leaves and the subsequent effect on cell division and endoreduplication remain entirely unknown. With this project, we aim to expand our current knowledge on these growth-regulating proteins.

Doelstelling:

For BB, it was shown that its cleavage leads to its destabilization. During this project, we will functionally characterize cleaved substrates of DA1 by exploring their post-proteolytic fate, such as degradation by the proteasome. In addition, we will mutate these genes and hereby generate uncleavable mutants of these DA1 substrates and explore the importance of their cleaving during leaf growth and development. For this, we will generate mutant Arabidopsis lines and phenotype them on the macroscopic and microscopic level. Finally, by developing and applying a novel sensor-tracking system, we will pinpoint with confocal microscopy where and when during leaf development DA1 cleaves its specific substrates and hence generate a spatio-temporal map of DA1-mediated cleaving. This system will also allow us to quantify the effect of DA1-mediated cleaving on cell division and endoreduplication for each substrate.

During this project, the student will get the opportunity to acquire a broad spectrum of techniques, ranging from imaging and phenotyping (macroscopic and microscopic, light and confocal) to common and more advanced molecular skills, such as Golden Gate cloning, DNA and RNA extraction, plant transformation, recombinant protein production, in vitro cleaving assays and protein degradation assays.

Locatie:

VIB Department of Plant Systems Biology

22511: Molecular mechanism of bioactive aromatic compounds in plants: cis-cinnamic acid as case study

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

Probleemstelling:

Plant growth and development is tightly regulated by the phytohormone auxin. We recently found that the naturally occurring molecule cis-cinnamic acid (c-CA) can perturb auxin homeostasis by interfering with auxin transport in the plant. Treating plants with c-CA results in the inhibition of primary root growth and proliferation of lateral roots. The altered root architecture can give plants an advantage under water or nutrient depleting conditions making c-CA an excellent candidate for the application in agricultural practice. To resolve the molecular mode of c-CA action and obtain a mechanistic insight into its perception further research is necessary.

Doelstelling:

During your master thesis you will be involved in functional characterization of some of the early c-CA response genes. You will work with the model plant Arabidopsis thaliana and analyze primary and lateral root growth. The relative role of specific biochemical pathways will be studied by means of mutants blocked in particular steps of the pathway, as well as by the use of specific drugs to inhibit particular enzymes. Finally, you will help in the functional characterization of genes that could play a role in the c-CA signaling pathway.

Locatie:

PSB Campus Ardoyen, Technologiepark 71, 9052 Ghent

Onderwerp voorbehouden voor Ellen Martens

22414: Onderzoek naar de relatie tussen verschillende vormen van natuurbeleving en draagvlak voor natuurbehoud bij jongeren

Promotor(en): Maurice Hoffmann
Begeleider(s): Ilse Simoens
Contactpersoon: Ilse Simoens
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:

Nog onbeslist voor:

Aantal studenten: 1

Aantal masterproeven: 1

Motivering voor deze opleiding:

Probleemstelling:

Kan natuurbeleving en de beleving van de positieve welzijnseffecten hiervan op jongeren een mindshift teweeg brengen die voor een verbreedt draagvlak voor biodiversiteit zorgt en duurzaam gedrag verhoogt? Dit is de vraag die we in dit onderzoek centraal stellen. Hierbij willen we de verschillende vormen van natuurbeleving belichten alsook de vernieuwde dynamiek in natuurbeleving met meer aandacht voor wilde natuur bekijken en deze verschillen in kaart brengen in relatie tot van draagvlak voor natuurbehoud en duurzaam-gedrag.

Doelstelling:

Deze studie start met een literatuur studie en het opstellen van een enquête. Aan de hand van een brede enquête bij studenten en een focusgroep met studenten zullen de gegevens voor dit onderzoek verzameld worden. Dit materiaal zal de student in staat stellen de verbanden tussen de verschillende vormen van natuurbeleving en draagvlak voor natuur te onderzoeken.

Locatie:

INBO, Brussel, campus Ledeganck

Website:

Meer informatie op: www.inbo.be (from January 2020 onwards)

Onderwerp voorbehouden voor nvt

22436: Patterns and rates of species evolution in tropical rain forests

Promotor(en): Lars Chatrou

Begeleider(s): Lars Chatrou

Contactpersoon:

Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie

Niet behouden voor:

Nog onbeslist voor:

Aantal studenten: 1

Aantal masterproeven: 1

Motivering voor deze opleiding:

Probleemstelling:

Tropical rain forests are the most species-rich terrestrial ecosystems, containing astonishing numbers of species in almost any group of organisms. This master thesis dives into the evolutionary build-up of this diversity. There is a long-standing debate on the pattern of species accumulation in tropical rain forests over evolutionary time, known as the museum vs. cradle debate. The museum hypothesis goes back to Alfred Russell Wallace, who proposed that tropical forests accumulated species over long periods of time due to their age and climatic stability. Ledyard Stebbins coined Wallace's idea the 'museum hypothesis', and suggested that the climatic stability is connected to low extinction rates and the survival over evolutionary time of archaic forms. Contrasting with the museum model, is the model of rapid speciation in clades, so-called radiations. This model, coined the 'cradle hypothesis' would necessarily involve extinction rates that are elevated compared to those associated with the museum model. An excellent plant group for testing these hypotheses is the family Annonaceae, containing ca 2500 species of trees and lianas that almost exclusively are found in tropical rain forests on all continents. In recent years we have learned a lot about the phylogenetic relationships within this plant family. Also, we know that the common ancestor of the family was around some 100 million years ago. However, we only have a limited understanding of patterns of diversification (speciation minus extinction) that gave rise to the present-day diversity. The reasons for this are twofold: first, our efforts to estimate the age of Annonaceae are seriously hampered by lineage-specific heterogeneity of molecular substitution rates. Indeed, processes at the level of DNA have a huge impact on our understanding of large-scale processes covering millions of years. The second cause is the incompleteness of species sampling in most family-wide analyses so far. Tree shape of the two main clades of the Annonaceae, the subfamilies Annonoideae (1400 species) and Malmeoideae (900 species), is very different. Our preliminary results suggest that the species in the Malmeoideae have accumulated at an even pace, which would be consistent with the museum model. Phylogenetic patterns in the Annonoideae, on the other hand, appear more radiation-like with periods without traceable speciation being followed by abrupt and fast bursts of speciation. Your task will be to further explore evolutionary ages and diversification patterns in the light of these observations. You will bring together data from several data sets and from online data repositories, and gathered a

data set containing all species of Annonaceae, for which sequence data of multiple plastid markers are available. Using mainly Bayesian statistical approaches you will infer phylogenies and clade ages, and infer diversification patterns.

Doelstelling:

Questions that you will focus on in your project are: - do pattern and rates of species evolution in Annonaceae conform to the museum model or the cradle model? - does the accumulation of species over evolutionary time follow a pattern that is universal for the entire family, or do clades within the family have different diversification patterns? - do diversification patterns differ among the major continents containing tropical rain forests (South America, Africa, Asia)? - are differences in patterns and rates of species evolution, if present, attributable to species characteristics, for example of flowers or fruit? - how large are the uncertainties of the results, and what is the effect of using different assumptions in the analyses? Techniques that you will use are: - bioinformatics and phylogenetics: data gathering, aligning, likelihood and Bayesian phylogenetics, including inference of ages and diversification patterns. The ability to use R would be helpful, but isn't required and can be learned during the project. Also, no preliminary knowledge of Bayesian phylogenetics is required but will help. By far the most important is enthusiasm for, and an interest in, biological disciplines like evolutionary biology, botany, biogeography, and a feel for data analyses.

At the Systematic and Evolutionary Botany lab, we encourage the publication of master thesis results in a peer-reviewed scientific journal.

Locatie:

Ledeganck

Onderwerp voorbehouden voor Robbe Strybol

22287: Pheromones inhibit the hatching of diapausing Anostraca (Crustacea: Branchiopoda)

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

Probleemstelling:

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

Doelstelling:

Locatie:

22472: Plants as a medicine for sexual, reproductive and urogenital problems and improvement, a Congolese experience (in Belgium)

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

Probleemstelling:

Migrant communities often hold on to their cultural preferences of herbal medicines. Also, after migration, they often maintain traditional concepts on health and illness. The use of medicinal plants is widespread in the Democratic Republic of Congo (hereafter referred to as DR Congo), largely due to an insufficient primary healthcare system.

It is known that this use of medicinal plants is at least partly continued among people from Congolese descent in Belgium.

As sex, fertility and reproduction are seen as very important in Sub-Saharan Africa, the use of a significant part of the available medicinal plants is related to these concepts. However, data on the use of medicinal plants for these purposes in DR Congo and among the Congolese migrant communities is lacking.

In this master dissertation, an ethnobotanical study will be conducted on the use of medicinal plants among the Congolese migrant communities for sexual, reproductive and urogenital problems and improvement.

Doelstelling:

The goal of this master thesis is to make an overview of the medicinal plants used for reproductive health care.

Through interviews with people from Congolese descent in Belgium, it will be investigated which plants are used, what these plants are used for and how they are used. Besides this, the underlying reasons why the Congolese community use these plants in Belgium will be investigated.

A voucher collection of dried plant specimens and possibly a living plant collection will be made up.

The collected plants will be identified up to the species level, applying a variety of techniques. For some plants the study of morphology and comparison with herbarium specimens (Plantentuin, Meise) may suffice, other will need to be identified by sequencing selected genetic markers and BLAST search in databases with publicly available nucleotide sequences.

Locatie:

Brussels (interviews, plant collecting), Ledeganck / Coupure (analyses)

22471: Pollen evolution in response to drought in wild relatives of the sweet potato (Convolvulaceae)

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

Probleemstelling:

Sweet potato ranks among one of the sixth most important crops for human diet. Recently, in the face of climatic emergency, it has been targeted as a potential famine crop, for its resilience to harsh environmental conditions, and high nutritional value. However, the evolution and biogeography of sweet potato and its wild relatives is still poorly understood, in particular the impact of climatic change on the morphology and ecological niche of the species.

Highly aperturate pollen has been suggested to be an adaptation to xeric environmental conditions. Apertures are areas on the walls of a pollen grain, where the wall is thinner and/or softer and the pollen tube is able to break through the (elsewhere very tough) pollen wall. It is hypothesized that a high number of apertures in the pollen grains allow a faster germination of the pollen tube, and therefore benefit a quicker reproductive cycle when the environmental conditions are unfavourable (e.g. drier and hotter). Yet, this has not been formally tested in a large scale evolutionary framework in any group of plants.

This project will focus on a group of wild relatives of the sweet potato which cover a wide range of habitats, from tropical forests to savannah and desert-like environments, and with an exceptional variation in the number and disposition of the apertures on their pollen grains, from 3 to well over 90 apertures. This makes it a perfect model group of plants to formally investigate in an evolutionary context, if the adaptation to drier and hotter environments could be at the heart of the development of high number of apertures in pollen grains. In addition, it will, in a broad sense, contribute to a better understanding of the impact of changing environmental conditions in the morphology and reproductive biology of the sweet potato wild relatives.

Doelstelling:

Investigate the evolution of high number of apertures in the tropical family Convolvulaceae, particularly subfamily Convolvuloideae, in a phylogenomic framework. The methodology will involve genome skimming of c. 200 species, phylogenetic analyses and character reconstruction of pollen and ecological characters - these will be extracted from available taxonomic literature and an extensive pollen dataset already compiled by Dr. Ana Rita Simões who is collaborating in the project, and with expertise in the plant group. Pollen acetolysis and SEM imaging may be conducted to fill in certain species gaps in the dataset.

Techniques and analyses methods that the student will use

- Scanning electron microscopy
- DNA sequencing (genome skimming)
- Bioinformatics tools for genome assembly
- Phylogenetic methods for tree inference and character evolution

Locatie:

Ledeganck

Onderwerp voorbehouden voor Ine de Man

22431: Pollutants and cryptic species: can toxicants alter the microbiome of cryptic species and influence their abiotic tolerances?

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

Probleemstelling:

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.

Doelstelling:

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.

Locatie:

22486: Population genetics and shell colour polymorphism in the introduced land snail *Theba pisana* (O.F. Müller, 1774)

Promotor(en): Frederik Hendrickx, Thierry Backeljau
Begeleider(s): Karin Breugelmanns, Brigitte Segers, Gontran Sonet, Carl Vangestel, Heinz KÄ¶hler
Contactpersoon: Thierry Backeljau
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1

Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

The land snail *Theba pisana* (O.F. Müller, 1774) ("zandslak" in Dutch) was introduced into northwestern Europa from the Mediterranean Basin. In NW Europe the species is mainly found in sandy dunes and ruderal terrains. The species is characterised by a remarkable shell colour polymorphism consisting of dark spiral bands of various intensities on a white to light brown background. In the context of a European project we are studying the ecological and population genetic patterning, and eventually determinants, of this colour polymorphism in NW Europe. Preliminary results suggest that about 70% of the shell colour variation is explained by climatic factors and the density of the vegetation. Yet, it is expected that also predation and colonisation history may contribute. Against this background there is a need for population genetic data to (1) reconstruct colonisation histories, (2) detect eventual founder effects, (3) explore possible clinal variation and signatures of adaptation in DNA markers, (4) establish the genetic basis of the shell colour polymorphism, and (5) explore the possible intereference of epigenetic factors in the expression of shell colour variation (e.g. phenotypic plasticity). In addition it would be interesting to compile similar shell colour polymorphism data for related, sympatric, species such as *Cochlicella acuta*, *Ceruella virgata*, etc.

Doelstelling:

Within the research theme outlined above, the purpose of this thesis is to conduct a mtDNA sequence analysis of *Theba pisana* in Belgium (and other areas in NW Europe). This should provide a first indication of the colonisation history and possible founder effects. In addition, the idea is to correlate mtDNA variation with environmental factors to look for possible patterns that might reflect signatures of adaptation. Finally, a first attempt will be made to explore in parallel nuclear DNA SNP variation via RAD-seq analyses. The thesis will hence include a good deal of lab work, even if fieldwork will be necessary as well. A research visit to the University of Tübingen may be required as well.

Locatie:

RBINS, OD Taxonomy and Phylogeny, Vautierstraat 29, 1000 Brussels

Onderwerp voorbehouden voor Ward Langeroot

22371: Quantifying grassland restoration potential: can we track down soil phosphorus availability with vegetation spectra?

Promotor(en): Lander Baeten, Frieke Vancoillie
Begeleider(s): Iris Moeneclaey
Contactpersoon: Iris Moeneclaey
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

The restoration of degraded ecosystems is an explicit target in Europe's 2020 Biodiversity Strategy, which focuses on halting the worldwide loss of biodiversity. The United Nations even declared 2021-2030 as the decade of ecosystem restoration. Species-rich semi-natural grasslands have experienced dramatic losses due to the intensification of agricultural land use, and are therefore in the critical need for restoration. Soil phosphorus availability, a legacy of past fertilization, is key in the recovery of such vegetation. Phosphorus is especially persistent in the soil and is known to determine community recovery. Measuring soil phosphorus is generally done by soil sampling and lab analyses, but this technique is labor intensive, expensive and provides low spatial coverage. Therefore, there is a need to develop more cost efficient approaches for assessing grassland restoration potential, preferably at a larger scale.

Doelstelling:

Spectral measurements of the vegetation can provide such a new approach, as they are quick and easy to make. However, this technique needs further development and validation. The detection of phosphorus in the vegetation poses particular methodological challenges. Furthermore, making quantitative predictions about soil phosphorus from concentrations in the vegetation, also requires detailed insights into the usage of phosphorus by plants and plant communities.

This master thesis aims at investigating if and how we can use vegetation spectra to track down soil phosphorus availability. It will be linked to an ongoing PhD project, in which we already set up an experiment with typical grassland species growing along a soil phosphorus gradient. Practical work will involve taking spectral measurements with state-of-the-art technology, measuring plant traits and harvesting biomass. The subject can further be developed depending on the

interests of the student; own input and ideas are especially encouraged!

Locatie:

Campus Gontrode, Campus Coupure

Website:

Meer informatie op: www.ugent.be/bw/environment/en/research/fornalab/Projects/ecological-restoration

22400: Restoration of floodplain forests with the European black poplar along the river Meuse on the Dutch-Belgian border. Evaluation of a re-introduction

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

Probleemstelling:

European black poplar (*Populus nigra* L.) is a key species of the floodplain forest, which is the natural vegetation type on riverbanks in Western Europe (Habitat Code. H91E0). In common with many other European countries, floodplain areas in Belgium were subjected to urbanization. Native poplar stands were replaced by agriculture or by cultivated poplar plantations consisting of a narrow range of euramerican (*P.x canadensis*) and interamerican (*P. interamericana*; *P. deltoides* x *P. trichocarpa*) hybrids. Exotic gene flow may have profound effects on the evolution of the native black poplar and a potential consequence is the increased extinction risk of the native species. In 2001, a species reintroduction project was set up and black poplar trees were planted along the riverside of the Meuse (Dilsen-Stokkem). These trees have now reached the reproduction stage, producing pollen and seeds that might contribute to the colonization of the gravel banks of the Meuse. This project aims to evaluate this re-introduction process. More specifically, this study aims to answer the following questions: Are the black poplar trees reproductive? Do they produce viable seeds of pure *Populus nigra*? What is the genetic origin of the poplar seedlings that can be found on the gravel banks? Our methods combine field work with greenhouse experiments (seed experiments) and molecular genetic methods in the lab (paternity analysis on the species level). The final aim is to evaluate the re-introduction project and to produce guidelines for the restoration of floodplain forests with black poplar populations along the river Meuse at the Dutch-Belgian border.

Doelstelling:

This project combines field-work (a few days in June and a few days in September – October), DNA-analysis in the lab under assistance of an INBO lab technician (at ILVO-Melle), greenhouse experiments (at ILVO – Melle) and statistical data-analysis.

Locatie:

INBO, Geraardsbergen, Melle; Ledeganckcampus

Website:

Meer informatie op: www.inbo.be (from January 2020 onwards)

Opmerkingen:

Useful references: Vanden Broeck A., Storme V., Cottrell J.E., Boerjan W., Van Bockstaele E., Quataert P., Van Slycken J. (2004). Gene flow between cultivated poplars and native black poplar (*Populus nigra* L.): A case study along the river Meuse on the Dutch-Belgian border. *Forest Ecology and Management* 197(1-6):307-310.

22372: Restoring semi-natural grasslands: how does soil phosphorus shape the trajectory of community development?

Promotor(en): Lander Baeten, Kris Verheyen
Begeleider(s): Iris Moeneclaey
Contactpersoon: Iris Moeneclaey
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:

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

Probleemstelling:

The restoration of degraded ecosystems is an explicit target in Europe's 2020 Biodiversity Strategy, which focuses on halting the worldwide loss of biodiversity. The United Nations even declared 2021-2030 as the decade of ecosystem restoration. Species-rich semi-natural grasslands have experienced dramatic losses due to the intensification of agricultural land use, and are therefore in the critical need for restoration. Soil phosphorus (P) availability, a legacy of past fertilization, is central to the recovery of such vegetation. Phosphorus is not only very persistent in the soil, but is also a key limiting nutrient that is likely to determine how communities recover. Understanding the specific contribution of phosphorus to the trajectories of vegetation recovery under field conditions is, however, complicated in several ways, e.g. because vegetation change is influenced by other environmental factors as well and because species composition (and abundance) is not very well controlled. Well-designed community experiments are thus needed to further unravel the role of phosphorus in the context of grassland restoration.

Doelstelling:

This master thesis aims at investigating trajectories of plant community development along a gradient in phosphorus availability. Plants of twenty species are grown as monocultures and as communities of different (functional) composition, to determine the individual plant responses and community dynamics along the phosphorus gradient. These patterns will be linked to the traits and strategies of the species involved to make more general inferences about the recovery trajectories of grassland communities (trait-based approach). This work will be linked to an ongoing PhD project, in which we already set up the experiment, so that the thesis can get a head start and directly start measuring important responses (plant-level biomass, traits). The subject can further be developed depending on the interests of the student; own input and ideas are especially encouraged!

Locatie:

Campus Gontrode, Campus Coupure

Website:

Meer informatie op: www.ugent.be/bw/environment/en/research/fornalab/Projects/ecological-restoration

22491: Revealing the African origin of *Lactarius*

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

Probleemstelling:

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

Doelstelling:

An important goal of this study is to describe the new African subgenera. This will be done based on morphological and molecular tools. The aim is to reveal the unique morphological features of the infrageneric taxa. The student will use herbarium material but might also participate in a mycological expedition to West-Africa in order to collect more specimens. Fieldwork in Europe is also necessary in order to get a good view on the existing subgenera in temperate regions and to define the differences with the African lineages. Microscopy will constitute an important part of this work, resulting in description and illustration (by drawings and by photographs) of the relevant characters.

Locatie:

Onderwerp voorbehouden voor Phaedra Lagaet

22433: Sansevieria @ the pub

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

Probleemstelling:

Sansevieria (mother-in-law's tongue, devil's tongue) is a well-known plant found in many homes and brown pubs (bruin café). They are often used as window decoration due to their low maintenance requirements. Sansevieria trifasciata is the most widely cultivated species. In Africa, Madagascar and southern Asia, there are about 70 wild species of Sansevieria, however.

Species of Sansevieria was recently placed in synonym with Dracaena, belonging to the asparagus family (Asparagaceae), and phylogenetic studies have been conducted in the past based on both chloroplast and nuclear markers. The boundaries between species still remain vague and difficult to establish.

Based on Illumina sequence reads, produced by the research group Systematic and Evolutionary Botany, a more in depth phylogenetic analysis can be performed.

Genomic data, derived from 50 species, is available to perform Chloroplast (Cp) genome assembly and in addition, the same data can be used for skimming the nuclear genome to locate and characterize single nucleotide polymorphism (SNP). These SNP's can consequently be used as potential barcodes to help identify species of Sansevieria, a tool that would be very helpful for plant breeders.

Doelstelling:

The goal is to engage in comparative genomics and phylogenetics of Sansevieria. You will familiarize yourself with the species of Sansevieria and assemble and annotate the available genomic data. In addition, potential barcodes can be extracted from the generated data, and tested for their use in phylogenetic analyses of the genus.

Objectives

- Learn bioinformatic tools in command line
- Assemble and annotate chloroplast genomes of species of Sansevieria
- SNP mining to select for potential barcodes for species
- Perform comparative genomic and phylogenetic analyses

Skill building

- Become comfortable in using bioinformatic tools in command line, as well as phylogenetic tools

Locatie:

Ledeganck

22476: Seasonal dynamics in carbon sequestration in high Arctic tundra: a meta-omics approach

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

Probleemstelling:

It is estimated that up to 50 % of the global soil organic carbon is buried in Arctic permafrost. Today, the high Arctic tundra biome still acts as an important global carbon sink due to the positive balance between photosynthesis by plants and cryptogams and the slow, microbially mediated degradation of newly produced and old organic matter that accumulated in the soils over millennia. However, with climate change being amplified in the Arctic, tundra biomes might become a carbon source rather than a sink as a result of two processes. First, higher temperature results in thawing of the permafrost and increased microbially mediated degradation of the ancient organic matter, and hence a release of the greenhouse gases CO₂ and CH₄ into the atmosphere. A second and less well known cause may be that most Arctic regions will be affected by a more extended and thicker snow cover during autumn, winter and spring. Given that snow cover acts as a thermal insulator for the soils, this in turn facilitates the microbial breakdown of organic matter at near 0 °C temperatures. Based on automatic measurements it has been shown that microbially mediated CH₄ production during the cold period is at least as high as during summer, with slowly dropping CH₄ emissions during winter and a short peak at spring onset. Importantly, increased snow cover can result in a shortening of the summer growing season for photoautotrophs, and thus tipping the balance of tundra from being a carbon sink to a source. However, microbial activity under snow cover remains largely unexplored and it is unclear which (groups of) microorganisms (e.g., methanogens, methanotrophs) are active and control carbon cycling in different types of tundra.

Doelstelling:

This MSc thesis will make use of a unique dataset collected along a gradient from dry to wet tundra in Svalbard during three seasons (spring, summer and winter). Samples from the three seasons will be studied using metagenomics and metatranscriptomics sequencing approaches to study the up- and downregulation of genes involved in carbon and nutrient cycling. These data will be combined with field-based measurements of CH₄ and CO₂ fluxes during the three seasons. The results of this study will help to better predict carbon emissions under future climate change scenarios.

Locatie:

camus Sterre

22451: Species of *Russula* from a drumlin archipelago in the northeastern USA

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

Probleemstelling:

Since December 2012, a fungal inventory has been conducted at the Boston Harbor Islands National Park Area (BHI), the only drumlin archipelago in the USA. This documentation resulted in over 900 collections, of which 313 have been identified to species level, accounting for 172 species. For identification, DNA was isolated from rice grain-sized pieces of fruiting bodies and sequenced the internal transcribed spacer (ITS) "barcode" region of the ribosomal DNA.

Doelstelling:

The goals of this master's project are: (1) to provide detailed data on species of the genus *Russula* (Fungi, Basidiomycota, Agaricomycetes) at the BHI; (2) to record information about their distribution, habitat, and dates of fruiting; and (3) to provide documentation for these species via voucher specimens that will be deposited at the Farlow Herbarium. The genus *Russula* is composed of 750 species, of which 334 species are reported from the USA. Unfortunately, many taxa are poorly known, due to short, incomplete diagnoses of taxa; the lack of extensive studies of the genus *Russula* in North America; and the lack of molecular

data. Because of their interrelationships with woody plants and mycophagous fauna, *Russula* species are important components of woodland ecosystems. To date, 40 collections of *Russula* have been sampled at BHI, of which 11 are identified to species level, good for 7 species. Interestingly, the ITS sequences of a majority of these *Russula* collections are <97% similar to any *Russula* sequence available in NCBI GenBank, suggesting that we could be dealing with either undescribed species or species that have been described but never sequenced. However, in addition, through both legacy taxonomic assignment and common misidentification, many sequences from North America are mislabeled as European species. This master's project is necessary for accurate identification of BHI collections for which the ITS sequence is <97% similar to any *Russula* sequence, including comparison with existing description and types as well as multi-locus sequencing for phylogenetic placement.

Locatie:

22406: Study the contribution of labile carbon and different sediment types on growth of the most abundant Oligochaete worm in the river Scheldt (Limnodri)

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

Probleemstelling:

Benthos in the river Scheldt likely is of crucial importance for overwintering birds. Benthos densities and biomass (mainly detritivorous Oligochaetes) have strongly decreased recently and so have overwintering birds. Even today we cannot precisely explain what has triggered these abrupt changes in benthos densities nor what shapes current spatial differences in benthos densities. A promising way forward is to look at a specific fraction of the detritus, the labile carbon, which is considered the food of the benthos.

This master thesis wants to:

1. reveal spatial patterns in labile carbon in mudflats of the Scheldt and link these to densities of Oligochaetes.
2. perform standardized growth experiments on a) a standard substrate with different levels of added labile carbon and b) sediment collected at different stations and different times of the year to study both labile carbon content and growth rates of worms
3. research goal 1 will be triplicated (3 different temperatures) to construct growth curves of *Limnodrilus* which can be used to calculate benthos production in the Scheldt river.

Doelstelling:

The study involves some field work in the river Scheldt, lab work at the Raymonde de Larochelaan 1, Sint-Denijs-Westrem (building of VMM) and lab work in the INBO laboratories at Gaverstraat 4 Geraardsbergen.

Locatie:

VMM, Gent, INBO, Gaverstraat 4, 9500 Geraardsbergen, Ledeganckcomp^{ex}

Website:

Meer informatie op: www.inbo.be (from January 2020 onwards)

22355: Studying the role of the anterior olfactory cortex in olfactory curiosity

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

Probleemstelling:

Curiosity refers to the intrinsic tendency of all animals to explore the unknown. The type of curiosity which is evoked by the novelty of sensory stimuli, is referred to as perceptual curiosity. Across animal species, stimuli never encountered before elicit arousal and evoke distinct orienting behaviours. How the brain initiates exploration in response to novel stimuli is currently not well understood and the mechanism of stimulus novelty detection remains to be identified.

We have previously established an olfactory perceptual curiosity paradigm in mice, based on the spontaneous sniffing response to novel stimuli. The ability to recognize a novel stimulus is extremely fast, taking less than 100ms. In order to accomplish such rapid detection, the brain needs to perform a remarkably efficient computation which allows for a memory-based classification of incoming sensory stimuli. Moreover, novel stimuli familiarize after few exposures, indicating rapid nonassociative learning in olfactory brain areas.

Olfactory perception begins with the binding of airborne odorant molecules to the olfactory receptors in the nasal epithelium. The axons from receptor cells expressing the same olfactory receptor project to one or two olfactory glomeruli, where they connect to the dendrites of mitral and tufted (M/T) cells, the major output projections of the olfactory bulb (OB). M/T cells project to subsequent cortical processing areas, namely the anterior olfactory nucleus (AON) and the piriform cortex (PCx) via the lateral olfactory tract fibre bundle. In addition to these feed-forward connections from the OB to olfactory cortical areas, both the AON and PCx also send feedback projections to the OB.

Doelstelling:

Our unpublished data demonstrate that the AON has a unique neural response properties to novel stimuli, which subsequent stages of olfactory cortex do not have. Hence, we hypothesize the AON is critically involved in mediating the effects of novel stimuli on the brain. In the master thesis, we will experimentally test this hypothesis using a pharmacological approach. We will chronically implant a novel miniaturised device, developed in the lab, to repeatedly infuse the GABAA agonist muscimol into the AON, while animals are performing the olfactory perceptual curiosity paradigm. We expect that this experimental manipulation will disrupt the spontaneous sniffing response to novel stimuli.

Locatie:

kapeldreef 75, 3000 Leuven

Onderwerp voorbehouden voor Robin De Plus

22475: Taxonomic and functional turnover in microbial mat communities in an East Antarctic lake

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

Probleemstelling:

Antarctic lakes are hotspots of biodiversity and primary production amidst the polar deserts in their catchments, because of the availability of liquid water (below lake ice cover). Benthic microbial mats are the most conspicuous life forms in these lakes. These mats consist of structured assemblages of Cyanobacteria and in some case mosses, which provide a substrate for and interact with other photo-autotrophs such as diatoms and green algae, as well as heterotrophic bacteria, protozoans and micro-invertebrates. A few millimeters to centimeters below this photosynthetic active layer, bacteria remineralize organic matter in anoxic conditions. Released nutrients are efficiently recycled by the photo-autotrophs in the microbial mats, resulting in a higher primary production compared with that in the (ultra)oligotrophic surrounding lake water. Recent studies in the PAE research group using high-throughput sequencing of specific marker genes uncovered an unknown diversity and a high amount of endemism in various phyla and supergroups in Antarctic bacteria and micro-eukaryotes. These studies, as well those based on more classical genetic fingerprinting approaches, also revealed a depth zonation in microbial communities in response to decreasing light availability and quality as well as disturbance by lake ice formation. The functional potential of these organisms and how biochemical pathways vary with lake depth is however still unknown. We hypothesize that benthic mats at shallow depths are more subjected to lake ice

disturbance and UV radiation, while at greater depth heterotrophic processes dominate biological activity.

Doelstelling:

In this MSc project samples collected along a depth gradient in a lake from Skarvsnes (Lützow-Holm Bay, Enderby Land) in East Antarctica will be studied using shotgun sequencing on an Illumina HiSeq platform. This will result in billions of sequences containing genomic information of (micro)eukaryotes, bacteria and DNA viruses. The student will process the metagenomics data using an in-house bioinformatics pipeline and combine the output with field measurements of the carbon and nitrogen cycles. The project will result in a better understanding of the functioning of microbial mats, and a biochemical model for carbon and nutrient dynamics along a depth gradient in Continental Antarctic lakes.

Locatie:

campus Sterre

22382: Testing a dispersal front: do newly founded populations of the digger wasp *Bembix rostrata* have different traits?

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

Probleemstelling:

The last few years we have experienced very dry and hot summers in Belgium. This can have serious consequences for local biodiversity. However, some species profit from these changes in weather: the distribution of southern species, or species that live in arid habitats, is often expanding. The edge of this expanding distribution, or dispersal front, is an interesting phenomenon to study eco-evolutionary dynamics, as individuals get sorted in space by their tendency to disperse and selection might act differently on these individuals at the dispersal front.

Last summer (2019), several new populations of the digger wasp *Bembix rostrata* (Harkwesp) were discovered in Belgium, a solitary wasp that lives in sandy habitat and is adapted to live in arid circumstances.

Doelstelling:

This topic will investigate several populations of *Bembix rostrata* in Flanders, with a focus on the newly discovered populations. The main research question will be if these new populations differ in their traits from long-established populations. Depending on the interest of the student, the focus can be on phenotypic traits, behaviour, molecular research (microsatellites), parasite community or a combination.

Locatie:

campus Ledeganck

Onderwerp voorbehouden voor Moyra Delafonteyne

22480: The complete botanist: integrating herbarium taxonomy, high-throughput sequencing and phylogenetics of tropical trees

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

Probleemstelling:

Tropical rainforests are home to an astonishing species diversity in almost any group of organisms. Unlike in Europe, a significant part of the tropical diversity is still to be discovered and described. A robust knowledge framework of the systematics of tropical plants is important. Firstly, up-to-date species descriptions and identification keys provide baseline data for the assignment of biodiversity hotspots, an important concept in conservation. Furthermore, groups of organisms for which the taxonomy and the phylogenetic relationships are well-known, provide model groups for downstream studies in, for example, ecology, evolutionary biology and genomics.

This project revolves around the genus *Klarobelia*, belonging to the plant family Annonaceae. *Klarobelia* contains 13 species of tropical rain forest trees in Central and South America. *Klarobelia* is a recently described genus (1998), but the taxonomic revision has not been published in a peer-reviewed journal. Also, phylogenetic relationships of the species are unknown. You will bring together existing data, as well as produce new data, that will lead to a publication in a peer-reviewed scientific journal.

The project offers you the possibility to become a complete botanist who has become acquainted with a variety of techniques to study patterns of plant diversity in the tropics, as well as the evolutionary history behind those patterns.

Doelstelling:

The goal is to learn several techniques for describing plant diversity in the tropics and testing hypotheses about their phylogenetic relationships. These techniques involve:

- Morphological studies of herbarium specimens
- Preparation of identification keys
- GIS techniques to study geographic distributions
- DNA sequencing techniques (genome skimming by Illumina sequencing)
- Bioinformatic tools for sequence assembly
- Phylogenetic methods

The techniques mentioned equip you with a set of tools that would enable the testing of further hypotheses, e.g. related to the evolution of characters, on biogeography, or the evolution of climatic preferences. During the preparation of this thesis, it is up to you to decide what kind of hypothesis you would like to test.

Locatie:

22428: The enigmatic species diversity of Cape Verdian cone snails revisited: an integrative taxonomic approach to elucidate real species diversity

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

Probleemstelling:

Cone snails (family Conidae) are an enigmatic taxon of marine gastropods which have attracted attention from a diverse scientific audience. On the one hand, several Conidae produce extremely complex mixtures of chemicals to capture prey, and some of these chemicals may have potential for biomedical applications. On the other hand, there are several geographic regions where cone snails display an astonishing morphological diversity. The Cape Verde islands undoubtedly provide the pinnacle of such diversity, which is generally assumed to result from one or more adaptive radiations, enhanced by the diversity of geographical and habitat characteristics of the Cape Verde islands and embayments. At present, more than a hundred (sub)species of Conidae from the Cape Verde islands have been described, and new species are still being discovered. Many of these species are considered endemic to the Cape Verde islands. From an ecological perspective, these Conidae provide a puzzling example of the sympatric occurrence of multiple closely related lineages; it is rule rather than exception to find several (sometimes > 6) species living together within a single bay.

Cone snail taxonomy has long relied exclusively on morphological characteristics of the shell, in combination with geographic and habitat specificity. Indeed, consistent morphological shell phenotypes are found in particular locations and habitats, and there is little or no evidence for hybridisation among them, supporting the view that these are indeed different species. More recently, morphological characteristics of the feeding apparatus, more specifically of the radula, have been included as diagnostic species characters. It was not until after 2010 that phylogenetic analyses based on DNA sequences entered the arena of cone snail taxonomy. Initially, these approaches, often based on single marker genes, helped to resolve some long-standing taxonomic issues within this family. In 2017, however, a phylogenetic study based on complete mitochondrial genome sequences of a multitude of Cape Verdian morphospecies shook the scientific community of cone snail specialists and amateurs, proposing a radically different classification and lower species diversity compared to the prevailing morphology-based ones, and contradicting the partly intuitive view of many field workers on species delineation and diversity. This mitochondrial genome-based classification did not attempt to combine genetic data with morphological or ecological (habitat preferences) information, thus causing considerable controversy among more 'traditional' taxonomists as well as field biologists and amateur-malacologists, who not only focus on consistent morphological differences, but also claim consistent differences in habitat choice between different morphotypes.

What is direly missing in this debate is a holistic view that integrates DNA-based with morphology-based taxonomy and with ecological information. Moreover, the focus in DNA-based studies on cone snails has been almost exclusively on mitochondrial marker genes or genomes, whereas congruence (or lack thereof) between mitochondrial and nuclear markers has hitherto not been well investigated.

Doelstelling:

Current thesis topic therefore aims to a) perform phylogenetic analyses of multiple mitochondrial and nuclear marker genes of a range of Cape Verdian cone snails, and b) compare and integrate the resulting molecular insights with morphological and ecological data.

The student will perform DNA extractions and PCR on tissue samples of cone snails. (S)he will perform single-marker gene based phylogenetic analyses as well as produce concatenated 'consensus' trees based on the information of the different nuclear and mitochondrial marker genes. (S)he will also assist in morphologically vouchering the specimens used for molecular analysis, and will integrate molecular, morphological and ecological information to provide a basis for a more holistic revision of the taxonomy and diversity of Cape Verdian cone snails.

Locatie:

Campus Sterre en campus Ledeganck.

22408: The evaluation of agri-environment schemes to increase insect biodiversity

Promotor(en):	Maurice Hoffmann, Luc De Bruyn
Begeleider(s):	Luc De Bruyn, Marc Pollet
Contactpersoon:	Luc De Bruyn
Goedgekeurd voor:	Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:	
Nog onbeslist voor:	
Aantal studenten:	1
Aantal masterproeven:	1
Motivering voor deze opleiding:	

Probleemstelling:

A recent study received a lot of media attention, showing a 75% decline of flying insect biomass over the last 27 years. Insects play countless roles in ecosystem functioning. Hence, loss of insect biodiversity and biomass will provoke cascading effects in ecosystems (e.g. food webs, nutrient recycling, ...) and can impact ecosystem services (e.g. pollination, pest control, ...). Increased agricultural intensification plays an important role in explaining this decline.

The European Partridge project (<https://northsearegion.eu/partridge/>) aims to improve the agricultural landscape which should increase biodiversity by 30% over 4 years. Through agri-environmental schemes, farmers sow flower strips and create beetle banks that should provide more food for Partridge chicks and increase insect biodiversity in general. The aim of the present study is to assess the effectiveness of these measures.

Doelstelling:

Tasks:

- Fieldwork
 - April – September in Ramskapelle and/or Isabellepolder
 - Survey of insects with traps (pit falls, sticky traps, pan traps, ...) and/or transect walks
- Lab
 - Identification of trapped insects
 - Statistical analyses

Locatie:

INBO, Brussel

Website:Meer informatie op: www.inbo.be (from January 2020 onwards)**Onderwerp voorbehouden voor nvt**

22482: The evolution of floral scent in tropical rain forest trees

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

Probleemstelling:

Flowering plants dominate tropical ecosystems, and in many cases these plants require their pollen to be moved via a pollinator such as a bee, beetle, or butterfly, to the flowers of another individual plant of the same species in order to successfully reproduce. This is no small feat in a tropical rain forest. Plants are densely packed together, yet due to the incredible biodiversity and heterogeneity of plant communities of tropical forests, individuals of the same species may be separated by many meters and other plant species. Flowers use combinations of visual and olfactory cues to attract and manipulate insects as pollinators. In the low and variable light within and below the canopy of the rain forest, olfactory chemical cues (floral odour) play a particularly important role in attracting appropriate pollinators.

Very little is known about the chemical composition of floral odours for species of Annonaceae, a family of tropical rain forest trees and lianas. The majority of the species which have had their floral scent described by human perception in the literature are described as sweetly fruity or as ripe, rotten, or fermented fruit. The fruity odour of a number of species has been linked to attraction of beetle pollinators, with the general assumption being that these fruity, fermented odours mimic actual rotting fruits, duping the beetle pollinators into visiting the flowers while in search of brood sites.

A line of research has started recently in the Systematic and Evolutionary Botany lab, and you can be part of that. This project offers the possibility to do fieldwork in Bangladesh, and sample the floral scent of several species Annonaceae. At Ghent University, these scent samples will be analysed and interpreted.

Doelstelling:

The goal is to learn several techniques for sampling and analysing the volatile organic compounds that make up the scent of flowers. Also, you will acquire experience with analytical tools to analyse the data in a phylogenetic context. These techniques involve:

- Headspace sampling of floral scent
- Gas chromatography–mass spectrometry (GC-MS)
- Transformation of volatile organic compounds into characters for evolutionary analysis.
- Phylogenetic methods

Locatie:Ledeganck, veldwerk in Bangladesh

22468: The evolution of sexual dimorphism in Monarch flycatchers

Promotor(en): Matthew Shawkey, Liliana D'Alba Altamirano
Begeleider(s): Michaël Nicolai
Contactpersoon:
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:

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

Probleemstelling:

Monarch flycatchers (Monarchidae) are a diverse family that show strong sexual dimorphism. However, this dimorphism is not consistent in that sometimes differences occur in colours, ornaments (e.g. a larger tail), or both. Are they synergistic, mutually exclusive, or is there no pattern at all? It is not known what the relationship between these traits are, nor how they evolved.

Doelstelling:

In this thesis the student would visit the collections of the RBINS (Royal Belgian Institute of Natural Sciences) and the RMCA (Royal Museum for Central Africa) to take morphological measurements as well as colour measurements of flycatchers present in the collections. These measurements will, in conjunction with ecological data, be used in a comparative framework to test how these sexually dimorphic traits evolved and possibly identify drivers for either selection towards ornaments, colours or both. Similar evolutionary patterns have evolved multiple times in birds and the student is free to propose another model organism.

Locatie:

Campus Ledeganck

22478: The functioning and diversity of cryptogamic biological soil crusts and their role in the 'Greening of the Arctic'

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

Probleemstelling:

Biological soil crusts (BSCs) are the first colonizers of exposed substrates after glacial retreat in which they act as ecosystem engineers through soil stabilization and the regulation of soil temperature. They are also essential for nurturing Arctic terrestrial environments poor in organic matter by fixing atmospheric nitrogen and carbon. The colonization of bare soils by BSCs is therefore considered to be the initial process of a succession ultimately leading to the 'Greening of the Arctic' and the succession to shrub tundra. BSCs are to a varying degree composed of cyanobacteria, eukaryotic microalgae, lichens, mosses, fungi, and heterotrophic bacteria. The relative dominance and taxonomic composition of these groups appears to depend on the microtopography and the physical and geochemical characteristics of the underlying substrate soils. The objective of this MSc project is to investigate the effects of bedrock type, nutrient concentrations and microtopography on the composition, development and functioning of microbial communities and BSCs in west Svalbard and Nordaustlandet along transects of developmental stages in glacier forefields. Svalbard has a high geological diversity at a relatively small spatial scale, making the region an ideal study site for this type of research.

Doelstelling:

The student will use high-throughput amplicon sequencing of functional and taxonomic marker genes in combination with metagenomics to study the taxonomic composition and functional potential of BSCs. These data will be integrated with vegetation surveys, a digital elevation model developed using drone images and geochemical and mineralogical characteristics of the substratum soils. Ultimately, these data will help predicting the rate and direction of early responses of polar deserts to climate change and their altered ecological and biogeochemical functions.

Locatie:

campus Sterre

22388: The molecular basis of cell size sensing in diatoms

Promotor(en): Wim Vyverman, Koen Sabbe
Begeleider(s): Darja Belišová

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

Probleemstelling:

Diatoms are one of the most successful groups of microalgae in aquatic ecosystems. In the last decades they have received increasing interest of scientists trying to understand how they impact the functioning of aquatic ecosystems, but also in an industrial context as they have great potential to produce interesting biomolecules. Like many algae, diatoms alternate vegetative and sexual phases in their life cycle. Importantly, their average cell size in population slowly declines during the vegetative growth. This is related to the peculiar structure of diatom's rigid (siliceous) cell wall. The cell wall has a box and lid structure, with one part (the lid or epitheca) being slightly larger than the other part (the box or hypotheca). During the mitotic cell division the two parental thecae become the new epithecae of the daughter cells, whereas the smaller hypothecae are synthesized de novo, which results in a decreased cell size. If this size reduction would go on indefinitely, the cells would become too small and die. To avoid this, diatoms have developed a capability to sense their own size. Once the cells reach species specific size threshold, they transform into mature cells which are capable to keep dividing mitotically or reproduce sexually to restore their initial size. How diatoms control their life cycle and monitor the cell size remains to date unknown.

Doelstelling:

In the PAE lab, we investigate this size sensing mechanism and how it translates into changes in their behavior. To accelerate this development, we established a new model system, *Cylindrotheca closterium*, in which we can routinely and controllably reduce cell size and symmetry by cutting of the long ends of the cells. Given the universal occurrence of cell size sensing in diatoms, we expect that the fundamental control mechanism is strongly conserved. We will search for the potential candidate genes using reference genomes of two diatom models developed in the lab, namely *C. closterium* and *Seminavis robusta*, and by performing comparative analyses of their transcriptomes above and below the SST. We expect to find highly conserved genes coding novel hypothetical proteins related to mitotic spindle formation, cytoskeleton dynamics during mitosis and cell cycling that may be involved in size sensing. For in-vivo tests of the selected candidates, we will use advanced Gibson assembly cloning to prepare plasmids with genes of our interest fused to GFP (green fluorescent protein), express them in *Cylindrotheca closterium* and finally localize the expressed proteins within the cell. We are mostly interested in altered expression and localization of the proteins during different stages of the cell cycle and in cells with modified size. In this MSc project we will use basic and advanced molecular biology techniques such as GO enrichment analysis, PCR, cloning, cell transformation, fluorescent microscopy and flow cytometry.

Locatie:

22368: The more the merrier?

Promotor(en): Yves Van de Peer, Eylem Aydogdu Lohaus
Begeleider(s): Tian Wu, Annelore Natran, Lucas Prost, Quinten Bafort
Contactpersoon: Quinten Bafort
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Whole genome duplication (WGD) or polyploidisation provides an organism with an extra copy of the genome. As this copy is entirely redundant it has the potential to evolve new functionality. Consequently polyploidy is considered to be a major factor contributing to (plant) evolution. Nevertheless polyploidisation is a rather stressful event as the extra copy of the genome hampers cell division and causes considerable transcriptional and epigenetic upheaval. Several lines of evidence suggest that polyploid success is somehow linked to environments that are considered to be stressful to their lower ploidy ancestors. Three non mutually exclusive hypotheses have been proposed to explain this link: 1) stressful conditions promote polyploid formation, 2) polyploidisation causes an immediate fitness advantage allowing polyploids to grow where their ancestors cannot survive 3) polyploids have an increased evolvability and consequently adapt faster to a changing environment. In this thesis we will focus on the second hypothesis. Immediate changes of polyploidisation such as a change in cell size and geometry and gene expression changes are supposed to create a niche shift which can either be an advantage when the environment changes or can allow the polyploids to disperse and spread in regions that are inaccessible to their the lower ploidy ancestors. This initial ecological differentiation is hypothesised to reduce interploidy competition and can consequently be a first step in the establishment of a polyploid species.

Doelstelling:

First we will grow diploid and neopolyploid plants along gradients of different environmental variables in order to quantify this niche shift. Secondly we will use competition assays to study how interploidy competition affects the amount of niche differentiation and to test whether the polyploids can establish themselves and out-compete their ancestors. The use of genetically divergent lines will allow us to test whether certain types of environments (e.g. toxic, mutagenic or nutrient poor) confer a consistent advantage to a specific ploidy level. All experiments will be conducted on the greater duckweed *Spirodela polyrhiza*, a small aquatic plant with short generation time.

Lab work involves: Culturing of *Spirodela polyrhiza*, PAM, image analysis (measuring plant and population growth) and flow cytometry. There is a possibility to do molecular work as well.

Locatie:

VIB zwijnaarde

22442: The role of bioactive phenylpropanoids in plant growth and development

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

Probleemstelling:

Tightly regulated phytohormone balances are crucial to steer plant growth and development. We recently found that the naturally occurring phenylpropanoid *cis*-cinnamic acid (*c*-CA) perturbs auxin homeostasis by interfering with auxin transport in the plant. Treating plants with *c*-CA increases auxin levels in the root, resulting in the inhibition of primary root growth and proliferation of lateral roots. The altered root architecture can give plants an advantage under water or nutrient depleting conditions making the compound an excellent candidate for application in agricultural practice. Besides *c*-CA, several other bioactive phenylpropanoids are currently being studied in our lab. The focus of our research lies specifically on the investigation of the physiological role and the molecular mechanisms of these compounds in steering plant growth and development.

Doelstelling:

During your master thesis you will mainly work with the model plant *Arabidopsis thaliana*. You will treat plants with different bioactive phenylpropanoids and perform a detailed analysis of the obtained phenotypes, focusing on primary and lateral root growth. In parallel you will use available insensitive *Arabidopsis* mutants to characterize the molecular players involved in the signaling cascade activated by the compound of interest. The project will combine *in vitro* growth assays with molecular techniques (e.g. PCR, mass spectrometry, metabolomics and confocal microscopy).

Locatie:

PSB Campus Ardoyen

22426: The role of CBP-1 and BLI-4 in the delay of senescent pathologies in axenically cultured *C. elegans*

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

Probleemstelling:

Aging, a universal phenomenon in the animal kingdom, causes senescent pathologies which in turn lead to morbidity and death. In aging *Caenorhabditis elegans*, various pathologies develop over time, including tissue deterioration in the pharynx, gonads, neurons and intestine, as well as lipid retention and the formation of uterine tumors. Interventions that delay or prevent such pathologies are expected to extend lifespan.

Many breakthrough discoveries in field of aging were made in the nematode *C. elegans* as this tiny worm has many characteristics that make it a great model organism such as: a very short lifespan, simple anatomy, ease of handling, and no major ethical concerns. It has been observed that worms show an impressive lifespan doubling when they are cultured under conditions of axenic dietary restriction (ADR), a dietary regimen in which *C. elegans* is grown in the absence of its normal bacterial food, i.e. in a nutritious sterile culturing medium. Worms under ADR display increased stress resistance, metabolic rate, mitochondrial mass, and mitochondrial efficiency. It is not clear yet, whether age-related pathologies are delayed in ADR worms or whether these worms can survive these pathologies for a longer time in the absence of bacteria.

Doelstelling:

Our lab recently showed that the genes *cbp-1* and *bli-4* are required for ADR longevity as RNAi knockdown of these genes shortens the long ADR lifespan back to control levels. We wonder whether age-related pathologies are accelerated to the same extent in these animals. If this is the case, *cbp-1* and *bli-4* are new modulators of the aging rate in *C. elegans*.

To analyze age-related pathologies we will use Nomarski DIC microscopy combined with image analysis (uterine tumors, gonad and intestinal atrophy) as well as histochemical staining, fluorimetry or protein separation techniques (vitellogenin/yolk accumulation, lipid retention).

Locatie:

campus Ledeganck - 2e fase - 4e verdieping

22386: The role of microorganisms in the flocculation of sediments

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

Probleemstelling:

Planktonic microorganisms are not only single cells floating in the water column, sometimes they prefer a social life, forming multicellular or multispecies aggregates embedded in their matrix of polymeric substances named Extracellular Polymeric Substance (EPS) or Transparent Exopolymer Particles (TEP). Because EPS and TEP are sticky, they trap other microorganisms and fine sediments, enhancing bioflocculation.

Since the deepening, widening and dredging activities started in the Scheldt estuary, the Suspended Particulate Matter (SPM) dynamics have changed. We know that an increase of SPM negatively affect photosynthetic organisms, when light becomes a limiting factor. However, little is known about how phytoplankton and other microorganisms themselves can affect SPM dynamics, by changing SPM properties through their metabolic activities and the release of TEP and EPS.

Doelstelling:

The objective of this master thesis is to study the effects of the microorganisms on the bioflocculation processes. The student will perform lab experiments to test the effects of turbulence, nutrients, salinity, SPM and plankton composition in the flocculation processes. The experiments will be performed in a flocculator chamber with a camera system that will records the floc formation and size dynamics. The flocs will be analyzed using image analysis techniques. In addition, using microscopy and high-throughput sequencing, the plankton community composition (especially phytoplankton and heterotrophic bacteria) linked to the flocs will be identified.

Locatie:

22438: The structure of aquatic food webs from important coastal habitats

Promotor(en): Anna-Maria Vafeiadou, Tom Moens
Begeleider(s):
Contactpersoon: Anna-Maria Vafeiadou
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie

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

Probleemstelling:

Stable isotope analyses on invertebrates can provide useful information on the carbon resource and the organic matter pathways, as well as on the position of an organism in the trophic web ('you are what you eat' concept). Despite their high abundance and diversity, benthic meiofauna have so far been largely understudied in terms of their role in the food web. Within the project framework, we have collected invertebrates from a range of tropical aquatic habitats, including keystone habitats such as mangrove forests and seagrass beds, which are considered important carbon sinks.

Doelstelling:

This study aims to quantify the contribution of different organic matter sources from important coastal habitats to the meiobenthic organisms using natural stable isotope analysis. Meiobenthos will be identified to species or functional groups in order to approach the real trophic diversity, aiming to compare trophic pathways between different sites and habitats. The stable isotope approach will be combined with an ecological modelling approach (Ecosim) to explore whether differences in the isotopic signatures can also reflect structural differences in the food webs. We anticipate that there is a large trophic diversity in aquatic benthic communities, which is important for sustaining the biodiversity and the functioning of benthic ecosystems.

Locatie:

22383: The use of cereal winter food plots by the threatened Yellowhammer

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

Probleemstelling:

Due to agricultural intensification, farmland birds have declined in Western-Europe. For granivorous species a shortage of seed food in winter results into a lowered winter survival. Sowing or leaving cereal field plots to provide alternative food in winter has been shown to be a valuable conservation measure. Preliminary research indicated that the location of the plots in the landscape might influence the effectiveness. Therefore, a good understanding of how the birds use the plots is crucial. In the West Flemish Heuvelland and around Beveren aan de IJzer, cereal strips and patches are left during winter already for several years. One of the target species is Yellowhammer, one of the most threatened farmland birds in Flanders. Field observations indicated that not all patches are used at the same rate. Sometimes all birds are grouped in a few plots, on other occasions they are more evenly spread.

Doelstelling:

The aim of the present study is to assess how the quality, location and spatial composition of the strips and patches in the landscape influences the visitation rate and patch use by the birds. The student will assess bird movements with a recently developed technique. Birds will be netted and a tiny Bluetooth chip will be attached to the birds. This chip records which birds visit which plots. In addition the student will carry out field visits to record the birds behaviour. Quality indicators of the cereal patches and potential landscape drivers will be measured in the field or deduced from detailed maps (GIS).

Locatie:

Campus Ledeganck + INBO

Website:

Meer informatie op: https://www.west-vlaanderen.be/sites/default/files/2017-12/GEELGORS_soortactieplan%20W-VL_2015.pdf

Opmerkingen:

As the project implies a high level of mobility, a driving license is recommendable.

22341: Towards eradication of hidden hunger: optimizing metabolic engineering strategies

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

Probleemstelling:

Scope

Worldwide micronutrient malnutrition, or hidden hunger, affects more than 2 billion people. Hidden hunger can be defined as a lack of essential vitamins and minerals which causes severe developmental issues, especially in infants and woman of reproductive age. High consumption of rice in a monotonous diet is linked to hidden hunger. The seeds contain a high amount of calories but lack most essential minerals and vitamins including carotenoids (provitamin A), folates (vitamin B9) and iron (Fe). Biofortification, the enhancement of micronutrient content of food crops, through genetic engineering could potentially help to alleviate this global burden (Blancquaert et al., 2015; De Lepeleire et al., 2018; De Steur et al., 2015). The success of biofortification, however, depends on the efficient usage of DNA elements to ensure sufficient expression and translation of genes of interest. During this proposed thesis, new elements that enhance gene expression will be identified and their mode of action will be elucidated.

Doelstelling:

Aim

The aim of the project is to identify novel elements that enhance gene expression in rice and to elucidate their mode of action. This will serve to enhance the success rate of future biofortification approaches. The effect of different DNA elements will be tested using a luciferase assay in rice protoplasts. The protoplasts will further be used to elucidate the respective modes of action using translational/transcriptional inhibition assays. Further, we will transform Arabidopsis with several DNA elements to study the mode of action in stable transformants. Knowledge retrieved here will be extrapolated to other crops and bring fundamental insight in the (post)-transcriptional regulation of gene expression. It will further prove a stepping stone to the future world of synthetic biology.

Techniques involved

Transient transformation (rice protoplasts); Agrobacterium mediated plant transformation (Arabidopsis); DNA/RNA isolation; PCR; Q-PCR; in vitro plant growth; Luciferase assay; Western blotting; Translational/transcriptional inhibition assays; molecular cloning, in vitro plant growth.

References

Blancquaert, D., Van Daele, J., Strobbe, S., Kiekens, F., Storozhenko, S., De Steur, H., ... Van Der Straeten, D. (2015). Improving folate (Vitamin B 9) stability in biofortified rice through metabolic engineering. *Nature Biotechnology*, 33(10), 1076–1078.

De Lepeleire, J., Strobbe, S., Verstraete, J., Blancquaert, D., Ambach, L., Visser, R. G. F., ... Van Der Straeten, D. (2018). Folate Biofortification of Potato by Tuber-Specific Expression of Four Folate Biosynthesis Genes. *Molecular Plant*, 11(1), 175–188.

De Steur, H., Blancquaert, D., Gellynck, X., Strobbe, S., Lambert, W., & Van Der Straeten, D. (2015). Status and market potential of transgenic biofortified crops. *Nature Biotechnology*, 33(1), 25–29.

Locatie:

Website:

Meer informatie op: www.fpb.ugent.be

22418: Transport and impact of microplastics in marine food webs

Promotor(en): Carl Van Colen, Ann Vanreusel
Begeleider(s): Carl Van Colen, Lidia Lins Pereira, Ulrike Braeckman
Contactpersoon:
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:

Nog onbeslist voor:

Aantal studenten: 1

Aantal masterproeven: 1

Motivering voor deze opleiding:

Probleemstelling:

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 modes have been shown 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. However, at present we know very little about what affects the uptake of microplastics by marine organisms and the possible role of seafloor biota in removing microplastics from marine food web through burial. Additionally, 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 is limited.

Doelstelling:

In this thesis, you can investigate the presence of microplastics in sediment-dwelling organisms collected across European coastlines, execute experiments that quantify the accumulation and removal of microplastics in food webs, as well as examining factors that possibly affect the ingestion of microplastics in marine organisms, such as size, shape, colour and colonization of microbial communities.

Locatie:

campus sterre

22492: Under the spell of a ring - species delimitation in two morphologically similar lineages from different continents within the genus *Lactifluus*.

Promotor(en): Annemieke Verbeken, Eske De Crop

Begeleider(s):

Contactpersoon:

Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie

Niet behouden voor:

Nog onbeslist voor:

Aantal studenten: 1

Aantal masterproeven: 1

Motivering voor deze opleiding:

Probleemstelling:

The 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 parziale, 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.

Doelstelling:

Locatie:

22373: Understanding the molecular networks underlying *Caulobacter* induced growth promotion of *Arabidopsis*

Promotor(en): Sofie Goormachtig

Begeleider(s): Amber Lampens

Contactpersoon: Amber Lampens

Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie

Niet behouden voor:

Nog onbeslist voor:

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

Probleemstelling:

Plant growth promoting rhizobacteria (PGPR) have regained scientific interest during the last decades as they might be implemented in agriculture as part of a sustainable and ecologically sound fertilization system. In the lab, a microbiome study on maize grown in cold conditions guided the establishment of a collection of potentially growth promoting micro-organisms. One of these species, a *Caulobacter* strain, is the subject of this project. It has been shown before in the lab that this bacterial strain promotes plant growth in both maize and *Arabidopsis thaliana*, the latter allowing more in depth molecular and functional studies. More specifically we are interested in the potential link between bacterial perception and plant growth promotion, since we have preliminary data suggesting the involvement of a specific plant co-receptor in this beneficial plant-microbe interaction.

Doelstelling:

During the project the role of this plant co-receptor and closely related members of the same family in bacterial induced plant growth promotion will be investigated in depth. Candidate receptors are selected via the screening of a receptor mutant collection for an aberrant phenotype, i.e. a significant decrease or complete loss of growth promotion upon inoculation with the *Caulobacter* strain. This thorough functional study will include both phenotypic and molecular experiments in order to get a broad view on the link between perception and growth promotion. To this end, we will check if the same phenotype, loss of growth promotion, can be detected upon inoculation of the receptor mutant lines with different PGPR. Furthermore, different environmental conditions and bioassays will also be tested in order to investigate how general (or specific) the involvement in growth promotion is. Molecular experiments will include the elucidation of the expression pattern of the receptors by making fusion constructs with a fluorescent marker gene followed by a microscopic investigation of these plants. The constructs can further be used in complementation experiments using the mutant lines. Since this family of receptors works as dimers and cross-phosphorylation is crucial for activation of the receptor and initiation of downstream signaling, the phosphorylation status of the receptors will be checked upon inoculation. Furthermore, protein-protein interaction studies could be performed on the most promising receptor pairs.

Together these experiments will aid us in gaining insights in the very early bacterial perception events that eventually influence the plant growth promoting phenotype. In the end we will elucidate the functional link between perception and growth promotion.

Locatie:

Campus Ardoyen, PSB

Website:

Meer informatie op: www.psb.ugent.be

Onderwerp voorbehouden voor Marjon Braem

22338: Unraveling the effect of a novel virus resistant trait on honey bee health.

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

Probleemstelling:

Honey bees are under pressure due to abnormal high death rates, especially during the winter. There are several possible explanations for the increased mortality, but the infestation by the *Varroa destructor* mite and the viruses that this ectoparasite transmits are generally seen as the most important ones. Previous research, based on a 6 years breeding program in Flanders showed a successful selection for virus resistance of honey bees. This trait, so-called 'suppressed in ovo virus infection' (SOV) is heritable through the genotype of the queen. Ongoing research also indicates that the SOV trait both reduces the virus infection load as the number of infected bees over all live stages of the honey bee.

Doelstelling:

The purpose of this topic is to improve our understanding on virus resistance and the implications for honey bee health. The student will conduct various

infection studies on in-vitro reared honey bees in different life stages and for different viruses. By measuring virus replication and the anti-viral responses using qPCR the effect of the SOV trait can be better understood. The student will link these findings with the current understanding on honey bee health.

Locatie:

campus sterre

22434: Unravelling alternative organic matter production pathways of aquatic invertebrate communities

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

Probleemstelling:

While photosynthesis derived organic matter is usually thought to be the main source of energy in aquatic food webs, other pathways can also offer alternative resources, such as chemo-autotrophic or methane based metabolic pathways. Methane production is known to be a critical energy source for organisms living in specific extreme environments, where photosynthesis is not an option or is limited. However, the role of chemo-autotrophic or methane based pathways in sedimentary coastal habitats remains largely unexplored. Stable isotope analysis is a powerful tool to detect the contribution of CH₄ as a resource in food webs.

Doelstelling:

In this study, we aim to quantify their contribution to benthic food webs in various aquatic habitats (e.g. mangroves, seagrass beds) in highly productive coastal environments, i.e. the tropical Gazi Bay area at the coast of Kenya and salt marsh vegetations in the Schelde Estuary. The study involves specific tracer incubation experiments to quantify the importance of the different carbon flows in aquatic food webs of different habitats within the sampling site in combination with natural stable isotope analyses of the benthic communities. We will compare ¹³C assimilation by different meiobenthic species and/or functional benthic groups from the tracer experiment to unravel the potential role of chemo-autotrophy and methane production as different pathways in aquatic ecosystems.

Locatie:

22413: Unravelling the M³A phenomenon (Mysterious Monastery Medetera Aggregations) in eastern Spain

Promotor(en): Maurice Hoffmann, Marc Pollet
Begeleider(s): Marc Pollet, Luc De Bruyn
Contactpersoon: Marc Pollet
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Back in 2016 an extraordinary phenomenon came to my attention: photographs showed an enormous number of adult flies clustering on the walls and ceilings of the entrance to the cloisters of a monastery in the Salamanca Region, eastern Spain. The space is known locally as "[Las Cuevas de los Mosquitos](#)" which implies that it is a regular, presumably annual, event. As it occurs in June it is interpreted as aestivating behaviour, with the adults protecting themselves from the unfavourable conditions (hot dry summer) between emergence and later activity such as oviposition. A small sample taken in the monastery contained only one species of long-legged fly, *Medetera saxatilis*, which is widespread rather arboreal species in Europe.

This truly special situation – basically an open air lab – allows detailed research. Indeed, different questions come to mind easily: which species are we dealing with, and are both sexes represented? Why is this species aggregating in this monastery and is this behaviour exceptional (is it only observed here, or does the species aggregate in other sites as well (similar buildings, cellars, caves, ...)? When does the species show this behaviour and what does it do beyond its aggregation phase, (i.e., does it leave the building again, or does it simply die)? What does it do during its aggregation phase (i.e., does it feed or not)? How does

it enter the building and how fast does the aggregation build up? Has climate change an effect on this phenomenon (e.g., do the flies arrive earlier nowadays as compared to earlier on)? Etc ...

Doelstelling:

This field study is best conducted by means of short visits to the site during the entire activity period of the species. Videorecording or photo analysis might certainly contribute to establish densities and movements. Regardless of this exceptional behavior, however, carrying out this research will ultimately encompass financial resources that should be provided by the student him/herself.

Profile: we are looking for an all-round biologist with an interest for entomology and insect behavior. (S)he is accurate in his/her observations and data handling, thinks out-of-the-box, is creative and communicative. Having an adventurous nature is considered an asset ...

Locatie:

INBO, Brussel, campus Ledeganck

Onderwerp voorbehouden voor nvt

22303: Vitamins in plant life: The regulatory role of vitamin B9 (folates) and folate binding proteins

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

Probleemstelling:

Folates are indispensable for the growth and developments of all living organisms. Deficiency of folates leads to several developmental anomalies in not only humans, but also in plants. As it is mainly the plant based diet that fulfils the folate requirements in humans, understanding folate metabolism in plants is important not only to expand our understanding, but also to increase staple crop folate levels, which in general is very low. Folate biofortification by overexpressing biosynthetic enzymes in rice has been successful, but combining it with transgenic expression of bovine folate binding protein (FBP) proved critical for the durability of the enhanced folates (Blancquaert et al., 2015). This triggered the quest for identification of a plant based FBP, which can optimally be employed in folate biofortification programs. Recently, a novel FBP has been identified in Arabidopsis, which upon expression in yeast resulted in higher folate uptake (Puthusseri et al., 2018). Our effort has led to the identification of several FBPs (Mishra et al., submitted for publication), many of which are critical in plant physiology, like HSP100 chaperone, which helps plant combat high temperature stress (Mishra and Grover, 2015). This project aims at purifying higher quantities of the novel plant FBP as well as HSP100. On one hand, the folate binding capacity of this FBP and how it helps cells in retaining folates will be assessed. On the other hand, the effect of folate on chaperone activity of HSP100 will be assayed employing in vitro chaperone activity assays. This project will boost the existing folate biofortification efforts as well as unveil the importance of folates in plant thermotolerance, which may become important in view of global climate change.

Doelstelling:

We will transform the appropriate bacterial host with a plasmid containing the novel plant FBP and HSP100 cDNAs, with N-terminus tag. A single positive clone will be selected for protein expression/purification. Appropriate growth conditions and induction parameters will be optimized to express as much soluble protein as possible; involving selection of the most suitable expression temperature and inducer concentration among a series of different temperatures/concentrations tested. Once the desired level of soluble FBP protein is attained in the bacterial cells, the recombinant protein will be purified using Ni-NTA beads affinity-based chromatography. Soluble protein will be dialyzed and dissolved in an appropriate buffer to ensure stability under long-term storage and activity. HSP100 chaperone activity assay will involve testing the effect of this chaperone on the activity of a restriction enzyme under denaturing high temperatures. Supplementing the reaction with folate will reveal its effect on HSP100 chaperone activity. If time allows, we will also transform Arabidopsis with a construct containing the FBP.

Locatie:

Campus Ledeganck

Opmerkingen:

Research is part of an international collaboration.

22447: When genomes team up - effects of genome doubling and merging on fitness and gene expression

Promotor(en): Olivier De Clerck, Yves Van de Peer
Begeleider(s): Quinten Bafort, Lucas Prost
Contactpersoon: Lucas Prost
Goedgekeurd voor: Master of Science Biology, incl. Educatieve Master Biologie
Niet behouden voor:
Nog onbeslist voor:
Aantal studenten: 1
Aantal masterproeven: 1
Motivering voor deze opleiding:

Probleemstelling:

Polyploidization, the doubling of the entire genome inside the nucleus of an cell, is considered a major factor contributing to evolution, especially in plants. In fact, all angiosperm species are ancient polyploids. Following a genome doubling event, dynamic changes occur at the genomic and transcriptomic levels. In polyploids formed through hybridization (allopolyploids), the merging of two different genomes may have additional effects on gene expression and consequently on fitness. These changes have been studied in several natural systems (*Tragopogon* sp., *Clarkia* sp., *Gossypium* sp., etc.). However, lack of immediate comparison between polyploids and their diploid ancestors due to subsequent evolution hinders direct observation of the allopolyploidization effects on gene expression.

Doelstelling:

To counteract such constraints on evolutionary hypotheses, we are carrying out an experimental evolution with the green microalgae *Chlamydomonas reinhardtii*. Haploid strains are evolving in different conditions. After several generations of divergent evolution an allodiploid strain will be formed using both haploid strains. This newly-formed diploid will contain both genomes.

Direct comparison of gene expression and fitness of parental haploids and the neodiploid will then be possible. Questions on the effects of genome merging and doubling on fitness and gene expression will be investigated, such as:

- i) does the presence of both genomes in the diploid produce a transgressive phenotype allowing it to increase its fitness in both conditions?
- ii) is the expression pattern of parental haploids conserve in the newly-formed diploid, grown in the same conditions?
- iii) is the fitness of a neodiploid in condition B lowered by the presence of a genome adapted to condition A, when compared the parental haploid adapted to condition B?

Lab work will mainly consist of microalgae culturing, treatment applications on experimental strains, competition and adaptation assays and RNA extraction. The student will then use bioinformatics tools to analyze the transcriptomic data which enable us to draw conclusion on allopolyploidization effects on gene expression.

Locatie:

campus Sterre, S8; VIB,Zwijnaarde

Onderwerp voorbehouden voor Antoine Van de Vloet