

2016 FAME symposia

Abstracts

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symposium 1: Global change and biodiversity: impact and mitigation

Biodiversity, ecosystem function, and environmental change

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Namur

For the past 20 years, research on biodiversity and ecosystem functioning (B-EF) has only implicitly considered the role of environmental change. In this talk, I present two perspectives on the re-introduction of environmental change drivers in B-EF research. The first perspective considers environmental change drivers as instigators of B change. Using model simulations, I illustrate that different environmental change drivers cause different B-EF trajectories and so predicting the functioning of ecosystems facing changes in B cannot be done without explicitly accounting for the underlying environmental change driver. Next, I present data from a recent meta-analysis that confirm a key prediction made by the models: environmental change can severely affect EF while leaving B unaltered but leaving compositional signals. The second perspective considers environmental change drivers as the context within which the effect of initial B on EF can be examined. I present a recent study that shows how the effect of environmental context on B-EF relationships can be predicted from direct effects on species growth and the same interactions prevailing in reference conditions. Finally, I show some examples of how re-introducing environmental change drivers improves experimental control over community composition and structure. This should help obtaining mechanistic insight about how multiple aspects of B relate to EF, and how B and EF relate in food-webs.

Phosphate stripping by hypolimnic oxygenation of Lake Ouderkerk: a highly effective measure to control cyanobacterial blooms

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Lake Ouderkerk is a dimictic sand extraction pit near Amsterdam (the Netherlands) with a poor water quality. Due to high phosphate concentrations in the water layer, the lake suffers yearly from blooms of green algae and Cyanobacteria (blue-green algae). The sediment of the lake is P-rich and during stratification the hypolimnion becomes anoxic due to the high biological oxygen consumption. As a result large amounts of phosphate are mobilised from the sediment to the water layer. Since 2010 cold water from the hypolimnion is extracted for the sustainable cooling of buildings in the direct surrounding of the lake. After use the extracted P-rich water from the hypolimnion is returned into the epilimnion of the lake. To prevent a further deterioration of the water quality due to this additional circulation of phosphate, the hypolimnion is oxygenated to stimulate phosphate binding by the iron-rich sediment. The effects of hypolimnetic oxygenation on the water quality and the development of phytoplankton were studied during a 6 years monitoring program. The results reveal that oxygenation strongly decreases the release of phosphate into the hypolimnion which together with the epilimnic fixation of phosphate by pelagic micro-algae, has resulted in a strong decrease of the total-P concentrations in the lake water. As a consequence, growth of algae is strongly reduced and Secchi depth (water transparency) has strongly increased.

The polar lacustrine microbiome: centres of endemism under changing climates

E. Verleyen ⁽¹⁾, W. Vyverman ⁽¹⁾, B. Van de Vijver ⁽²⁾, M. Sweetlove ⁽¹⁾, E. Pinseel ⁽¹⁾, B. Tytgat ⁽¹⁾, K. Sabbe ⁽¹⁾ and the CCAMBIO consortium ⁽³⁾

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Nowhere is climate change more visible than in the Arctic and parts of Antarctica, making them the most critical reference regions for the detection and understanding of global change and its effects on biodiversity. Particularly polar lakes appear to respond quickly to changes in temperature in the form of longer ice-free periods, increased primary production and declining water levels. Because polar lakes are dominated by microbial organisms, understanding the processes shaping spatio-temporal dynamics in microbiome composition is of key importance to predict future changes in their function, as well as to assist conservation planning under changing climate regimes. Our large-scale taxonomic inventory of high-latitude lake ecosystems based on high-throughput sequencing of environmental DNA, microscopy and

culture-based approaches revealed that climate-related environmental variables, such as air surface temperature and lake water salinity exert a strong influence on the diversity and distribution of eukaryotic and prokaryotic communities. We also observed strong biogeographical and macroecological patterns in the microbial communities, which are remarkably congruent with multicellular organisms. This suggests a common evolutionary history between microbial organisms and plants and animals. For well-studied taxa such as diatoms, evidence indicates that lakes in the Antarctic Realm share few species with those from environmentally similar lakes in the (sub)-Arctic. This suggests a high level of endemism as well as other key features of canonical island biota, including a marked taxonomic imbalance in the Antarctic flora. Comparison with Miocene freshwater diatom deposits shows the loss of a more temperate flora with a distinct Gondwana signature in the Antarctic, resulting from lineage sorting in response to past climatic changes since the onset of Miocene cooling. These observations form compelling evidence for the combined role of historical as well as contemporary processes such as climate change in shaping polar lacustrine microbiomes. Our results also call for increased attention to prevent human introductions of microorganisms in the Antarctic and the subsequent homogenization of the microbiomes in these relatively pristine ecosystems.

From carbon source to carbon sink: strong reduction of greenhouse gasses by rewetting of agricultural peatlands and restoring peat moss vegetation

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Globally, many wetlands including peatlands have extensively been drained for agricultural use, resulting in severe land subsidence and loss of important ecosystem services such as carbon (C) sequestration, flood protection and water purification. To halt land subsidence, these peatlands are rewetted by increased rainwater storage or sub-optimal surface water supply. Previous reports show that increasing water storage already transforms drained peatlands into considerable sources of methane (CH₄). Furthermore, rewetting of former agricultural peatlands is expected to cause eutrophication due to the high nutrient availability in the soil, which may compromise the restoration of C sequestration by negatively influencing the regrowth of peat forming vegetation such as *Sphagnum* spp.

We compared C fluxes of a rewetted former agricultural drained peatland in the Netherlands with its control situation, and additionally used a controlled laboratory approach to study potential side effects of rewetting with P and HCO₃⁻ rich surface water compared to rainwater. Besides, we tested measures that may reduce negative side effects, including topsoil removal and the application of *Sphagnum* spp.

After removal of the nutrient-rich topsoils, rewetting led to much lower P and N mobilisation and much lower C (CH₄, CO₂ and DOC) emissions. Supply of P-rich water resulted in further eutrophication and algal blooms, whereas HCO₃⁻-enrichment by surface water not only stimulated P release and C emissions, but also strongly reduced the vitality of Sphagnum mosses.

We conclude that rewetting of drained peatlands and applying Sphagnum greatly reduces CO₂ emissions without increasing CH₄ fluxes. Besides, topsoil removal will, at least in initial stages, strongly reduce the emission of nutrients and greenhouse gases. The storage of rainwater rather than surface water is preferred to reduce mineralisation rates and enable Sphagnum growth. In order to optimize the total C balance, the removed topsoil should be re-used in subsiding agricultural peatland areas.

Disentangling interactive effects of past and present environmental changes on forest herbs in a multi-factor experiment

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Herbaceous plant communities represent a key part of functional biodiversity in forests. The diversity within and across these communities can reflect past and current ecosystem conditions. This is especially the case for ancient forests, where understorey species share a typical set of functional and life-history traits. Clearing of these forests for agricultural purposes results in a loss of this typical flora, even after re-establishment of a post-agricultural forest. The floristic composition of post-agricultural forests still bears the imprint of the past land-use for many decades, only allowing rapid colonizers with associated functional traits to establish in such sites. Nutrient stocks in these forest soils can be elevated for long time periods as a result of the past agricultural practice. Aside from land-use history, other environmental drivers such as light availability, climate change and nitrogen deposition will codetermine the developmental trajectory of understorey communities. Some of these drivers such as changes in light availability due to a shift in forest management act on a local scale. Others such as climate change affect ecosystem changes globally. Nitrogen deposition is an environmental driver that varies on a regional scale affecting ecosystem functioning by acidification and eutrophication. We developed an unprecedented multi-factor field experiment to disentangle interacting effects of land-use legacy, climate warming, light availability and enhanced nitrogen availability on herb layer communities. Model plant communities were planted in soils collected from post-agricultural and ancient forests stratified along wide temperature and nitrogen deposition gradients across Europe. These experimental units are represented as mesocosms: a part of a natural environment brought under relatively controlled conditions. We hypothesize that the model herb layer communities will

develop differently with former land-use and light availability as the major drivers of change.

Modelling marine species distributions in a changing world

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Typically species distribution modelling assumes that the species is in equilibrium with its environment, which is not the case for invasive species and for species sensitive to a changing climate. In addition, to ensure that distribution models adequately capture the ecological niche of the organism we need to use relevant predictors, proper model validation and appropriate algorithms and settings. For marine species the uncertainty in predictor selection and parameter settings is probably even larger than for terrestrial organisms whose ecological is mostly much better studied. In this presentation, I will show how these issues can be researched using a benchmark dataset, MarineSPEED. This dataset consists of distribution records for 524 marine species from a wide variety of taxa and ecoregions. I will also illustrate the need for proper background selection, spatial thinning and the propagation of uncertainty with a case study modelling the niche and distribution of invasive seaweeds in Europe through time and space.

The need for large-scale distribution data to estimate regional changes in species richness under future climate change

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Species distribution models built with geographically restricted data often fail to capture the full range of suitable conditions for the species. Using such models to predict distribution shifts under environmental change may produce biased projections. However, restricted-scale models have certain advantages, most notably the

potential to include a larger sample of taxa for which distribution data is available and to provide finer-resolution projections that are better applied to conservation planning than forecasts of broad-scale models. We examine the circumstances under which the projected shifts in species richness patterns derived from restricted-scale and broad-scale models are most likely to be similar. The distribution of butterflies in Finland, Belgium/Netherlands and Spain was modelled based on restricted-scale (national) and broad-scale (continental) distribution and climate data. Models were calibrated with present-day climate data and projected under future climate change scenarios to assess potential changes in species richness. In Finland, species richness was projected to increase strongly based on restricted-scale models and to decrease slightly with broad-scale models. In Belgium/Netherlands, restricted-scale models projected a larger decrease in richness than broad-scale models. In Spain, both models projected a slight decrease in richness. We obtained similar projections based on restricted-scale and broad-scale models in Spain because the climatic conditions available here covered the warm part of the distributions of the species better than in Finland and Belgium/Netherlands. Restricted-scale models that fail to capture the warm part of the distributions of the species produce biased estimates of future changes in species richness when projected under climatic conditions with no modern analogue in the study area. We recommend the use of distribution data beyond the boundaries of the study area to capture the part of the species response curves reflecting the climatic conditions that will prevail within that area in the future.

Acknowledging biotic interactions and traits improve predictions for biodiversity in a warmer climate

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Understanding how global changes impact species losses and gains (local extinctions and invasions) is critical for predicting effects of global change on biodiversity. Arctic tundra ecosystems are encountering the most rapid climate warming on the Earth. This warming may radically alter tundra plant diversity by inducing species losses and gains. At the same time tundra plant growth is controlled by mammalian herbivores, but it remains unknown whether herbivores amplify or mitigate impacts of climate warming on diversity. Here, I present results of an experimental field study, which tested how warming and herbivores affected species losses and gains. Our results also illustrate how functional traits can be used to predict species sensitivity to local extinctions in a changing environment.

Evaluating realistic conservation management scenarios in an Afrotropical biodiversity hotspot using a novel, individual-based modelling platform

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Given rising food demands, the application of conservation approaches focusing on the protection or creation of large habitat areas will increasingly be constrained by land availability and socio-economic issues, especially in the tropics. Biodiversity conservation, hence, requires alternative management strategies that effectively improve the persistence of populations constrained to smaller habitat fragments. One potentially realistic option is to effectively connect subpopulations through dispersal, allowing them to function as one larger, more resilient population capable of tracking environmental variation in space (i.e. the creation of 'habitat networks'). However, evaluation of the effectiveness of such networks is challenging, as it requires predictive models that can capture the effects of management on functional connectivity. Spatially explicit population models (SEPMs) potentially meet this requirement but in most applications the dispersal process is modelled unrealistically which may render predictions unreliable. In addition, progress yet has to be made to take into account temporal variation in environmental suitability in scenario evaluation. Given forecasted rates of climate change this likely is crucial. For instance, habitat protection may appear to be sufficient for a species to persist under the assumption of a stable climate but in reality, habitat corridors may be required that allow the species to shift its range. RangeShifter is a recently developed SEPM that allows dispersal to be modelled mechanistically and here we illustrate how this likely is crucial in scenario evaluation. Simulations of the spatial population dynamics of an Afrotropical forest bird species, for instance, revealed that patches added to a habitat network compromised population persistence in some of the existing patches by acting as disperser sinks. Current work seeks to improve robustness of predictions and we are applying RangeShifter at a large spatial extent (Eastern Arc Mountains) for multiple species and, for the first time, taking into account effects of climate change.

Survival in a feast-famine environment: Resource utilization and storage in cold-water coral *Lophelia pertusa*

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Coral reefs are not limited to shallow, tropical seas. Cold-water Scleractinian corals (CWCs) likewise secrete calcium carbonate skeletons and construct deep-water reefs which provide habitat for a multitude of organisms. CWC reefs play a major role in carbon cycling in the deep-sea, but their high productivity and diversity stands in sharp contrast to the scarcity of available resources. Organic matter is exported from surface ocean to deep sea in rare short peaks creating feast feeding conditions intermitted by long famine periods. This natural environmental gradient might be enforced due to global change, likely resulting in lower export production. Further, climate change and ocean acidification potentially increase CWC energetic demands, which requires efficient energy storage and use. Determining CWCs resource use is therefore important to predict resilience and conserve their functional role in shaping this deep-sea ecosystem. In a stable isotope tracer experiment we simulated a feast-famine sequence to understand the resource processing and allocation in the most common CWC species *Lophelia pertusa*. The uptake of an algal food peak was followed over four weeks by weekly measurements of (a) coral-produced dissolved inorganic carbon (DIC), dissolved organic carbon (DOC), and particulate organic carbon and nitrogen (POC, PON) and (b) biweekly measurements of ¹³C and ¹⁵N storage into bulk coral tissue and specific biogeochemical pools such as fatty acids and amino acids. Our results indicate that *L. pertusa* invests energy from a short food peak directly to build new biomass, and store excess carbon in organic storage pools. Stored resources, however, are depleted to almost 50% within four weeks of starvation, via continued metabolization of food carbon through respiration and organic carbon release in terms of mucus. Resource availability, utilization and energy allocation of those ecosystem engineers are discussed as key factors to study resilience towards global climate change.

Effects of plant diversity on the stability of natural grassland ecosystem functioning

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The hypothesis that a greater species diversity leads to a greater stability of ecosystem functioning has been a point of debate for decades. The increasing effects of climate change, climate extremes in particular, and the current biodiversity crisis makes this one of the most relevant research topics in current vegetation sciences and ecology. However the bulk of research is done in relatively small scale in situ and ex situ experiments, where species compositions are manipulated and monitored over time. This study aims to upscale research into diversity-stability relations to natural real-world ecosystems. Therefore data sets on vegetation, climate, functional traits and remote-sensing are combined to observe these relations over larger temporal and spatial scales in several natural grassland ecosystems in the Netherlands with natural dune grassland ecosystems in particular. Our findings suggest that the diversity-stability relationships found in biodiversity experiments hold across larger temporal scales in natural unmanipulated ecosystems. Based on long-term species composition and remote sensing data, we show that over years with climate extremes, ecosystem productivity of dry dune grassland communities was significantly more stable with higher plant species richness. These results remain consistent when environmental variation across sites is taken into account. Again, the same positive diversity-stability relationship seems to hold at increasingly larger scales, up-scaling this study to a broader range of grassland ecosystems in the Netherlands. This research explores the opportunities given by the use of large data sets and new monitoring techniques and our results underline the important role of plant species diversity in maintaining ecosystem functioning in a changing world.

Creating a super-Daphnia to control toxic cyanobacterial blooms by manipulating its gut microbiome

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Microcystis (cyanoHABs) are a problem for drinking water production as many of the drinking water sources contain cyanobacterial toxins. Additionally, these cyanoHABs produce large amounts of particulate and dissolved organic matter concentrations in the feed water that interfere with the water production (blocking of filter systems and an increased chemical demand). The aim of this research project is

to create super-Daphnia that are resistant to microcystin toxins by manipulating its gut microbiome as recent research by Macke et al. (in review) revealed that the gut microbiome plays a crucial role in the resistance of Daphnia to cyanobacteria. When she transplanted the microbiome from the tolerant strains to the sensitive strains, the sensitive strains became resistant to toxic Microcystis. These super-Daphnia will then be applied to control toxic Microcystis blooms in water sources used for drinking water production. Firstly, a selection of different freshwater ecosystems in Flanders will be screened and inventoried for zooplankton microbiome composition, phytoplankton and toxins. Secondly, Daphnia donor genotypes will be acclimatized to Microcystis by exposing them to a diet of Microcystis. By adapting the donors, bacterial taxa involved in digestion of cyanobacterial cells will be favored and will provide increased resistance to Microcystis. As such, we will obtain a pool of gut microbiomes which can, after extraction, be inoculated to more susceptible Daphnia genotypes to improve their resistance. Thirdly, the recipient Daphnia will be inoculated with the donor gut extract in order to achieve the super-Daphnia. And lastly, the proof-of-concept of our super-Daphnia will be validated through a mesocosm experiment. Additionally, different time points of inoculation of the super-Daphnia will be examined in order to obtain insight into the ideal timing in possible preventive (before bloom) and curative (during bloom) approaches.

Help from above - Boosting yield and conservation value in cacao production by doing nothing?

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Apart from pressures from changing environmental conditions and increases in pest incidence, cacao production has been shown to be limited by cacao pollinator abundance. Cacao pollinators can occur in several habitat types such as the water holding leaf axils of tank bromeliads (Bromeliaceae). Epiphytic bromeliads can naturally occur in cacao plantations of the new world, but are often removed by the farmers who falsely assume them to be parasitic. By comparing plantations with and without bromeliads and experimental manipulations, this research focusses on uncovering the potential positive effects of maintaining bromeliads within cacao plantations on the potential yield, and on general insect biodiversity associated to bromeliads.

symposium 2: Emerging infectious diseases

How spatial data can help in the battle against emerging infectious diseases

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Over the last decades, new challenges have emerged for public health authorities worldwide as global changes facilitate both the introduction, establishment and spread of invasive vector species and the emergence/resurgence of the diseases they transmit. As a result, we have seen a significant increase in some of the worlds most prevalent mosquito- and tick-borne diseases. Tropical diseases transmitted by invasive Aedes-mosquitoes, such as chikungunya fever, dengue and recently also ZIKA, are expanding worldwide, whilst in the Northern hemisphere tick-borne infections such as Lyme disease are booming. For example, in 2013 the CDC increased the estimated annual diagnoses of Lyme disease by a factor of ten from 30,000 to 300,000; a similar phenomenon was observed in the Netherlands. Several factors contribute to this situation. Vectors and the pathogens they carry are travelling further, faster and in greater numbers than ever before due to tourism and transportation of goods. Changing climatic factors can accelerate the invasion or transmission process whilst changing environments, human interventions and habits can lead to a higher exposure to the vectors. Spatial data can help us in predicting invasions and outbreaks and getting prepared for them, not only by mapping the current known distribution of the vector and/or pathogen but also by predicting their future spread, making gap analyses to identify knowledge gaps and modelling the seasonality to guide control methods. Two examples will be highlighted: the spread of two invasive mosquito species accompanied by an increase in Dengue cases, and the remarkable increase in reported Lyme disease cases.

Tropical infectious disease in Europe: reconstructing the emergence of urinary schistosomiasis in Corsica (France).

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Snail-borne diseases affect more than 300 million people worldwide but also lead to economic losses and mortality in livestock. Especially developing countries are affected but due to globalization and climate change the distribution of snail-borne diseases is shifting northwards. New introductions of disease are linked with increasing human migration as illustrated by the recent outbreak of urinary schistosomiasis in Europe. Successful establishment depends, however, on the presence of a suitable snail host, which is tightly linked with climate and environmental change.

With molecular tools we aim to reconstruct the source of introduction into Corsica and characterize the local intermediate snail host. Larval schistosome stages isolated from patients that became infected in Corsica were characterized with 17 microsatellite markers and compared with isolates from Mali and Senegal. Similarly, populations of the local snail intermediate host, *Bulinus truncatus*, from Corsica were genotyped using next-generation sequencing technology and compared with populations from Senegal, Cameroon and Egypt. Comparative phylogeographic analyses are conducted and possible introduction scenarios will be discussed. Given the fact *Bulinus truncatus* is endemic in southern Europe, close monitoring of putative transmission sites is highly recommended.

Update on Lyme disease in Belgium

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Lyme borreliosis is a multisystem infectious disease caused by infection with spirochetes of the *Borrelia burgdorferi sensu lato* (s.l.) complex, transmitted to humans by the bite of infected ticks. It is the most common tick-borne disease in Europe. Clinical manifestations of infection include dermatological (typical rash called erythema migrans), rheumatologic, neurological or cardiac symptoms. In the early stage of the disease, diagnosis is based on clinical symptoms only. Laboratory tests (ELISA confirmed by Western Blot) are necessary to confirm a diagnosis of later stage infection. Treatment of Lyme borreliosis consists of appropriate antibiotics and should be started as soon as possible for full clinical recovery. The duration of treatment depends on the stage of illness. Surveillance of Lyme disease in Belgium is based on three sources of information. A network of sentinel laboratories

weekly reports the number of positive serological tests for *B. burgdorferi*. The yearly number of persons hospitalized for Lyme disease is monitored through the hospitals minimum clinical datasets. And the incidence of erythema migrans is estimated based on repeated studies carried out by a sentinel network of general practitioners. Up to 2015, none of the systems identified a significant increase in the incidence of Lyme disease in Belgium.

Report from the European OneHealth/EcoHealth Brussels workshop 2016

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The European OneHealth/EcoHealth workshop brought together people from different communities in science, policy and practice to exchange experience and views, to discuss opportunities and challenges for integration and practice. Experienced OneHealth/EcoHealth experts, networks and projects from different countries within Europe but also beyond, like developing countries in the South, contributed to the workshop, as well as representatives from the CDB-WHO State of Knowledge review and the EU. The program of the workshop provided a combination of topical and generic integrative sessions. In the topical sessions, specialists exchanged experiences from their specialized fields and projects, whilst also addressing the generic OneHealth/EcoHealth perspective. In the generic part of the program all participants jointly discussed experiences, opportunities and challenges surpassing more restricted topical foci. This also built upon a survey that preceded the workshop in which a wide range of relevant experts from science, policy and societal practice participated to give their perspective on the OneHealth/EcoHealth ambition. Together we formulated key lessons learned and key steps forward messages. This may develop in a European OneHealth/EcoHealth Community of Practice.

Elemental changes along a spatial gradient: does it impact zooplankton-parasite interactions?

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Eutrophication has played a crucial role as a driver of local, regional and global changes in C, N and P biochemistry of aquatic ecosystems. This severely impacts the availability and quality of the phytoplankton, which further scales up in the food web. As many aquatic grazers perform best under a fixed availability of nutrients, this altered availability and quality of the phytoplankton food can impact zooplankton life history traits directly (growth, mortality) or indirectly (predation, immune defences). Although often neglected, defences against parasites are important as they regulate host density or susceptibility to predation. Here, we focused on how a spatial gradient in nutrient availability impacts the interaction between the zooplankton (*Daphnia magna*, *Daphnia pulex*, *Simocephalus vetulus*) and its parasites. More specifically, we monitored the response of two different groups of parasites based on their association with the host: parasites that live inside the host (endoparasites; tight association) and outside (epibionts) the host. We expected stronger effects of phytoplankton food parameters on endoparasites as are they critically depending on the host nutritional state. We monitored changes in phytoplankton C, N- and P-concentration of 61 ponds in Flanders and related this to several host and parasite parameters. Our results indicate a more pronounced impact of food quantity on epibionts, which contrasts with our initial hypothesis. We present different mechanisms that might have contributed to this observed pattern.

symposium 3:

Functional biodiversity

Biodiversity and ecosystem multifunctionality in European forests

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Numerous experiments have shown that biodiversity can drive multiple ecosystem functions simultaneously (ecosystem multifunctionality). However, we still have a poor understanding on how biodiversity is related to multifunctionality in more natural, nonexperimental ecosystems, such as mature forests. Using data from the FunDivEUROPE forest plot network, we investigated how tree diversity is related to ecosystem multifunctionality at different spatial scales. At local scales, we found that forests with a high number of tree species support many ecosystem functions at moderately high levels, but only very few functions were as high as in best performing monocultures. This was driven by a Jack of all trades mechanism: the mixing of different tree species specialized in different functions ensures that in diverse communities, each desired ecosystem function is supported at reasonably high levels, although top levels of individual ecosystem functions are only found in monocultures. Using simulation analyses, we also found that at larger spatial scales, forest landscapes consisting of sites that are dominated by different tree species (i.e. a high beta-diversity), landscape level ecosystem multifunctionality was highest, as different tree species supported different functions in different sites of the landscape. In summary, tree diversity can support multifunctionality in European forests, although the exact relationship depends on the spatial scale and on the desired levels of ecosystem function delivery.

Tree growth in strict forest reserves: local stand density more important than tree species diversity

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Mixing effects on tree growth and stand production have been abundantly studied, mostly in (young) plantation forest or in (former) production forest. Most of the studies looked at the effects of tree species diversity while controlling for stand density and stand structure. Strict forest reserves, i.e., protected forests left for free development without human interference, offer unique opportunities for studying the effects of diversity in tree species combined with diversity in stem density, stand structure, tree age, ... We used data from repeated inventories in ten strict forest reserves in the Netherlands and northern Belgium to study the growth of pine and oak. We investigated how the basal area growth of individual trees is affected by the species diversity, stem size diversity, and stand density of their local neighbourhoods. Crowding exerted by neighbour trees was more important in explaining tree growth than neighbourhood diversity, particularly for pine. For small oaks, tree growth was related to the size diversity of the neighbours. In conclusion, we saw no overall diversity-growth relationship for the oak and pine trees growing in the structurally diverse temperate mixed forest stands of our study. The growing site conditions, tree size, and local density explained a considerable part of the variation in growth; the relative importance of tree diversity was small.

Impact of species diversity and facilitation on exotic plant invasions in the Brazilian Cerrado

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The complementary use of various resources is an important mechanism for the co-existence of plants. This may explain why nutrient-poor ecosystems, where plant growth is limited by multiple resources, are often very rich in plant species. And because no individual species can access the entire pool of a limiting nutrient, this mechanism may also explain why nutrient-poor co-limited ecosystems are normally rather resistant to alien plant invasions. However, there are notable exceptions to this general rule, including the large-scale invasion of African grasses in the extremely species-rich Brazilian Cerrado. We performed field studies and greenhouse experiments to improve understanding of this process of exotic invasion. Field observations showed that the invasive species occur under nitrogen limited conditions

(low N:P ratio in community biomass), field fertilization experiments showed that they particularly respond to phosphorus increase, and a biodiversity experiment in the greenhouse demonstrated that the invasive species could benefit from a species diversity effect on root enzyme activity to overcome the low phosphorus status of the Cerrado soil. The latter biodiversity effect observed in the greenhouse could be supported with field data. Hence, invasion of the exotic grasses is controlled by interactions between soil phosphorus, species diversity and interspecific facilitation.

The effect of stress dispersal on the relationship between regional diversity and metacommunity functioning

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The differential distribution of environmental stressors in a metacommunity can create a high among-community diversity, with potential consequences for productivity. However, the dispersal of environmental stressors can both reduce and increase stress levels. Therefore, it can be expected to modify the relationship between among-community (also named beta-) diversity and productivity. To investigate this, we designed a full-factorial marine micro-algae microcosm experiment with five biota and four stress-dispersal levels in a two-patch metacommunity. Because one of the two patches was treated with an environmental stressor (atrazine), biota dispersal created a realistic gradient of beta diversity. The relationship between beta-diversity and metacommunity productivity was determined every 4 days. In treatments with stress dispersal, a higher stress-induced beta-diversity led to higher metacommunity productivity at the start of the experiment, but a lower metacommunity productivity in the middle and at the end. These relationships were the result of regional processes as biota dispersal led to source-sink dynamics from the more-productive non-stressed community to the less-productive stressed community. As a result, beta-diversity and metacommunity productivity decreased. Afterwards, the growth of the dispersed stress-tolerant species in the stressed community increased productivity, inverting the relationship between beta-diversity and metacommunity productivity. In communities without stress dispersal, a higher stress-induced beta-diversity led to higher metacommunity productivity at the end of the experiment. This relationship was the result of local dynamics by which the strongest competitor almost reached monodominance in the non-stressed communities that were not affected by stress dispersal. As a result of this monodominance, beta-diversity was high, while the nearly absence of interspecific interactions in the non-stressed community led to an increasing metacommunity productivity. Many communities today suffer exposure to and effects from environmental stressors. Our results show that the dispersal of these stressors affects the relationship between stress-induced beta-diversity and metacommunity productivity.

Cryptic diversity matters: ecological and functional differences in a marine nematode cryptic species complex

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Cryptic species - species which have been classified as a single species because of their morphological similarity but are genetically distinct - have been found worldwide, in many different taxa and often occurring sympatrically. These cryptic species are so similar in their morphology and physiology that a high degree of ecological similarity and hence of functional redundancy is expected. Management or conservation plans rarely consider cryptic diversity and may therefore be biased, because (a) the distributions and population sizes of individual cryptic species may be more restricted than that of the morphospecies complex as a whole, and (b) ecological differences between cryptic species may be more substantial than anticipated. In the cryptic nematode species complex of *Litoditis marina* (Sudhaus, 2011), at least ten cryptic species have been found. The autecology of four of them has been studied and has revealed that they have different preferences for environmental factors such as salinity and temperature, different dispersal abilities and differences in their resource utilization. Moreover, we have tested whether ecological differences between the cryptic species could potentially translate in functional differences. *L. marina* can substantially impact the decomposition process of algal wrack. We demonstrated that species-specific effects on the decomposition process indeed exist. As a result, each cryptic species may have a (partly) unique role in ecosystem functioning, and the loss of cryptic species may thus cause changes in ecosystem functioning. These ecological and functional differences emphasize the importance of including cryptic species diversity in the assessment of anthropogenic impacts on communities, on ecosystem functioning and on conservation management.

On shaky ground: soil food web structure and drought sensitivity are too uncertain to predict climate change effects on carbon sequestration.

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Heathlands are semi-natural ecosystems able to store large quantities of carbon in their soils, making them valuable ecosystems to mitigate climate change by trapping atmospheric CO₂. The functional diversity of the microbial decomposer community determines its ability to break down the variety of soil organic matter substrates and hence the rate of carbon turnover vs sequestration. Therefore, since biodiversity is crucial for ecosystem processes such as carbon cycling, global climate change forms

a major threat. However, the consequences of drought for soil carbon sequestration in heathlands are highly uncertain due to knowledge gaps concerning the soil food webs structure and a lack of basic data on relative drought tolerances.

Using a generalized Lotka-Volterra model of the soil food web, we illustrate how these uncertainties lead to varying drought-induced changes in carbon sequestration. Changes are positive when secondary consumers (predators) are most sensitive to drought and negative when primary consumers (decomposers) are most or equally sensitive compared to secondary consumers. These drought-induced carbon sequestration changes range from 10% for mild drought stress, 40% for medium drought stress and up to 100% for severe drought stress. Apart from drought sensitivity, also food web structure creates different trends and ranges of change in carbon sequestration due to drought. The two most important parameters accounting for this additional variation are the fungal formation-degradation ratio of polyphenolic carbon compounds and the feeding behavior of the secondary consumers.

We conclude that the uncertainty associated with the structure and drought tolerance of the heathlands soil food web creates a lot of variation in drought-induced changes in carbon sequestration. Predicting how drought stress affects soil carbon budgets is thus at present impossible and data on drought tolerances, predator feeding behavior and decomposer contribution to the polyphenolic pool are urgently needed to do so.

Effects of land use legacies and contemporary environmental changes in determining functional trait distribution changes.

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www.forestreplot.ugent.be

Organism functional traits, in conjunction with the abiotic environment, underpin the delivery of ecosystem services. Understanding how plant traits, such as specific leaf area (SLA), vegetation height, and seed mass, are affected by contemporary environmental changes is key to managing future service delivery. Theory suggests that trait distributional changes due to contemporary environmental change will also interact with legacies of land use. This interaction may occur because communities are on trajectories of change engendered by previous management interventions, and especially because community processes of dispersal and selection are fundamentally related to plant traits. Until now, the potential for this interaction has rarely been tested. Here, we elucidate the arguments as to why it is important to consider the past when projecting the future. We then present results, from temperate forest understorey resurveys in Europe, across contemporary gradients of nitrogen deposition and climate, for the effects of land management legacies and environmental changes on the community weighted mean (CWM) and range of trait values. We

show, in line with previous research on biodiversity responses, that there is limited CWM trait change in SLA, vegetation height and seed mass across all datasets. However, this overall CWM value hides substantial trait change across the datasets, that can be related particularly to land management legacies, and sometimes to environmental change. There is limited evidence for interactions among contemporary environmental changes and land management interventions. However, for mean SLA the direction of trait changes to rates of precipitation alteration depends on how forests were managed in the past. These patterns were apparent even after controlling for potential covariates, such as species richness at the time of the first survey, and underlying site differences as indicated by Ellenberg Indicator Values. The implications of these results will be discussed.

symposium 4: Ecological and evolutionary genomics

Genomic evidence for ameiotic evolution and genetic exchanges in the bdelloid rotifer *Adineta vaga*

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Loss of sex is an evolutionary dead end for metazoans, but bdelloid rotifers, micro-invertebrates abundantly found in semi-terrestrial habitats such as lichens and mosses, challenge this view having persisted asexually for millions of years. We found that the genome structure of the bdelloid lineage *Adineta vaga* is indeed incompatible with conventional meiosis. At gene scale, the genome is tetraploid and comprises anciently duplicated segments and less divergent allelic regions. However, in contrast to sexuals, the allelic regions are rearranged and sometimes found on the same chromosome. Such genomic architecture impedes meiotic pairing, confirming their ameiotic evolution. Instead, we found abundant evidence of gene conversion, limiting the accumulation of mutations in the absence of meiosis. Gene conversion may occur during mitotic recombination repair of broken DNA following cycles of desiccation and rehydration experienced by bdelloids in their temporary habitats. Indeed during desiccation the genome of *A. vaga* is broken in hundreds of DNA fragments that get repaired once rehydrated. In the genome of *A. vaga* 8% of the genes are likely of non-metazoan origin and probably acquired horizontally. These genes appear to be functional and many of those involved in resistance to desiccation have been acquired through HGT. Moreover, combining nuclear and mitochondrial markers, we demonstrated recently intra- and inter-specific genetic exchanges within the lineage *A. vaga* suggesting a non-meiotic recombination mechanism. Whether genetic exchange via HGT is a key innovative mechanism in those eukaryotes allowing adaptation in the absence of sex is an important question we are investigating currently.

The manuscripts presenting these results are published in *Nature* (Flot et al., 2013), in *Journal of Evolutionary Biology* (Hespels et al., 2014) and in *Current Biology* (Debortoli et al., 2016).

Genomic signatures of rapid evolution during range expansion of the dainty damselfly (*Coenagrion scitulum*)

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Many species are expanding their range polewards, and this has been associated with rapid phenotypic change. Yet, it is unclear to what extent this reflects rapid genetic adaptation or neutral processes associated with range expansion, or selection linked to the new thermal conditions encountered. Neutral changes can occur when during subsequent colonisation events, new populations are established from a subset of the source population. Yet, also trait changes are expected at the edge. For example, flight ability may both increase in response to selection driven by the process of range expansion as well as by antagonistic selection to counter potential reduction in flight ability at suboptimal thermal regimes. To disentangle these processes, we studied the genomic signature of range expansion in *Coenagrion scitulum*. Common garden breeding experiments already suggested that edge populations of this damselfly have evolved during the process of range expansion. Using 4950 newly developed genomic SNPs we were able to study the genomic structure across the range expansion area and linked this to the rapidly evolved phenotypic differences between core and (newly established) edge populations. Most edge populations were genetically clearly differentiated from the core populations and all were differentiated from each other indicating independent range expansion events. We identified one SNP under consistent selection in four of the five edge populations and showed that the allele increasing in frequency is associated with increased flight performance. We also detected a genomic signature of adaptation to the newly encountered thermal regimes, reflecting a pattern of countergradient variation. Overall, this study highlights how a strategic geographic sampling design and the integration of genomic, phenotypic and environmental data can identify and disentangle the neutral and adaptive processes that are simultaneously operating during range expansions.

Connectivity the Southern Ocean: population genomics of icefish

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The teleost fauna of the Southern Ocean is dominated both in terms of abundance and biomass by icefish of the suborder Notothenioidei. These fish are a rare example of a marine adaptive radiation with more than 120 extant species. Their diversification concurred with key adaptations to a cold, stable environment. Rapid environmental changes and increasing anthropogenic pressures, however, may affect their diversity and call for sound management and conservation measures. Characterizing genetic structuring in time and space is an important prerequisite to define targets for such measures. The oceanographic system of the Southern Ocean is dominated by the Antarctic Circumpolar Current that is connected to local gyres and fronts. While this current in conjunction with long pelagic larval phases may act as homogenizing force between populations, other factors such as habitat discontinuity or local adaptation can increase genetic differentiation. Current reduced genome representation approaches such as restriction-site associated DNA (RAD) sequencing enable characterization of markers on a genome wide level even in non-model species. We use these techniques to infer large and fine scale patterns of contemporary population structure in icefish and relate observed signals in genomic variability to potential driving forces of connectivity, such as ocean current systems.

Unravelling the evolutionary history of a parallel adaptive radiation of *Calosoma* beetles in the Galpagos archipelago.

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An intriguing and remarkable feature of adaptive radiations within archipelagos is that often phenotypic equivalent species can be found along similar environmental gradients on different islands. It remains however a contentious debate whether each island community has reached similar endpoints either by i) true independent parallel evolution, ii) a single speciation event followed by migration of each species across the archipelago (species sorting) or iii) introgression of adaptive alleles (allele sorting).

Pinpointing behavioral responses during mating using differential gene expression in the female brain of cichlid fish

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The development of ecological and/or behavioural changes associated with the speciation process drive the diversification of the ancestral gene pool into separate gene pools, whose integrity is subsequently maintained by reproductive isolation. How such genomic changes can be linked to the species' mate recognition system and to their mating behaviour remains unknown. For mouth brooding cichlids it is well documented that the process of mate choice and mating behaviour is largely determined by female choice. Therefore we analysed differential gene expression patterns in six brain regions of female fishes of *O. nasuta* and *O. ventralis* (two of the four described *Ophthalmotilapia* species) once they laid their first egg after mating with a conspecific or a heterospecific male. As control experiments, we assessed gene-expression profiles in the brains of females exposed to different experimental setups that never involved any exposure to males. Our RNAseq data revealed that, regardless of the treatment, different brain regions showed very distinct gene-expression patterns, confirming that each brain region modulates different biological processes. Within each brain part, differential gene expression patterns observed for *O. nasuta* and *O. ventralis* females that mated with a conspecific male, are species specific. Moreover, we observed that the differential gene expression pattern in the brain of female *O. ventralis* was different depending whether she had mated and reproduced with a conspecific or a heterospecific male. Surprisingly, differentiation in gene expression between the treatments was most pronounced in the cerebellum, a brain region where the production of hormones involved in mating is assumed to be low. Functional annotation of these genes will reveal the nature of the genetic processes that are responsible for mate choice and mating in these fishes.

No anonymity for fish: tracing sole juveniles arriving at the Belgian nursery combining genomics, otolith microchemistry and otolith shape analysis

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To improve sustainability, fish stocks need to be monitored at an ecologically meaningful scale. Therefore fisheries management requires to understand population structure. However it is difficult to measure connectivity between populations especially because early-life stages cannot be tagged due to their small size. Success of larval dispersal is the key to connectivity between spawning grounds and nurseries. *Solea solea* is among the most economically valuable fish species in the North Sea, yet little is known about its population dynamics. In the present study, we investigate the geographical origin of young-of-the-year sole arriving at the Belgian nursery. Previous studies showed that genomic markers, otolith microchemistry and shape can reveal fine scale population structure for other fish species. We ran a sampling campaign and genotyped more than 400 juveniles of sole using the double digest Restriction Site-Associated sequencing (ddRAD) technique. Five hundred high quality Single Nucleotide Polymorphic sites were retained and used to define population structure at a fine spatial (≤ 50 km) and temporal scale (2013-2014). Outlier tests were run to identify markers that could be used for traceability and might show signatures of local adaptation. In addition to the genomic approach, otolith microchemistry and shape were used to reveal small scale population structure. Combining the three different traceability measures increased our assignment power. Results show that southern North Sea populations of sole are highly connected, and that those caught off the Belgian coast are closely related to the Eastern English Channel populations. Improving the discrimination of subpopulations of fish would allow a better traceability of fish products and sustainable management of the resources.

The ghost of competition: experimental evolution with spider mites.

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Local adaptation is one opportunity to avoid extinction from environmental changes. Given that species are living in communities, this competition might have an impact on local adaptation. Here, the effect of the presence of a competitor on the local adaptation of spider mites (Tetranychidae) is investigated during experimental evolution. In this research, the ecological and evolutionary dynamics are explored. We found that those populations under competition performed significantly worse compared to those without. However, more surprisingly after outcompeting the competitor, the increase in fitness was significant and resulted in even a higher fitness than the populations without this initially interspecific competition. On the other hand, no differences in the ecological dynamics were revealed. This suggests that a delayed response of competition is possible and might not always result in changes in population densities.

Food availability affects the strength of mutualistic host-microbiota interactions in *Daphnia magna*.

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The symbiotic gut microbial community is generally known to have a strong impact on the fitness of its host. Nevertheless, it is less clear how the impact of symbiotic interactions on the hosts fitness varies according to environmental circumstances such as changes in the diet. We aimed to get a better understanding of host-microbiota interactions under different levels of food availability. We conducted experiments with the invertebrate, experimental model organism *Daphnia magna* and compared growth, survival and reproduction of conventionalized symbiotic *Daphnia* with germ-free individuals given varying quantities of food. Our experiments revealed that the relative importance of the microbiota for the hosts fitness varied according to dietary conditions. The presence of the microbiota had strong positive effects on *Daphnia* when food was sufficient or abundant, but had weaker effects under food limitation. Our results indicate that the microbiota can be a potentially important factor in determining host responses to changes in dietary conditions.

Population genomic analysis of European introduced populations of the African-clawed Frog, *Xenopus laevis*.

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Due to both deliberate and accidental introductions, invasive African Clawed Frog (*Xenopus laevis*) populations have become established worldwide. Moreover, invasive *X. laevis* populations have been reported to negatively impact local biota by e.g. reducing reproduction and increasing predation pressures on native prey organisms. With INVAXEN we investigate the INVasive biology of XENopus *laevis* in Europe. More precisely, we aim to study all relevant aspects of the invasion ecology and adaptive ability of this species in order to develop a robust predictive species distribution model. A mitochondrial DNA survey of specimens collected across the invaded French and Portuguese area demonstrated that native phylogeographic lineages have contributed differently to invasive European *X. laevis* populations. In Portugal, genetic and historical data suggest a single colonization event involving a small number of individuals from the south-western Cape region in South Africa. In contrast, French invasive *X. laevis* encompass two distinct native phylogeographic lineages, i.e. one from the south-western Cape region and one from the northern regions of South Africa. Moreover, the lack of population structure based on nuclear DNA suggests a potential role for admixture within the invasive French population. Here, we evaluate to which extent RAD-tag genotyping-by-sequencing method is appropriate and applicable for the further investigation of population differentiation among and within the invasive and native *Xenopus laevis* populations.

symposium 5: Urban ecology

The role of plants in an urbanizing world? Monitoring the ecosystem services of urban green through geo-technology

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The prospected growth in urban population and progressive global warming will put huge pressure on the quality of the environment in densely populated areas. Sustainable development and management of urban areas is hence crucial to guard the living quality in our future cities. In this context the role of plants is vital. Indeed, it is widely acknowledged that vegetation plays an important role in the functioning of ecosystems and consequently in the provisioning of ecosystem services to society. Despite this, quantitative spatial explicit data on the environmental effects of plants in an urban(ized) context are scarce such that current policy support tools such as environmental models do only partly address the effects of urban green. Through integration of remote sensing technology, Geographic Information Systems and in situ observations, in spatial explicit modeling routines we explore how, and to what extent, different plant species and/or plant assemblages contribute to ecosystem services. Our aim is to provide nature-based solutions, referring to the use of nature in tackling today's environmental challenges such as climate change, environmental pollution, water resources management, and natural disaster risk management. As such we want to support the use of vegetation/green infrastructure in the design, organization, management and spatial planning of urbanized regions, thereby improving the resilience of our ecosystems.

Effects of a heterogeneous and highly urbanized landscape on gene flow in a coastal amphibian metapopulation

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Dispersal is a crucial process in metapopulation persistence, both in terms of colonization-extinction dynamics and as a means to counter genetic drift and inbreeding in local demes. To investigate effective dispersal in a coastal dune metapopulation of Natterjack Toad (*Epidalea calamita* Laurenti), 256 larvae in four potential subpopulations were genotyped with 11 microsatellites. The grey dunes they inhabit are rare natural features on the Belgian coast. They are separated by urban areas and surrounded by agricultural fields. Because spatial landscape heterogeneity is expected to influence dispersal and genetic structure, we analyzed which landscape features affect functional connectivity and to what degree. Sixty landscape resistance scenarios were assessed using two different approaches. Our results revealed a genetic structure which was clearly not influenced by distance alone and source-sink dynamics among subpopulations. Urbanized areas seemed to hinder dispersal as well as surfaces with higher vegetation. On the other hand, distant subpopulations appeared functionally connected by the beach. Estimates of genetic diversity and effective population size further supported the landscape genetic results.

Leaf bacterial community composition in urban environments

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The leaf surface habitat, also known as the phyllosphere, supports diverse bacterial communities shaped by plant factors and environmental conditions. Phyllosphere bacteria affect the host plant (eg preventing colonization of plant pathogens), are capable of degrading or detoxifying atmospheric pollutants and are an important source of bacterial particles in the atmosphere. We will present the results of three of our studies in which the bacterial communities of the phyllosphere of a common evergreen climber (ivy) and a common tree species (London plane) in and around Antwerp (B) were assessed. A culture-independent approach based on high-throughput 16S rRNA amplicon sequencing was used to determine the bacterial community structure of the phyllosphere. Leaf bacterial communities differ greatly between urban and non-urban locations, as we observed a shift in several of the dominant taxa on ivy (eg *Beijerinckia* and *Methylocystaceae* were most abundant in the non-urban phyllosphere, whereas *Hymenobacter* and *Sphingomonadaceae* were

dominating the urban ivy phyllosphere). The relative abundances of eight of the ten most dominant taxa correlated well with leaf magnetism, a proxy for the metallic compounds of particulate matter and related with traffic and industrial activity. Within the urban premises, the phyllosphere microbial composition of 53 plane trees could not be linked with the PM proxy, instead, motorized traffic intensity and leaf characteristics correlated well with the abundances of several taxa. An ongoing experiment in urban, industrial and rural sites shows rapid colonization of introduced ivy plants, with shifts in community composition towards (up to now) quite stable, site-specific bacterial communities in the phyllosphere. It is clear that urbanisation affects the phyllosphere microbial composition, but, up to now, the identification of the most important drivers for this effect remains uncertain.

Impact of an urban tree crown on the local distribution of atmospheric dust (PM10) inside an urban street canyon in Antwerp, Belgium

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Besides the direct impact of urban trees on atmospheric particles through dry or wet deposition on their surfaces, tree crowns will influence the aerodynamics of their surroundings, indirectly impacting the local distribution of atmospheric particles. Nevertheless, tree crowns are often represented very rudimentary in three-dimensional air quality models. We, therefore, evaluated the influence of tree crown characteristics on the local ambient PM10 concentration and resulting leaf-deposited PM10, using the three-dimensional computational fluid dynamics (CFD) model ENVI-met and ground-based LiDAR imaging. The modelled leaf-deposited PM10 mass was compared to gravimetric results within three different particle size fractions (0.23, 310 and ≥ 10 μ m), obtained from 20 sampling locations within the tree crown. Modelling of the LiDAR-derived tree crown resulted in significantly altered atmospheric PM10 concentrations near the tree crown. Although this model study was limited to a single tree and model configuration, our results demonstrate that improving tree crown characteristics (shape, dimensions and LAD) affects the resulting local PM10 distribution in ENVI-met. An accurate tree crown representation seems, therefore, of great importance when aiming at modelling the local distribution of atmospheric particles.

Taxonomic, functional and phylogenetic metacommunity ecology of zooplankton along urbanization gradients

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As human population size increases and cities become denser, several urban related selection pressures increasingly affect species composition in both terrestrial and aquatic habitats. Yet, it is not well known whether and how urbanization influences other facets of biodiversity, such as the functional and evolutionary composition of communities, and at what spatial scale urbanization acts. Here we used a hierarchical sampling design in which urbanization levels were quantified at seven spatial scales (ranging from 50 to 3200m radii). We show that urbanization gradients impose a strong selection pressure on zooplankton species traits, which in turn affects phylogenetic composition of the entire metacommunity, but only when considering urbanization at the smallest spatial scale (50m radius). Specifically, small cladoceran species dominated in more urbanized ponds whereas large-bodied, strong competitors prevailed in less urbanized systems. We also show that trait and phylogenetic metrics strongly increase the amount of variation in α -diversity that can be explained by degree of urbanization, environmental and spatial factors. This suggests that the mechanisms shaping α -diversity in our study system are mediated by traits and phylogenetic relatedness rather than species identities. Our study indicates that accounting for traits and phylogeny in metacommunity analyses helps explaining seemingly idiosyncratic patterns of variation in zooplankton species composition along urbanization gradients. The fact that urbanization acts only at the smallest spatial scale suggests that correctly managing environmental conditions locally has the power to counteract the effects of urbanization on biodiversity patterns. The multidimensional approach we explore here can be applied to other systems and organism groups and seems to be key in understanding how overall biodiversity changes in response to anthropogenic pressures and how this scales up to affect ecosystem functioning.

Untangling possible relationships between urbanization and the eco-evolutionary dynamics of the land snail *Cepaea nemoralis*

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Species eco-evolutionary dynamics can be strongly influenced by anthropogenic disturbances. In the SPEEDY project (SPatial and environmental determinants of Eco-Evolutionary DYnamics: anthropogenic environments as a model) the impact of such a disturbance is explored via a gradient of urbanization across a broad range of different taxa.

Here, we study the relation, if any, between urbanization and phenotypic and/or population genetic variation in the pulmonate land snail *Cepaea nemoralis*. This species is common across Flanders and occurs in three basic colour morphs (brown, pink and yellow) with various degrees of brown shell banding. Firstly, we performed a shell morphometric analysis to explore whether degree of urbanization correlates with the species phenotypic shell characteristics such as size, shape, shell thickness, shell strength and colour pattern. Secondly, we used mtDNA Sanger sequencing (COI) and Restriction-site Associated DNA sequencing (RAD-seq; a Next Generation Sequencing technique) to obtain genome-wide population genetic information for exploring population structuring, gene flow and possible signatures of selection. In addition, the DNA sequence data will be correlated with the phenotypic data. Furthermore, in a community analysis the impact of urbanization on the biodiversity of land snails was assessed by means of α , β and γ diversity. Overall, these data will be compared at various levels with data for other organisms surveyed by the SPEEDY project. In this way the SPEEDY project aims at uncovering overarching patterns of effects of urbanization upon local biota.

symposium 6:

Long term ecosystem research

Long-term ecological research in strict forest reserves in Flanders (Belgium) : what have we learnt so far?

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Strict forest reserves are forest sites that are deliberately left for free development. No human interventions are allowed, so natural dynamics can fully re-develop. These sites are not only important for biodiversity, but are also important reference sites for scientific research. In a selection of sites, intensive studies on vegetation dynamics are ongoing. We present some of the most striking and relevant results on forest dynamics and their consequences for ground vegetation and dead-wood related biodiversity.

FORBIO: overview of five years of research in a large tree biodiversity experiment

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Mixed forest plantations are expected to deliver more ecosystem services than monocultures and to do so in a more stable way. Although more and more studies looked into diversity effects in mature forest, mixing effects in the early stages of mixed forest plantations are still poorly understood. FORBIO is a tree diversity experiment in Belgium that serves as a model platform to study the effects of tree species diversity and composition on forest ecosystem functioning throughout the different stages of forest development. The main objective of this talk is to present an overview of the main results after five years of research on various ecosystem properties and functions, including primary production and tree architecture, resistance to crown damage, crown arthropod community composition, and nutrient cycling.

The Kenya Long-Term Exclosure Experiment (KLEE): large mammals as drivers of savanna dynamics

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In arid and semi-arid rangelands worldwide, livestock share the landscape with native plants and animals. Much of this land suffers from degradation caused by inappropriate land management. Although there has been considerable research on the effects of stocking densities on range ecosystems, there is relatively little known on the separate and combined effects of different herbivore guilds on each other and on the vegetation they share. This information is vital if we are to make informed decisions about the future of wildlife on the grazing lands of Africa. Therefore, an experimental study was set up in 1995 in a Kenyan savanna, whereby 18 four-hectare exclosures allow herbivory by six different combinations of cattle, wildlife, and mega-herbivores (elephants and giraffes). In these exclosures, soil, microbial, plant, invertebrate, and vertebrate responses to these experimental treatments are monitored. In this talk, I will present some of the main results so far, including the impact of herbivore treatments on soil nutrient cycling and stoichiometry, grass-tree interactions and interactions between cattle and livestock. This large-scale long-term exclusion experiment demonstrates how different guilds of large mammals are important drivers of ecosystem dynamics and allows us to address fundamental issues in ecology, including induced compensation and competition.

The Integrated Carbon Observation Network (ICOS) in Belgium an overview

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ICOS, the Integrated Carbon Observation Network, is a pan-European research infrastructure that aims to provide long-term data on the European carbon cycle, greenhouse gas budgets and their perturbations. High-quality data are needed to understand underlying mechanisms and to make meaningful predictions for the future. Quantifying present-day sources and sinks of carbon and their fluxes are key to informed policy making.

ICOS (www.icos-ri.eu) integrates atmosphere, ecosystem and ocean monitoring networks. Measurements are carried out on ecosystems sites, on tall atmospheric towers and on oceanic platforms and vessels.

Belgium is well-represented within the European network. It hosts no less than six ecosystem stations on different ecosystems (pine and mixed forests, heathland, agricultural land and coppice culture), one atmospheric station and three oceanic stations (two vessels and a buoy). Furthermore Belgium is co-host of the Ecosystem Thematic Centre that coordinates the ecosystem network.

ICOS has an open data policy and encourages everyone to use its data for purposes ranging from scientific research over education to policy making. All Belgian ICOS stations are open for collaborations and complementary on-site research. This presentation gives an overview and update on the research activities in the Belgian ICOS stations and how you can access ICOS data through the Carbon Portal.

Long term monitoring in the Sea Scheldt estuary: the baseline for ecological system understanding and a driver for research questions

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Since the nineties a long term integrated monitoring is set up in the Scheldt Estuary within the Belgian-Dutch framework of MONEOS. Within this framework all the data is centralised within Scheldemonitor.be an webbased information portal with validated long term data. As such, the Scheldt Estuary is one of the Belgian LTERsites with a huge amount of information which has documented a recent dramatic shift in the ecosystem. One of the observed shifts in the food web in the upper stretch of the estuary has been a decline of macrobenthic communities and avifauna, and the return of fish and epi- and hyperbenthos. This system shift has coincided with a sudden improvement in water quality and rising oxygen levels. However to understand this shift, insight is needed in ecological functioning and relations among trophic groups. In an ongoing project, INBO investigates the trophic interactions and energy fluxes that characterize the new ecosystem state in the upper Sea Scheldt so as to better understand the benthic - pelagic coupling. This will help us to better understand the functioning of the Sea Scheldt ecosystem altogether and provide input for sustainable management.

Long-term forest vitality assessment via real-time growth and sap flow measurements

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Forests provide a multitude of ecosystem services. They couple for instance soil with atmosphere and are therefore an important link in climate regulation. Global change is directly and indirectly impacting these forest functions. While data from several large-scale forest monitoring initiatives confirm that our forest are changing, it remains challenging to make a well-founded and prompt judgement on the vitality of our forests because the mechanisms underlying such changes remain poorly understood. Having a better mechanistic understanding about the status of a forest would allow forest managers to act more proactively and would assist in making important forest management decisions.

Beech (*Fagus sylvatica* L.) and oak (*Quercus robur* L.) trees are currently being monitored in the experimental forest Aelmoeseneie (LTER site Gontrode) using plant sensors. The basic setup installed on each study tree (five beech and four oak trees) includes one dendrometer and one sap flow sensor. With these sensors diel patterns of tree growth and sap flow are continuously measured and in real-time visualised using the PhytoSense cloud software. Combination of both measurements together with plant modelling will allow the development of a process-based and real-time tree vitality indicator. By using the best upscaling method and/or by networking several trees (i.e. TreeWatch.net) it should become possible to assess the vitality of an entire forest stand.

Multiple nitrogen saturation indicators yield contradicting conclusions on improving nitrogen status of temperate forests in five LTER-Belgium/ICP Forests sites

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Nitrogen (N) depositions in European forests are decreasing, while there were local signs of initial recovery from acidification during the past three decades. These two global change processes both affect total N levels and often occur simultaneously, hence complicating mechanistic explanations for changing European forest N status. We aimed to test the hypothesis that forest N status in northwest Europe has started to improve. We evaluated the evolution of multiple N saturation indicators in five ICP Forests Level II plots (also LTER-Belgium sites) in northern Belgium, using long-term soil solution and foliage datasets. The DON:TDN ratio in soil solution

increased overall in the O horizon (mean 0.279 ± 0.463 , slope $0.023 \pm 0.037 \text{ y}^{-1}$) and in the mineral soil (mean 0.134 ± 0.78 , slope $0.007 \pm 0.051 \text{ y}^{-1}$) between 2005 and 2014. The molar DOC:NO₃⁻ ratio in soil solution increased in three plots in the O horizon (mean 6.84 ± 22.15 , slope $0.58 \pm 1.92 \text{ y}^{-1}$) and in four plots in the mineral soil (mean 2.07 ± 25.32 , slope $0.06 \pm 5.76 \text{ yr}^{-1}$) between 2002 and 2014. The ratio of N and phosphorus (P) concentrations in foliage remained unaltered between 1999 and 2013. Changes in the soil solution chemical composition thus confirmed an improvement in forest N status, despite sustained high NO₃⁻ concentrations, but biotic recovery appeared pending. This questions if common critical DOC:NO₃⁻ limits are stringent enough for European forest soils. Clearly, insight in forest recovery from N saturation requires a multiple indicator approach, and further monitoring of foliar N:P levels alongside these soil processes is needed to monitor the evolution of European forest N status.

The site of the Botanic Garden Meise: a potential LTER-site

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The site of the Botanic Garden Meise is a 92 ha large domain in the vicinity of Brussels. It has been assembled from (parts of) two historic castle domains. For more than 75 years it has been housing very large plant collections, as well as a research institute dedicated to botany, forming one of the largest botanic gardens in Europe but also a main tourist attraction nearby Brussels. Some areas are highly disturbed, either for the maintenance of the collections and of the infrastructure, or by the high number of visitors. There are also less managed or more natural areas, however. Varied terrestrial and aquatic ecosystems and habitats occur, among which valuable woody (semi-)natural areas, and also differentially managed grasslands. Within the domain in Meise, detailed biodiversity research and monitoring has been done for several taxonomical groups, as well as phenological research, some of it over multiple decades. This was facilitated by the large in-house expertise and knowledge of various groups of organisms. It has shown that the site is a biodiversity hotspot for different kinds of organisms. Part of this research also investigates the effects of the management methods on the biodiversity, while historical factors are also considered. Recently, a wireless network of high-tech sensors has been installed in the domain in order to demonstrate the impact of trees on the microclimate. More importantly, there is a willingness to further develop the research infrastructure and to participate to long term ecological research/monitoring projects. We think that the site has several assets which contribute to its potential as LTER site, while an increasing number of visitors might contribute to the socio-economic aspect of studies made at the site.
