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ABSTRACTS

Abstracts are given in the alphabetical order of the first author. If multi-authored: presenting author of a lecture underlined.
Poster Presentation

Infrageneric classification of Lipocarpha and allied genera (Cyperaceae) based on morphological, developmental and molecular evidence

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Molecular phylogenetic analyses of Lipocarpha (Cyperaceae) based on nuclear ribosomal ETS1f and plastid rpl32-trnL and trnH-psbA markers are presented. Separate gene trees as well as a species tree were constructed using the assembled data. Results indicate a polyphyletic Lipocarpha consisting of a paraphyletic core Lipocarpha s.s. in which the monotypic Volkiella is included, and a small separate clade with species formerly placed in the genus Rikliella. Core Lipocarpha s.s. consists of six clades, which can be distinguished based on morphological characters. Developmental data for Lipocarpha rehmannii indicates that this species is not a true Lipocarpha. The genus Lipocarpha is a clade of Cyperus sensu Linnaeus, and is here lumped in Cyperus subg. Cyperus and new names and/or combinations for Lipocarpha and Volkiella are presented.

Oral Presentation

Dictyota embryogenesis: a complementary model to study the establishment of polarity

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Zygotes of brown algae serve as a practical model system for the establishment of polarity in plant systems. Traditionally the effort is almost uniquely allocated to fucoid algae, while polarization of the zygotes of the Dictyotales remains obscure. Fucoid eggs are homogenous protoplasts that show no sign of cell polarity. Only after fertilization using environmental cues (e.g. light) and the point of sperm entry as informational cues the zygotes establish the point of rhizoid differentiation, defining both the polarization axis and the pole of germination at the same time. In contrast the determination of the polarization axis and the determination of pole identity are temporally separate and functionally distinct processes in the polarization process of Dictyota. Fertilization leads to an almost instant actin-myosin dependent elongation which reveals the polarization axis. No influence of the direction of light or the sperm entry site was found on the determination of the axis. In contrast several lines of evidence back the hypothesis that the axis is maternally determined. The apical-basal pattern is only completed when the embryo decides based on environmental cues as light which pole has to commit to the rhizoidal cell fate leading to the holdfast. Interestingly this completion of polarization may either occur in the unicellular zygote or in the multicellular embryo depending on the culture conditions. The mechanistic basis of the striking level of developmental plasticity in the polarization process is under investigation. Given the availability of cultures, we suggest Dictyota as a practical system for developmental research which might serve as a complementary source of insights on polarization and patterning.
Poster Presentation

**Gap analyses to support ex situ conservation of genetic diversity in Magnolia, a flagship group**

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Worldwide about one third of all plant species is estimated to be threatened with extinction. The Global Strategy for Plant Conservation (GSPC) is a plan to save plants that has been adopted by governments worldwide. Unfortunately, the global loss of plant diversity receives relatively little attention from politicians and media, and insufficient financial resources are allocated to reverse the trend of loss. Given the urgent need for action and limited resources, the conservation and research community must work together to identify and prioritize conservation activities.

Plant conservation activities include an integrated mix of *in situ* (on-site) and *ex situ* (off-site) actions. *In situ* conservation protects species in their native habitat, while *ex situ* efforts ensure plant material is secure and available for research, education, and ultimately reintroduction of species to wild population if and when needed. Botanic gardens increasingly support *in situ* conservation, and they play a leadership role in *ex situ* conservation efforts. Target 8 of the GSPC calls for at least 75 % of threatened plant species to be present in *ex situ* collections, preferably in the country of origin, and at least 20 % available for recovery and restoration programs by 2020. Only *ex situ* collections that are genetically diverse and well-documented are able to directly support *in situ* conservation by providing seeds or plants needed to reintroduce extirpated populations. Yet Target 8 does not specify to what extent the *ex situ* collections of a particular species should be representative of the genetic diversity of the species. This is in contrast to GSPC Target 9 stating that 70 % of the genetic diversity of crops and their wild relatives should be conserved.

Research on *ex situ* conservation of genetic diversity of crops and their wild relatives is progressing, yet little information is available to identify and build the genetic diversity of *ex situ* collections of threatened plants. By analyzing where gaps in *ex situ* collections and research exist relative to diversity hotspots of threatened species, it is possible to identify and prioritize action. We undertake a gap analysis of *ex situ* collection needs in the genus *Magnolia*, a relatively well-known and valuable genus. Results indicate three main areas of biodiversity (China, Vietnam and Colombia) for the endangered *Magnolia* taxa. The present paper provides a critical overview of recent conservation activities carried out in the genus *Magnolia* throughout the world, focusing on genetic diversity analyses of the species.
Poster Presentation

Global analysis of the threatened mangrove trees species

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Understanding the relation of socio-economic effects on mangrove ecosystems is crucial to the development of new tools to protect and conserve this vulnerable ecosystem. So far, however, there has been little discussion about which species of mangrove can be affected by socio-economic influences on a global scale. Therefore, we ask the following questions: Which mangroves tree species are more affected by human pressure? In which countries are they located? Which impacts are influencing that scenario of species threatened? In order to answer these questions, we used neural networks called Self-Organizing Maps (SOM), because it is an efficient tool for geovisualising high-dimensional data. In addition, SOM approximate the probability density function of input data and it has been used as an alternative to traditional statistical methods to efficiently deal with datasets ruled by complex, non-linear relationships. The input data are the distribution of plant species that contain the presence/absence data for each country extracted from the Mangrove Reference Database and Herbarium (Massó i Alemán \textit{et al.}, 2010), which includes the World Atlas of Mangroves (Spalding \textit{et al.}, 2010) amongst other data. We also included the IUCN database that shows the species that are at risk. We confronted this information of threatened species distribution with socio-economic country indicators such as population density, mangrove degradation, coastal population size and density, aquaculture surface, etc. In short, the contribution of this work is to analyse the socio-economic influences on mangroves on a global scale using SOM techniques. SOM are widely used by researchers in several areas of science, but were seldom used by plant ecologists. All in all, we can have new methodological approaches using the Mangrove Reference Database and Herbarium focusing on a global scientific and policy impact.

References


Explaining large-scale patterns of diversity and determining the processes that have generated these patterns is a major goal of evolutionary biologists, ecologists, and conservation biologists. For groups which lack a fossil record, we are entirely dependent on the extant diversity to infer the historical evolutionary processes that resulted in the present-day diversity patterns. Phylogenies, in combination with auxiliary information (e.g. morphology, physiology and ecological traits) and species distributions have the potential to elucidate the evolutionary process. I will present data on diversification of marine macroalgae. Seaweeds provide food and create habitats for a huge number of marine organisms, yet little is known about their evolutionary history and the current day distributions of the individual species. Data availability, e.g. inadequate diversity estimates, geographical sampling bias, uncertainty about phylogenetic relationships and divergence times, as well as methodological issues related to historical biogeography, make that scenarios of macroalgal diversification have rarely been tested explicitly. By integrating parametric models in historical biogeography and ancestral state reconstructions of ecological niches I test the hypotheses that: 1.) the Australian algal flora acted predominantly as a donor region from which species dispersed in the Cenozoic; 2.) the diversification of typical tropical families is a relatively recent phenomenon coinciding with thermal stratification of the oceans, increased herbivory and tectonic activity in the Oligo-Miocene boundary; 3.) an important element of warm temperate flora’s is derived from a tropical flora in response to an increased latitudinal sea surface temperature gradient from the mid-Eocene onwards. I make use of global algal phylogenetic datasets developed over the last decade in my research group and integrate these data with species distribution models and divergence time estimates to explore the evolution of ecological niches.
Variation of functional traits in steppic savanna vegetation along a copper gradient in Katanga (DR Congo)

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The Katangan copper belt is formed of more than 200 hills positioned along an arch between Lubumbashi and Kolwezi. At the top of these hills, the copper concentration in the soil can reach more than 10,000 ppm and decreases from top to bottom to reach 100 ppm in the surrounding plain. Because of the harsh conditions (six months long dry season, metal pollution, annual fire), a very specialized flora, composed of, among others, 32 strict and 33 broad endemic species, has been selected in these environments.

The aim of our work is to investigate a large number of functional traits on these plants and to highlight their variation along an environmental gradient. For the moment we have investigated 38 species along five parallel transects on the hill of Fungurume V.

We have shown that, along a gradient from 100 to 6600 ppm of Cu and from 10 to 655 ppm of Co, traits like height and leaf area decrease while SLA increases. Life form and type of storage organs also show differences with a decrease of xylopods and an increase of annual plants when the copper concentration gets higher. Furthermore, for the leaf area and plant height, we show that this variation originates from both intraspecific variation (10 and 23% respectively) and turnover of species.

Further studies are in progress to include seventy-five more species which will allow us to calculate functional diversity index and give us a general overview of the assembly mechanisms of these communities. We will also test if the intraspecific variation is due to phenotypic plasticity or has a different origin (genetic or epigenetic).

Applying the General Lineage Concept of species to Asian Hydrangea

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Hydrangea, a woody genus with several well known ornamental representatives, shows a disjunct distribution. It occurs in the temperate regions of eastern Asia and eastern North America, extending southward into the tropics of both hemispheres. In the most recent revision of the Asian representatives of the genus (Wei and Bartholomew in FOC, 2001) both authors explicitly disagree on the number of recognizable Asian species, due to the presence of several morphologically variable species complexes.

This study aims at unraveling these species complexes using both modern molecular techniques and more traditional morphological observations. Combining these different forms of data will allow us to delimit independent evolutionary lineages within Asian Hydrangea. These independent lineages can be recognized as separate species under the general lineage concept of species, and will allow insight into the processes driving speciation in Asian Hydrangea.
The majority of temperate herb species have very limited capacity to disperse beyond local boundaries, mainly because of their small size and seeds that lack clear traits for dispersal. This syndrome is particularly prevalent in grasslands and other open habitats. Yet, a significant number of these grassland species appear to be fairly common or widely distributed within urbanized landscapes. Several explanations can be conceived for this apparent paradox: either natural dispersal is sufficient after all (natural dynamics), the species’ populations reflect lingering relics (no dynamics), or they are provided with some new form of dispersal (human dynamics). Using molecular markers (AFLPs), we investigated differentiation among populations within four species of small, annual clovers from Belgian coastal dune grasslands (Trifolium dubium, T. campestre, T. micranthum and T. scabrum). In the rare T. micranthum, we found convincing evidence of region-wide gene exchange through human land use (most probably, exchange of seeds with machinery or compost). Population differentiation patterns of the other three species also showed very little genetic signatures of natural processes (such as isolation-by-distance), suggesting similar processes to be at work here. Therefore, we consider the regional population genetic structure of small, immobile herbs to be structured by human (instead of natural) dynamics more often than is currently suggested.
Ceratopteris richardii (C-fern): a model system for investigating tissue-specific cell wall architecture and metabolism

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Plant cell walls are dynamic and complex materials that play important roles during plant growth and development. They are exploited commercially as textile fibres, industrial raw material (paper, wood) and as a source of renewable biomass for energy production. The suitability of cell walls for specific applications depends largely on their properties and architecture. There is considerable evidence that cell wall polysaccharides show taxonomic variation although the understanding of how polymer structure is integrated with cell wall properties and plant evolution is limited. Cell wall models (Type I, II and III) have been suggested for different plant groups. However, such a classification neglects variation in polysaccharide content between cell types within organs and most notably does not relate to all plant species. Furthermore, primary and secondary cell walls are traditionally distinguished, but in fact, there are no clear boundaries between these wall types. The challenge now is to document tissue-specific aspects of cell wall composition and architecture in relation to plant growth and development. Integration of this knowledge with the emerging understanding of polymer functions will provide insight into the structural-functional relationships of specific configurations of cell wall polymers. In addition, an increased knowledge of the tissue-specific cell wall diversity that exists within different plant lineages is necessary to understand how specific tissues evolved.

C-fern is a specially derived strain of Ceratopteris richardii, a homosporous fern with a free-living photosynthetic non-vascular haploid gametophyte generation and a dominant diploid sporophyte generation. Although the gametophyte and sporophyte share the same genetic constitution (with the exception of differences in chromosome number), they display clear functional and structural differences. These characteristics offer novel opportunities to study aspects of plant cell wall biology, including some research topics that cannot be addressed in flowering plants. For example, it is possible to examine if specific cell wall polymers that are associated with complex tissues or structures in the sporophyte are also present in the morphologically less complex gametophyte. Moreover, ferns, along with lycophytes, are the only extant land plants in which root hairs (sporophyte) and rhizoids (gametophyte) occur in the same species. While rhizoids and root hairs probably share similar functions it is not known if they share similar mechanisms of growth and development. In conclusion, C-fern offers a range of new possibilities for cell wall research.
Invited lecture

**Plant community ecology: old questions, new paradigms?**

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While the concept of ‘community’ has lost much of its substance in the modern ecological literature, the renewed interest in community ecology is currently reviving some old questions. Recently, the old debate about the organismic vs individualistic view of plant communities has been resolved by considering a hierarchical filtering of species pools. This reconciliation is the result of merging findings of hierarchy theory, niche-based and neutral theories to explain vegetation patterns by multi-scale environmental filters, global biogeographic processes and local biotic interactions (plant-plant competition and facilitation, interactions with microbial and animal communities). The ‘integrated community’ concept could benefit from considering also some overlooked paradigms, such as Grime’s CSR strategies and integrated synusial phytosociology.

Based on four founder assumptions, phytosociology cannot be considered anymore as a science of the past and reduced to a pure descriptive approach. Even though the reviving interest for vegetation classification is mainly due to political reasons (need for ‘habitat’ typologies at regional, national and international levels for conservation purposes), phytosociological databases and theories have proved to be useful to address modern scientific questions.

New concepts, linked to population ecology, have recently emerged and become very popular in plant community ecology, such as plant functional traits, or metacommunity. Nevertheless, other very promising concepts linked to ecosystem dynamics, such as ecological resilience and adaptive cycles, remain widely overlooked so far.

From a methodological point of view, important progress has been achieved in the unified definition of diversity indices (taxonomic, phylogenetic and functional; alpha, beta and gamma), fidelity indices and ecological indicator values. Molecular approaches allow the emergence of new research fields (phylogeny of communities, belowground components of plant communities, biotic interactions with microbial and herbivore communities). The combination of observational, experimental and modelling approaches is key to understand vegetation patterns and processes. Dynamic modelling of vegetation, featuring its spatial-temporal hierarchical organization, is a promising way to predict future changes in terrestrial ecosystems subjected to accelerated climate and land-use changes.
National estimates of the abundance of plant species and their change are important for the formulation of evidence-based conservation policy; in guiding land management decisions and in quantifying and predicting changes in the ecosystem services. Spatial and temporal unevenness in recording effort confounds analysis and the taxonomic biases of recorders skew the results. One common approach to reducing unevenness in recording effort is to aggregate records into large spatial units, often 100 km$^2$. However, plants and other organisms tend to have clumped distributions and are not randomly distributed. This is caused by intrinsic factors such as the plant’s ability to disperse and extrinsic factors such as soil conditions and competition.

An alternative approach to estimating grid square occupancy has been investigated on the vascular plants of Great Britain. This was achieved by selecting well-surveyed 4 km$^2$ grid squares from the pool of all records and from these it was possible to extrapolate occupancy probabilities to the whole area. Grid squares were selected by setting a minimum threshold for the recording effort for each grid square based upon the number of species recorded and the number of surveys. The spatial distribution of plants was modelled for these selected sites using variography and then kriging was used to interpolate across the whole area. This gives a spatially explicit, minimally biased estimate of the grid square occupancy.
In the last few years, an increasing body of evidence has highlighted the role of functional traits as reliable predictors of species resistance to disturbance (Gamfeldt and Kallstrom 2007) and response to environmental gradients (Pakeman et al. 2009). As intraspecific traits variability is a necessary condition for species to adapt to environmental changes (Albert et al. 2010) studying intraspecific functional traits variation along environmental gradients is a major issue in a context of global change.

In this context, the aim of our study was to evaluate the intraspecific variability of functional traits along an environmental gradient of water availability at local scale. Calcareous grasslands species are present along a xeric gradient from mesophilous grasslands to more xerophilous grasslands. Changes of exposure (from north to south), slope and soil depth (from less than 2 cm to more than 15 cm) can lead to differences of water availability for plants along the gradient.

Our three study sites were located in south Belgium. On each site, we marked 100 plots along a gradient of xericity. We observed the presence or absence of four study species known to be present along the whole gradient. We then randomly selected 60 individuals of each species in plots where they were present. On each individual we measured the maximum vegetative height (MVH) and we collected two leaves in order to measure the specific leaf area (SLA, one side area of a fresh leaf divided by its oven-dry mass) and the leaf dry matter content (LDMC, leaf oven-dry mass divided by its water-saturated fresh mass). The exposure, slope and soil depth was measured in each plot.

Results showed the intraspecific variability of the maximum vegetative height, the specific leaf area, the leaf dry matter content along a gradient of slope, exposure and soil depth. Main implications for species resistance to disturbance and climate change adaptation will be discussed.

References
Comparative approach of functional ecology of *Fallopia japonica, F. sachalinensis* and *F. ×bohemica* in Belgium

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The hybrid complex of Asiatic invasive knotweeds (genus *Fallopia*) presents a major interest in ecology. Although *F. japonica, F. sachalinensis* and their hybrid *F. ×bohemica* display the same lifeform and distribution area, their invasiveness differ. *F. sachalinensis* is much less invasive and rarer than the other two taxa. Study of the functional traits of the members of the complex may allow to determine which traits underlie invasive success of invasive knotweeds.

During my thesis, I tested if *F. sachalinensis* presented a specific combination of functional traits that could explain its lower invasive success. In particular, I examined traits involved in resource capture and use, such as SLA, architecture, foliar nutrient concentrations and litter decomposition rate. Three methods were used: *in situ* comparisons in sites where the taxa coexist, common garden experiments in semi controlled conditions, and a litterbags experiment.

Results highlighted the particular strategy of *F. sachalinensis* regarding resource capture and use, as well as its less adaptive plastic responses for some traits. Although *F. sachalinensis* has higher shoots and bigger leaves, it is less ramified and has less leaves, resulting in a lower total leaf area. Regarding nitrogen use efficiency, it shows lower nitrogen resorption, producing a nitrogen-rich litter that decomposes faster than that of the other taxa. On the other hand, the litter of *F. japonica* decomposes very slowly and immobilizes nitrogen. Coupled with an efficient nitrogen resorption, it contributes to the high competitive ability and invasive success of *F. japonica*. The hybrid does not display transgressive variation and is similar to *F. japonica* for functional traits and plastic responses. However, the limited number of accessions that we studied does not allow to conclude that the hybrid does not show transgressive variation in its whole introduction area.
We here present an overview of our ongoing population genetic research in the ancient rainforest tree *Symphonia globulifera*. The species is widely distributed in tropical forests of Africa and America, which it has colonized by trans-oceanic dispersal about 15 – 18 Ma ago. We used sequences of plastid DNA (psbA-trnH intergenic spacer) and of the internal transcribed spacer of nuclear ribosomal DNA (ITS) and nuclear microsatellites (SSRs) to investigate the population genetic structure of the species on both continents and at the within-population level. In America, we observed a clear phylogeographic signal of Andean uplift; Amazonian populations showed weak phylogeographic structure despite large geographic distances, and Mesoamerican populations were much more strongly differentiated, which can be related to region-specific topographic and climatic conditions. In Africa, gene pools detected in Benin, West Cameroon and São Tomé bear signs of a bottleneck approximately dated to the Last Glacial Maximum (LGM) using Approximate Bayesian Computation, whereas an older bottleneck was found in South Cameroon and Gabon, suggesting a genetic effect of Pleistocene cycles of forest contraction. In the latter region, cpDNA indicated wide-ranging long-term persistence of the species both inside and outside of postulated forest refugia and a four times further-ranging pollen than seed flow, which probably enabled rapid recovery of population sizes after the LGM. Our study also suggested ecotypic differentiation – coastal or swamp vs. terra firme ecotypes – in African *Symphonia globulifera*. Spatial genetic structure was stronger in African than in American populations, which can tentatively be linked to distinct pollen and seed dispersal syndromes in distinct parts of the species range. We are currently developing next-generation sequencing approaches to examine transatlantic gene flow and adaptation to micro-environmental gradients.
Application of the phylogenetic informativeness method to chloroplast markers:
a test case of closely related species in tribe Hydrangeae (Hydrangeaceae)

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In evolutionary biology appropriate marker selection for the reconstruction of solid phylogenetic
hypotheses is fundamental. One of the most challenging tasks addresses the appropriate choice of
genomic regions in studies of closely related species. Robust phylogenetic frameworks are central to
studies dealing with questions ranging from evolutionary and conservation biology, biogeography to
plant breeding. Phylogenetic informativeness profiles provide a quantitative measure of the
phylogenetic signal in markers and therefore a method for locus prioritization. The present work profiles
phylogenetic informativeness of mostly non-coding chloroplast regions in an angiosperm lineage of
closely related species: the popular ornamental tribe Hydrangeae (Hydrangeaceae, Cornales, Asterids).
A recent phylogenetic study denoted a case of resolution contrast between the two strongly supported
clades within tribe Hydrangeae. We evaluate the phylogenetic signal of 13 highly variable plastid
markers for estimating relationships within and among the currently recognized monophyletic groups of
this tribe. A selection of combined loci based on their phylogenetic informativeness retrieved more
robust phylogenetic hypotheses than simply combining individual markers performing best with respect
to resolution, nodal support and accuracy or those presenting the highest number of parsimony
informative characters. We propose the rpl32-ndhF intergenic spacer (IGS), trnV-ndhC IGS, trnL-rpl32
IGS, psbT-petB region and ndhA intron as the best candidates for future phylogenetic studies in
Hydrangeae and potentially in other Asterids. We also contrasted the phylogenetic informativeness of
coded indels against substitutions concluding that, despite their low phylogenetic informativeness,
coded indels provide additional phylogenetic signal that is nearly free of noise. Phylogenetic
relationships obtained from our total combined analyses showed improved resolution and nodal
support with respect to recently published results.
Keynote lecture
Towards an understanding of the evolution and radiation of angiosperms

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With over 250,000 species, flowering plants belong to the world’s most dominant evolutionary lineage, trailing only insects in named species diversity. Despite the enormous biodiversity, fossil evidence indicated that flowering plants are a rather young group in evolutionary terms compared to gymnosperms and ferns. The rapid radiation of flowering plants, which Darwin referred to as an “abominable mystery” has led to intense interest among scientists in explaining the causes of diversification in this clade. The use of molecular data and continuously improving bioinformatics yield new opportunities to better understand how and when angiosperms have taken over the dominant position around much of the globe relative to gymnosperms and ferns. Diversification analyses, divergence time estimates and historical biogeography demonstrate that evolutionary lineages in flowering plants did not gradually accumulate but are rather the result of abrupt changes in diversification rate.

Poster Presentation
Does shape matters?
A global vulnerability assessment of fragmented mangrove forests against climate changes

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Mangrove forests are amongst the world’s most productive ecosystems. They serve many ecological functions, such as nursery habitat for juveniles of pelagic species, trapping sediment transported from upland towards the sea, and protecting shorelines against ocean surges and wave action. However, mangroves forests are under severe threat globally due to biotope degradation and land use change causing fragmentation of mangrove area. Fragmented mangroves have a higher edge to area ratio, which would affect the environmental conditions prevailing within its perimeter. Larger edge ratios entails that the area of mangroves forest exposed to external conditions is larger in relative and absolute terms; this would in turn increase the exposure to ocean waves and might even affect the food web through increased accessibility to opportunistic and eurytopic predators within the mangrove ecosystem. This condition might be unfavourable for mangrove species that are solely dependent on well conserved and integer mangroves, living far from the edge. As an example, the mangrove rivulus (Kryptolebias marmoratus) could be susceptible to effects of mangrove fragmentation. The aim of this study is to determine the global status and trends of mangrove forest fragmentation. Results on the status of global fragmentation of mangroves will be viewed in the light of scenarios on climate change and sea level change put forward by the Intergovernmental Panel on Climate Change (IPCC). We expect in this research to evaluate the vulnerability of mangroves to fragmentation against the backdrop of climate change. In order to achieve our objectives, we will use the distribution of the world’s mangroves that were mapped by Giri et al. (2011) and these data will be inserted into a Geographical Information System (GIS) and analyzed using the ArcGIS software. The findings of this ongoing study should ultimately identify impacts on mangroves of the combined effects of fragmentation and climate change. If particular areas of high vulnerability can be indicated, management considerations can follow.
GIS analysis of climate change impacts on threatened mangrove trees

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Some climatic limits of mangroves are already known, however, there has been little discussion about the climatic variables that can explain the distribution of certain mangrove tree species. The past twenty years have seen increasingly rapid advances in the field of species distribution models (SDMs) of plants and animals. However, limitations related to the input distribution data still preclude the use of SDMs in many practical applications. For instance, correlating climate data to the global distribution of mangroves was never attempted (but see Quisthoudt et al., in press). Moreover, historical correlation analysis of the climate data from the past, present and future scenarios could give us better understanding of aspects of climate change on mangroves. The aim of this paper is to analyse certain unstudied effects of climate change on threatened mangrove tree species. In order to obtain our results it will be necessary to pursue the following steps: Firstly, it is necessary to update the Mangrove Reference Database and Herbarium and insert it into a Geographical Information System (GIS). The Worldclim database will provide the historical climate while collecting temperature, precipitation and bioclimatic variables that will be used to characterize environmental changes on the species (e.g. Avicennia rumphiana, Heritiera fomes, Pelliciera rhizophoreae in Polidoro et al.). The methodology is basically to extract the value of a climate variable in Worldclim based on a set of point features (species locations) and export the values to a GIS attribute table. The exploratory analysis will be done using the geostatistical analysis tools of the software ArcGIS 10. We expect to produce results in support of the assessment of climate change impacts and to identify the climate variables that have an influence on mangrove species distribution.

References
Tackling convergent evolution, radiation and paraphyly: towards a modern classification of the giant genus *Cyperus*

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Originally, Cyperaceae species with flattened spikelets and distichous glumes were placed in the genus *Cyperus*. However, we now know that this morphology has independently evolved in other Cyperaceae genera, while reversal to spiral glumes has occurred in multiple *Cyperus* lineages. There has been disagreement whether to recognize *Cyperus* as a single large genus (c. 950 species) or to segregate it into c. 14 genera. Segregate genera in *Cyperus* s.l. have been delimited based on a single or a combination of characters, but molecular phylogenetic data demonstrated convergent evolution in several key characters. Using molecular phylogenetic data, we reconstructed a phylogenetic hypothesis of *Cyperus* s.l. The ancestor of *Cyperus* is a perennial with C3 photosynthesis, and spikelets with distichous glumes shedding individual fruits. Three segregate genera, differing by having spiral glumes (*Kyllingiella, Oxycaryum*) or spikelets dispersing as a single unit (*Courtoisina*), are derived from the C3 *Cyperus* s.s. ancestral morphology and were recently merged into *Cyperus*. A large (c. 760 species) monophyletic clade rapidly radiated from an ancestor, with an anthelate inflorescence and distichous glumes, which switched to C4 photosynthesis in the last 10 mya. Diversification has been accompanied by reductions leading to spikelets bearing single flowers (*Alinula, Ascolepis, Lipocarpha, Volkiella*), multiple origins of lateral nutlet orientation (*Kyllinga, Pycreus, Queenslandiella*), and evolution of sterile lower flowers (*Remirea, Sphaerocyperus*). To resolve the paraphyly of *Cyperus* and provide a classification reflecting evolution, we are revising generic delimitation, to recognize a single large genus *Cyperus* and delimit infrageneric taxa for clades supported by morphology.

Next generation transcriptomics elucidates brown algal sexual reproduction genes

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Brown algae have served extensively as model organisms for algal life cycle studies and sexual reproduction. Yet, little is known about the molecular basis of sex determination, gamete attraction and fertilization. To provide a better understanding of the molecular mechanisms underlying physiological differentiation, gamete recognition and fusion, we sequenced the transcriptome of male and female Ectocarpus siliculosus gametes using AB SOLiD Next Generation Sequencing technology. Despite being morphologically identical, digital expression analysis identified approx. 4700 differentially expressed genes between male and female gametes. Functional analysis was performed based on Gene Ontology (GO) and KEGG categories and provided valuable insight into complex transcriptome adjustment to diverse functions fulfilled by male and female gametes. Several new genes and pathways with a putative function in the recognition and attraction process were identified, providing foundations for more detailed research on the fertilization mechanisms and their evolution in brown algae.
Poster Presentation

Variation à l'échelle locale de la composition spécifique des communautés d'arbres dans une forêt tropicale du forestier central : rôle des facteurs édaphiques et topographiques

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Dans beaucoup d'études écologiques des forêts tropicales dans le monde, le rôle de substrat sur l'organisation spatiale des peuplements végétaux est de plus en plus pris en compte et certains travaux ont montré l'impact des variables édaphiques sur la répartition spatiale des espèces dans les tropiques. Cependant de telles études demeurent rares dans les forêts des environs de Kisangani.
Les forêts de la Réserve de Yoko qui font l'objet de cette étude sont établies sur des substrats hétérogènes et à topographie contrastée (pente, bas de pente et plateau).
Dans cette étude, nous avons évalué l'impact de la microtopographie de terrain sur la diversité, la composition spécifique et la structure des peuplements arboréscents de deux zones (une située sur un plateau sableux et l'autre sur un substrat argileux à topographie contrastée) dans la Réserve forestière de Yoko.
Keynote lecture

Evolutionary mechanisms in colonizing plant populations

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In a rapidly changing world, human activities offer opportunities for many plant species to colonize new areas. Increasingly, it is recognized that colonization can be accompanied by different ecological and evolutionary processes, acting over relatively short periods of time. When populations colonize novel environments, individuals’ phenotypes will depend on a combination of different, non-exclusive processes, including phenotypic plasticity (PP), local adaptation (LA), environmental maternal effects (EME) and genetic drift (GD) (Monty and Mahy 2009b). Despite these processes have long been studied independently, few attempts have been made to simultaneously address the importance of those processes in plant colonization.

Here, we present a set of related studies aiming at disentangling the role of PP, LA, EME and GD in Senecio inaequidens (Asteraceae) in southern France, where it was introduced at a single wool-processing site in the late 19th century. We used seeds from populations growing in contrasted climates to explore the phenotypic variation related to climate. We performed several common garden experiments (Monty et al. 2009, Monty and Mahy 2009a, 2010), as well as a reciprocal sowing experiment with gardens under Mediterranean and Pyrenean climates (Monty et al. in revision). We analyzed climatic phenotypic variation in germination, growth, reproduction, leaf physiology and survival. We characterized genetic structure in the studied populations using AFLP.

We found consistent genetic differentiation in growth traits but no home-site advantage, thus weak support for LA to climatic conditions. In contrast, genetic differentiation showed a relationship to colonization history. PP in response to climate was observed for most traits, and it played a particularly important role in leaf trait variation. EME mediated by seed mass influenced all but leaf traits under harsh climate. Heavier, earlier-germinating seeds produced larger individuals that eventually produced more flower heads throughout the growing season. However in a milder climate, EME were negligible. Our different studies suggest that phenotypic variation in response to climate depends on various ecological and evolutionary processes associated with geographical zone and life history traits. Therefore, we argue that a “local adaptation vs. phenotypic plasticity” approach, as often considered in the literature, is not sufficient to fully understand what shapes phenotypic variation and genetic architecture of colonizing populations.

References
Keynote lecture  
**Metal hyperaccumulating plants**

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Metalliferous environments were among the first environments where selective pressures, and adaptations, have been highlighted. Many questions about the ecology, evolution and speciation of metallicolous taxa, including the strange metal-accumulating species, are still unresolved. I will first review the recent discoveries of genes involved in metal accumulation, with the point of view of an ecologist. I will then examine what is known about the genetic relationships among populations of metallicolous taxa, as well as between metal-adapted and related unadapted taxa. Finally, I will conclude in showing different approaches to study adaptations to metalliferous soils at the level of the populations.

Keynote lecture  
**Speciation in Fungi**

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The comprehension of the process by which the current 1.5 million or more fungal species have arisen, is one of the central and persistent challenges in mycology. Among the numerous recently discovered (complexes of cryptic) species many appear consistent with allopatric divergence. Sympatric speciation, however, is also possible under certain conditions. Recent models of sympatric speciation in fungi are discussed and examples are illustrated. The evolution of reproductive barriers, be it pre- or postmating, between diverging populations is a critical step in speciation. Natural selection against maladaptive hybridization can drive the evolution of reproductive isolation in sympatric taxa. Natural selection for reinforced premating isolation is widely recognized, also in Homobasidiomycota, but reinforcement of postmating barriers, like hybrid inviability, remained controversial. In the example of the Ascomycete Neurospora it is shown that hybrid fruiting body abortion increases maternal fitness. Other factors that influence speciation in fungi, such as host-symbiont co-evolution, host shifts, hybridization and asexuality are also discussed.
The rare *Helosciadium repens* is strongly influenced by management and climate

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The rare *Helosciadium repens* (Jacq.) W.D.J. Koch is a small creeping umbellifer. It is mentioned under its former name *Apium repens* (Jacq.) Lag. in annex II and annex IV of the Habitat Directive of the European Union (Directive 92/43/EEG), listing the species of community interest in need of strict protection. This species is rare and endangered throughout its natural distribution area (mainly atlantic northwest Europe). In Belgium, which lies in the core of its distribution, only five populations subsist. In four of them, demographic monitoring was carried out six times a year from 2003 to 2007, recording the total number of ramets, as well as the germination, flowering, seed setting and clonal growth in permanent plots. At the same time several parameters relating to management regimes were recorded, namely vegetation height, openness of the vegetation, pit depth as a measure of trampling intensity caused by grazers, covering by dung, as well as groundwater levels near the plots. Climatological data were obtained from official meteorological stations in the vicinity. The influence of these external parameters on the demographic parameters was analysed.

During the course of this study, the management regimes in three of the four populations were markedly altered, due to a number of reasons, which has resulted in dramatic decreases of these populations. Our measurements have shown that especially the vegetation height relates negatively to the number of ramets per area, as well as to the flowering. This variable can explain the observed collapse of the populations. The openness of the vegetation and the degree of trampling are also negatively related with the number of ramets; however, they show a strong positive relation with seed production. The groundwater level is also a very important parameter for the total population: a high groundwater level correlates with high total numbers of ramets, especially of adult vegetative individuals; however there is a negative correlation of the groundwater with the germination. Climate variables affect the number of ramets less strongly, but they are very important for the flowering of *H. repens* in Belgian populations: high temperatures and high numbers of sunshine clearly result in a higher flowering, and this is also the case to a lesser extent for the precipitation. The seed production, however, is influenced merely by the temperatures.

These results show clear but complex interactions of the management and of climate variables with the fate of the populations of *Helosciadium repens*. 
Towards a protocol for management of genetic variation of *ex situ* living plant collections

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Worldwide about one third of all plant species is threatened with extinction. Botanical gardens play a key role in conservation of plant diversity, and as is stated in Target 8 of the GSPC, at least 75% of threatened plant species should be present in *ex situ* collections. However, only about 30% of globally threatened plant species are currently held in living collections. These have to be genetically representative, but information about the genetic diversity present in such collections is scarce, although it is estimated that diversity is low in numerous species. Moreover, besides the many studies and initiatives for specific taxa, our knowledge about genetic diversity of threatened plant species in general is quite restricted. This lack of insight in genetic diversity of threatened plant species heavily contrasts with the broad knowledge about crops and their wild relatives. We still have a long way to go to study genetic diversity in threatened plants, conserve an important part of this diversity in *ex situ* collections, define which percentage of genetic diversity might be feasible and/or desirable to aim for, and finally make this available for conservation and restoration projects.

Within this specific project at Ghent University, we aim to compare genetic diversity between wild populations and *ex situ* collections of three distantly related Angiosperm groups with different life histories and growth forms. A range of genomic tools (barcoding, microsatellites, AFLP, RAD sequencing) will be applied to wild and *ex situ* individuals of selected species of the flagship groups *Hydrangea*, *Magnolia* and Cactaceae to enable rapid characterization of genetic variation, providing 1) support of specific conservation actions, and 2) general guidelines and a protocol on genetic management for acquiring accessions for *ex situ* collections, to be used by collectors and botanical gardens worldwide in the framework of achievement of Target 8 of the GSPC.

Inbreeding depression and environmental stress in *Silene vulgaris*

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Inbreeding is a common process in small populations, with relevance for the evolution and conservation of species. However, most of the studies on the amount of inbreeding depression have been carried out under benign conditions in greenhouses or common gardens. We show for *Silene vulgaris* (Caryophyllaceae) that inbreeding depression is much stronger in a field population than in a common garden (47% compared to 17%). To study the effects of inbreeding under different conditions in more detail, a greenhouse experiment was conducted to study inbreeding depression under eight different stress treatments (e.g. drought, shade, nutrient deficiency, heavy-metal stress).
Diatoms from the Congo and Zambezi sister basins – a first overview

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The diatoms from the Congo and Zambezi basins have been little investigated due to the size and relative inaccessibility of the territory covered by these two basins. As African countries develop and experience a steady growth in population the monitoring of water resources is becoming more important. In the last three decades the diatoms have formed a critical part of the suite of bio-indicator organisms used by different countries, especially in the northern hemisphere. These organisms are excellent indicators of water quality as they respond quickly to changes in the environment and as each species has specific water quality requirements in terms of pH, dissolved salts and plant nutrients. Once these requirements are known they can be used to compile indices. Recently diatom material has been collected in both the Democratic Republic of the Congo and Zambia with the ultimate goal of establishing some form of diatom-based water quality metric. However, a first examination of this material has yielded a not unexpected result – the greater part of the diatom species encountered are unknown to science and others are described in obscure publications often with no reference collections available. Before the diatom species from these two basins can be used to infer water quality their identity needs to be confirmed or they need to be described. Only after this their ecological preferences can be ascribed and the species integrated into a water quality metric. This poster presents an overview of the diatom diversity from the Congo and Zambezi basins based on a selection of interesting species, including some new taxa, and outlines strategies to confirm identities based on the work of previous researchers.

Oral Presentation

Relative embryo length as an adaptation to habitat and life cycle in Apiaceae

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We analyzed the ecological significance of relative embryo length in Apiaceae and examined the factors driving the evolution of relative embryo length. We tested the hypothesis that seeds with large relative embryo length, because of more rapid germination, are beneficial in dry and open habitats and for short-lived species. We also analyzed to what extent delayed germination as a result of embryo growth can be considered a dormancy mechanism. Hypotheses were tested by correlating the relative embryo length with other plant traits, habitat and climatic variables. The adaptive nature of the relative embryo length was determined by comparing the performance of a pure drift, Brownian motion (BM) model of trait evolution with that of a selection–inertia, Ornstein–Uhlenbeck (OU) model. A positive correlation of the relative embryo length with germination speed and negative correlations with the amount of habitat shade, longevity and precipitation were found. An OU model, in which the evolution of longer embryos corresponded to a transition to habitats of high light, or to a short life cycle, outperformed significantly a BM model. The results indicated that the relative embryo length may have evolved as an adaptation to habitat and life cycle, whereas dormancy was mainly related to temperature at the sampling sites.
**Poster Presentation**

**ß-proteobacteria beyond legumes: endophytic Burkholderia in Rubiaceae**

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Symbiotic ß-proteobacteria not only occur in root nodules of legumes but are also found in leaves of certain Rubiaceae. The discovery of bacteria in plants formerly not implicated in endosymbiosis suggests a wider occurrence of plant-microbe interactions. Several ß-proteobacteria of the genus *Burkholderia* are detected in close association with tropical plants. This interaction has occurred three times independently, which suggest a recent and open plant-bacteria association. The presence or absence of *Burkholderia* endophytes is consistent on genus level and therefore implies a predictive value for the discovery of bacteria. Only a single *Burkholderia* species is found in association with a given plant species. However, the endophyte species are promiscuous and can be found in association with several plant species. Most of the endophytes are part of the plant-associated beneficial and environmental group, but others are closely related to *B. glathei*. This soil bacteria, together with related nodulating and non-nodulating endophytes, is therefore transferred to a newly defined and larger PBE group within the genus *Burkholderia*.

**Oral Presentation**

**Variation partitioning to control for anthropogenic impact on species composition in a tropical forest of central Africa**

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Non random spatial distribution of trees is the result of neutral vs. deterministic factors. Neutral models suggest that species are equally competitive, with spatial structures mainly due to dispersal limitation. Deterministic models consider species assemblages as the result of environmental processes. However, these processes have often included habitat variables only, without considering human disturbance which we know enhances the competitive advantage of heliophytic (light-demanding) species and therefore the floristic composition of phytocenoses. Based on charcoal abundance (used as an indicator of anthropogenic perturbation) species abundance, and environmental data, we applied modern variation partitioning methods to assess the relative impact of human disturbance on floristic patterns. Some signals of human influence have been found so far but conclusion cannot yet be established as further analyses are still on process.
Oral Presentation

Floral cups in Rubiaceae: a developmental approach

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According to a developmental model worked out by Leins and Erbar (2010), different kinds of floral cups such as perianth tubes, hypanthia, and also phenomena such as gynophores or androgynophores can be explained by the activity of annular or disc-shaped intercalary meristems in the floral axis, just below the respective whorl of floral primordia. In Rubiaceae, floral cups are present in the form of calyx and corolla tubes. In the past, based on ontogenetic investigation of the corolla tube, three developmental character states were defined: early and late sympetaly, and the transition between both. Moreover, it became clear that in some Rubiaceae, the corolla tube actually is a stamen-corolla tube. Despite these observations, it remained difficult to understand the varying superposition of the stamens on the corolla tube or at its base, or other corolla phenomena such as corolla splits. As for the calyx tube, few developmental data are available. Therefore, we studied the development of calyx, corolla and androecium in several species of Rubiaceae in order to test the developmental model for floral cups of Leins and Erbar.

Our observations make us conclude that a rubiaceous tubular corolla essentially consists of a combination of a corolla tube sensu strictu and a stamen-corolla tube, each formed from a proper annular intercalary meristem, and with, in some species, on top of these also a postgenitally formed corolla tube (by fusion of corolla lobes). Depending on the proportions of each, the stamens can be attached at the base of the tubular corolla or higher up. In species with corolla splits, the ontogeny of the tubular corolla affects the formation and position of the splits. Early sympetalal and the ‘transition’ between early and late sympetaly can also be explained by the activity of an underlying intercalary meristem.