

## **BORDER - Research on the biosynthetic origin of macrocyclic diterpenes of Euphorbiaceae - plants and/or endophytes?**

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**Abstract:** Terpenoids are a large and structurally diverse class of natural compounds, produced by a variety of plants. Among these, diterpenes occurring in plants of the Euphorbiaceae family are nevertheless of considerable interest due to their wide range of potentially valuable biological activities and their broad structural diversity. Enzymes and/or process involved in the biogenesis of lower diterpenes are poorly understood. In parallel, plant symbiotic fungi are known to produce the same or similar secondary metabolites as their host. The aim of BORDER project is to assess in which extent complex diterpenes considered as "plant metabolites" can be produced or modified by endophytes. The purpose is in one hand to understand the involvement of endophytes in the biosynthesis of these molecules founds in plants. And in a second hand to demonstrate that from an ecological point of view there is a transfer or-coproduction of secondary metabolites between to interspecies entities in symbiosis.

## **BROWSE - Browsing in treefall gaps: cross-interactions between large-bodied browsers and forest regeneration in French Guiana forests**

PI: Cécile RICHARD-HANSEN  
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**Abstract:** Since Redford's "empty forest" early warning about defaunation consequences on tropical forests, many studies uncovered several processes involved in complex interactions between the neotropical large fauna and forest structure and functioning, or modelled consequences of their disappearance. Most of these studies focus on the alteration of seed dispersal, seed survival, and seedling recruitment processes. The impact of direct predation of browsers on forest regeneration has received much less attention. We propose here to have a deeper insight in this process, particularly focusing on the role of treefall gaps in these interactions. We hypothesize that browsers particularly use them for feeding, because they are dominated by plants with nutritious and palatable leaves. Large neotropical herbivores (ungulates) have a frugivore-folivore diet, and browse mainly young leaves, on small trees up to the sapling stage. They may have a non-negligible and selective impact on the growth and survival rates of some species or functional groups of species, after the most critical survival stage of seedling to sapling transition. BROWSE, which will be the first step of a longer study, will focus on (1) comparing browsing intensity within and outside treefall gaps, and (2) to investigate the degree of selectivity of large browsers within treefall gaps. For the first question, all browsing signs will be counted in paired plots located within and outside treefall gaps. Second, within treefall gap plots, all browsed species, as well as all 20-150cm-high plants in a 10m radius around them, will be identified and measured to test for selectivity, and collected for further analyses. Functional traits will be obtained from existing databases and other ongoing studies. Plots' frequentation will be checked by video camera traps, to identify the species browsing, and document feeding and selecting behaviour. Our results will contribute to understanding of tree regeneration processes in tropical forest, and especially

of the understudied ecological role of large browsers in these processes. It will also enhance our currently very poor knowledge of the ecology of these hunted and endangered species, and provide baseline data for hunting and forest management.

### **BRYOTROP - Effects of simulated nitrogen deposition on the epiphytic bryosphere in a tropical rainforest**

PI: Vincent JASSEY  
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**Abstract:** Human-induced increase of nitrogen (N) threatens tropical forests, influencing their capacity to stock carbon (C), and thereby, mitigates climate change. How and to what extent elevated N deposition rates affect C processes such as C uptake and efflux in tropical rainforests still remain an open question. To address this question, we will take an integrated approach and test how N deposition affects C cycling in epiphytic bryophytes –a model-based ecosystem. Epiphytic bryophytes represent a substantial proportion of the green biomass in tropical forests and dominate in terms of C and N mass the canopy of tropical rainforests. Bryophytes, also known as the bryosphere, consist of living and dead mosses supporting a large diversity of microfauna, collectively comprising the moss food web that governs the rates of key N and C cycling processes (e.g. N<sub>2</sub> fixation, decomposition). Here, we will test how N addition affects C and N cycling in the bryosphere, and how in turn, the bryosphere affect C and N fluxes (leaching) to the forest floor. Particularly, we will explore how the moss food web composition control these processes. To do this, we will run in a lowland rainforest near Petit-Saut Dam (French Guiana) a field experiment where we will simulate different rates of N deposition from 0 to 50 kg N ha<sup>-1</sup> y<sup>-1</sup>, according to predictive N deposition models in South America. We will study how CO<sub>2</sub> fluxes, C and N leaching, N<sub>2</sub>-fixation by cyanobacteria, microbial diversity, and moss food web structure respond to N additions. Our results will provide vital knowledge on how the epiphytic bryosphere contributes to tropical forests C and N cycling, and especially, which mechanisms drive shifts in C and N cycling under high level of N deposition.

### **CANO4D-CAL - Dense canopy characterisation using coupled airborne and ground LiDAR, and implications for canopy monitoring over time**

PI: Nicolas BARBIER  
*AMAP, Montpellier, France*

**Abstract:** Detailed characterization of tropical forest structure and dynamics has become crucial to advance our understanding of carbon, water, nutrients and energy fluxes, as well as to characterize interactions between plants and with other organisms in the forest environment. LiDAR scanning is known for the fascinating amount of 3D data it can provide, but heavy implementation costs still hamper adding a 4th dimension, time, and hence completing the metrological revolution. We propose to calibrate a light, drone-based LiDAR scanner against data from reference airborne and terrestrial scanners, in order to pave the way towards this end. Additionally, by performing a high density acquisition over the area of the COPAS project, Nouragues station, French Guiana, we will deliver a range of 3D products that will be of great use to the research community, such as voxel maps of leaf area and plant

area density, tree topological and geometrical description as Quantitative Structure Models (QSMs), local biomass allometries for the most abundant species, etc.

### **CASMA - Comparative phylogenomic approach to study the origin of butterfly mimetism in Amazonia**

PI: Fabien CONDAMINE  
*ISEM, Montpellier, France*

**Abstract:** Amazonian butterflies are well known for their mimetism such as the genus *Heliconius* that practices Müllerian mimicry (two species come to mimic each other's warning signals). However, less is known on Batesian mimicry (a harmless species has evolved to imitate the warning signals of a harmful species), which is practiced by swallowtail butterflies of the genus *Papilio*. The project CASMA will explore the origin of Amazonian butterfly mimetism using a genomic comparative approach in a phylogenetic context. Relying on time-calibrated phylogenies for swallowtail butterflies (*Papilionidae*) and associated wing patterns of mimetic, non-mimetic and model (the ones that are imitated) species, we will reconstruct the evolution of wing pattern through time, allowing us to determine the timing of mimetism origin in the swallowtail lineages. More importantly, we want to explore the genomic architecture of adaptation in relation with mimetism evolution, by comparing mimetic species with non-mimetic species. For that goal, we are building a genomic dataset (low coverage whole genomes) for all genera of swallowtail butterflies to unravel the processes driving their evolution and ecological preferences. The project CASMA will take advantage of this genomic dataset to study the origin of Batesian mimicry in Amazonian butterflies. However, complete and annotated genomes are required to properly study gene ontology. This project will allow us to sequence two high-quality swallowtail genomes representative of Amazonian mimetic and non-mimetic species using a hybrid sequencing approach combining long and short reads. We will then perform resequencing on four pairs of mimetic and non-mimetic species. Such genomes coupled to our resequencing dataset (plus the genomes already acquired) will illuminate the role of genomic changes along the phylogeny with a focus on the natural selection and gene evolution involved into Batesian mimicry.

### **DIGS - Diversification of an ancient Guiana Shield lineage of fossorial frogs**

PI: Antoine FOUQUET  
*LEEISA, Cayenne, French Guiana*

**Abstract:** The processes at work in the diversification of megadiverse biotas, such as Amazonia, have fascinated biologists for centuries. Amphibians represent a key group to understand these processes because they display unique patterns of species richness and endemism. Some frog lineages in Amazonia, such as *Otophryinae*, are both endemic and very ancient, and their study can yield crucial insights into the understanding of vertebrate diversification in the region. Moreover, the genera in this group underwent drastically distinct evolutionary trajectories (stream-associated/diurnal/exotrophic tadpole vs. fossorial/nocturnal/direct development) that led to the acquisition of remarkable anatomical features, some of which unique among amphibians, which have puzzled phylogeneticists for decades. We will determine the spatiotemporal aspects of the diversification of *Otophryinae*

and investigate the paleogeographic events that could have triggered ecomorphological divergences in the group. A combination of molecular, acoustic and anatomical data will be used to delineate species and their respective distributions. We will also use  $\mu$ CT-scans and geometric morphometrics to investigate osteological characteristics and shape evolution, notably the ones linked to fossoriality. This will lead to the description of several newly detected species (some already detected through preliminary barcoding analyses). Mitogenomic and multiple nuDNA loci will be then used to establish a time-calibrated species tree in order to investigate the historical biogeography and the evolutionary history of anatomical features linked to fossoriality. Most of the material spanning the entire range of the focal group is already available thanks to a large collaborative effort involving scientists with extensive expertise in amphibian phylogenetics and diversification of Amazonian taxa.

### DREAM - Drought recovery mechanisms in a tropical forest

PI: Megan BARTLETT  
*Princeton University, USA*

**Abstract:** Climate change is predicted to increase drought in tropical forests, with important consequences for global carbon dynamics and biodiversity. Recent work has elucidated traits that maintain plant function and limit damage during drought, but also shown that many trees survive drought but undergo years of reduced growth and heightened mortality rates, even though conditions are favorable again. Here we are proposing to conduct the first study to link the mechanisms underlying recovery in plant physiological function to species differences in growth and mortality rates following a severe drought. We will use census data from the Paracou research site to identify species that varied strongly in mortality after the exceptionally severe 2008 drought, and assess these species for their ability to recover function (i.e., embolism resistance and water transport) in their leaves and stems. We will then evaluate correlations between these recovery traits and the traits underlying other drought resistance strategies, as well as species growth and survival rates in the decade following the 2008 drought. This research will advance our understanding of the physiological mechanisms that drive plant recovery from drought, and potentially improve our predictions for the impacts of global change on the carbon dynamics and community assembly of Amazonian forests.

### PIXIE - Bordered pits provide a mechanistic understanding of embolism resistance in branch and leaf xylem of tropical rainforest trees from French Guiana

PI: Patrick HEURET & Steven JANSEN  
*AMAP, Montpellier, France & Institute Systematics Botany and Ecology, Ulm University, Germany*

**Abstract:** Vulnerability to drought-induced xylem embolism is a key parameter for drought tolerance of vascular plants, especially in areas that will experience an increase in drought intensity and frequency associated with climate change. However, the anatomical and chemical determinants of embolism by gas entry are poorly understood, with marginal data

relating to tropical species. Although the mechanism of “air-seeding” via openings in secondary walls of conduits (i.e., bordered pits) has been described many times, our mechanistic understanding remains simplistic and suffers from a lack of detailed observations of bordered pit membranes. An in-depth structure-functional approach is also needed to better understand the occurrence of xylem embolism in leaves, which are frequently assumed to be more vulnerable to hydraulic failure than branches. Based on anatomical observations and hydraulic measurements for samples from the same tree, we aim to explain interspecific variability in xylem embolism resistance by vessel and bordered pit characteristics. Measurements will be conducted for a total of 25 species from French Guiana. We will take advantage of the expertise in electron microscopy at Ulm University for pit membrane observations. We expect that our anatomical observations such as pit membrane thickness will largely explain the variation in xylem embolism resistance, both at the leaf and branch level, for tropical rainforest trees that experience seasonal drought. An improved mechanistic understanding of drought tolerance and hydraulic failure is especially relevant given current concerns about climate change and predicted shifts in Amazon rainfall.

### **POLYMIM - The ecological and genomic basis of polymorphic mimicry in Heliconius butterflies**

**PI:** Mathieu CHOUTEAU  
*EDB, Toulouse, France*

**Abstract:** The proposed study aims to further our understanding of the rich biodiversity of French Guiana by combining ecological field experiments and genomic techniques to explore the biological basis of local adaptation. The proposed experiments will allow us to determine if fine-scale and regional variation in warning colours is driven by predators and thereby the result of local adaptation. Through whole genome sequencing of *Heliconius* with different warning colorations, we expect to identify narrow genomic regions associated with colour pattern variation. We will directly compare the ecological and genomic results to results from other *Heliconius* species to determine if the same selection pressures and genetic mechanism are responsible for mimetic polymorphisms in *H. doris* and other *Heliconius* species. Collectively this study will provide a better understanding of the processes that drive patterns of biodiversity in Amazonia.

### **RESERVOIRS - The role of Neotropical birds as potential reservoirs of infectious diseases**

**PI:** Javier PEREZ-TRIS & Christophe THEBAUD  
*Complutense University of Madrid, Spain & EDB, Toulouse, France*

**Abstract:** Biodiversity is heterogeneously distributed at the local scale: a few common species often account for a substantial fraction of the individuals, while most species are rare. Common species usually stand out as central nodes in ecological networks, thereby playing key roles in the long-term persistence of species assemblages. In Neotropical birds, an important but poorly known function of common species may be acting as reservoirs of infectious diseases. In bird-diverse Neotropical rainforest, natural selection favours the evolution of generalist avian pathogens, which are capable of thriving in a large diversity of

bird hosts, due to a combination of dilution effects (lowered Darwinian fitness of specialist pathogens faced with diverse incompetent hosts) and amplification effects (increased transmission rates of generalist pathogens taking advantage of diverse competent hosts). Thus, the most common bird species may play a central role in the epidemiology of Neotropical pathogens if they score the highest pathogen prevalence, sustain more intense infections, or take specialist pathogens in their component communities (the pathogen assemblage that affects a single host species). We will use avian malaria parasites and different avian viruses to test these ideas. Specifically, we will test for a correlation between bird relative abundance and (i) pathogen prevalence, (ii) intensity of infection, and (iii) host contribution to nestedness of host-pathogen networks (the pattern in which pathogen component communities form ordered subsets of each other, making specialist pathogens interact with generalist hosts). By analysing these features of bird-pathogen interactions, this project will aim to improve significantly the understanding of disease dynamics in Neotropical ecosystems, expanding current paradigms with new conceptual perspectives and unprecedented data.

### **SYMBIOSYNTHESIS - Bacterial defensive symbionts associated with ants in Amazonia: evolutionary and ecological factors impacting the diversity of bacterial genes in the biosynthesis of polyketides and non-ribosomal peptides**

**PI:** Christophe DUPLAIS & Corrie MOREAU  
*ECOFOG, Kourou, French Guiana & Field Museum of Natural History, Chicago, USA*

**Abstract:** This project aims to study the chemical defense provided by endo- and exosymbiotic bacteria associated with ants by correlating for the first-time the bacterial chemical diversity with phylogenetic and ecological factors of the host. Instead of using time consuming traditional techniques for isolating bacteria and bacterial natural products, here we use a novel molecular approach that targets specifically bacterial genes involved in the biosynthesis of polyketides (PK) and non-ribosomal peptides (NRP). Since these natural products are among the most bioactive antimicrobial chemical families with applications in medicine and of high interest for understanding the evolution of chemical defense of microbial symbionts, we propose to evaluate the diversity of PK and NPR biosynthetic genes as a proxy of the bacterial chemical diversity of these secondary metabolites. We will focus on several species of ants (N=24) in French Guiana having distinct evolutionary histories, different diets, and with different nesting habitats (primary forests vs cities). This sampling strategy will help us to better understand which factors impact the diversity of PK and NRP biosynthetic genes. The project will provide new insights into the chemical defense of symbiotic bacteria associated with ants in an evolutionary and ecology framework, and it will also guide future bioprospections for drug discovery in Amazonia.